

BrainVision Analyzer 2.0 User Manual

Version 002

23 June 2008

CE

Imprint

BrainVision Analyzer

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Version of the user manual: 002

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Contents

	About this manual
1	Intended Use
2	About the software
2.1	Product identification
2.2	CE marking
2.3	Application environment
3	Introduction
4	Installation
5	Getting started and working with the Analyzer
5.1	The new user interface of the Analyzer
5.2	Creating and editing a workspace
5.3	Applying a transform
5.4	Explanation of terms: primary and secondary history data
6	Segmentation
7	User-specific preferences
7.1	Configuring preferences
7.2	Customizing the graphical user interface
7.2.1	Skins
7.2.2	Docking
7.3	Configuring the EEG view settings
7.3.1	View settings: Introduction
7.3.2	Category-related view settings
7.3.3	Node-specific view settings
7.4	Configuring administrator rights (Administration command)
8	Montages
9	Views (EEG display modes)
9.1	Views: Introduction
9.2	The EEG views in detail
9.2.1	The butterfly view
9.2.2	The grid view
9.2.3	The head view
9.2.4	The mapping view
9.2.5	The standard view

9.2.6	The time-frequency view
9.2.7	The 3D view
9.3	Overlaying of different data sets
9.4	Additional view functions
10	Automation using history templates
11	Macros
12	Transforms
12.1	Transforms in the Dataset Preprocessing group
12.1.1	New Reference
12.1.2	Pooling
12.1.3	RMS/GFP (Root Mean Square/Global Field Power)
12.1.4	CSD (Current Source Density) interpolation
12.1.5	Rectify
12.1.6	Edit Channels
12.1.7	Level Trigger
12.1.8	Linear Derivation
12.1.9	Formula Evaluator
12.1.10	Change Sampling Rate
12.2	Transforms in the Artifact Rejection/Reduction group
12.2.1	Complex Demodulation
12.2.2	IIR Filters
12.2.3	Band-Rejection Filters
12.2.4	Artifact Rejection
12.2.5	Data Inspector
12.2.6	Ocular Correction ICA
12.2.7	Ocular Correction
12.3	Transforms in the Frequency and Component Analysis group
12.3.1	ICA (Independent Component Analysis)
12.3.2	FFT (Fast Fourier transform)
12.3.3	Wavelets
12.3.4	Inverse FFT
12.3.5	Wavelet Extraction
12.3.6	PCA (Principle Component Analysis)
12.4	Transforms in the Segment Analysis Functions group
12.4.1	Peak Detection
12.4.2	LRP (Lateralized Readiness Potential)
12.4.3	ERS/ERD (Event-Related Synchronization/Desynchronization)
12.4.4	Grand Average
12.4.5	Segmentation
12.4.6	Average

12.4.7	Baseline Correction
12.4.8	DC Detrend
12.5	Transforms in the Comparison and Statistics group
12.5.1	t-Test
12.5.2	Cross Correlation
12.5.3	Data Comparison
12.5.4	Covariance
12.5.5	Coherence
12.6	Transforms in the Special Signal Preprocessing group
12.6.1	LORETA
12.6.2	MR Correction (MRI scanner artifact correction)
12.6.3	CB Correction (pulse artifact correction)
12.7	Transforms in the Others group
12.7.1	Data Cache
12.7.2	Edit Markers
12.7.3	MATLAB®
12.7.4	Topographic Interpolation
13	Add-ins
13.1	Marker Navigation
13.2	Analyzer Video
13.3	Generic Data Header
13.4	LORETA
14	Transient transforms
14.1	3D Map
14.2	Current Source Density (CSD)
14.3	LORETA
14.4	Fast Fourier transform (FFT)
14.5	Map
14.6	Zoom
15	Export components
15.1	Simple export components
15.1.1	Besa Export
15.1.2	EDF Export
15.1.3	Markers Export
15.1.4	Generic Data Export
15.2	Complex export components
15.2.1	Area Information Export
15.2.2	Peak Information Export
15.3	Additional export components: LORETA

16	Importing data, positions and markers
16.1	Importing data
16.1.1	Besa format
16.1.2	Generic Data Reader
16.2	Importing markers and channel positions
17	Printout
18	Graphical export
19	Appending multiple raw data sets
20	Solutions
21	Analyzer help
Appendix A	Raw data on removable media
Appendix B	Electrode coordinate system
Appendix C	Markers (time markers)
Appendix D	Keyboard shortcuts
Appendix E	Installing a network license (USB)
Appendix F	Command-line parameters
Appendix G	Shortcuts to raw data
Appendix H	BrainVision Electrode Files

About this manual

This user manual describes the EEG analysis software BrainVision Analyzer.

The user manual is part of the software product. It is essential to follow the instructions in the manual in order to use the software correctly and as intended. You should therefore read this user manual in its entirety.




The user manual is aimed at medical research staff.

TARGET GROUP

The user manual contains specific information that you need in order to install and work with BrainVision Analyzer. The functions and settings of the software are described in detail.

CONTENTS OF THE USER
MANUAL

The **Note** symbol  draws your attention to additional information relating to a topic.

NOTE SYMBOL

Please notify us of any errors or faults you come across when reading the user manual or using the software. In such cases, please contact:

NOTIFICATION OF
ERRORS

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1 Intended Use

BrainVision Analyzer is intended for use with human beings.

It is used to analyze ExG signals (including raw EEG data, spontaneous EEG analyses and evoked potentials) and sensor data on a PC. The ExG signals and sensor data are recorded using separate programs (BrainVision Recorder, for example) and stored in the user's file system. The ExG signals are obtained and recorded exclusively through the recording program used, not through BrainVision Analyzer.

The ExG signals and sensor data are analyzed exclusively for research purposes. The software must not be used for therapy, diagnosis, the monitoring of bodily functions or any other diagnostic or therapeutic purposes.

The program may only be used by doctors or trained staff.

2 About the software

2.1 Product identification

Product name:	BrainVision Analyzer
Manufacturer:	Brain Products GmbH Zeppelinstraße 7 D-82205 Gilching (Munich) Phone: +49 8105 73384 - 0 Fax: +49 8105 73384 - 33 Website: http://www.brainproducts.com Email: Analyzer2@brainproducts.com
Classification according to Directive 93/42 EEC (MDD), Annex IX, Rule 12:	Class I
DIN EN 62304 classification:	Class A – “No injury or damage to health is possible”
UMDNS code:	16-307, Analysis Software for EEGs and Evoked Potentials
GMDN code:	35 163

2.2 CE marking



The CE marking confirms that the product conforms to the essential requirements of the Medical Devices Directive 93/42/EEC (MDD), Annex I.

2.3 Application environment

The Analyzer is not an applied part and is not part of the patient environment.

3 Introduction

The first version of BrainVision Analyzer was released in 1997 for the analysis of EEG data. Since then, numerous modules and calculation methods have been added to the system. Given the continuous advances in both hardware and software technology, after ten years the time came to base the system on a new technology in order to give BrainVision Analyzer the benefit of these advances. The result is BrainVision Analyzer 2.0, which offers new functionality in addition to all the features of the previous version. These include the following:

- The Analyzer is able to read and process the EEG data of numerous EEG amplifiers from well-known manufacturers.
- History trees log every single operation applied to the EEG data. Templates can be created based on these operations, allowing further trees to be created automatically. The parameters of operations can be modified subsequently, and subsequent operations are adjusted automatically.
- As a result of the implementation of OLE Automation and Microsoft .NET interfaces, the Analyzer can be controlled by other programs.
- The various different parts of the Analyzer have a modular structure. These include reader, transformation, montage, export, display and add-in components. By adding new components it is possible to dynamically expand the Analyzer's functionality. Brain Products works to develop new components on an ongoing basis. All interfaces are open, which gives expert users the opportunity to develop their own components. Alternatively, users can have such components developed for them. The integrated Basic interpreter and the fact that transforms and add-ins can be written in any .NET language make it possible to program these applications quickly and with great flexibility.
- A new view concept based on the XML description language also offers flexibility, allowing user interfaces to be customized. These user interfaces can also be used in users' own modules.
- A direct interface to MATLAB® ensures efficient, problem-free data interchange between the Analyzer and MATLAB®/EEGLab. MATLAB® scripts can be used in history trees and added to templates. (A valid MATLAB® license is required on the computer for this function, which is not part of the Analyzer.)
- The LORETA module is used for source localization. It offers a graphical display and allows virtual channels to be calculated based on what are known as "regions of interest" and further processed using the methods offered by the Analyzer.

4 Installation

BrainVision Analyzer generally does not conflict in any way with programs that are already installed. However, Brain Products GmbH will only guarantee perfect interaction in cases where the compatibility of the relevant programs has been tested. This applies both to the BrainVision Analyzer software and the Microsoft Windows® XP/Vista operating systems, provided no changes have been made to the supplied configuration of the operating system (including official service packs and updates).

The system has the following hardware and software requirements:

SYSTEM REQUIREMENTS

- Windows® XP Service Pack 2 or Windows® Vista
- Minimum configuration: Intel Pentium IV or higher, 512 MB of RAM, 8 GB hard disk, graphics card with 64 MB of RAM
- A monitor with a screen size of at least 21 inches (53 cm) when measured diagonally from corner to corner
- At least 256 MB of free RAM, possibly more, depending on the volume of data processed

To install BrainVision Analyzer, proceed as follows:

INSTALLATION STEPS

- Start Windows®.
- Insert the CD-ROM provided into one of your CD-ROM drives.
- If your computer is set up to autostart a CD-ROM, the menu that guides you through the installation will appear after a short time. Follow the instructions displayed.


If your computer is not set up to autostart a CD-ROM, proceed as follows when using Windows® XP:

WINDOWS® XP

- From the taskbar, choose **Start > Run**.
- Click the **Browse** button.
- In the **Browse** dialog box, select your CD-ROM drive and double-click the **setup.exe** file to open it. Follow the instructions displayed.

If your computer is not set up to autostart a CD-ROM, proceed as follows when using Windows® Vista:

WINDOWS® VISTA

- Click the **Start** button  on the taskbar, and then choose **All Programs > Accessories > Run**.
- In the **Browse** dialog box, select your CD-ROM drive and double-click the **setup.exe** file to open it. Follow the instructions displayed.

The wizard takes you through the installation:

INSTALLATION WIZARD

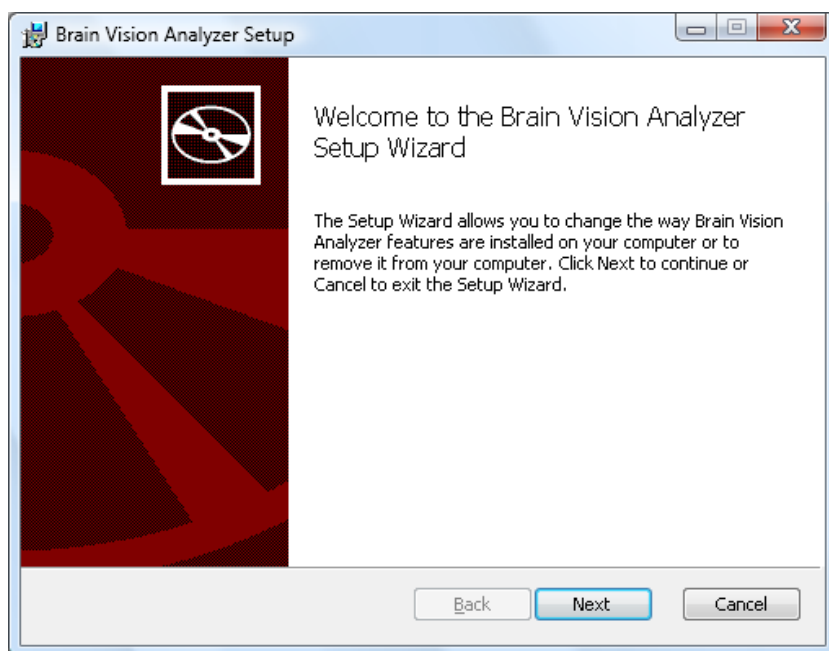


FIGURE 4—1 INSTALLATION WIZARD (A)

The wizard requires you to select the destination folder for the program:

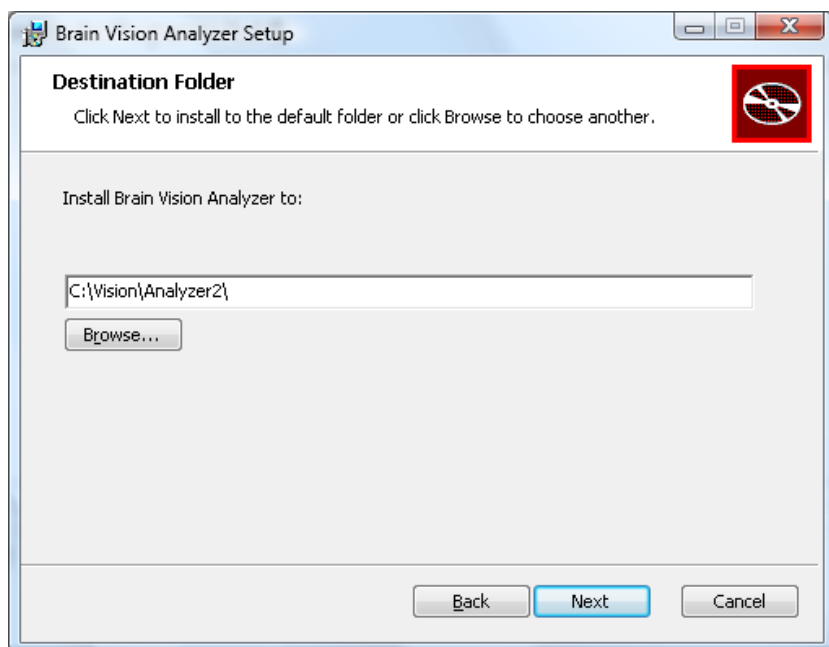



FIGURE 4—1 INSTALLATION WIZARD (B)

Before you start the Analyzer, insert the hardlock key provided into one of your computer's USB ports.

If you have a network license, you will find the instructions in Appendix E, “Installing a network license (USB)”.



Start the Analyzer by double-clicking the Analyzer icon . This appears on your desktop on completion of successful installation.

Alternatively, you can start the Analyzer by choosing **Start > Vision Analyzer** from the taskbar (Windows® XP, Vista).

5 Getting started and working with the Analyzer

5.1 The new user interface of the Analyzer

There are numerous new tools that make it easier to work with Analyzer 2.0.

The Analyzer 2.0 user interface has a new structure, incorporating a Ribbon. The functions on the toolbars and menus have been rearranged on the Ribbon. The Ribbon is subdivided into tabs. The **tabs** (figure 5—1) contain **groups** (figure 5—2), and a group contains a number of **command buttons** (figures 5—3 and 5—4).

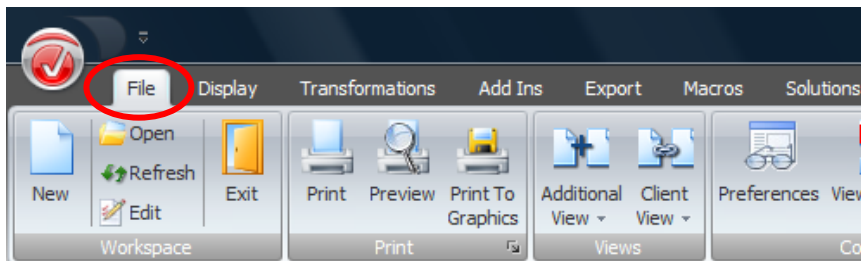


FIGURE 5—1 TAB

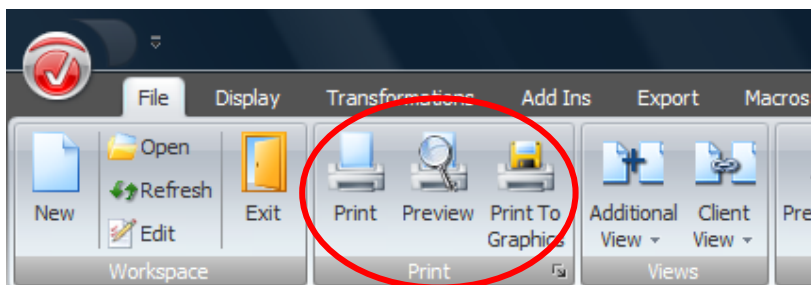


FIGURE 5—2 GROUP

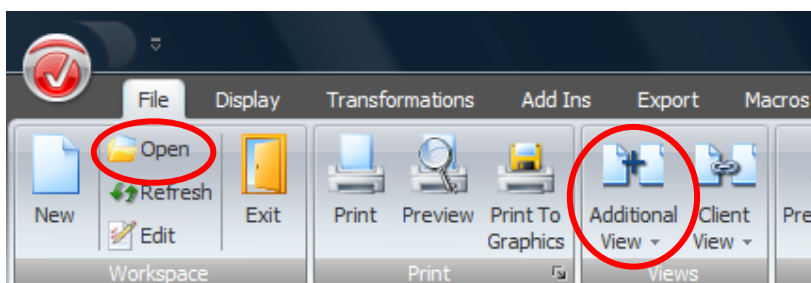


FIGURE 5—3 COMMAND BUTTONS

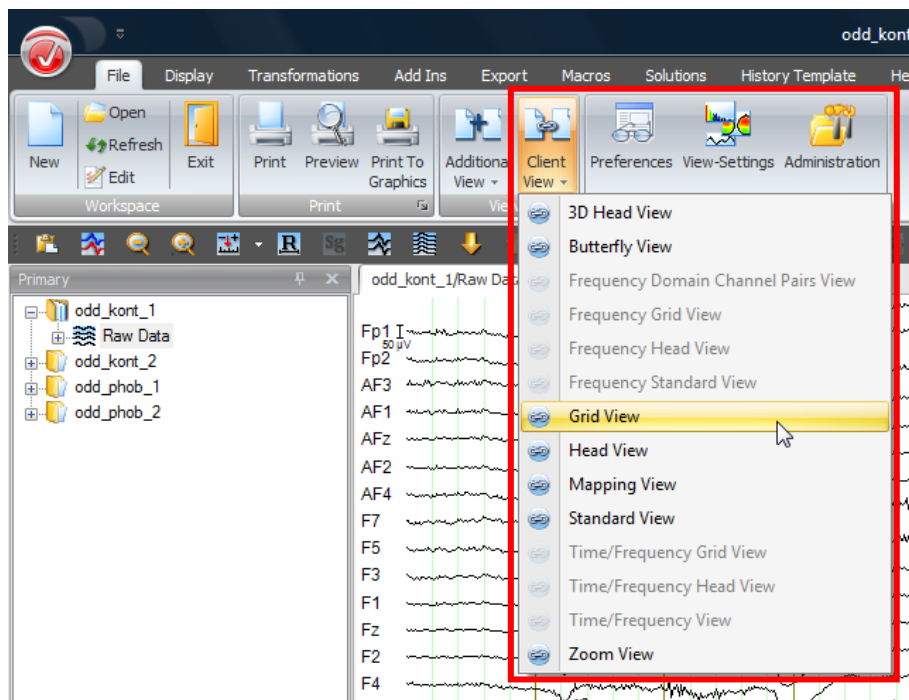


FIGURE 5—4 COMMAND BUTTONS

You can hide or show the Ribbon by double-clicking a tab.

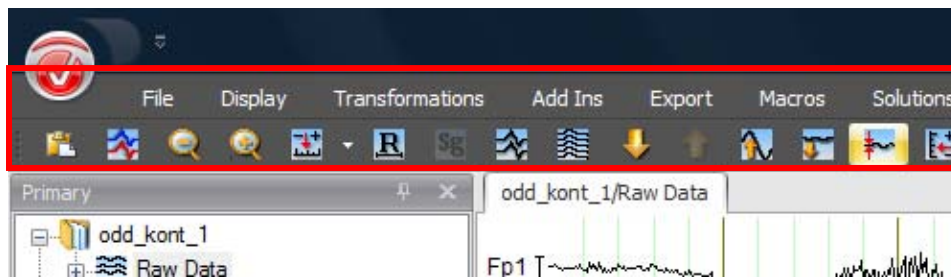


FIGURE 5—5 RIBBON HIDDEN

The Analyzer title bar contains the name of the EEG data set displayed.

TITLE BAR

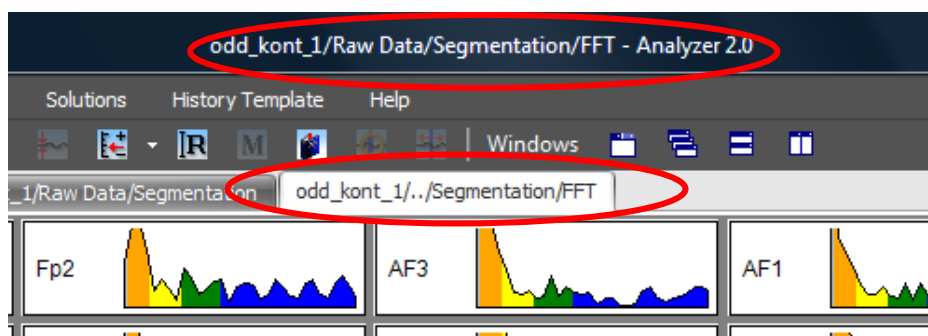


FIGURE 5—6 TITLE BAR

Docking allows you to arrange windows and bars dynamically and customize the user interface. You will find detailed information on the docking options available in section 7.2.2, “Docking”.

DOCKING

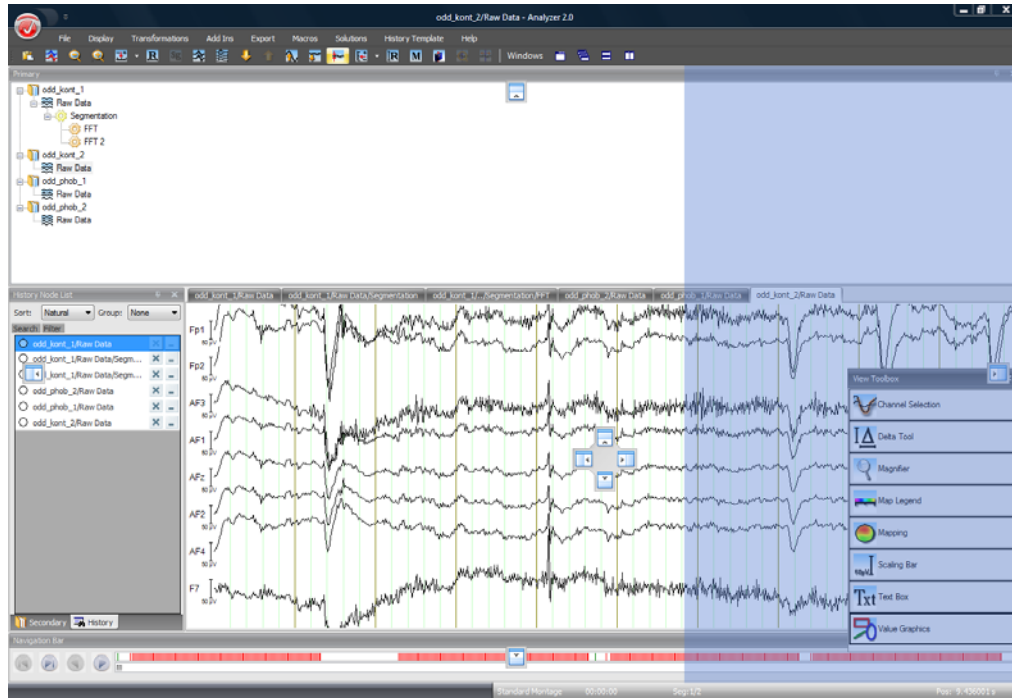


FIGURE 5—7 ARRANGING DOCKING ELEMENTS DYNAMICALLY

The **Analyzer button**, which is located in the upper left corner of the application window, contains the application’s main menu.

ANALYZER BUTTON



FIGURE 5—8 ANALYZER BUTTON

Next to the **Analyzer button** there is a control that displays the **Quick Access Toolbar**.

QUICK ACCESS TOOLBAR

You add a control to this toolbar by right-clicking the control on the Ribbon and then choosing the **Add to Quick Access Toolbar** command from the context menu that appears. You delete controls you have added by right-clicking the control and then choosing the **Remove from Quick Access Toolbar** command from the context menu.

If you prefer, you can display the Quick Access Toolbar below the Ribbon by choosing the **Show Quick Access Toolbar Below the Ribbon** command from the context menu.

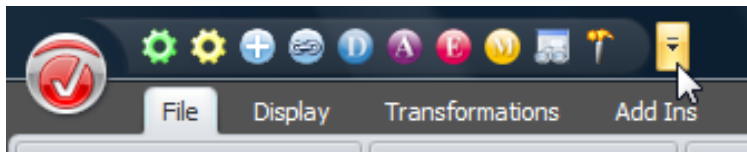


FIGURE 5—9 DISPLAYING THE QUICK ACCESS TOOLBAR, ADDED CONTROLS

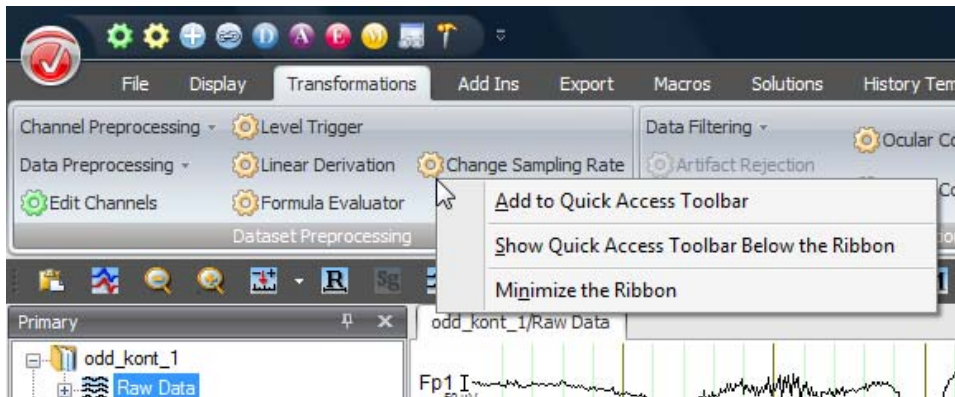


FIGURE 5—10 ADDING CONTROLS TO THE QUICK ACCESS TOOLBAR

When you move the mouse pointer over a control, a small box appears, containing a brief **TOOLTIP** description of the control.

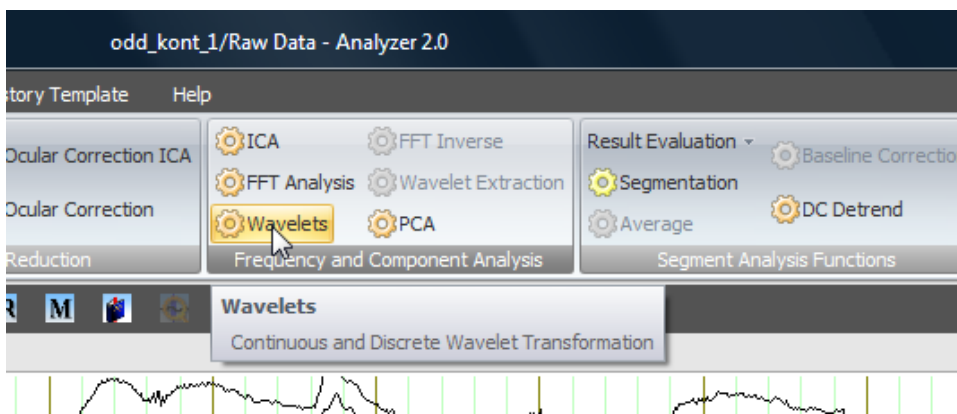


FIGURE 5—11 TOOLTIP

The menu bar, which is located along the top of the application window, contains the tabs.

MENU BAR

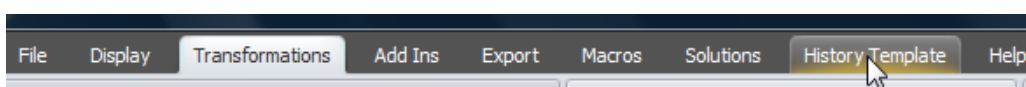


FIGURE 5—12 MENU BAR WITH TABS

The toolbar, which is located along the top of the application window just below the menu bar, allows you, for example, to increase or decrease the interval displayed or the number of channels displayed simultaneously.

TOOLBAR

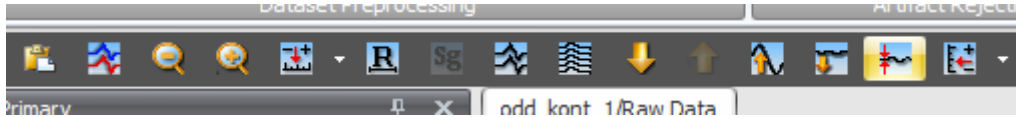





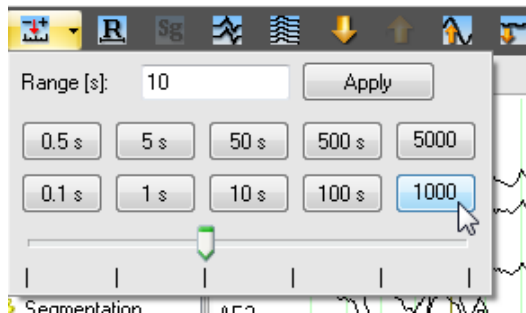


FIGURE 5–13 PART OF THE TOOLBAR

The toolbar contains the following buttons (see the table of keyboard shortcuts in Appendix D):





BUTTONS ON THE
TOOLBAR







-  **Copy:** Copies the current view to a clipboard.
-  **Overlay Data Set:** Overlays different data sets.
-  **Increase Interval:** Increases the interval displayed.
-  **Decrease Interval:** Decreases the interval displayed.
-  **Set Displayed Interval:** Sets the time scale;

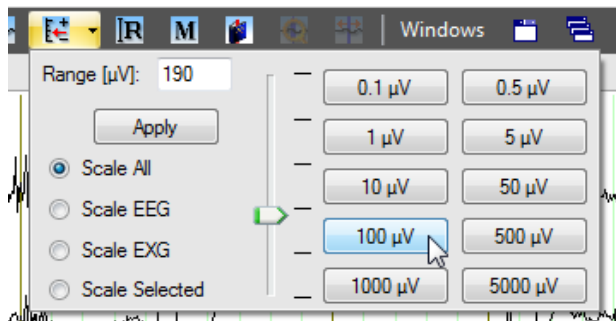


In the **Range [s]** text box, you specify the scaling range in ms. When you click **Apply**, your entry is applied to the data.

You can use the slider to change the scaling, or you can click one of the buttons (e.g. **10 s**) to apply the scaling associated with that button.

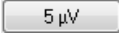
-  **Reset Interval** resets the interval displayed to the default value.
-  **Fit Segment:** Displays a single segment. This button is only available for segments that are small enough.
-  **Decrease Channels:** Decreases the number of channels displayed.
-  **Increase Channels:** Increases the number of channels displayed.






-  **Next Group:** Switches to the next channel group. This function is only available when the number of channels has been reduced.
-  **Previous Group:** Switches to the previous channel group. This function is only available when the number of channels has been reduced.
-  **Scale Up:** Increases the scaling (sensitivity).
-  **Scale Down:** Decreases the scaling (sensitivity).
-  **De/Activate the Baseline Correction:** Switches the baseline on and off.
-  **Set Scaling Range:** Allows you to scale the voltage.




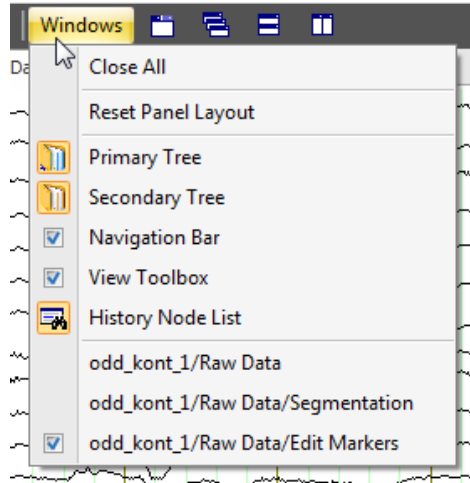
In the **Range [µV]** text box, you specify the scaling range in volts. When you click **Apply**, your entry is applied to the data.

If you select the **Scale All** radio button, your entry applies to all channels; if you select **Scale EEG**, it applies only to the EEG channels. If you select **Scale EXG**, it applies only to non-EEG channels. You distinguish between EEG channels and non-EEG channels by checking whether they have coordinates.

You can use the slider to change the scaling, and you can click one of the buttons (e.g. ) to apply the scaling associated with that button.

-  **Reset Scaling Range:** Resets the scaling to the original value.
-  **Marker Edit Mode:** The marker button displays the interactive marker editor.
-  **Bookmark Menu:** This button allows you to set a bookmark in the EEG and remove it again.
-  **Zoom To Selection** enlarges the selected range.
-  **Zoom from Selection** undoes the last zoom operation on a selected range.

-  The **Windows** button gives you the flexibility to display and arrange the various windows and other items in the application in a variety of ways. If there is a check mark next to an item's name, this item will be displayed.







Close All closes all the windows.

Reset Panel Layout returns the windows to their original layout.

All the built-in docking windows are listed after this. If you click one of these commands, you show or hide the corresponding window, depending on whether it is currently hidden or shown.

The section at the bottom of the menu lists all the open nodes. The active node has a check mark against it.

-  The **Use Tabbed MDI** button allows you to specify whether the data is to be displayed on tabs or in windows. If you opt for display in windows, you can use the following three buttons to arrange the windows:
 -  **Cascade Windows** cascades all the open windows one behind the other.
 -  **Tile Horizontal** arranges them horizontally one above the other.
 -  **Tile Vertical** arranges them vertically next to each other.

The status bar contains a number of sections that provide information about the montage, the interval displayed, the mouse position and the current workspace. STATUS BAR



FIGURE 5—14 PART OF THE STATUS BAR

You can use the status bar's context menu to choose which information is to be displayed.

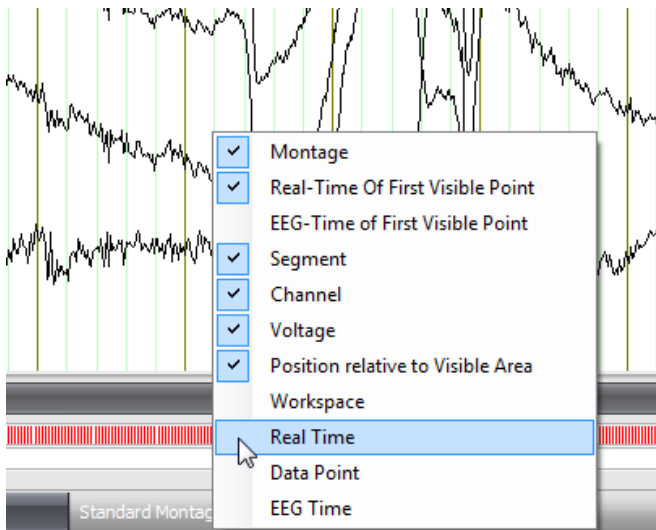


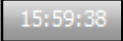
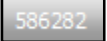
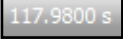


FIGURE 5—15 SELECTING THE STATUS INFORMATION

You can display the following status information:

- Standard Montage The **Montage** section indicates the montage type that is currently set. You will find more information on montages in chapter 8, "Montages".
- 15:59:30 The **Real-Time Of First Visible Point** section indicates the real time of the beginning of the EEG interval displayed.
- 00:01:49 The **EEG-Time of First Visible Point** section indicates the time position of the interval displayed in the EEG.
- Segment:1/1 The **Segment** section indicates the current segment number at the beginning of the EEG interval displayed. You will find more information on segments in chapter 6, "Segmentation".
- Chan: Fp1 The **Channel** section displays the name of the channel on which the mouse is positioned.
- Volt: 17.82227 µV The **Voltage** section indicates the voltage applied at this point.

-  The **Position relative to Visible Area** section indicates the time position on which the mouse is positioned, relative to the beginning of the EEG interval displayed or relative to a time zero marker, if one has been set. You will find detailed information on editing markers in section 12.7.2, “Edit Markers”.
-  The **Workspace** section indicates the name of the active workspace.
-  The **Real Time** section indicates the real time on which the mouse pointer is positioned.
-  The **Data Point** section indicates the data point on which the mouse pointer is positioned.
-  The **EEG Time** section indicates the time position on which the mouse pointer is positioned, relative to the whole EEG.

The navigation bar along the bottom allows you to navigate in the EEG.

NAVIGATION BAR

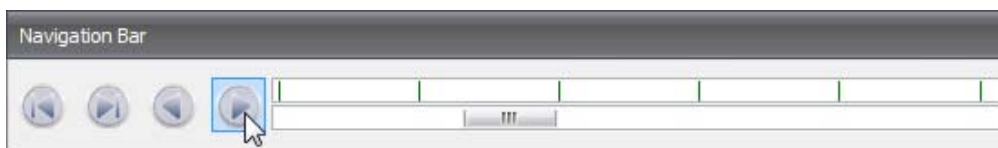






FIGURE 5—16 PART OF THE NAVIGATION BAR, WITH NAVIGATION BUTTONS, MARKER BAR AND SLIDER BAR

There are four buttons on the left-hand side of the navigation bar that allow you to move through the EEG on the time axis.

The buttons  and  take you one second forward or back, unless a section is $\leq 1s$, in which case they take you 100 ms forward or back.

The buttons  and  allow you to go forward or back by the interval displayed minus one second. That is because the successive intervals displayed overlap by one second.

The marker bar to the right of the buttons displays all the markers set in the EEG. Markers are time-related indicators such as stimuli, responses, comments, segment boundaries, DC corrections, etc.

The slider bar is located below the marker bar. The width of the slider in the bar represents the currently displayed section of the EEG, and the slider bar represents the entire EEG.

You can use the mouse to change the position of the slider. A different section of the EEG is then displayed based on the new position of the slider.

If you click any point on the marker or slider bar, the corresponding section of the EEG is displayed.

If you right-click the marker bar, a context menu appears. By choosing the commands on this menu to set and remove the check marks, you can either hide the entire marker bar (by removing the check mark against **Show Markers**) or select which types of marker you want to be shown.

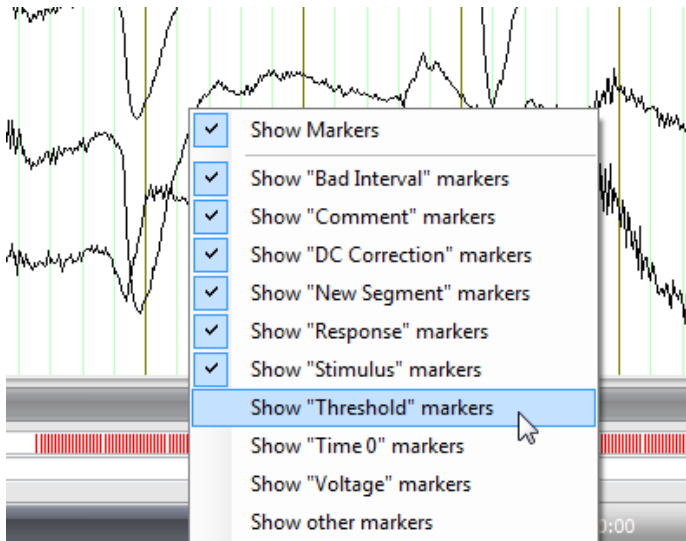


FIGURE 5—17 CONTEXT MENU FOR SHOWING AND HIDING MARKERS

The various EEG views are displayed by default in the form of tabs arranged above the EEG.

VIEW TABS

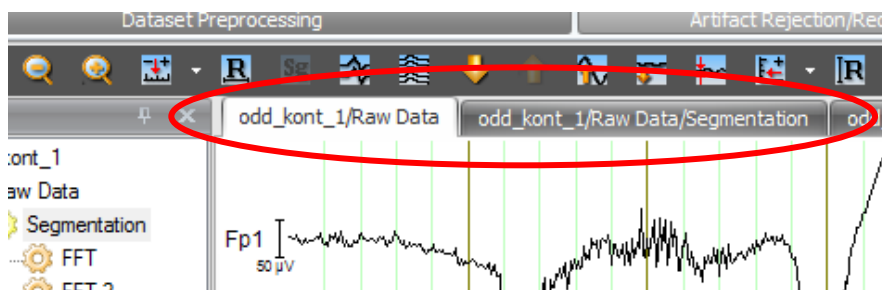


FIGURE 5—18 EEG VIEWS ON TABS

To close a view tab, click the cross on the right of the tab bar. You can use the arrows to switch between the different tabs.

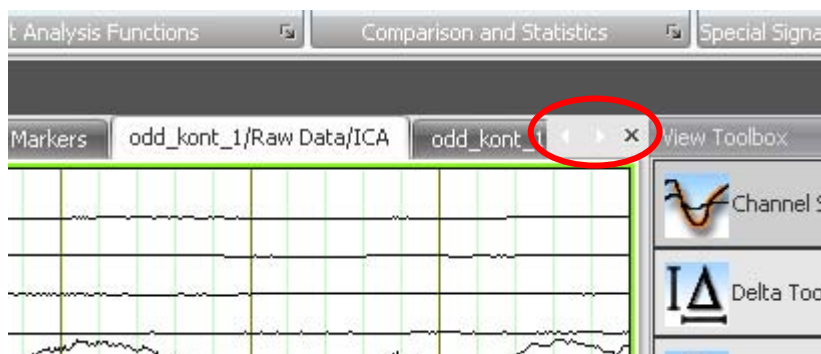


FIGURE 5—19 EEG VIEWS ON TABS

The History Explorer displays your history files. It is located on the left-hand side of the application window. HISTORY EXPLORER

The History Explorer contains the primary and secondary history data and a list of all the open history nodes.

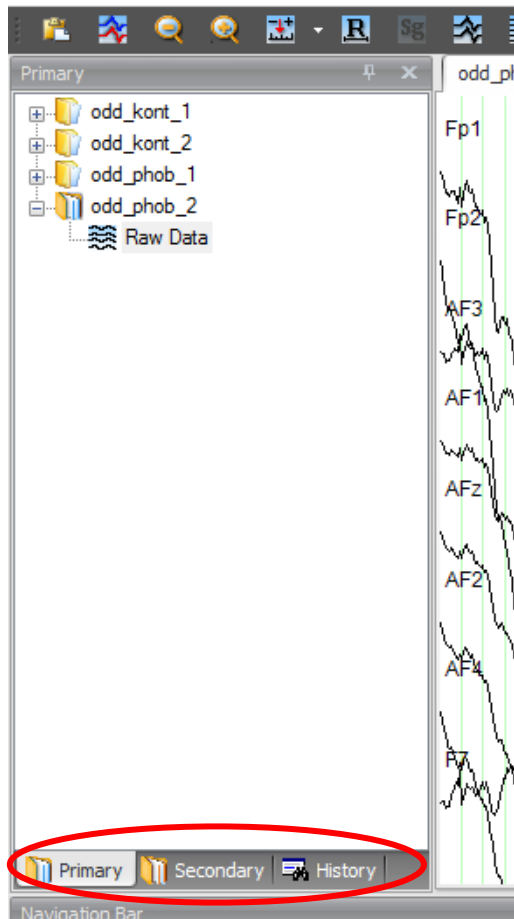


FIGURE 5–20 HISTORY EXPLORER WITH PRIMARY AND SECONDARY DATA AND THE HISTORY NODE LIST

Each history file is assigned a book icon.

If the book icon does not appear, this is either because the specified raw data folder is empty or because the Analyzer is not (yet) able to read the format of the EEGs stored in this location. If the latter is true, contact Brain Products GmbH and ask about the latest EEG readers.

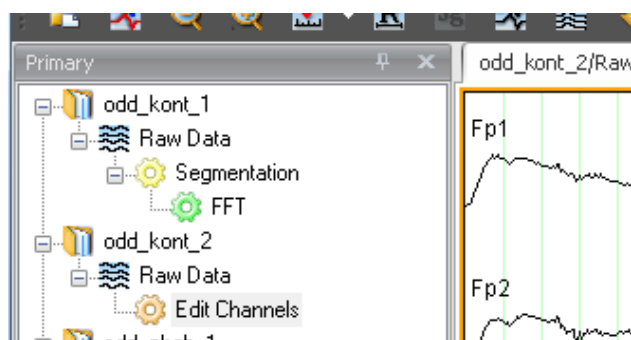



FIGURE 5–21 OPEN NODES IN THE HISTORY EXPLORER

To open a history file, click the icon  to the left of the book icon. If you double-click the icon, the corresponding EEG is displayed.

You close the history file by clicking the icon . This also closes all the data set windows associated with the file.

If you want to transfer the transforms you have run to a history file, open this history file. Ensure that the file contains the same channel names as the source file. Our example (figure 22 onward) concerns **odd_phob_1** and **odd_phob_2**. Position the mouse pointer on the icon of the transform to be transferred, and then press the left mouse button. Hold down the mouse button to drag the icon to the **Raw Data** icon of the second history file, and then release the mouse button to drop it there. The Analyzer automatically creates the corresponding history tree.

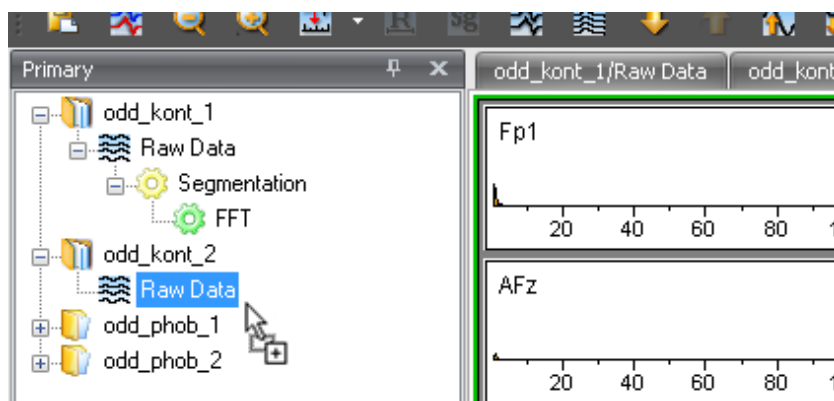


FIGURE 5—22 DRAGGING AND DROPPING TO GENERATE A HISTORY TREE (A)

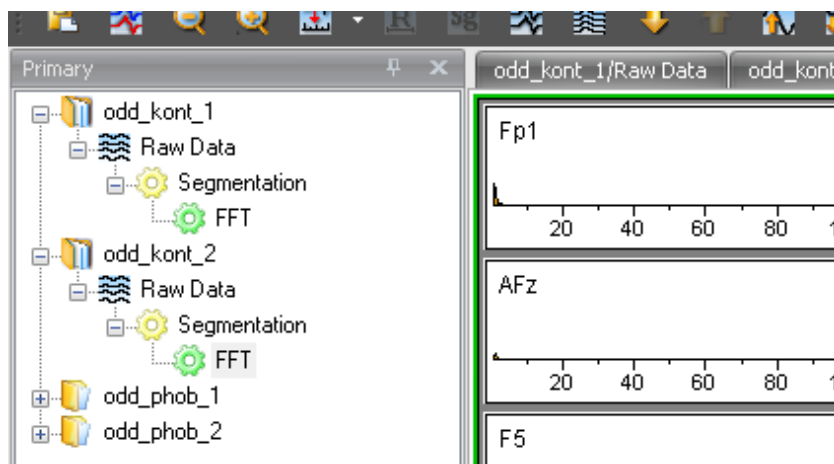


FIGURE 5—23 DRAGGING AND DROPPING TO GENERATE A HISTORY TREE (B)

In addition to transferring history information to other history files, you can also save history information in history templates. You will find more information on this in chapter 10, “Automation using history templates”.

The various data sets that make up a history file are known as history nodes. You can delete and/or rename these data sets.

If you right-click a book icon, the following context menu appears:

CONTEXT MENUS IN THE HISTORY EXPLORER

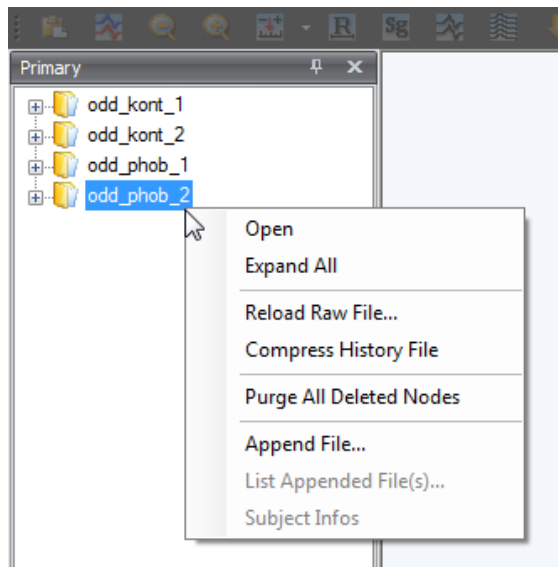


FIGURE 5—24 CONTEXT MENU OF A HISTORY DATA SET

- **Open /Close** opens or closes the data set.
- **Expand All** expands the entire history tree.
- **Reload Raw File...** removes all the nodes and reloads the raw data set.
- **Compress History File** compresses the history file. When you delete larger data sets (e.g. FFT), the history file may remain the same size. The Analyzer does not delete the data from the history file immediately for performance reasons.
- **Purge All Deleted Nodes** permanently removes all deleted nodes of the entire data set (to restore deleted history nodes, choose **Undelete a Child...** from the context menu of the corresponding raw data set or node).
- **Append File...** appends a raw EEG to the data set. When you acknowledge the warning that the transforms in the relevant history file are going to be lost, the **Append Files** dialog box appears. In this dialog box you select the raw data EEG to be appended. If you click **OK**, the first history file is modified and the second one is removed. The icon changes from a book into a stack of books.
- **List Appended File(s)...** contains a list of the raw EEGs appended to the data set.
- **Subject Infos** displays information about the subject (patient) that was obtained during recording.

If you right-click **Raw Data**, the following context menu appears:

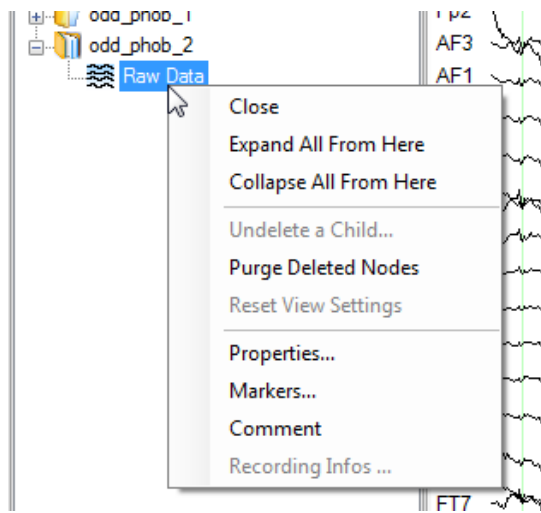


FIGURE 5—25 CONTEXT MENU OF A RAW DATA SET

- **Open/Close** opens or closes the corresponding window or tab.
- **Expand All From Here** expands the data set from this point.
- **Collapse All From Here** collapses the data set from this point.
- **Undelete a Child...** restores the most recently deleted node. You can repeat this operation as often as you like.
- To permanently remove (purge) all deleted nodes, choose **Purge Deleted Nodes**.
- **Reset View Settings** deletes all node-specific view settings.
- **Properties...** displays a window containing an overview of the data properties, such as the length of the data set and the sampling interval.
- **Markers...** displays a window containing an overview of the markers in the data set together with their properties.
- **Comment** adds a comment that can then be displayed using this function.
- **Recording Infos...** displays the information captured in the data set during the recording of the EEG.

If you right-click a node, the following context menu appears:

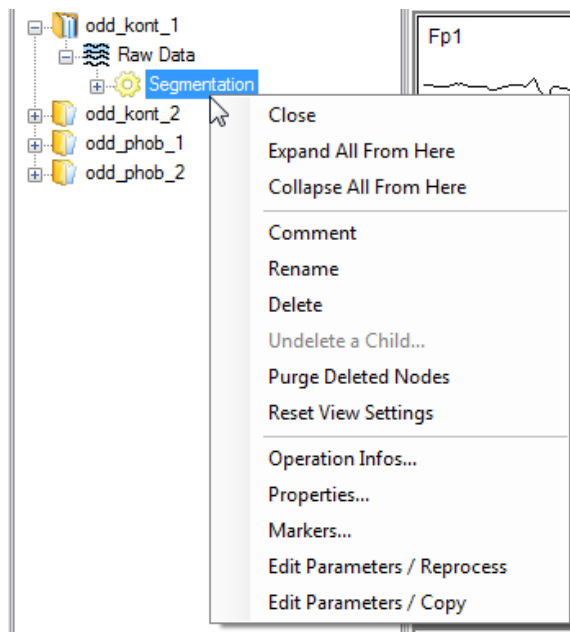


FIGURE 5—26 CONTEXT MENU OF A NODE

- **Open/Close** opens or closes the node as a window or tab.
- **Expand All From Here** expands the data set from this point.
- **Collapse All From Here** collapses the data set from this point.
- **Comment** adds a comment that can then be displayed using this function.
- **Rename** allows you to rename a node. Alternatively, you can click the node to select it and then press the **<F2>** key on your keyboard or click the history node text a second time after a few seconds. You can then edit the text. This function is the same as the one in Windows® Explorer.
- **Delete** deletes the node. Alternatively, you can press the **<Delete>** key on your PC keyboard.
- **Undelete a Child...** restores the most recently deleted node. You can repeat this operation as often as you like.
- To permanently remove (purge) all deleted nodes, choose **Purge Deleted Nodes**.
- **Reset View Settings** deletes all node-specific view settings.
- **Operation Infos...** displays the parameters with which the relevant transform was executed.
- **Properties...** displays a window containing an overview of the data properties, such as the length of the data set and the sampling interval.
- **Markers...** displays a window containing an overview of the markers in the data set together with their properties.

- **Edit Parameters / Reprocess** allows you to modify parameters of the associated transform. The original node is removed and replaced.
- **Edit Parameters / Copy** allows you to modify parameters. The original node is retained.

If you choose the **Edit Parameters / Reprocess** or **Edit Parameters / Copy** command, the parameters dialog box for the relevant node appears, containing the node's existing parameters.

On the parameters selected, it may not be possible to restore all child nodes. In such cases, what happens is similar to what happens in the case of a history template that cannot be executed any further for a similar reason.

If the parent node uses a semiautomatic view for parameter editing, its child nodes are saved hidden and not restored until the transform is completed. This also happens when the semiautomatic view is interrupted with **Suspend** (a corresponding message appears).



The **History Node List** contains all the open history nodes and allows the nodes to be sorted. The history nodes in the list are marked in the same color as the corresponding transform. Raw data is marked white.

HISTORY NODE LIST

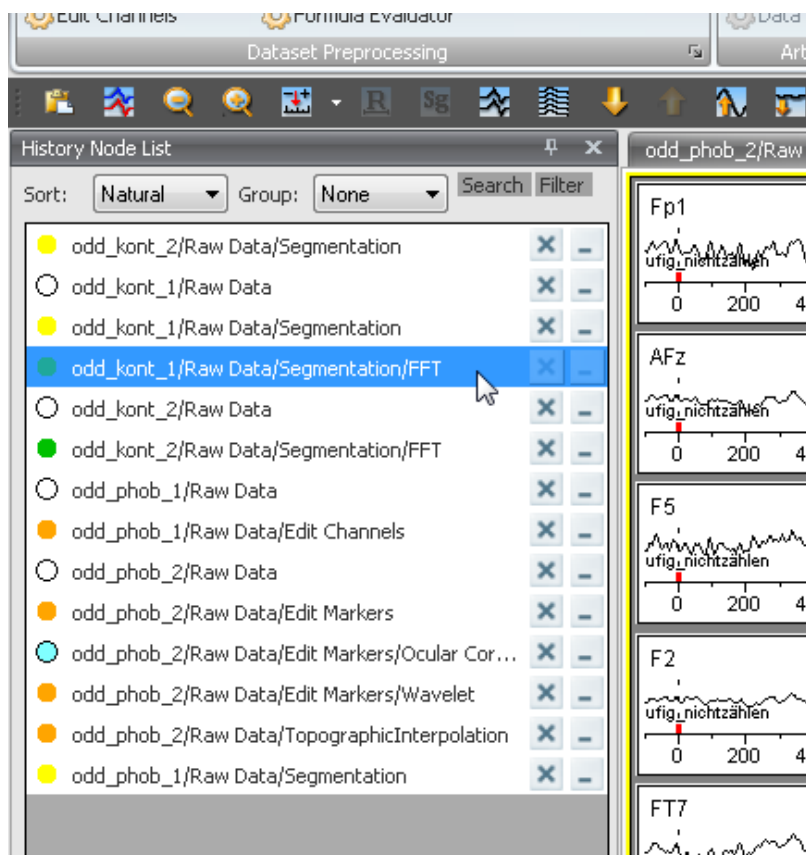





FIGURE 5—27 HISTORY NODE LIST

The History Node List has the following selection and display functions:

- If you double-click an item in the list, the corresponding node is activated.
- The cross button  to the right of each item closes the corresponding node.
- The button  minimizes the node or hides it temporarily.
- The button  maximizes the node or displays it again.
- **«Shift»** plus a mouse click allows you to select either a range of items or all of them.
- **«Ctrl»** plus a mouse click allows you to select multiple items.
- If you right-click one or more selected items, a context menu appears that allows you to close the selected nodes (**Close Selected Nodes**), hide them (**Hide Selected Nodes**) or display them (**Show Selected Nodes**).

When a large number of nodes are open, the following functions allow you to arrange them and maintain the best possible overview:

- The **Group** drop-down list box allows you to group the nodes in four different ways:

None means that the nodes are not grouped.

File groups them by file name.

Status groups them based on whether the node is open (i.e. it has the status **Displayed**) or closed (it has the status **Hidden**).

Type groups them by transform type.

- The **Sort** drop-down list box allows you to sort the nodes based on three criteria:

Natural sorts the nodes in the sequence in which they were opened.

Depth sorts the nodes by node depth. For the grouping criterion “Type”, for example, FFT nodes of the same depth appear one after the other.

Recursive sorts the nodes by path components (i.e. by the components separated by a forward slash). The file is ignored, and the paths are compared component by component from left to right until there is a difference or the end of the path is reached. In this case, the shorter of the paths is listed first. Consequently, the parent node is listed first within a file, followed by its child nodes.

The History Node List also offers a search and filter function:

- The search function allows you to find a specific node quickly. To use it, you click **Search**. A text box appears, in which you can enter a search string. The filter is incremental (the function progressively finds a match for the filter as you enter each character). When you press the **Return** key, all the search results are displayed.
- The filter function allows you to preselect nodes in order to limit the nodes displayed. Click **Filter**. A text box appears, in which you can enter the filter you want to apply. The filter is incremental (the function progressively finds a match for the filter as you enter each character). When you press the **Return** key, all the search results are displayed. The **Backspace** key broadens the selection again.

You can, for example, filter out all nodes that contain segmentation, select them and then close them all.

The **View Toolbox** window provides you with a number of different tools. You use them by dragging them onto the EEG using the mouse and dropping them there by releasing the mouse button.

VIEW TOOLBOX

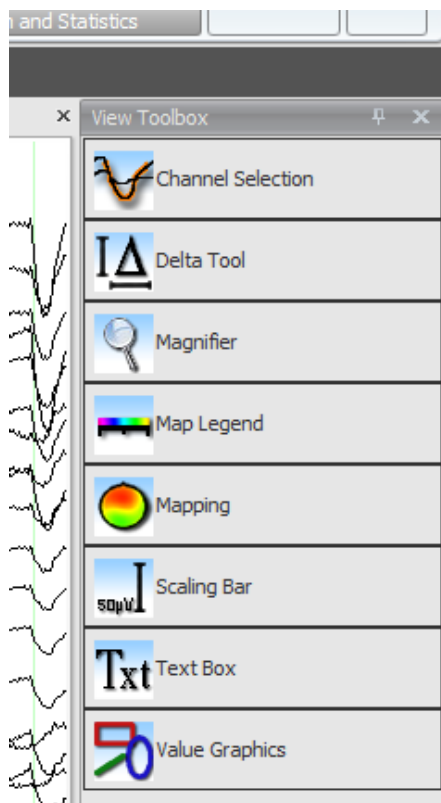



FIGURE 5—28 VIEW TOOLBOX WINDOW

You can make settings for each view tool by choosing **Settings...** from the context menu that appears when you click the drop-down button  on the tool's right-hand border.



The **Close Tool** command closes the tool.

The **Channel Selection** tool adds highlighting to a selected part of a channel. The tool is used purely for the purpose of highlighting.

CHANNEL SELECTION
TOOL

You change the width of the highlighting by moving the mouse pointer over it. Two blue arrows appear on its edges. Click one of these arrows, and drag it in the required direction.

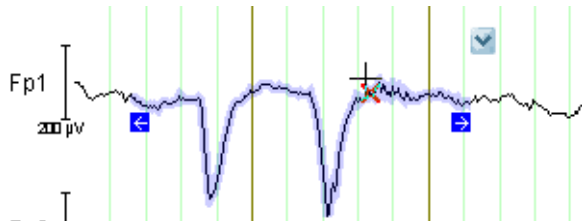


FIGURE 5—29 CHANNEL SELECTION TOOL IN THE VIEW TOOLBOX WINDOW

The context menu contains the following commands:

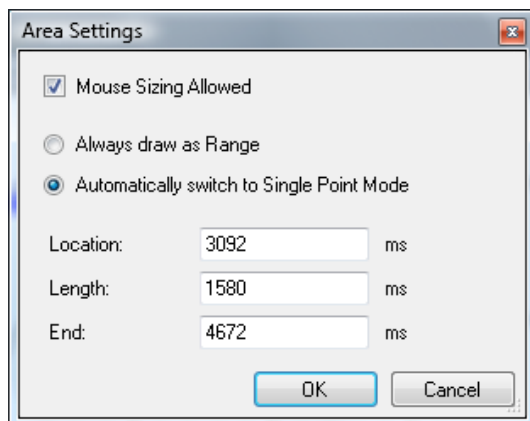


FIGURE 5—30 AREA SETTINGS DIALOG BOX

- **Lock Tool to Channel** locks the tool onto the channel.
- **Selected Area Settings...** opens the Area Settings dialog box, in which you can make the following settings:

If you select the **Mouse Sizing Allowed** check box, you allow the tool to be resized using the mouse.

If you select the **Always Draw as Range** radio button, a range is highlighted.

If you select the **Automatically switch to Single Point Mode** radio button, a single point is highlighted.

In the text boxes in the lower part of the dialog box, you can change the position (**Location**, **End**) and length (**Length**) of the highlighting. Note that the times you specify are rounded to the nearest data point.

The **Delta Tool** is for indicating differences in voltage and time values.

DELTA TOOL

When you drag the Delta Tool to a graph and release the mouse button there, the tool is fixed in that position. The tool remains tied to the mouse pointer. You can then set the position of the second point by moving the mouse pointer over the channels (not holding down the mouse button). The first point remains in its fixed position. You set the second fixed point with another click.

Note that both of the tool's points must always be on the same channel.

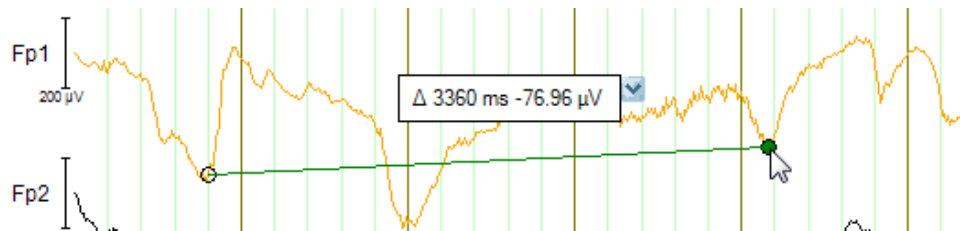


FIGURE 5—31 DELTA TOOL IN THE VIEW TOOLBOX WINDOW

You can reposition the left- and right-hand points of the tool by moving the mouse pointer over them. When the point turns green, click it and drag the tool to the required position.

Under **Settings...**, you can make the following settings:

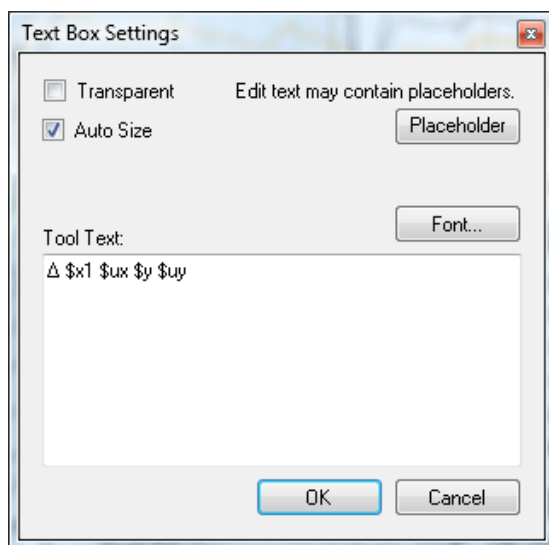


FIGURE 5—32 TEXT BOX SETTINGS DIALOG BOX (DELTA TOOL)

You can change the appearance of the tool's text box and edit the text displayed in the text box. You can specify any text and placeholders.

- \$x = difference in the x-axis direction
- \$y = difference in the y-axis direction
- \$ux = unit in the x-axis direction
- \$uy = unit in the y-axis direction

You can append single-digit numbers to the placeholders \$x and \$y that specify the decimal point to which the output is rounded (e.g. \$y3).

The **Transparent** check box makes the text box transparent. If you select the **Auto Size** check box, the size of the text box changes automatically to fit the length of the text. Otherwise, you can change its size as required. **Font...** opens a dialog box in which you can select the font to be used. In the **Tool Text** text box, you enter the text you want.

The **Magnifier** magnifies an EEG channel.

MAGNIFIER

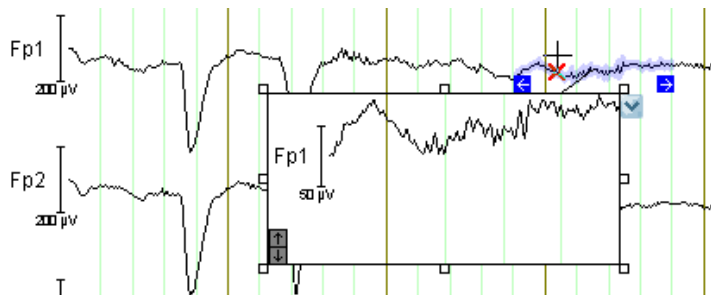


FIGURE 5—33 MAGNIFIER IN THE VIEW TOOLBOX WINDOW

You resize the tool by clicking it, grabbing one of its 8 small handles (rectangles) and dragging it until the tool is the right size.

The gray arrows in the lower left corner of the tool are for changing the vertical scaling. You can choose **Settings...** to display the settings of the view displayed in the Magnifier.

The **Map Legend** tool is used together with the **Mapping** tool to display the color scale of the maps.

MAP LEGEND

This tool supports the same settings as the Mapping tool. As with the Mapping tool, the data range for automatic scaling extends across the entire EEG section displayed.

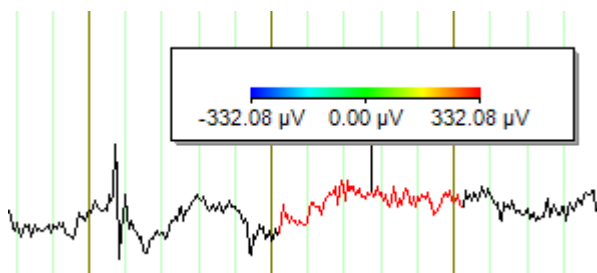


FIGURE 5—34 MAP LEGEND TOOL IN THE VIEW TOOLBOX WINDOW

The **Mapping** tool allows you to display maps in any position. The tool always displays a range across all channels. MAPPING TOOL

To resize the tool, click it. A total of 8 small handles (rectangles) appear around it. You resize the tool by dragging these.

You can choose **Settings...** to display the settings of the view displayed in the Magnifier. The view settings are the same as those of the map (see section 7.3.2, “Category-related view settings”), except that the number of maps is always “1”.

If you use the **Automatic Scaling** function, the entire EEG section displayed underlies the scale. As a result, all map tools use the same scale with uniform scaling settings regardless of their positioning.

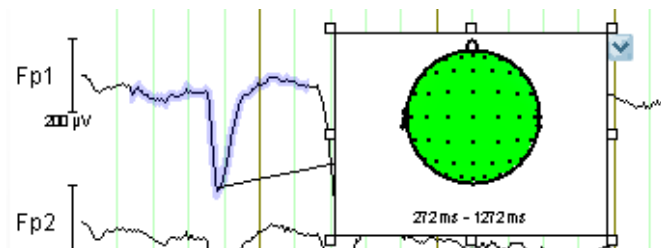


FIGURE 5—35 MAPPING TOOL IN THE VIEW TOOLBOX WINDOW

The **Scaling Bar** indicates the voltage values. The bar is always based on a specified point. SCALING BAR

You resize the tool by clicking it, grabbing one of its small handles (rectangles) and dragging it until the tool is the right size.

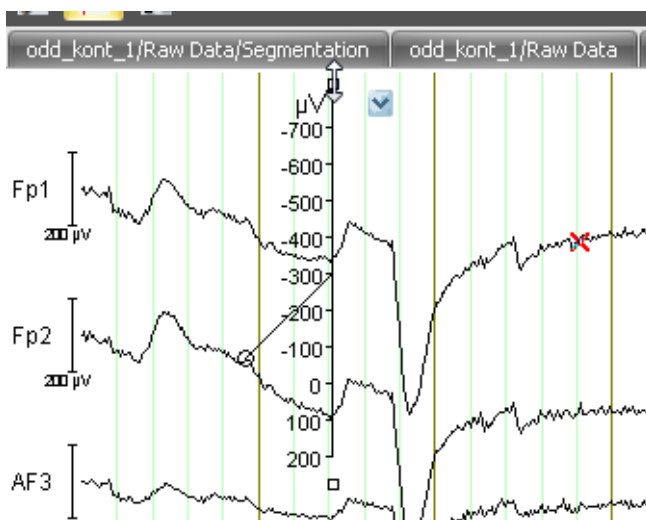


FIGURE 5—36 SCALING BAR IN THE VIEW TOOLBOX WINDOW

You can choose **Settings...** to display the **Bar Settings** dialog box:

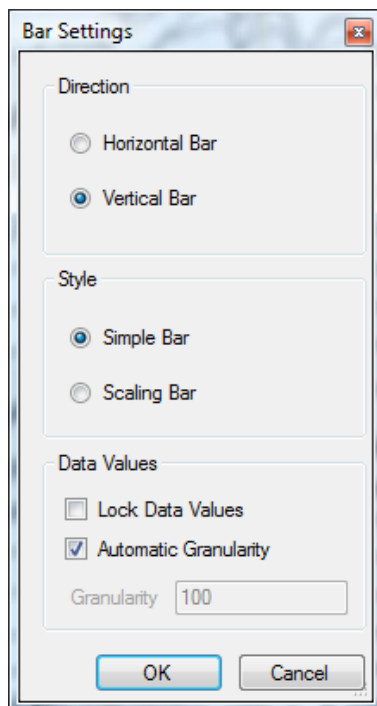


FIGURE 5—37 BAR SETTINGS DIALOG BOX

Under **Direction**, you specify the orientation of the Scaling Bar (horizontal or vertical).

Under **Style**, you choose between a simple bar (Simple Bar) or a bar that displays the values of the channel on which it is located (Scaling Bar).

If you select the **Lock Data Values** check box, the Scaling Bar is scaled as well. If you clear the check box, the bar retains its original size during scaling. If you select the **Automatic Granularity** check box, the intervals between two divisions on the scale are set automatically. If you clear the check box, you can enter a user-specific value in the **Granularity** text box.

The **Text Box** tool allows you to enter comments. You resize a text box by clicking it, grabbing one of its small handles (rectangles) and dragging it until the box is the right size. TEXT BOX TOOL

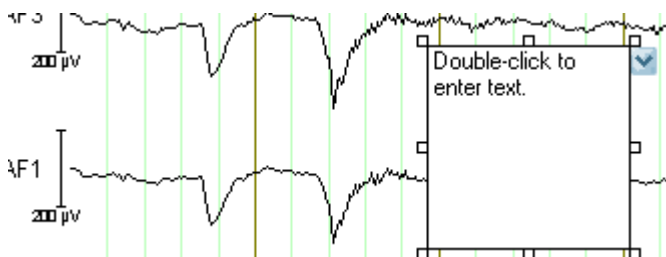


FIGURE 5—38 TEXT BOX TOOL IN THE VIEW TOOLBOX WINDOW

Under **Settings...**, you can make the following settings:

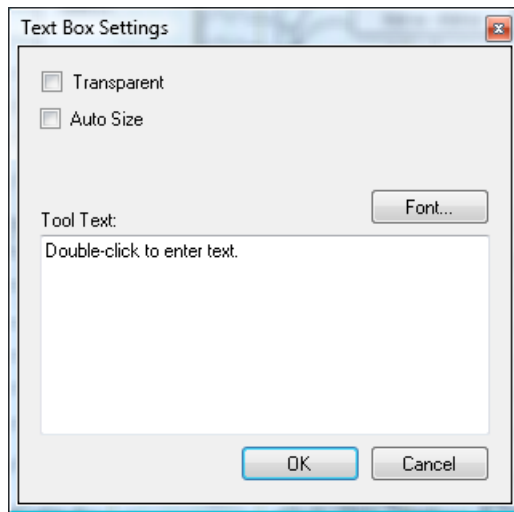


FIGURE 5—39 TEXT BOX SETTINGS DIALOG BOX (TEXT BOX TOOL)

The **Transparent** check box makes the text box transparent. If you select the **Auto Size** check box, the size of the text box changes automatically to fit the length of the text. Otherwise, you can change its size as required. **Font...** opens a dialog box in which you can select the font to be used. In the **Tool Text** text box, you enter the text you want.

The **Value Graphics** tool allows you to add simple drawing objects to the graph. When you drag the tool onto the graph, a context menu appears that allows you to select an ellipse (**Ellipse Tool**), a rectangle (**Rectangle Tool**), a line (**Line Tool**) or a curve (**Curve Tool**).

VALUE GRAPHICS TOOL

You resize the object by clicking it, grabbing one of its small handles (rectangles) and dragging it until the object is the right size.

The curve is a Bézier curve with four points.

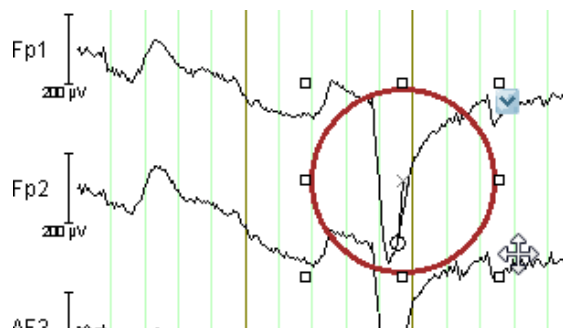


FIGURE 5—40 ELLIPSE OBJECT OF THE VALUE GRAPHICS TOOL IN THE VIEW TOOLBOX WINDOW

You can choose **Settings...** to open the **Value Graphics Settings** dialog box.

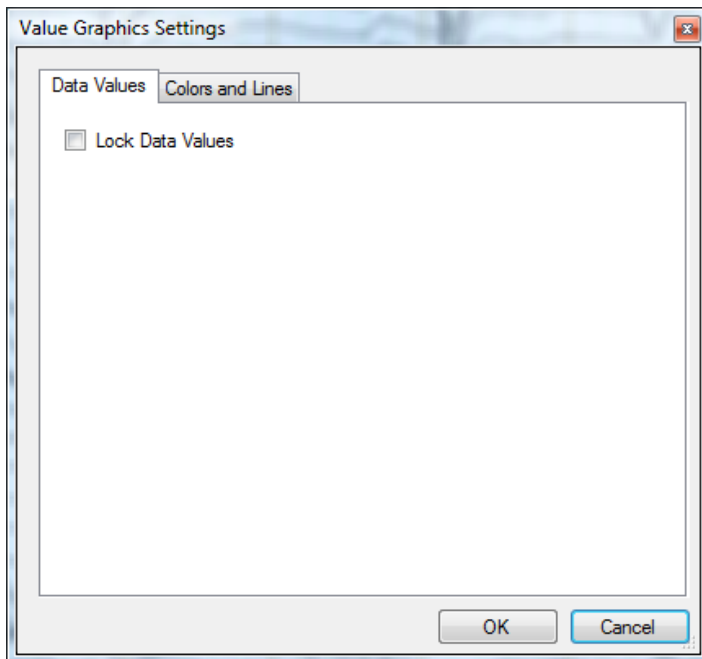


FIGURE 5—41 VALUE GRAPHICS SETTINGS DIALOG BOX, FIRST TAB

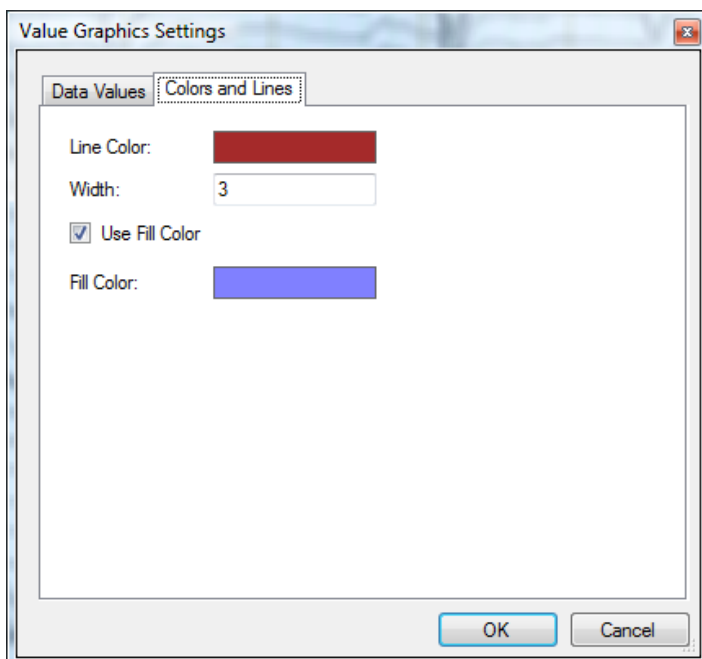


FIGURE 5—42 VALUE GRAPHICS SETTINGS DIALOG BOX, SECOND TAB

The **Lock Data Values** check box on the **Data Values** tab allows you to control the scaling of the drawing object. If you select it, the drawing object is including in scaling. If you clear the check box, the object retains its original size during scaling.

The **Colors and Lines** tab allows you to set colors and line widths.

5.2 Creating and editing a workspace

Start the Analyzer.

To create a workspace, click the **Analyzer button** and then **New**. Alternatively, click **New** in the **Workspace** group on the **File** tab. NEW WORKSPACE

The workspace allows you to enter the storage location for your history data.

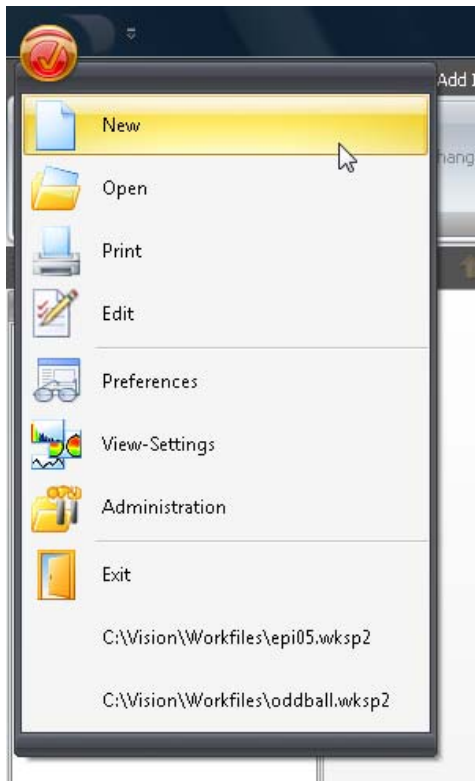


FIGURE 5—43 ANALYZER BUTTON, CREATING A NEW WORKSPACE

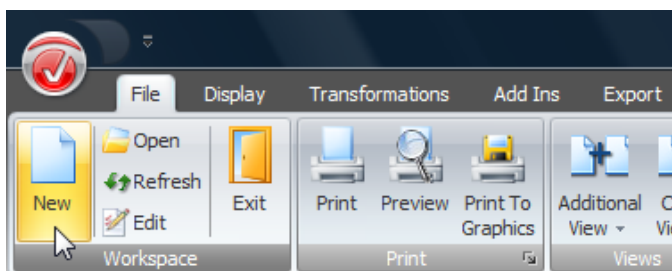


FIGURE 5—44 PART OF THE FILE TAB, CREATING A NEW WORKSPACE

The **Edit Workspace** dialog box appears. This allows you to specify the following folders, which you can either enter manually or select by using the **Browse...** button.

- **Raw Files:** This is the folder for the raw data. The files containing the recorded EEG data are referred to as the raw data.
- **History Files:** This is the folder for the history data. The history files contain all the processing steps (transforms) performed on the raw data. These files are displayed graphically in the History Explorer.
- **Export Files:** This folder contains the files you may want to export as the result of the analyses performed. Exported files are intended for further processing in other programs.

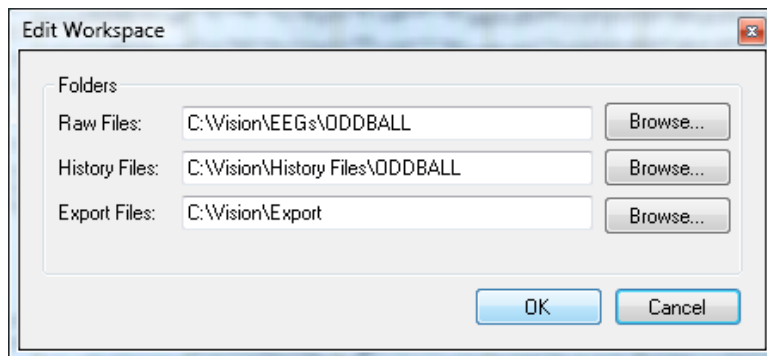


Figure 5—45 DIALOG BOX FOR CREATING A NEW WORKSPACE

Once you have made your settings, press the **⏏** key or click the **OK** button.

The **Save As** dialog box appears, which allows you to save the workspace file. Give the file a meaningful name, and then press the **⏏** key or click the **Save** button.

To open an existing workspace, click the **File** tab, then **Open**. A dialog box containing all the workspaces appears.

OPEN AND REFRESH
BUTTONS

The **Refresh** button on the **File** tab opens files that have just been added to the workspace without closing the existing files. This means that if you copy new data and/or history files to the folders of the workspace and then click **Refresh**, you can work with these files without having to interrupt your work with existing files.

To make changes to the storage locations for history data, click **Edit**. The **Edit Workspace** dialog box appears. You can then make the required changes to the folders.

EDITING A WORKSPACE

Once you have finished configuring the folders for your data, the raw data is analyzed, and a history file is created for each raw data file.

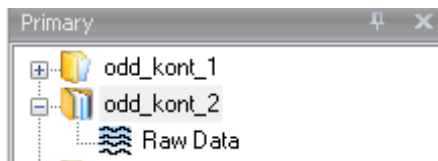


FIGURE 5—46 HISTORY EXPLORER WITH BOOK ICONS

Once you have successfully read in one or more EEG files, you can open a history file.

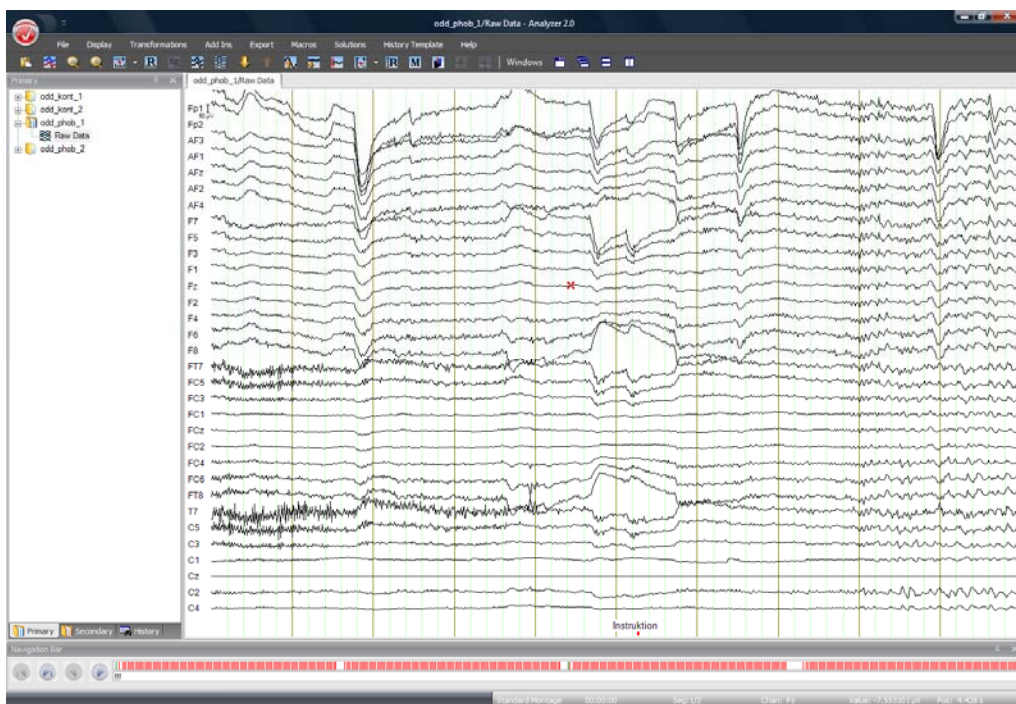


FIGURE 5—47 VISION ANALYZER WITH AN EEG LOADED

You can then navigate around the EEG and show and hide markers (see also section 5.1).

5.3 Applying a transform

You will find detailed explanations of the various transforms in chapter 12. You can undo all the transforms easily. Note also that the Analyzer never makes changes to the original EEGs.



To perform a simple operation by way of example, click the **Transformations** tab and choose **Data Filtering > IIR Filters** from the **Artifact Rejection/Reduction** group. The **Filters** dialog box appears, in which you can make various filter settings. Click the **OK** button in the dialog box.

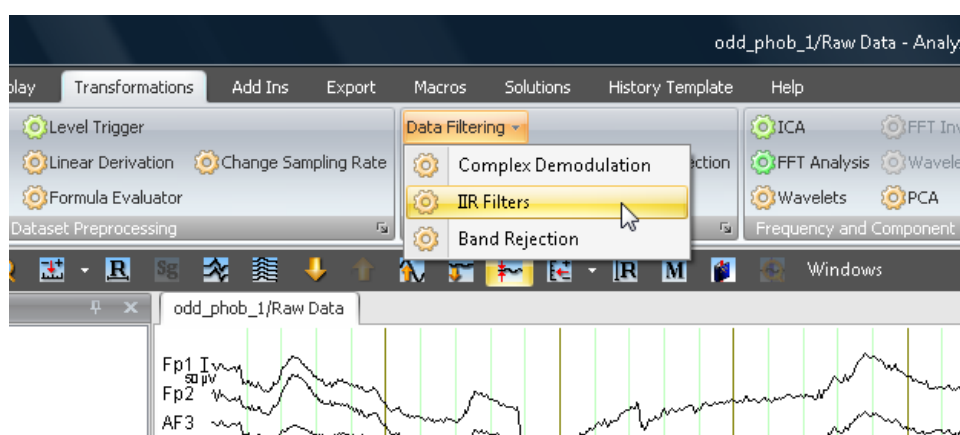


FIGURE 5—48 CHOOSING THE IIR FILTERS COMMAND

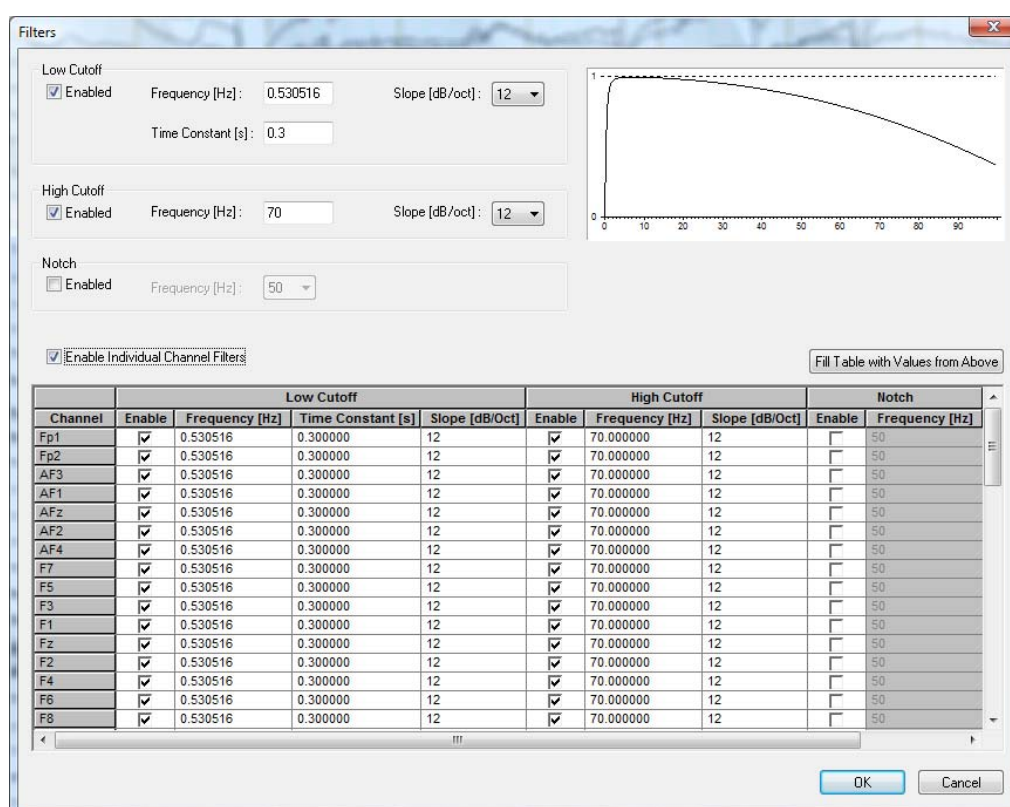


FIGURE 5—49 FILTER SETTINGS DIALOG BOX

A new window containing the resulting data set appears. An icon with the name **Filters** is added to the History Explorer.

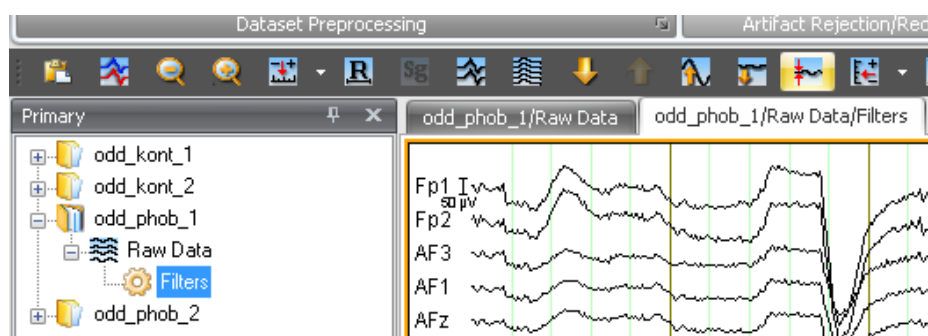


FIGURE 5—50 BRANCHED HISTORY TREE (A)

Then choose: **Transformations** tab > **Data Preprocessing** group > **RMS/GFP** command. A dialog box containing two list boxes appears. The list box on the left contains the available channels, and the one on the right contains the selected channels. To add a channel to the list box on the right, you double-click it in the list box on the left.

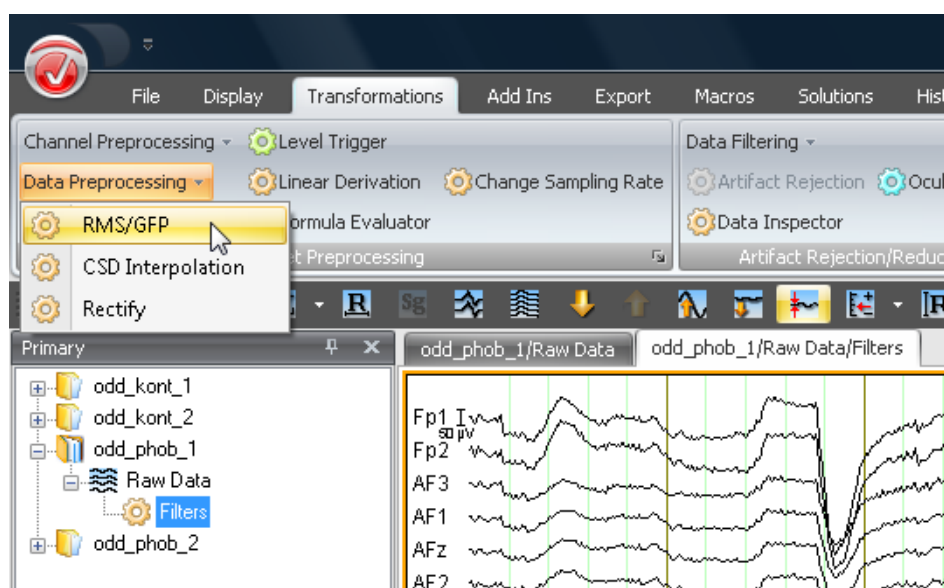


FIGURE 5—51 CHOOSING THE RMS/GFP COMMAND

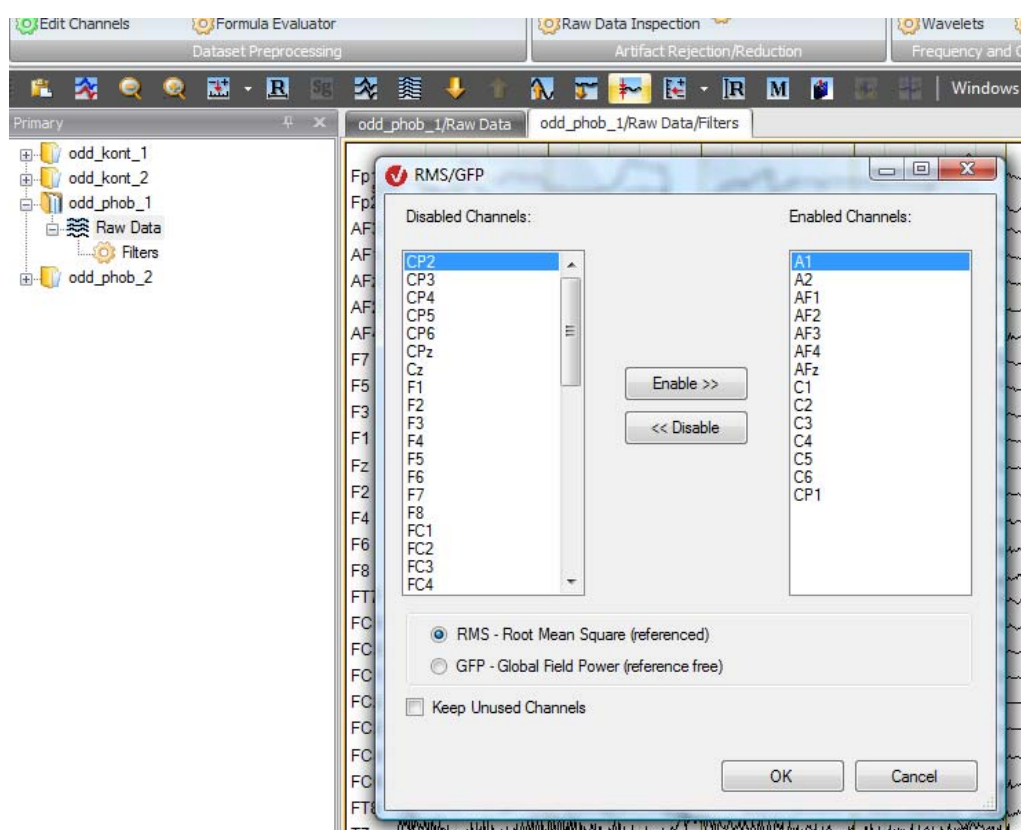


FIGURE 5—52 RMS/GFP DIALOG BOX

Click the **OK** button. A new data window containing the result of the operation appears. In the History Explorer, an **RMS** icon is attached to the Filters icon.

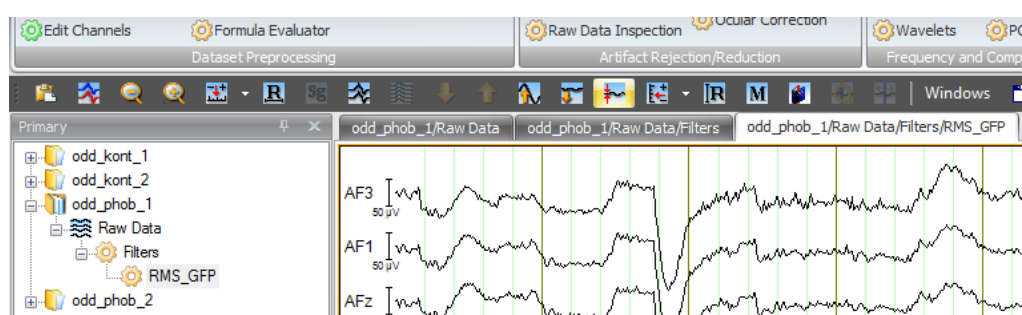


FIGURE 5—53 BRANCHED HISTORY TREE (B)

When you perform further operations, the corresponding icons are added to the history file.

You can create multiple branches from a data set. The analyses can be branched at any point.

If you want to perform analyses on your raw data that do not require filtering beforehand, display the raw data window by double-clicking the corresponding icon in the History Explorer. Choose the **Transformations > RMS/GFP** command. Select some channels, and then click **OK**. A new **RMS** icon appears under the **Filters** icon. The history list has branched.

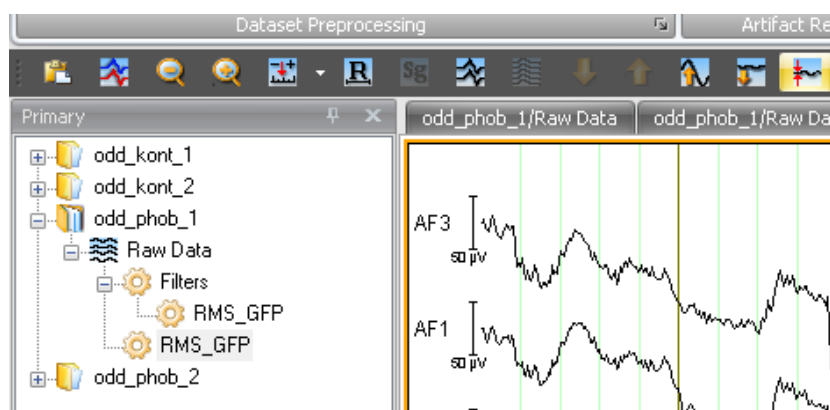


FIGURE 5—54 BRANCHED HISTORY TREE (C)

5.4 Explanation of terms: primary and secondary history data

There are two types of history data: primary and secondary data. The primary history data is located on the **Primary** tab on the left-hand side of the application window. It consists of a specific set of raw EEG data and the processing steps carried out on it (i.e. transforms applied to it).

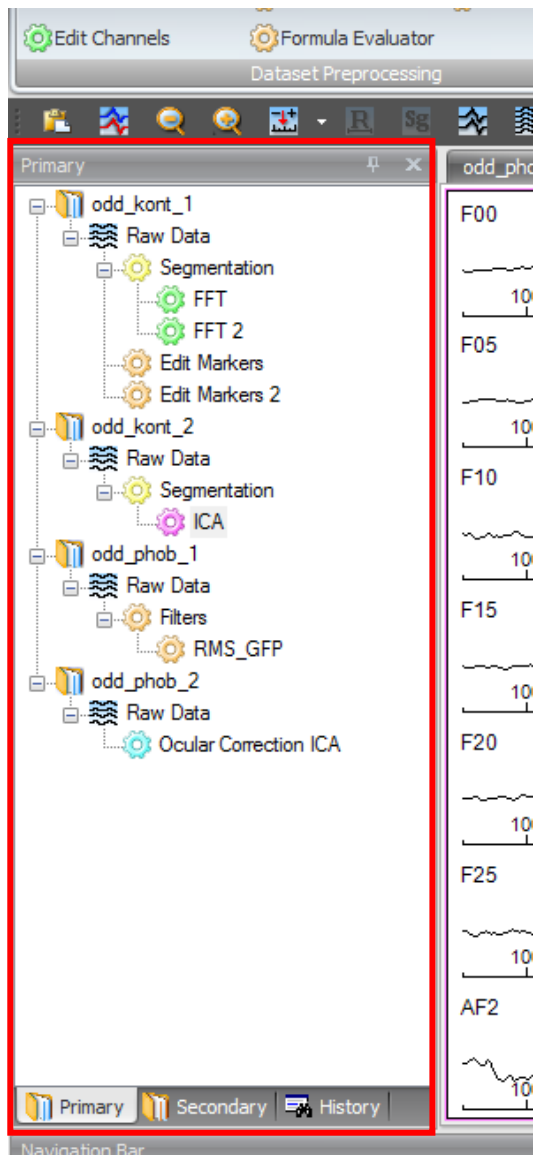


FIGURE 5—55 TAB FOR THE PRIMARY HISTORY DATA

The secondary history files, which are located on the **Secondary** tab, generally represent operations performed across multiple nodes of different primary history files. Consequently, secondary history files no longer have a unique link to a specific set of raw EEG data. One example of secondary history data is the **Grand Average** transform. (You will find detailed information on performing this operation in section 12.4.4.)

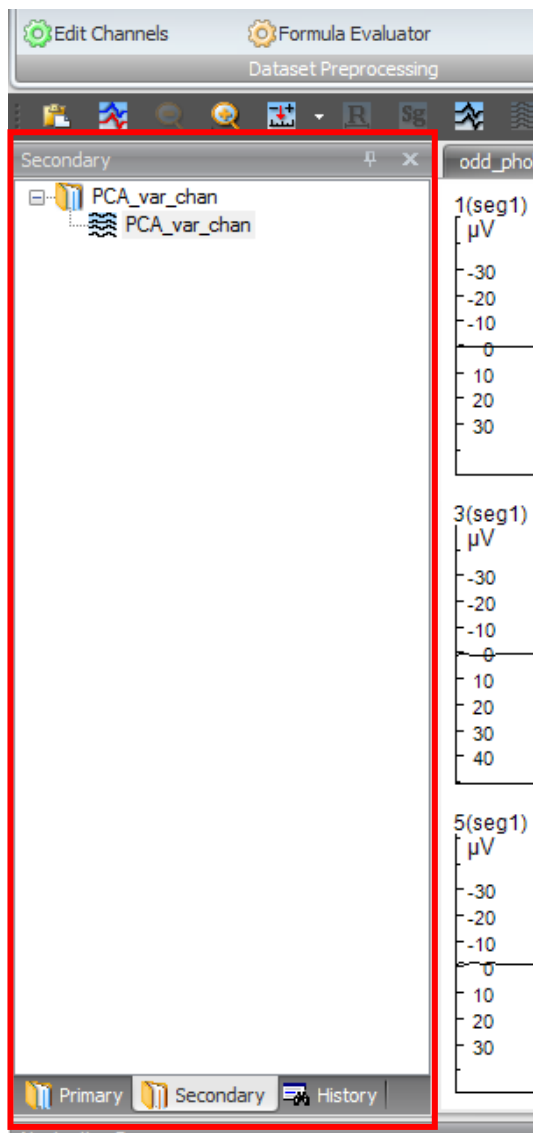


FIGURE 5—56 TAB FOR SECONDARY HISTORY DATA

You can rename or delete history files in the same way as history nodes. Note, however, that unlike secondary history files, you cannot rename or delete primary history files in the Analyzer.



6 Segmentation

The term “segmentation” is explained here because it comes up constantly in subsequent chapters.

Segmentation is the subdivision of the EEG into different segments. Segmentation can be based on a number of different criteria.

This manual uses the term segmentation in the following cases:

- As a preliminary stage in the analysis of evoked potential. Epochs of the same length are generated relative to a reference marker (a stimulus, for example). This results in a data set consisting of connected segments or epochs. Thanks to the extensive segmentation options offered by the Analyzer, it is also possible to calculate averages based on complex stimulus conditions (behavior-dependent conditions, for example).
- To prepare separate processing steps for different sections of an EEG, for example for the analysis of different stages before and after medication. In this case, sections are selected either manually or based on a fixed time scale and converted to new data sets in the history file. These can then be analyzed separately.

Depending on whether you are looking at a data set before or after segmentation, you can specify initial settings for montages and views (EEG display modes or views) when new data windows are opened.

You will find a detailed description of montages and views in chapter 8, “Montages”, and chapter 9, “Views”. You will find more information on segmentation in section 12.4.5, “Segmentation”.



7 User-specific preferences

7.1 Configuring preferences

To configure preferences for the user interface, click the **Analyzer button** and then **Preferences**. Alternatively, click the **File** tab then **Preferences** in the **Configuration** group.

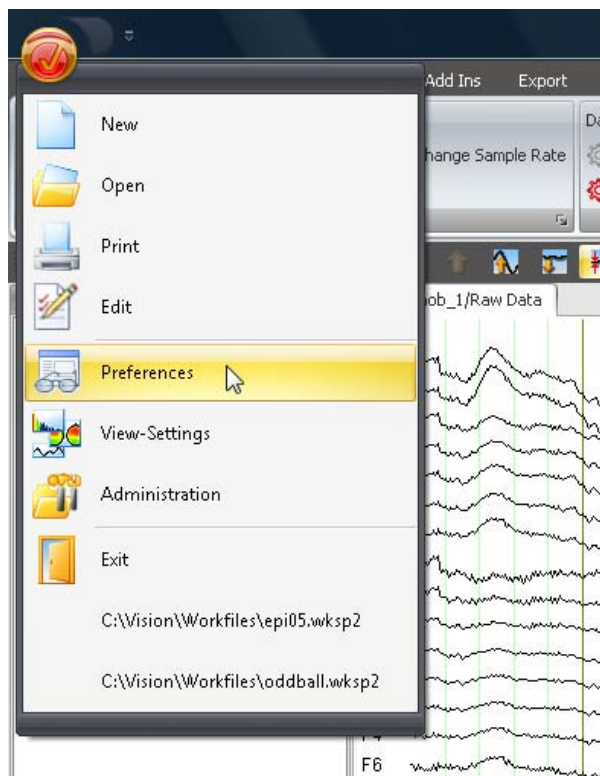


FIGURE 7—1 ANALYZER BUTTON, PREFERENCES COMMAND

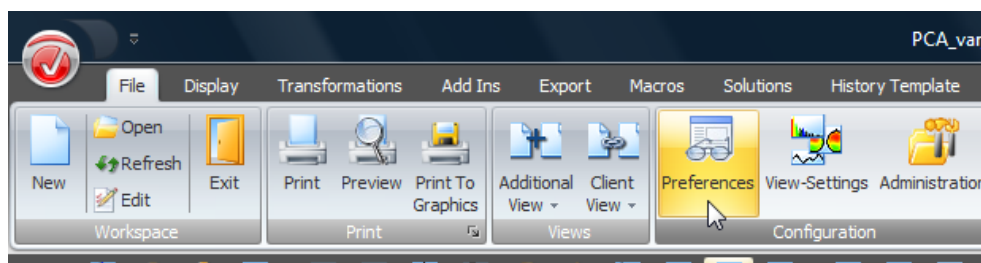


FIGURE 7—2 CONFIGURATION GROUP, PREFERENCES COMMAND

The **Preferences** dialog box appears. This contains the tabs **Views** (EEG views), **Scaling**, **Transformation Colors** (for assigning colors to the transforms), **Graphics Export/Output**, **Electrodes** and **General**.

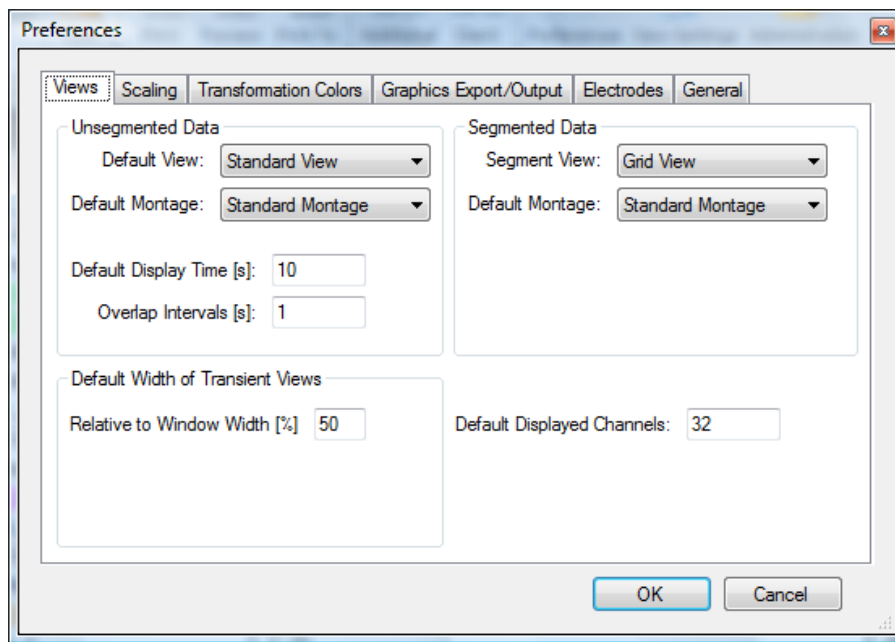


FIGURE 7—3 PREFERENCES DIALOG BOX, VIEWS TAB

The **Views** tab draws a distinction between unsegmented and segmented data (and offers the **Unsegmented Data** and **Segmented Data** group boxes).

VIEWS TAB

For both groups of data there is a drop-down list that allows you to set the standard view and standard montage (**Default View** and **Default Montage**).

In addition, in the **Default Displayed Channels** text box you can display the number of channels to be displayed by default.

For the unsegmented data, you can also display the default display time in seconds (in the **Default Display Time [s]** text box) and the overlap of the intervals in seconds (in the **Overlap Intervals [s]** text box).

The value in the **Relative to Window Width [%]** text box specifies the width of a transient view when it is opened. The value specifies the portion of the view occupied by the transient view.

The **Scaling** tab allows you to configure the initial parameters of the EEG views. It contains the **Time Domain Scaling** and **Frequency Domain Scaling** group boxes.

SCALING TAB

On this tab you can specify the time domain scaling and frequency domain scaling before and after averaging for newly opened view windows.

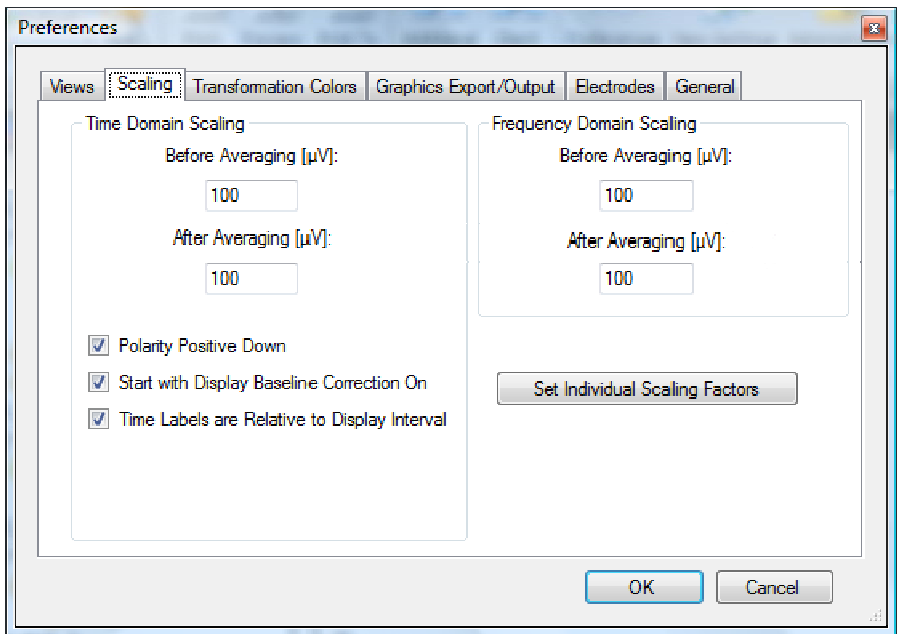


FIGURE 7—4 PREFERENCES DIALOG BOX, SCALING TAB

In the **Before Averaging [µV]** and **After Averaging [µV]** text boxes, you specify different scaling for before and after averaging.

For the time domain, the **Polarity Positive Down** function sets the polarity of the signal in the display. If you select the check box, the axis for positive measured values points down.

If you select the **Start with Display Baseline On** check box, the baseline correction function in the EEG view is activated by default.

The **Set Individual Scaling Factors** function allows you to specify the channels that are to be displayed attenuated. This is desirable for ECG channels, for example, since otherwise they encroach badly on the curves of the EEG channels. You enter the channel names and the associated scaling factors for the attenuation of the signals in the table below. The attenuation only affects the display of the data; it does not affect the data itself.

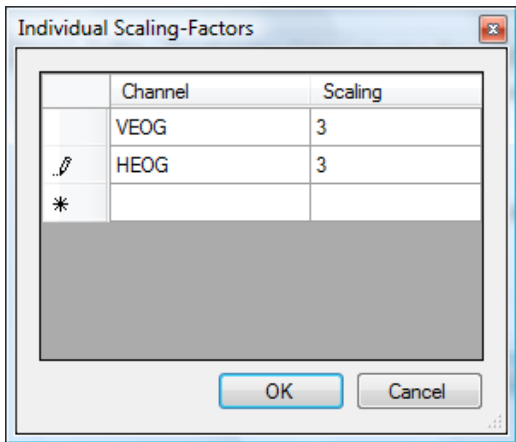


FIGURE 7—5 SCALING OF INDIVIDUAL CHANNELS

If you select the **Time Labels are Relative to Display Interval** check box, the times in views (in the labels of head maps, for example) are displayed relative to the EEG interval displayed. If the check box is not selected, these times are displayed relative to the beginning of the whole EEG. If the EEG has its own time scale defined by time zero markers, this time specification is ignored and the time scale is used.

The **Transformation Colors** tab allows you to assign colors to the individual transforms. These are used for the corresponding icon in the History Explorer, the commands on the Ribbon and in the frame of the EEG views.

TRANSFORMATION
COLORS TAB

You can assign colors in the table in the figure below.

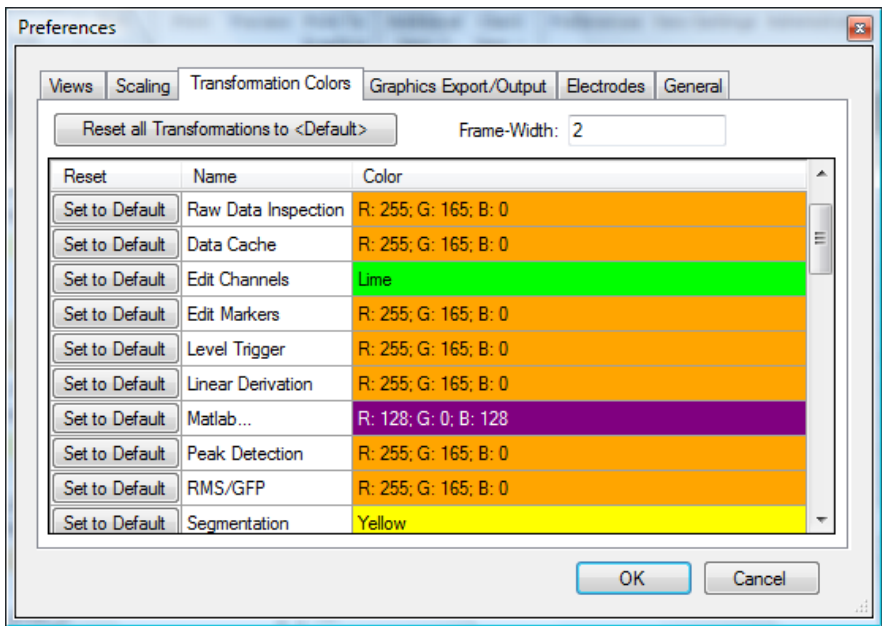


FIGURE 7—6 TABLE FOR ASSIGNING COLORS TO TRANSFORMS

If you repeatedly click a color strip in the **Color** column, a drop-down list containing the color selection dialog box appears.

The **Custom** tab contains the basic colors, and the **Web** tab contains predefined Web colors.

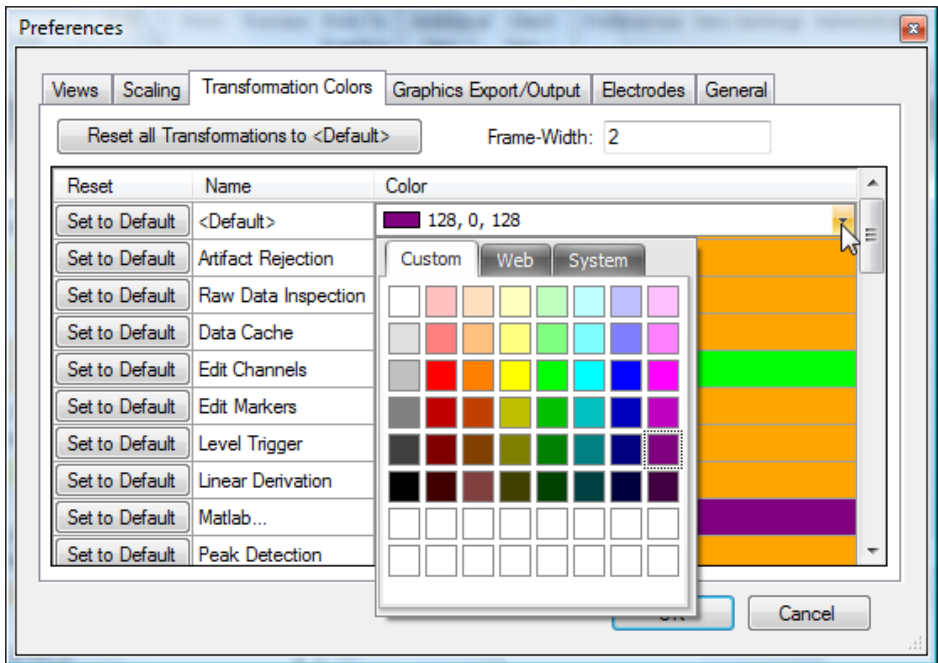


FIGURE 7—7 EDIT COLORS DIALOG BOX (A), BASIC COLORS

You can choose between basic (standard) colors and custom colors. You enter the latter by right-clicking a free box on the **Custom** tab. The **Edit Colors** dialog box opens. On the right-hand side of the **Edit Colors** dialog box, there is a color spectrum from which you can select the color you want. When you click the **Add to Custom Colors** button, the selected color is added to the **Custom colors** list. Click the **OK** button to close the dialog box.

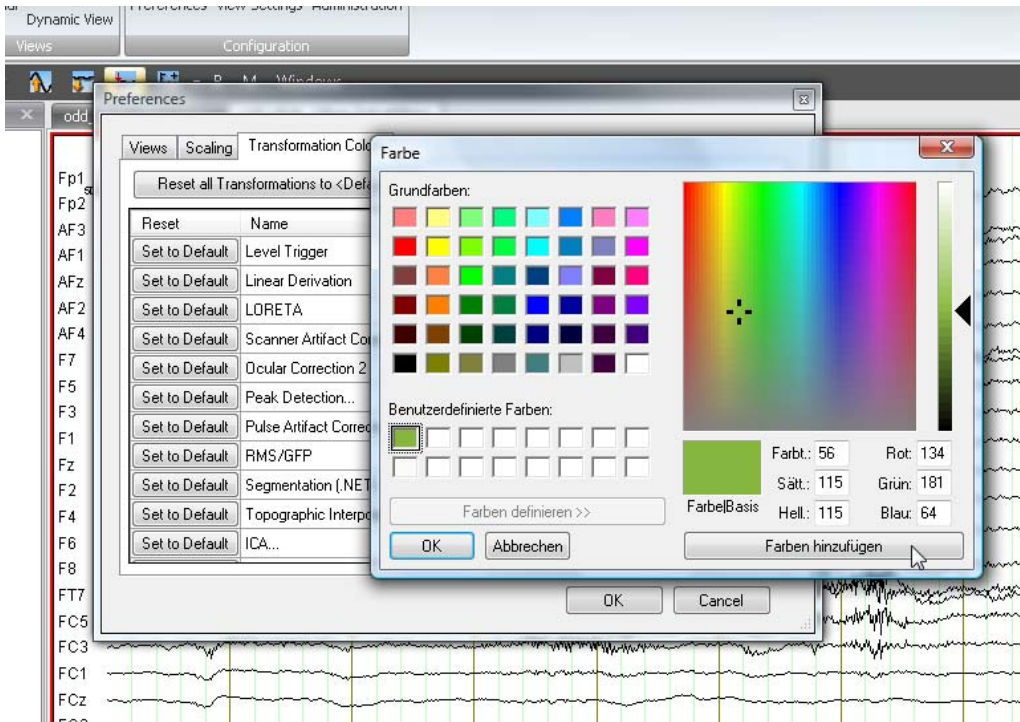


FIGURE 7—8 EDIT COLORS DIALOG BOX (B), CUSTOM COLORS

In the **Frame-Width** text box, you specify the width of the color frame around the EEG data window. This must be a value between 0 and 99.

If you click the **Set to Default** button, the color of the corresponding transform is set to the color value selected under **Default**. If you change the value **Default**, all transforms containing this value are changed.

If you click the **Reset all Transformations to Default** button, the value **Default** is applied to all transforms.

The **Graphics Export/Output** tab is described in chapter 17, “Printout” and in chapter 18, “Graphical export”.

GRAPHICS
EXPORT/OUTPUT TAB

On the **Electrodes** tab, you can specify a file containing electrode coordinate definitions. These coordinates are used if EEG data does not have coordinate specifications for its channels.

ELECTRODES TAB

By default, numerous electrode positions are predefined in the Analyzer. By specifying a separate electrode file, you can add to or replace these electrode positions. The format of this file is described in Appendix H. Note that a file containing the specification “Defaults = False” entirely replaces the Analyzer’s default coordinates. If a file does not contain this specification, the coordinates in the file are added to the default coordinates.

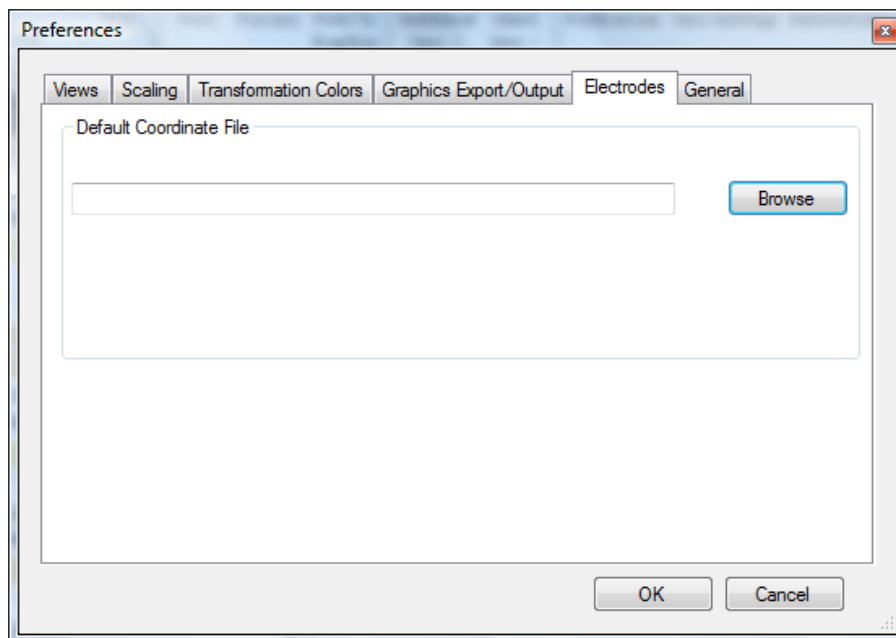


FIGURE 7—9 PREFERENCES DIALOG BOX, ELECTRODES TAB

On the **General** tab, you can specify the intervals at which the deleted nodes of a history file are to be purged. This is the same function you get when you choose the **Purge Deleted Nodes** command from the context menu of the history file. It prevents deleted nodes from accumulating over time and taking up storage space.

GENERAL TAB

The entry in **Purge Nodes every xxx days** specifies that the nodes are purged after this time elapses, at the earliest. In normal usage, the nodes are often there for a little longer because the automatic purging of the nodes is subject to additional checks.

The automatic purging of nodes is only carried out when you close the history file. This means that deleted nodes in history files that you never open are not automatically purged.

The setting you make for **Draw Background for Progress Bar** specifies whether the Analyzer window is displayed when a progress bar is active. This is part of the system in Windows® Vista. The setting **Auto** takes this into account and suppresses emulation by the Analyzer on Vista machines.

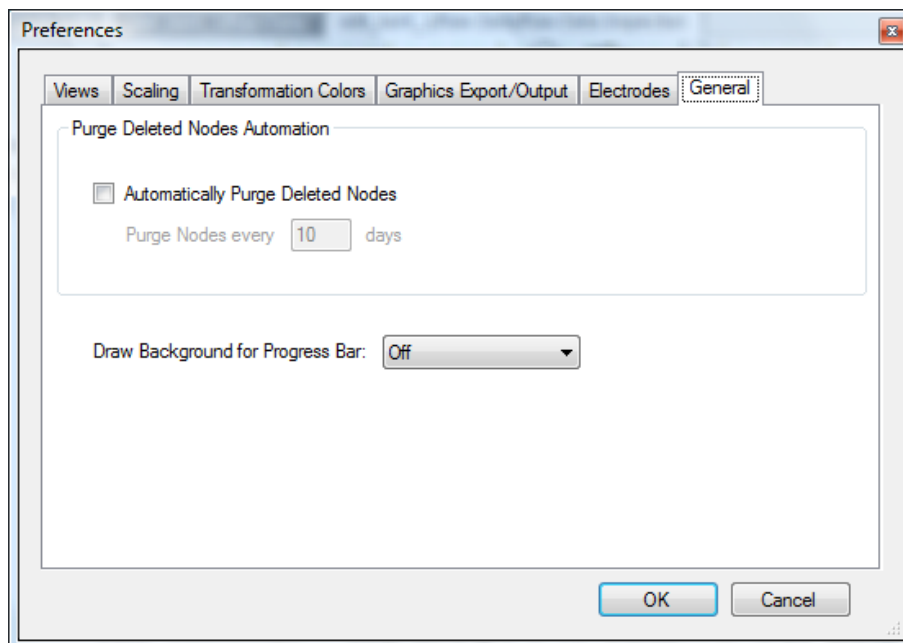



FIGURE 7—10 PREFERENCES DIALOG BOX, GENERAL TAB

7.2 Customizing the graphical user interface

7.2.1 Skins

To make changes to the graphical user interface of the Analyzer, click the **Display** tab and go to the **Skins** group.

You select a skin by clicking one of the skin buttons in the group. Alternatively, you can click the button  in the lower right corner of the group to get a detailed view.

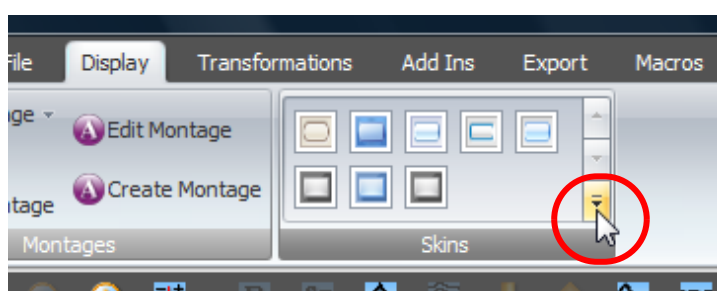


FIGURE 7—11 DISPLAY TAB, SKINS GROUP

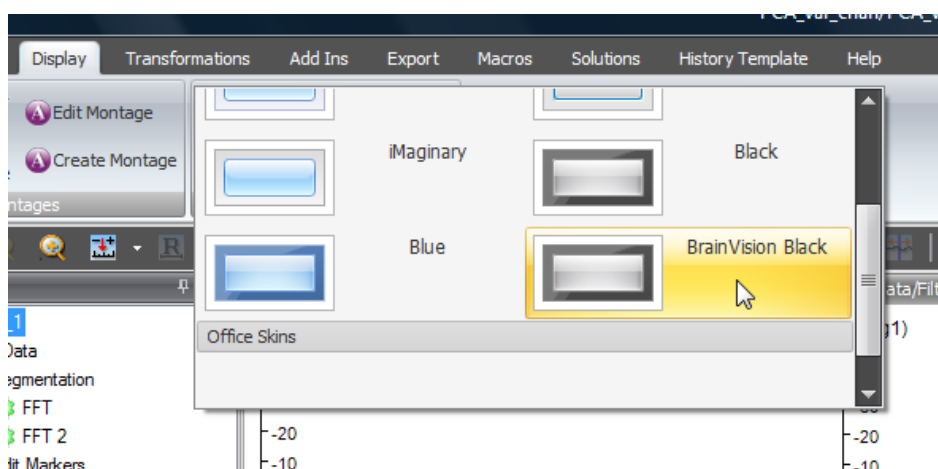


FIGURE 7—12 DISPLAY TAB, SKINS GROUP, DETAILED VIEW

7.2.2 Docking

The docking feature allows you to display the docking or tool windows and data to be analyzed clearly and arrange them flexibly. The docking windows can be fixed in position at any point in the application window and shown or hidden dynamically.



FIGURE 7—13 MAXIMUM DATA VIEW

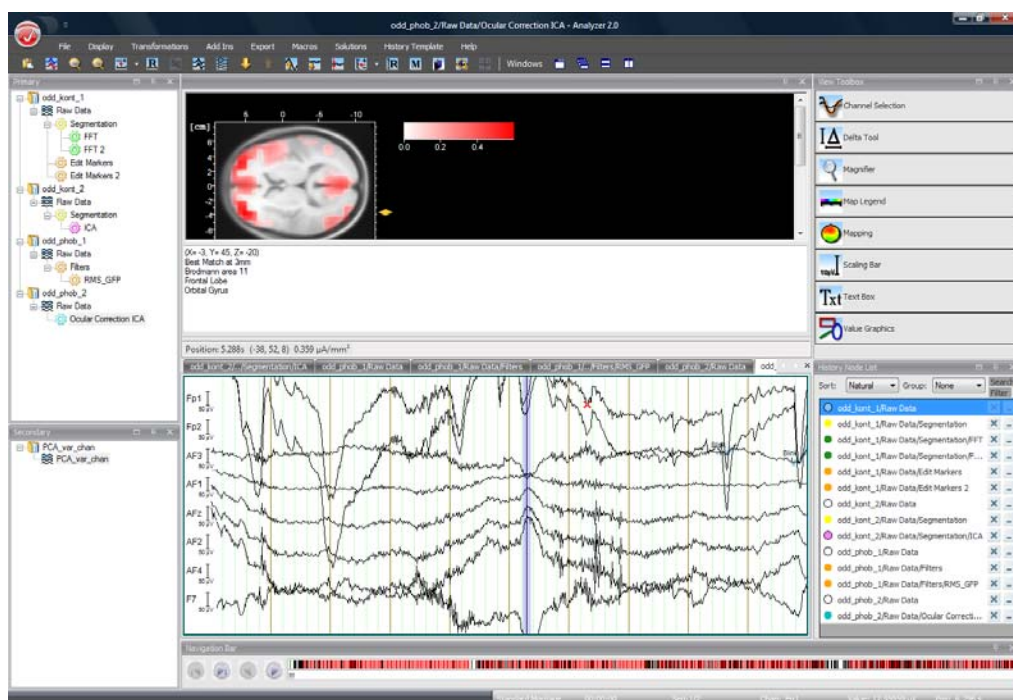







FIGURE 7—14 MAXIMUM PRODUCTIVITY

The docking window has a title bar containing its name and, depending on the settings specified, the following buttons, which allow you to hide, resize and close the window:

-  Anchors the docking window in a fixed position.
-  Shows or hides the docking window temporarily.
-  Maximizes the docking window.
-  Minimizes the docking window.
-  Closes the docking window.

The docking windows can be displayed in the modes “docked” or “undocked” (also known as “floating”). The docked mode also has the display modes “pinned” and “unpinned”.

MODES OF THE
DOCKING WINDOWS

In undocked or floating mode, the window is essentially left floating. It can be docked onto the outer or inner borders of the existing windows.

UNDocked/FLOATING
MODE

You can resize the floating window by dragging its borders.

In undocked mode, you can also move the windows outside the main window. This also allows you to work with more than one monitor.



FIGURE 7–15 FLOATING DOCKING WINDOW

In docked mode, each docking window has a pin button on the title bar. When you click the **DOCKED MODE** pin, it changes from horizontal (unpinned) to vertical (pinned) or vice versa.

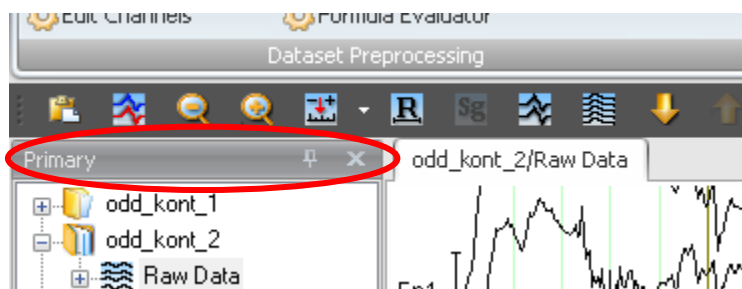


FIGURE 7—16 TITLE BAR OF A DOCKING WINDOW



Horizontal pin: The docking window is unpinned and is hidden when you move the mouse pointer outside it. In addition, a bar containing a button for each open window appears with the docked window. You display the hidden window again by positioning the mouse on the corresponding button on this bar. When you display the unpinned window again, it covers the data window behind it (figure 7—18).

PINNED

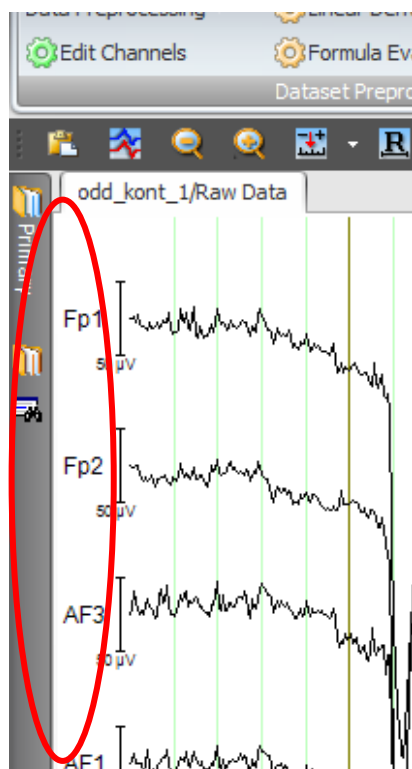


FIGURE 7—17 UNPINNED DOCKING WINDOW (HIDDEN)

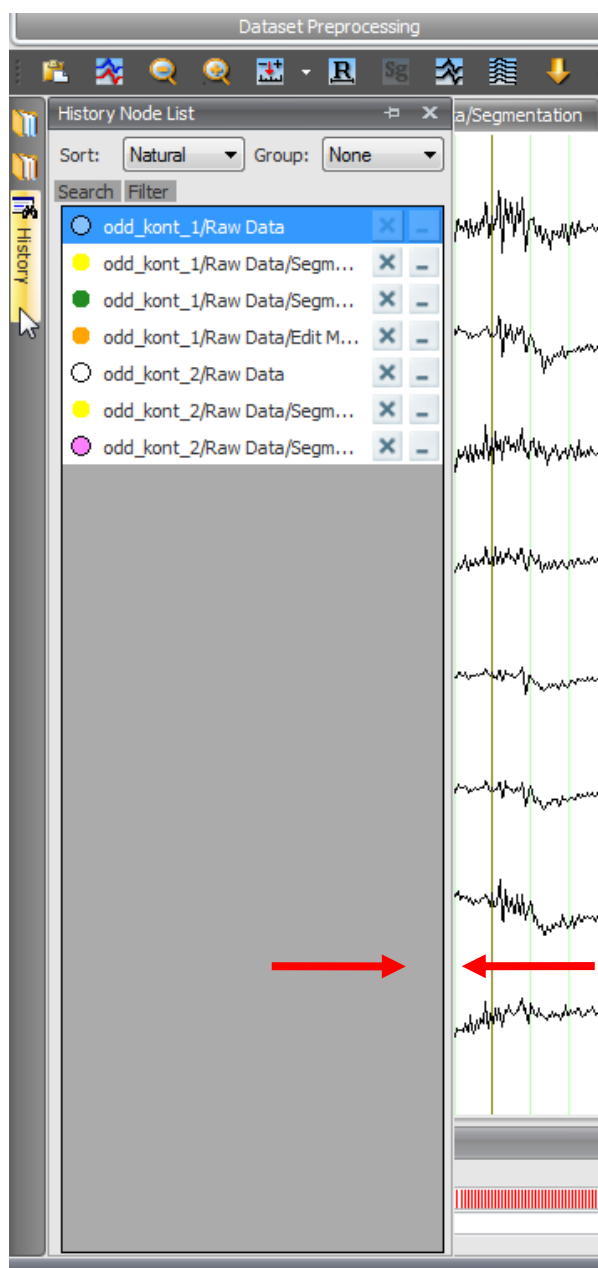


FIGURE 7—18 UNPINNED DOCKING WINDOW (SHOWN)

The position of an unpinned window cannot be changed. In other words, it is not possible to move the window using the mouse. In addition, the scope for resizing the docking window is limited because it is fixed to a window border.



Because of their horizontal orientation, the toolbar and navigation bar can only be docked onto the upper or lower border.



Vertical pin: The docking window is pinned and remains open. You can move the unpinned docking window by clicking the title bar and holding down the left mouse button.

UNPINNED

Several windows can be grouped together in a container. They either appear along the lower border of the container as tabs or arranged horizontally or vertically as subdivisions of the container. The container has the same modes as a docking window.

TAB CONTAINER AND
SPLIT CONTAINER

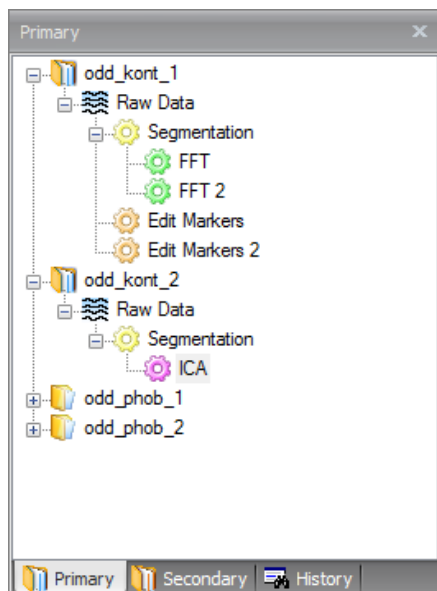


FIGURE 7—19 TAB CONTAINER WITH THREE TABS

With horizontally arranged docking windows, you can, for example, arrange the primary and secondary history data in the same way as in Version 1.0 of the Analyzer:

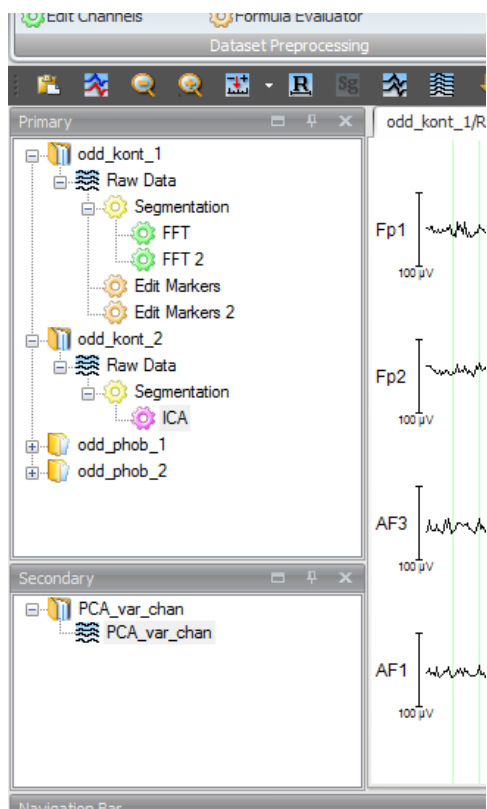


FIGURE 7—20 SPLIT CONTAINER WITH HORIZONTALLY ARRANGED DOCKING WINDOWS

When the Analyzer is started up for the first time, the docking windows are positioned as follows: The **Primary Data**, **Secondary Data** and **Node List** windows are docked onto the left-hand border of the application window, the **View Toolbar** window is docked onto the right-hand border, and the navigation bar to the lower border.

OPENING AND CLOSING
THE DOCKING WINDOWS

To open or close the different windows, click the **Window** button on the toolbar and select or clear the relevant check box.

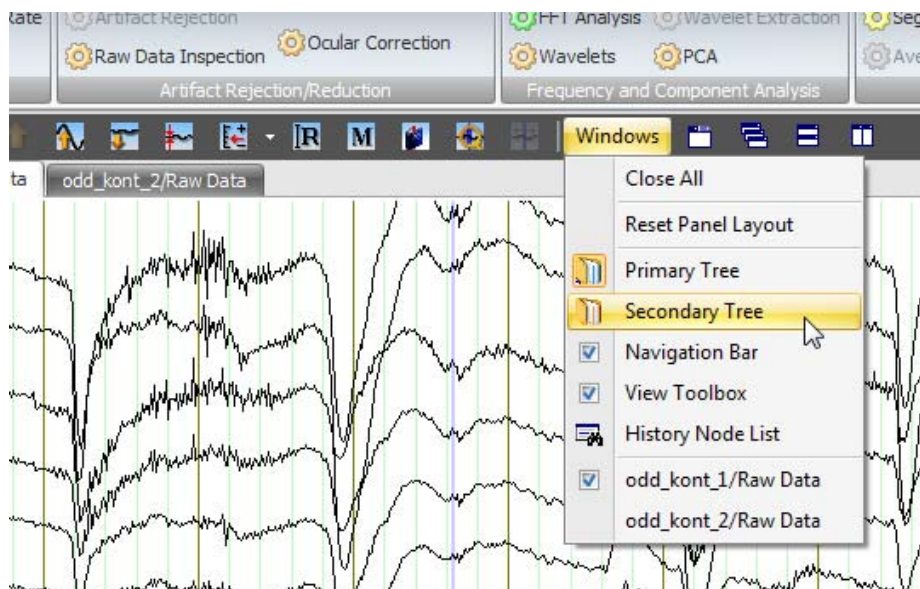


FIGURE 7—21 CONTEXT MENU FOR OPENING AND CLOSING THE DOCKING WINDOWS


To close the windows, you can also click the cross button on the right-hand side of the window's title bar.

You can choose **Windows > Reset Panel Layout** to reset the docking windows to their original layout.

RESETTING THE WINDOW
POSITIONS

You can position the docking window relative to the outer or inner borders of the available windows by using landing zones.

POSITIONING BY MEANS
OF LANDING ZONES

Note that a docked window can only be moved when it is in unpinned mode (i.e. with a vertical pin button: ).



You can move the unpinned docking window by clicking its title bar. By holding down the left mouse button, you can move the window around freely. If you position the mouse pointer on a landing zone, the position that the window can take up is highlighted in blue:

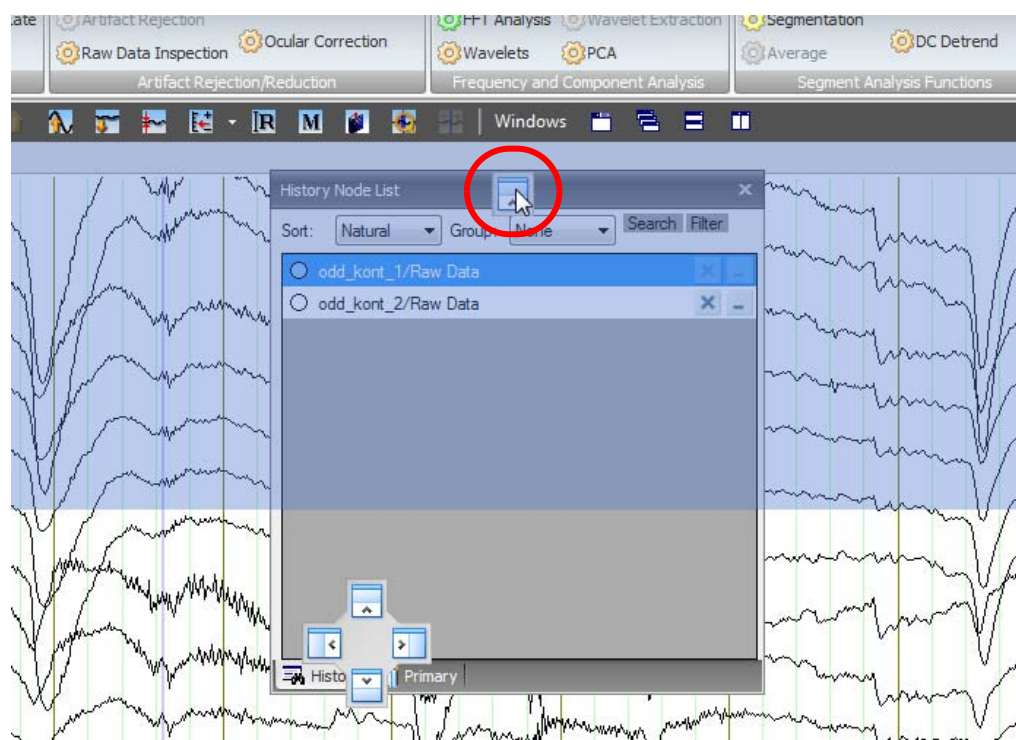


FIGURE 7—22 BLUE HIGHLIGHTING OF THE LANDING ZONES

The figures below show examples of the positioning of docking windows before and after docking:



FIGURE 7—23 BEFORE DOCKING (UPPER BORDER)

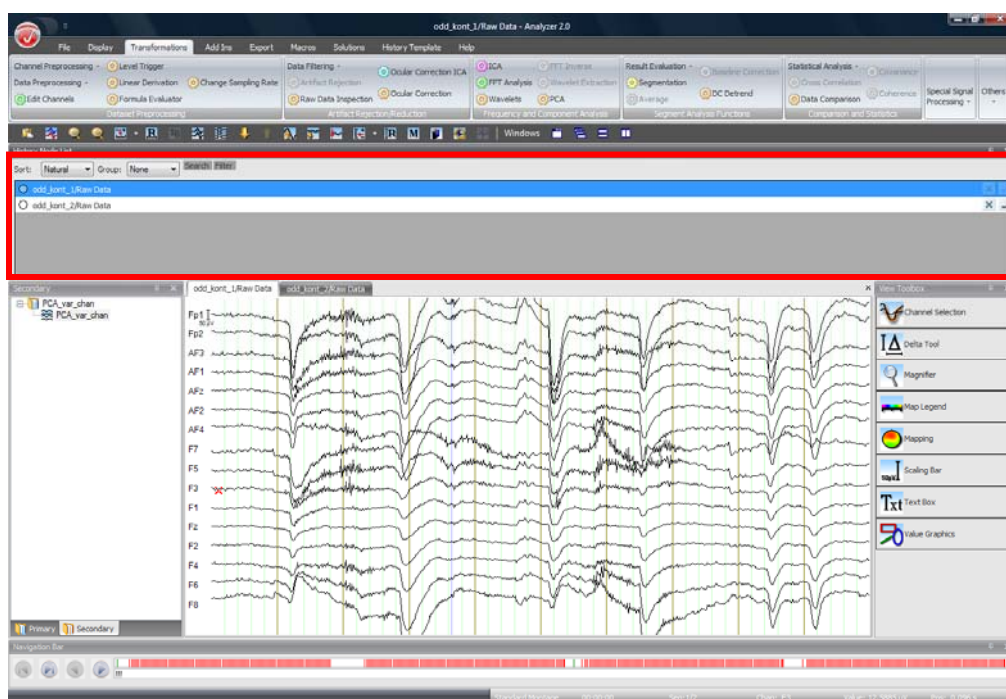


FIGURE 7—24 AFTER DOCKING (UPPER BORDER)

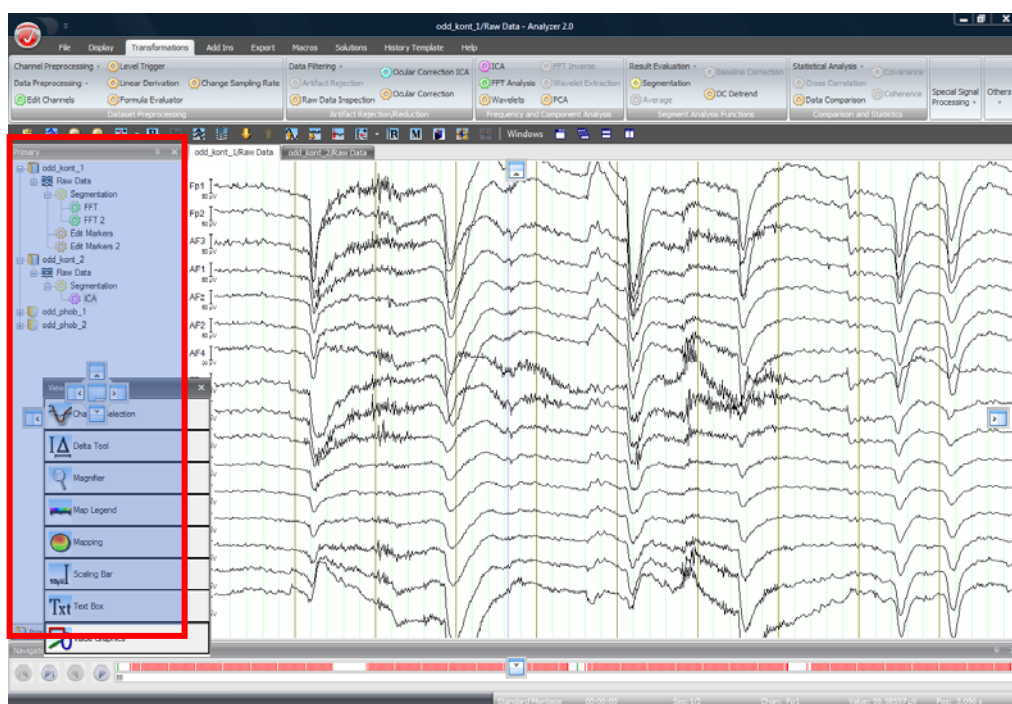


FIGURE 7—25 BEFORE DOCKING (INSERTION OF THE WINDOW AS A NEW TAB)

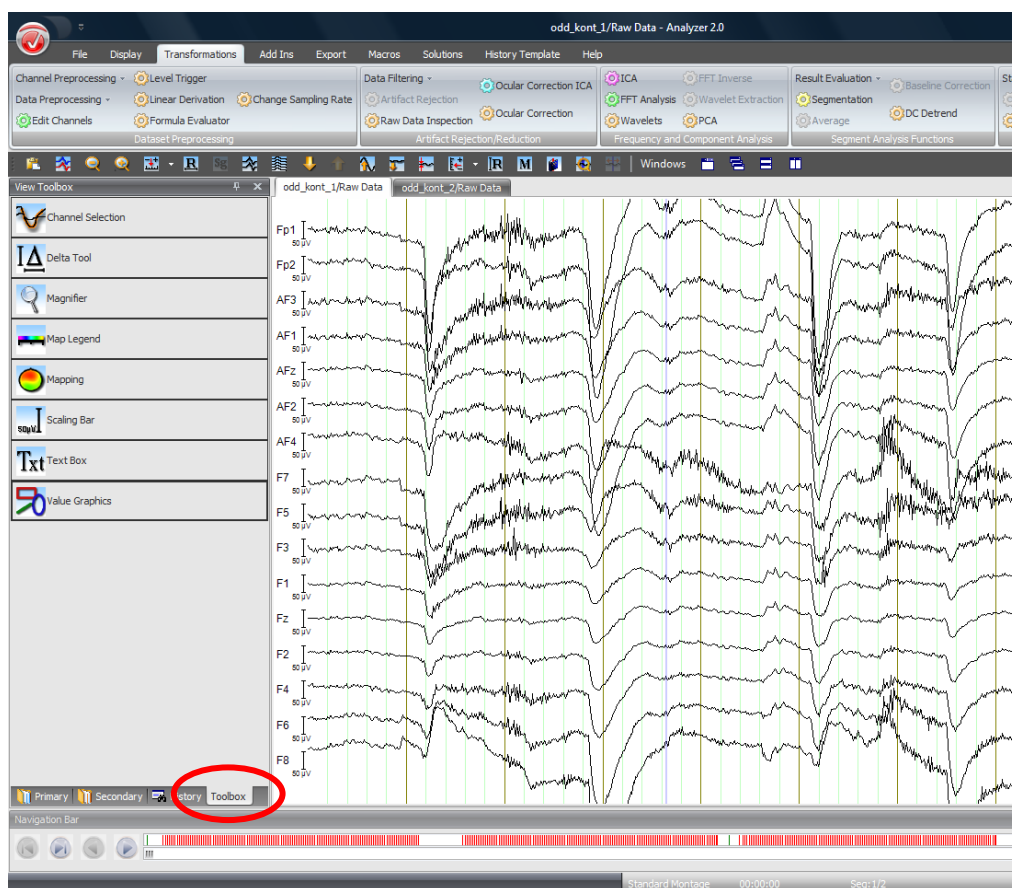


FIGURE 7—26 AFTER DOCKING (INSERTION OF THE WINDOW AS A NEW TAB)

7.3 Configuring the EEG view settings

7.3.1 View settings: Introduction

The EEG views offer a variety of ways of displaying EEG data on the screen. You can configure them using the view settings in order to display the EEG data how you want it. Views that display the data in a similar way are subdivided into view categories to make configuration easier. Thus, the grid views for time and frequency data belong to the same view category. All the views in a category can be assigned the same settings.

Distinctions are drawn between the factory settings of the view settings, the category-related view settings (default view settings) and the node-specific view settings.

The factory settings cannot be altered. They differ from one view category to the next. User-defined settings can easily be reset to the factory settings.

You can change the category-related view settings. They apply, in each case, to a single category of EEG views. Examples of categories are the standard view, grid view and map view. The node-specific view settings apply exclusively to the history node currently being processed.

The category-related view settings, which can be changed by the user, apply to all nodes displayed with views of a particular category – all standard views or all grid views, for example. You can display the category-related view settings by choosing **File > Configuration > View Settings**.

The node-specific view settings apply exclusively to the history node currently being processed. The settings are saved in the node and become available whenever you open the node. You display the node-specific settings by right-clicking any point in the current view and choosing the **Settings...** command from the context menu that appears.

Note that changes to the category-related view settings are also applied to open windows as soon as you close the dialog box by clicking **OK**.



You will find a detailed description of the EEG views in chapter 9, “Views”.



7.3.2 Category-related view settings

Click the **Analyzer button**, and then choose **View Settings**. Alternatively, click the **File** tab, then **View Settings** in the **Configuration group**.

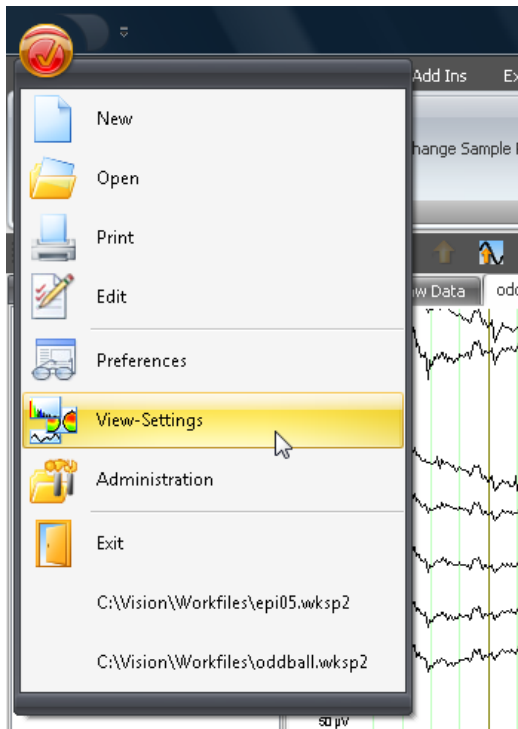


FIGURE 7—27 ANALYZER BUTTON, VIEW SETTINGS COMMAND

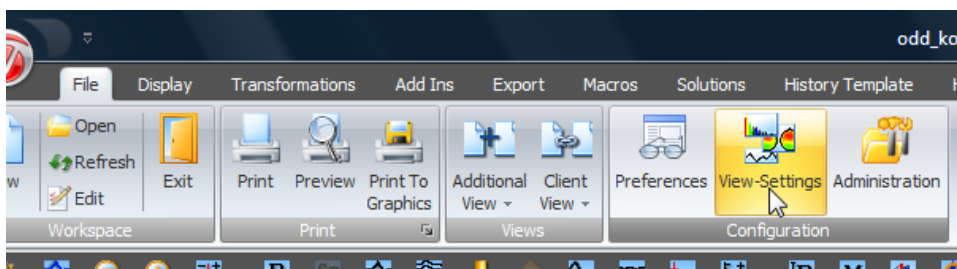


FIGURE 7—28 CONFIGURATION GROUP, VIEW SETTINGS BUTTON

The **Default View Settings** dialog box appears. All EEG view categories are listed alphabetically.

Click an item in the list. Seven tabs, which are identical regardless of which category you choose, appear in the dialog box. These allow you to make settings for the views.

Views that display nodes with different data types in the same way – the frequency grid view and time grid view, for example – are grouped together in the same view category. Consequently, all the tabs are always displayed, even if you want to make settings for the time grid view, for example.



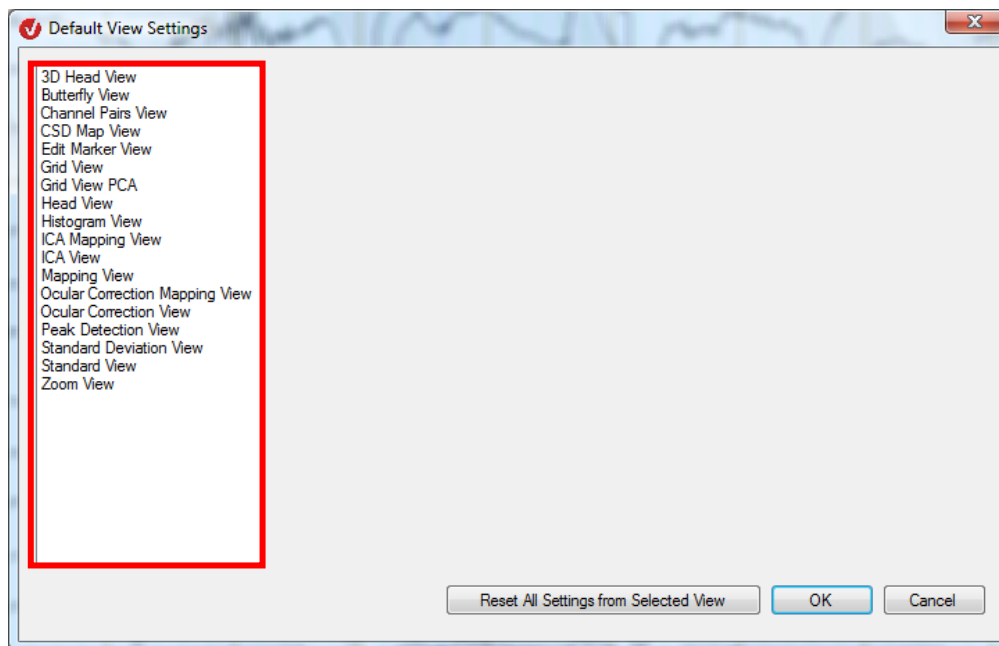


FIGURE 7—29 DEFAULT VIEW SETTINGS DIALOG BOX

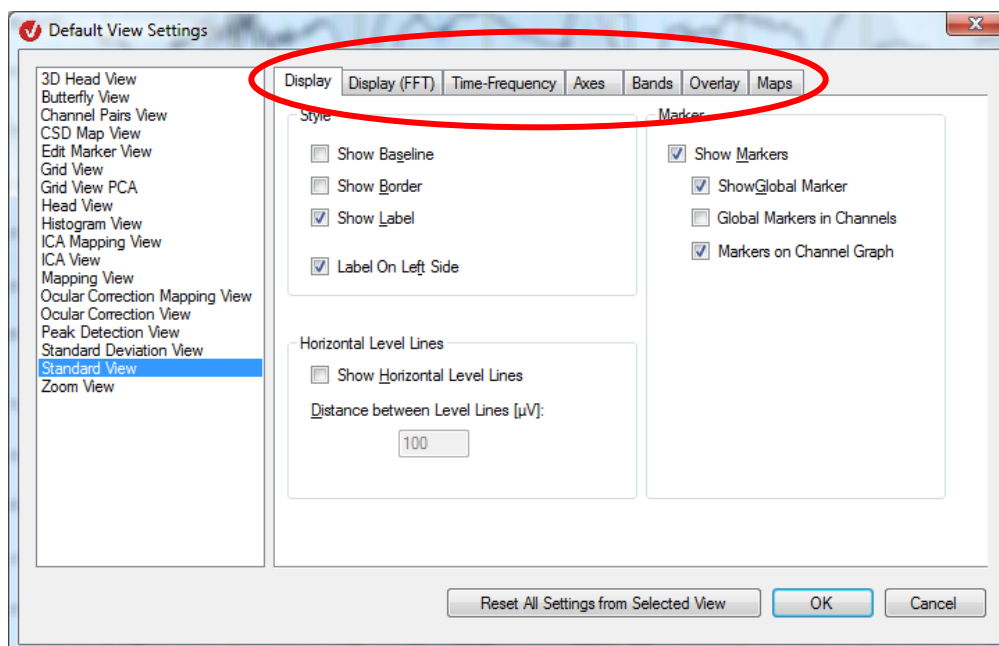


FIGURE 7—30 DEFAULT VIEW SETTINGS DIALOG BOX WITH TABS

The **Reset All Settings from Selected View** button resets the view settings of the currently selected view category to the factory settings for this category.

The **Display** tab contains the group boxes **Style**, **Marker** and **Horizontal Level Lines**.

DISPLAY TAB

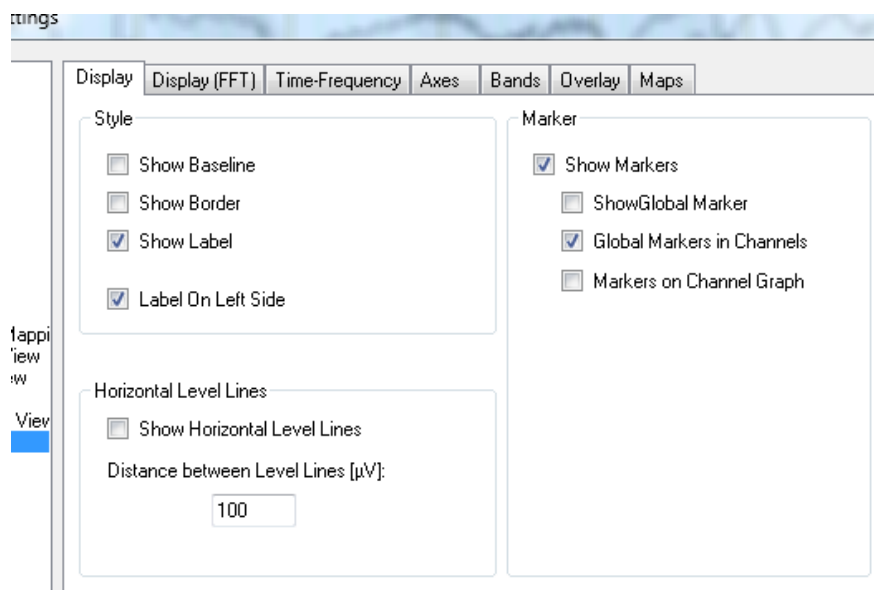


FIGURE 7—31 DEFAULT VIEW SETTINGS DIALOG BOX, DISPLAY TAB

In the **Style** group box, you can make the following settings:

STYLE GROUP BOX

- If you select the **Show Baseline** check box, the baseline is displayed.
- If you select the **Show Border** check box, the EEG graphs are truncated at the borders of the grid cells or channel ranges. An additional border appears around the cell in grid or head views.
- The **Show Label** check box allows you to show or hide the channel names.
- If you select the **Label on Left Side** check box, the channel names are displayed to the left of each channel.

The **Show Horizontal Level Lines** check box allows you to show or hide the horizontal level lines. In the **Distance between Level Lines [µV]** text box, you can enter the spacing between the horizontal level lines in µV.

HORIZONTAL LEVEL LINES GROUP BOX

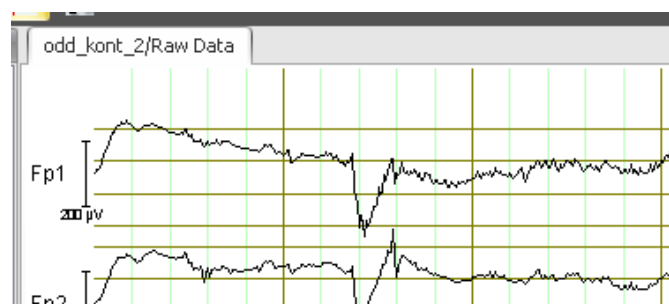


FIGURE 7—32 HORIZONTAL LEVEL LINES DISPLAYED

In the **Marker** group box, you can make the following settings:

MARKER GROUP BOX

- If you select the **Show Markers** check box, the markers set in the EEG are displayed. If the check box is selected, you can:
- Select the **Show Global Markers** check box to display the markers that are common to all channels (i.e. not limited to a particular channel)



FIGURE 7—33 GLOBAL MARKERS DISPLAYED

- Select the **Show Global Markers in Channels** check box to display the global markers at the level of the individual channels:

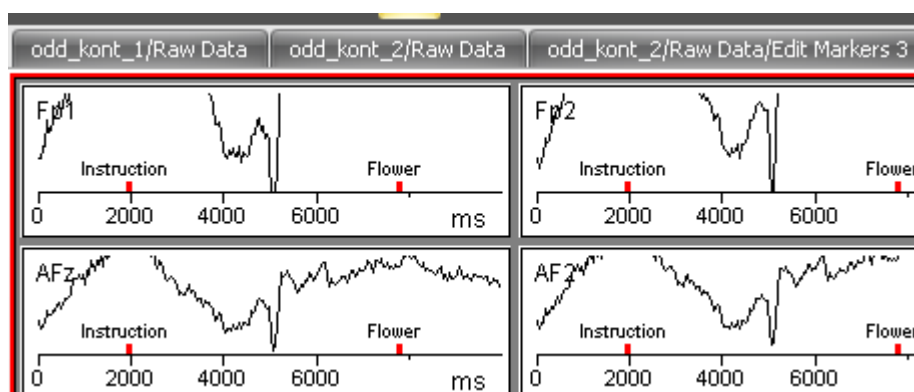


FIGURE 7—34 MARKERS DISPLAYED IN EACH CHANNEL

- Select the **Markers on Channel Graph** check box to display the markers of a channel on the graph of this channel:

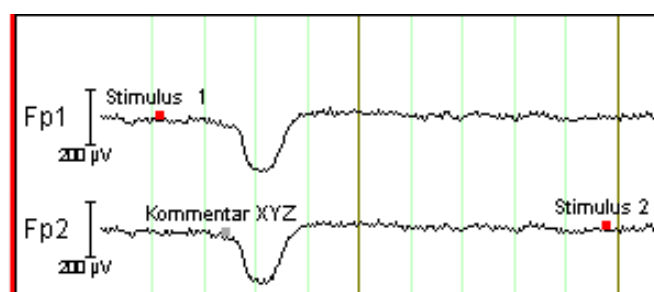


FIGURE 7—35 CHANNEL MARKER DISPLAYED ON THE GRAPH

The **Display (FFT)** tab contains parameters that are relevant to data in the frequency range.

DISPLAY (FFT) TAB

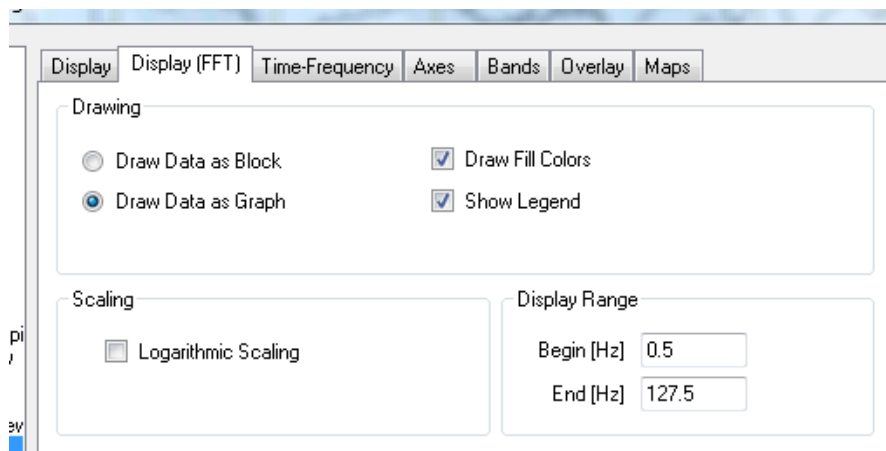


FIGURE 7—36 DEFAULT VIEW SETTINGS DIALOG BOX, DISPLAY (FFT) TAB

In the **Drawing** group box, you can make the following settings:

DRAWING GROUP BOX

- The **Draw Data as Block** and **Draw Data as Graph** radio buttons allow you to specify whether the points are to be drawn as discrete blocks or a graph.
- If you select the **Draw Fill Colors** check box, the area under the graph is filled with colors. The frequency bands set on the **Bands** tab are highlighted in color.
- If you select the **Show Legend** check box, the color legend is displayed.

In the **Scaling** group box, you can make the following settings:

SCALING GROUP BOX

- If you select the **Logarithmic Scaling** check box, logarithmic scaling is applied to the y-axis.
- If you select the **Show Scaling Bars** check box, the scaling bar is displayed.

In the **Display Range** group box, you specify the frequency range displayed in hertz.

DISPLAY RANGE GROUP BOX

The **Time-Frequency** tab is used for views that display data in the time-frequency domain. It contains the group boxes **Colors**, **Scaling** and **Satellite Graphs**. TIME-FREQUENCY TAB

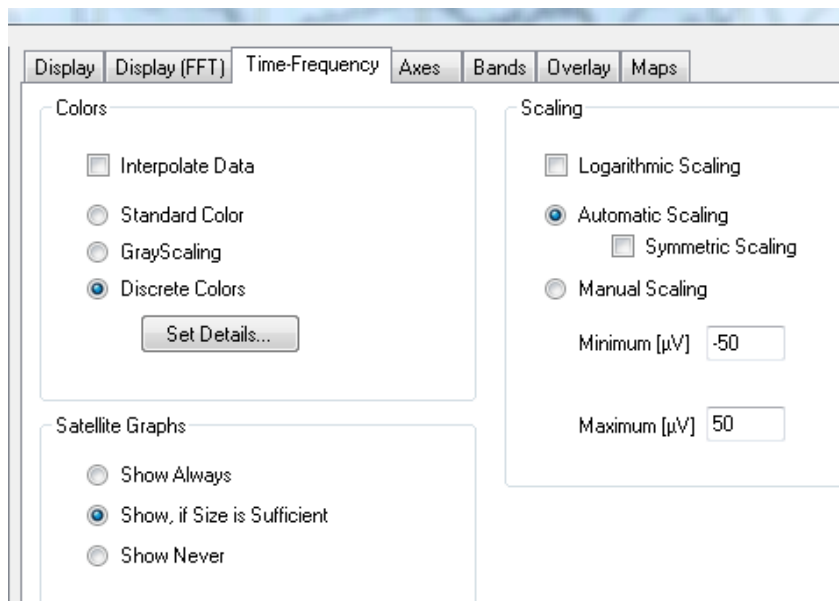


FIGURE 7—37 DEFAULT VIEW SETTINGS DIALOG BOX, TIME-FREQUENCY TAB

In the **Colors** group box, you can make the following settings:

COLORS GROUP BOX

- **Interpolate Data:** The data is interpolated in the time/frequency domain, resulting in continuous data display.
- **Standard Colors:** The standard color scale (blue-green-red) is used.
- **Grayscale:** Converts the color display to grayscales.
- **Discrete Colors:** Displays discrete colors.
- The **Set Details...** button displays the **Discrete Color Settings** dialog box. In this dialog box you can specify the colors values for positive and negative values (in the **Color for Positive Values** and **Color for Negative Values** list boxes). In the **Color Steps** text box, you specify the number of steps in the color scale.
- If you select the **Symmetrical Map Color** check box, the minimum and maximum voltage values both appear in the same color, while zero values are assigned the other color.
- If you select the **Zero is Darkest Color** check box, all zero values appear in black. If you clear it, they appear in white.
- If you select the **Draw Contour Lines** check box, each color step gets a contour line.

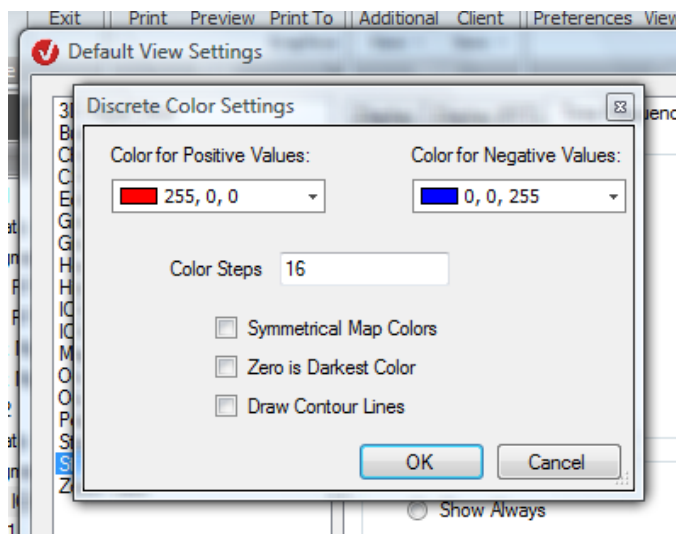


FIGURE 7—38 DISCRETE COLOR SETTINGS DIALOG BOX (ACCESSED FROM THE TIME-FREQUENCY TAB)

In the **Scaling** group box, you can make the following settings:

SCALING GROUP BOX

- If you select the **Logarithmic Scaling** check box, logarithmic scaling is applied to the y-axis.
- If you select the **Automatic Scaling** radio button, the optimum scaling is calculated automatically. If you also select the **Symmetric Scaling** check box, scaling limits are selected that ensure the value “0” is always in the middle of the color legend.
- If you select the **Manual Scaling** radio button, you can specify scaling manually by entering in the **Maximum** and **Minimum** text boxes the voltage interval covered by the color spectrum shown.

The radio buttons here allow you to specify whether the satellite graphs are always displayed (**Show Always**), never displayed (**Show Never**) or only displayed when there is enough space for them (**Show, if Size is Sufficient**).

SATELLITE GRAPHS
GROUP BOX

The **Axes** tab allows you to configure the x- and y-axes.

AXES TAB

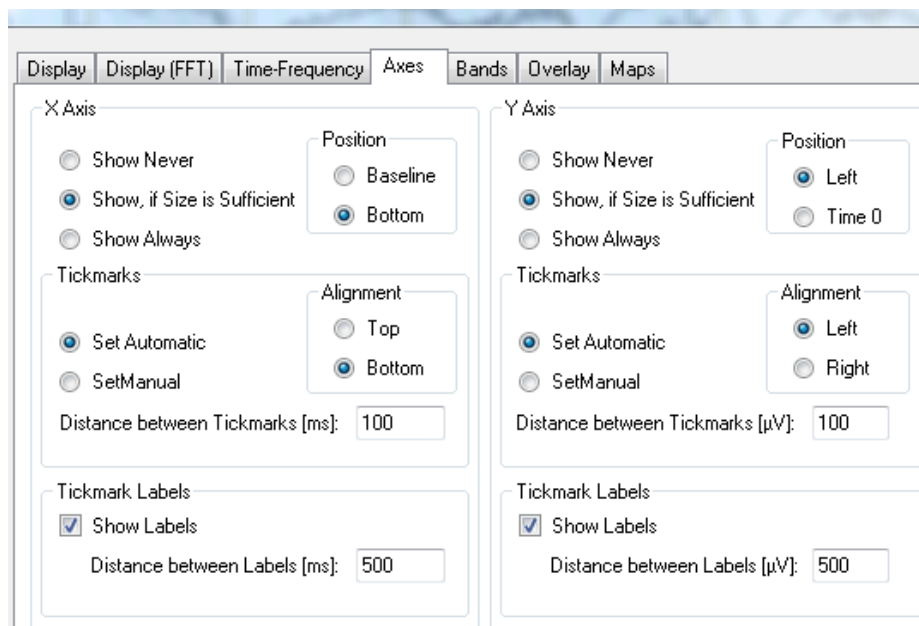


FIGURE 7—39 DEFAULT VIEW SETTINGS DIALOG BOX, AXES TAB

You can make the following settings separately for the x- and y-axes:

X AXIS AND Y AXIS
GROUP BOXES

The **Show Never**, **Show, if Size is Sufficient** and **Show Always** radio buttons allow you to specify whether the axis is not to be displayed, only to be displayed if there is enough space or always displayed.

- In the **Position** group box, you can specify the position of the axis: The x-axis can be positioned on the baseline (**Baseline** radio button) or along the lower border of the EEG (**Bottom** radio button). The y-axis can be positioned on the left (**Left** radio button) or at the zero point (**Time 0** radio button).
- Under **Tickmarks**, you set the intervals for the subdivisions of the axis. You can either have the intervals calculated automatically (**Set Automatic**) or set them manually (**Set Manual**). For the x-axis, you specify the interval in ms; for the y-axis, you specify it in μV . Under **Alignment**, you specify the alignment of the scaling marks: For the x-axis, you can specify alignment with the top (**Top** radio button) or bottom (**Bottom** radio button), and, for the y-axis, you can specify left alignment (**Left** radio button) or right alignment (**Right** radio button).
- Under **Tickmark Labels**, you use the **Show Labels** check box to specify whether and, if so, at what intervals the subdivisions of the axis are to be labeled. For the x-axis, you specify the interval in ms, and for the y-axis in μV .

On the **Bands** tab, you can set the frequency bands.

BANDS TAB

In the table, you can specify the color of a band, its name and where it starts and ends (in which columns from left to right) in hertz. You change the color of the band by repeatedly clicking a color strip in the **Color** column and displaying the color selection dialog by means of a drop-down list.

The asterisk allows you to insert a new row. You can delete rows from the table by pressing the **<Delete>** key.

All frequency ranges that are not defined in the table are displayed in black.

The **Apply to all Views** button applies the current settings for frequency bands to all other view categories. The histogram view (MR Correction transform) is an exception to this because it does not use the usual frequency bands.

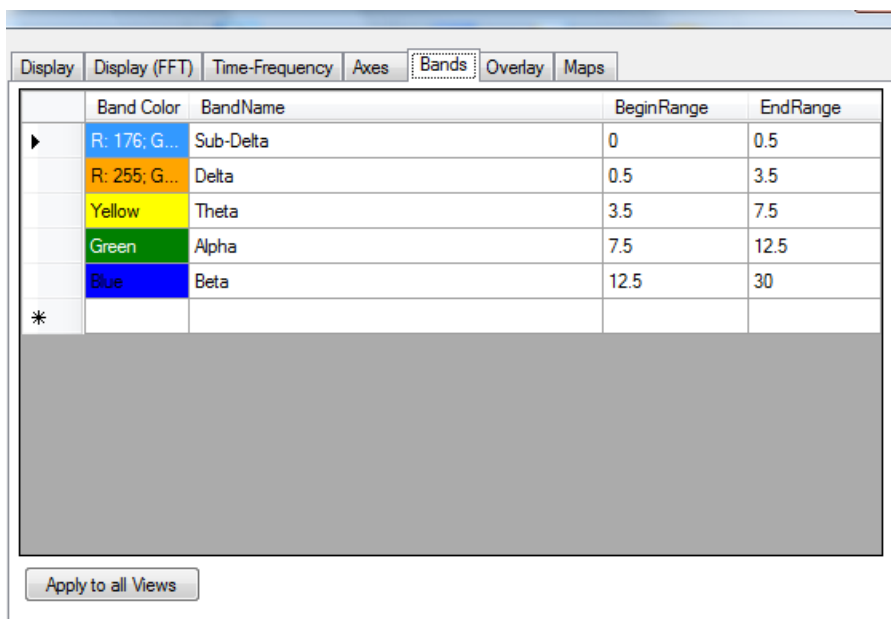


FIGURE 7—40 DEFAULT VIEW SETTINGS DIALOG BOX, BANDS TAB

On the **Overlay** tab, you can specify settings for overlaid EEG curves. The settings affect how the curves are displayed and labeled. They are made in a separate table for each curve. OVERLAY TAB

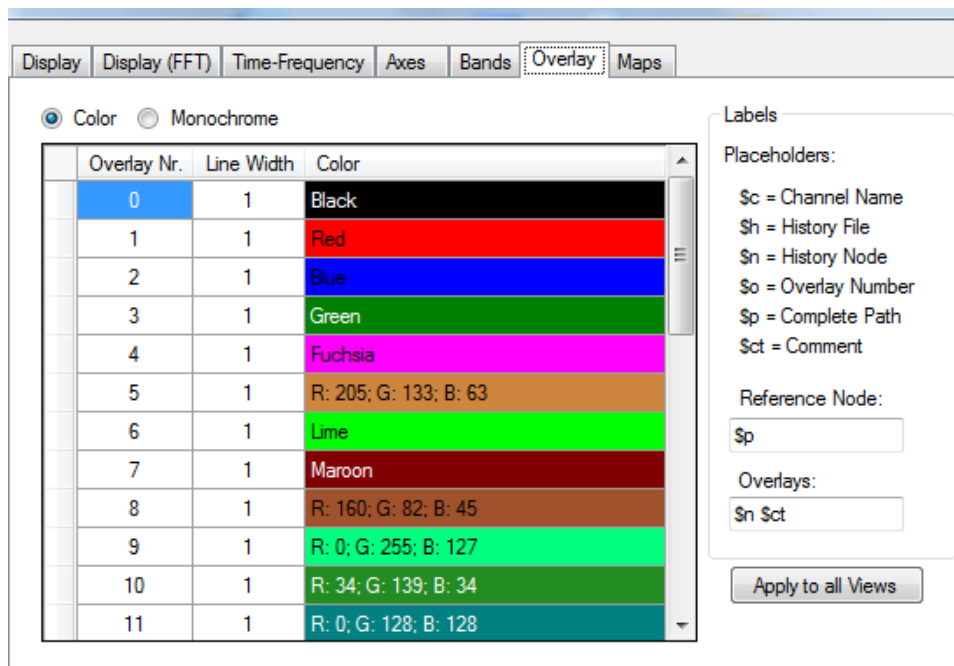


FIGURE 7—41 DEFAULT VIEW SETTINGS DIALOG BOX, OVERLAY TAB, COLORS OF THE FREQUENCY BANDS

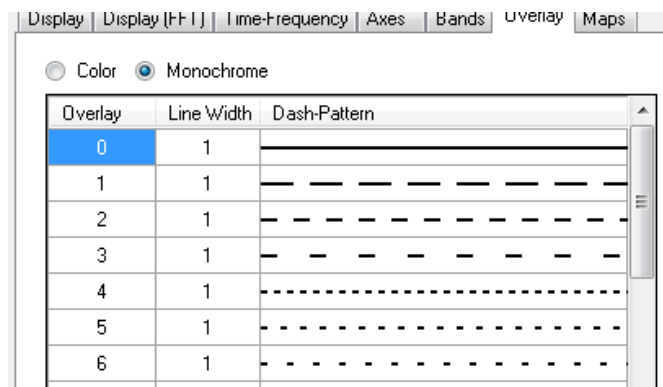


FIGURE 7—42 OVERLAY TAB, DISPLAY OF THE FREQUENCY BANDS USING MONOCROME LINES

The following options are available to you:

- You can choose between displaying the EEG curves in a single color using different line types (**Dash-Pattern** column) and displaying them in different colors (**Color** column). To do this, you select either the **Monochrome** or **Color** radio button.
- In the **Line Width** column, you specify the line width of the curves.
- In the **Reference Node** and **Overlays** text boxes, you enter the names of the reference channel and the overlaid channels. The entries in these text boxes only take effect if the data sets are overlaid (see section 9.3, “Overlaying of different data sets”).

- You can also use placeholders to name the channels (see under **Placeholders**). These are replaced with current values when the curves are displayed (i.e. with the name of the relevant data set). The following table lists the available placeholders:

Placeholder	Meaning
\$c	Channel name
\$h	Name of the history file
\$n	Name of the associated data set
\$o	Ordinal number of the curve
\$p	Full history path including all the intermediate steps from the raw EEG to the current data set

- The **Apply to all Views** button applies the current settings for overlays to all other view categories. The butterfly view and standard deviation view are exceptions to this because they use special overlay settings.

The **Maps** tab allows you to configure the topographic map display. It contains the group boxes **Interpolation**, **Scaling** and **Display**. MAPS TAB

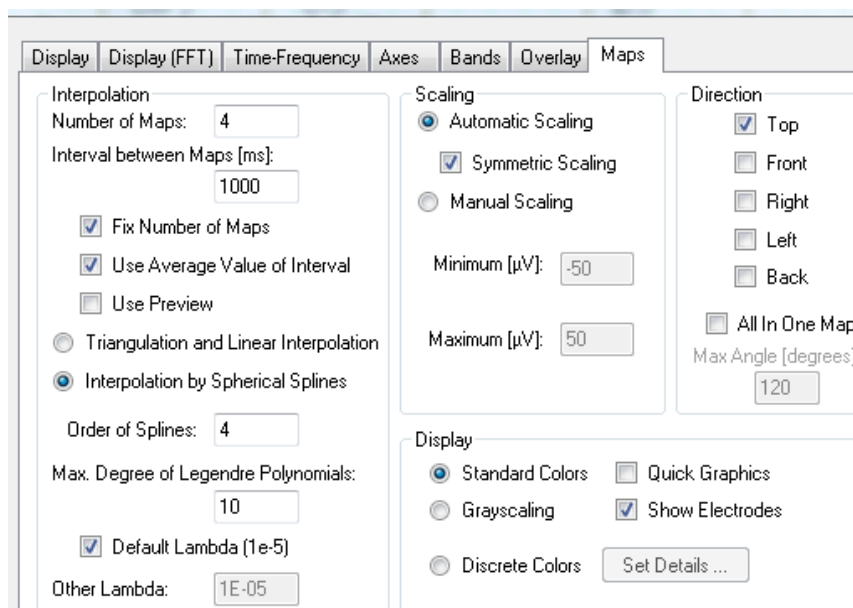


FIGURE 7—43 DEFAULT VIEW SETTINGS DIALOG BOX, MAPS TAB

In the **Interpolation** group box, you can make the following settings:

INTERPOLATION GROUP
BOX

- In the **Number of Maps** text box, you specify the number of maps to be displayed simultaneously.
- In the **Interval between Maps** text box, you specify the interval between two maps. For time data you specify this in milliseconds and for frequency data in hertz.
- **Fix Number of Maps** check box: There are two ways to specify the number of maps:

Directly, by entering a value in the **Number of Maps** text box and selecting the **Fix Number of Maps** check box

Indirectly, by entering a value in the **Interval between Maps** text box and clearing the **Fix Number of Maps** check box

- Select the **Fix Number of Maps** check box if you want to manually change the width of the total interval to be displayed in a mapping view. When you select the check box, the number of maps displayed is kept constant during scaling and the interval between them is adjusted accordingly. If you do not select the check box, the interval between the maps is kept constant and the number of maps is adjusted accordingly.
- If you select the **Use Average Value of Interval** check box, the average value of the selected interval is used to calculate the maps. If you leave the check box cleared, only the first point of the interval is used.
- If you select the **Use Preview** check box, a preview is created before the map is actually calculated. This can give a very quick impression of the map's color distribution. This option is useful when the map image has to be navigated quickly. You should clear this check box if you want to programmatically record an animation consisting of map screenshots.

The following radio buttons allow you to select algorithms for calculating the data:

- **Triangulation and Linear Interpolation:** You will find detailed information on this algorithm in section 12.7.4, "Topographic interpolation".
- **Interpolation by Spherical Splines:** You will find detailed information on this algorithm in section 12.7.4, "Topographic interpolation".
- If you opt for interpolation with splines, you enter the spline order in the **Order of Splines** text box and the maximum degree of the Legendre polynomial in the **Max. Degree of Legendre Polynomials** text box.
- If you select the **Default Lambda** check box, the default value of 10^{-5} ($1e-5$) is automatically accepted. If you clear the check box, you can enter a different value in the **Other Lambda** text box. You will find detailed information on this in section 12.7.4, "Topographic interpolation".

In the **Scaling** group box, you can make the following settings:

SCALING GROUP BOX

- If you select the **Automatic Scaling** radio button, the optimum scaling is calculated automatically. If you also select the **Symmetric Scaling** check box, scaling limits are selected that ensure the value “o” is always in the middle of the color legend.
- If you select the **Manual Scaling** radio button, you can specify scaling manually by entering in the **Maximum** and **Minimum** text boxes the voltage interval covered by the color spectrum shown.

In the **Direction** group box, you can select one or more different views of the map: **Top** (viewed from the top), **Front** (viewed from the front), **Back** (viewed from the rear), **Right** (viewed from the right) and **Left** (viewed from the left). You can define the view of the map by selecting the **All in One Map** check box and then specifying a maximum angle of view (in the **Max Angle [degrees]** text box).

DIRECTION GROUP BOX

The **Display** group box offers you the following options:

DISPLAY GROUP BOX

- **Standard Colors:** The standard color scale (blue-green-red) is used.
- **Grayscale:** Converts the color display to grayscales.
- **Discrete Colors:** Displays discrete colors.
- The **Set Details...** button displays the **Discrete Color Settings** dialog box. In this dialog box, you can specify the color values for positive and negative values (in the **Color for Positive Values** and **Color for Negative Values** list boxes). In the **Color Steps** text box, you specify the number of steps in the color scale.
- If you select the **Symmetrical Map Color** check box, the minimum and maximum voltage values both appear in the same color, while zero values are assigned the other color.
- If you select the **Zero is Darkest Color** check box, all zero values appear in black. If you clear it, they appear in white.
- If you select the **Draw Contour Lines** check box, each color step gets a contour line.
- In **Quick Graphics** mode, not every pixel in the map is calculated. Instead, only the values of the points of a rectangular grid with a specific resolution are calculated. Then each rectangle in the grid gets the calculated color. This results in a map that has a lower resolution but can be calculated much more quickly.
- If you select the **Show Electrodes** check box, the electrodes appear as small circles on the map.

The settings for the 3D map only appear for the “3D Head View” category. They allow you to configure the display of the 3D head. The dialog box contains the group boxes **Interpolation**, **Scaling**, **Display** and **Head**. 3D MAP SETTINGS

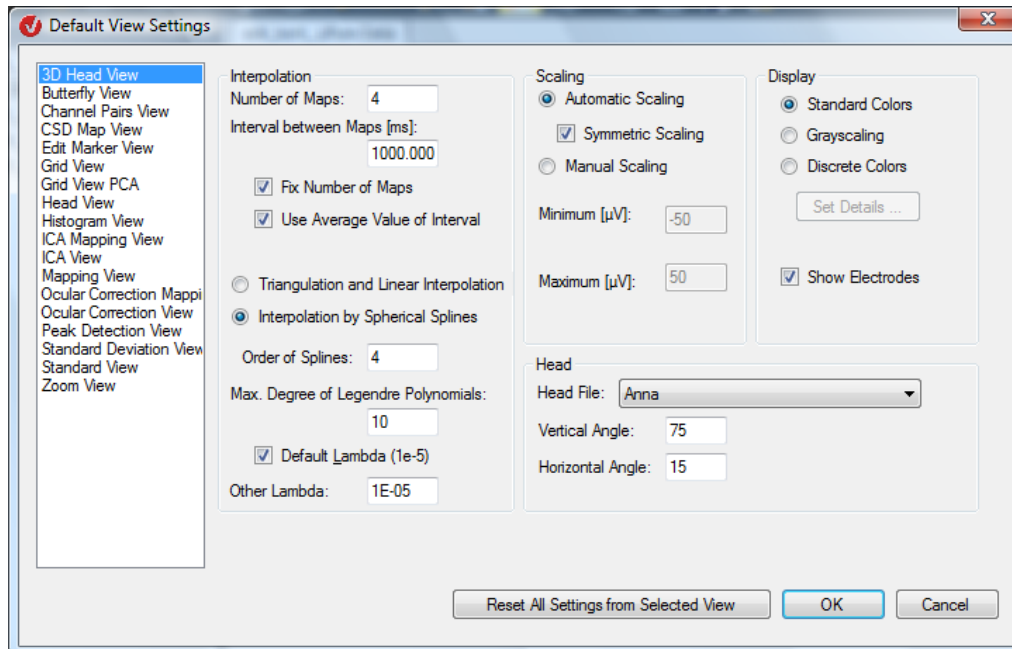


FIGURE 7—44 SETTINGS FOR THE 3D MAP

The group boxes **Interpolation**, **Scaling** and **Display** contain identical options to those on the **Maps** tab. The **Direction** group box on that tab does not appear here because the head can be rotated freely.

From the **Head File** drop-down list box, you choose the head to be displayed from the available head definitions. HEAD GROUP BOX

The **Vertical Angle** and **Horizontal Angle** text boxes allow you to specify the angle of view for the head.

7.3.3 Node-specific view settings

You display the node-specific settings by right-clicking any point in the current view and choosing the **Settings...** command from the context menu that appears. Our example concerns the history node **odd_phob_2/Raw Data**.

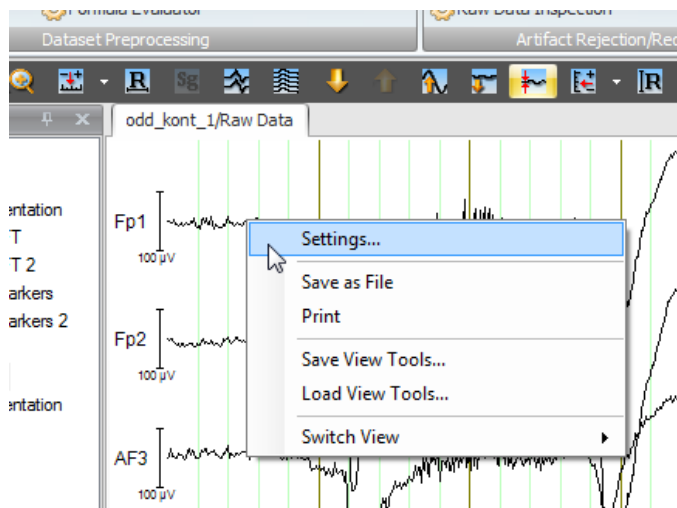


FIGURE 7–45 NODE-SPECIFIC CONTEXT MENU, SETTINGS COMMAND

The **View Settings** dialog box appears, which contains the node-specific settings for the view on the corresponding tabs. In our example of a standard view with time data, it contains the **Display** and **Overlay** tabs.

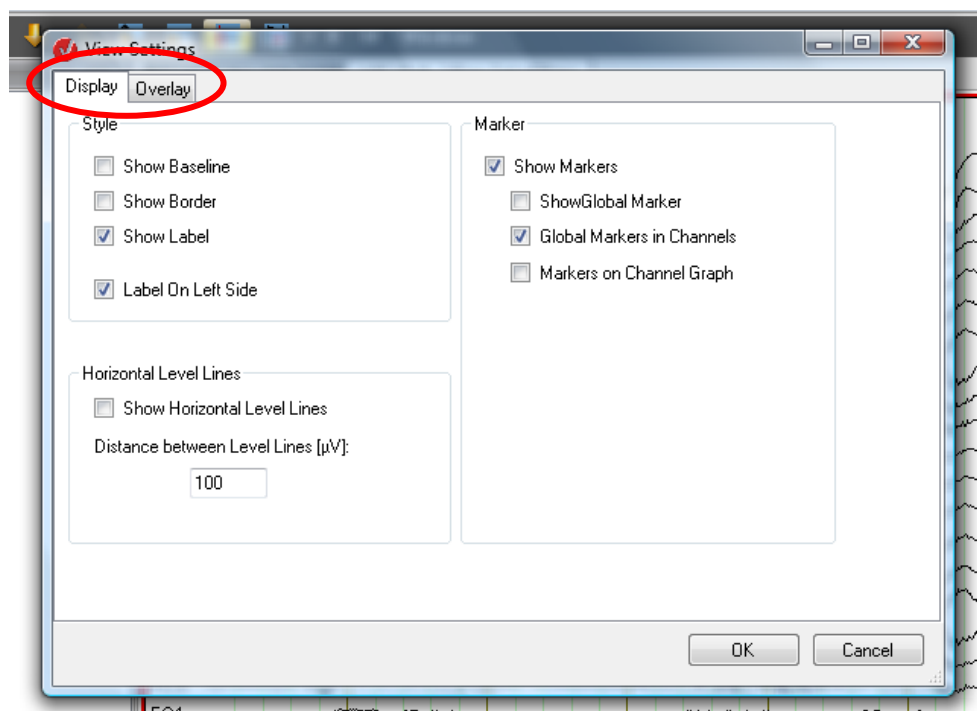


FIGURE 7–46 NODE-SPECIFIC VIEW SETTINGS DIALOG BOX

When you create a new node, it initially takes the category-related view settings (default view settings). The changes you subsequently make to the node's view settings always take priority over changes to the category-related view settings. If you make no changes at node level, the category-related view settings are used.

The node-specific settings are saved in the node and become available whenever you open the node. The node-specific settings apply only to the active view. You can thus display different views of the node using different settings each time.

By right-clicking and choosing the **Reset Settings** command from the context menu, you can delete from the node all the settings made at node level that apply to the currently selected view.

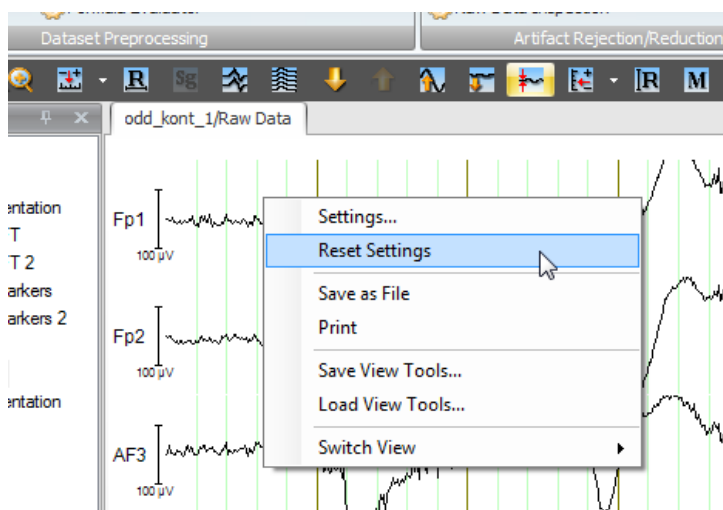


FIGURE 7–47 NODE-SPECIFIC CONTEXT MENU, RESET SETTINGS TO DEFAULTS COMMAND

7.4 Configuring administrator rights (Administration command)

Click the **Analyzer button**, and then choose **Administration**. Alternatively, click the **File** tab, then **Administration** in the **Configuration** group.

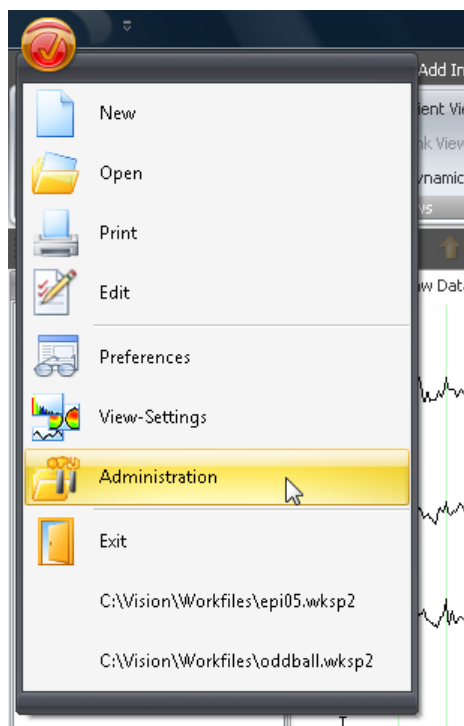


FIGURE 7—48 ANALYZER BUTTON, ADMINISTRATION COMMAND

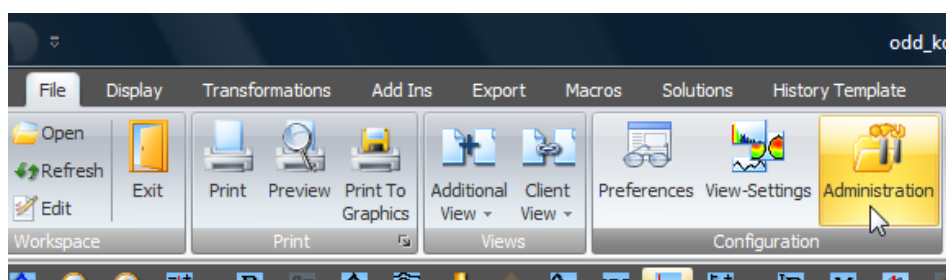


FIGURE 7—49 CONFIGURATION GROUP, VIEW SETTINGS BUTTON

The **Analyzer Administration** dialog box appears. This contains the tabs **Application Paths**, **Profiles** and **Component Search Paths**.

The **Application Paths** tab allows you to set search paths.

APPLICATION PATHS TAB

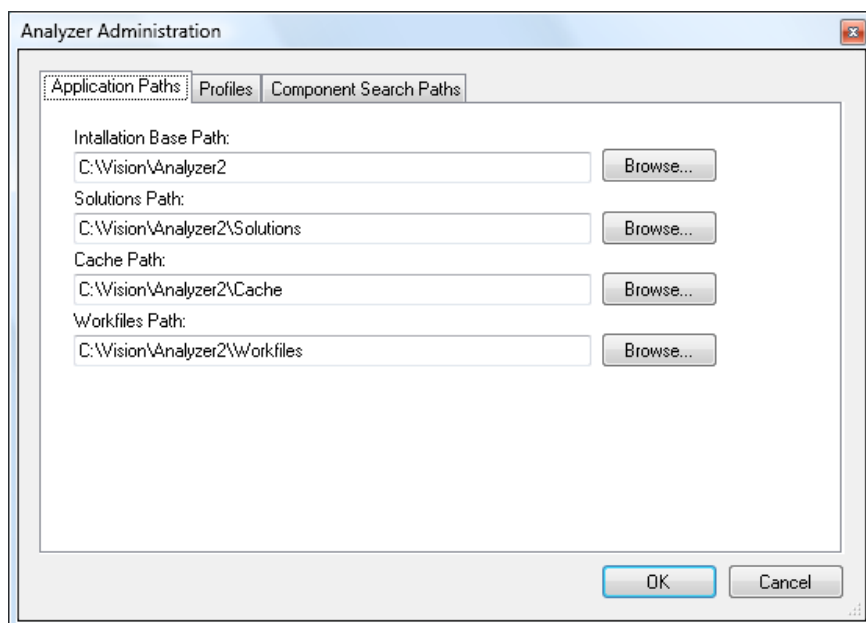


FIGURE 7—50 ANALYZER ADMINISTRATION DIALOG BOX, APPLICATION PATHS TAB

In the **Installation Base Path** text box, you specify the folder containing the application. In the **Solutions Path** text box, you specify the folder containing the solutions. In the **Workfiles Path** text box, you specify the folders for workspace files, macros and history templates.

The associated **Browse...** buttons allow you to select a folder.

The **Profiles** tab allows you to manage user profiles.

PROFILES TAB

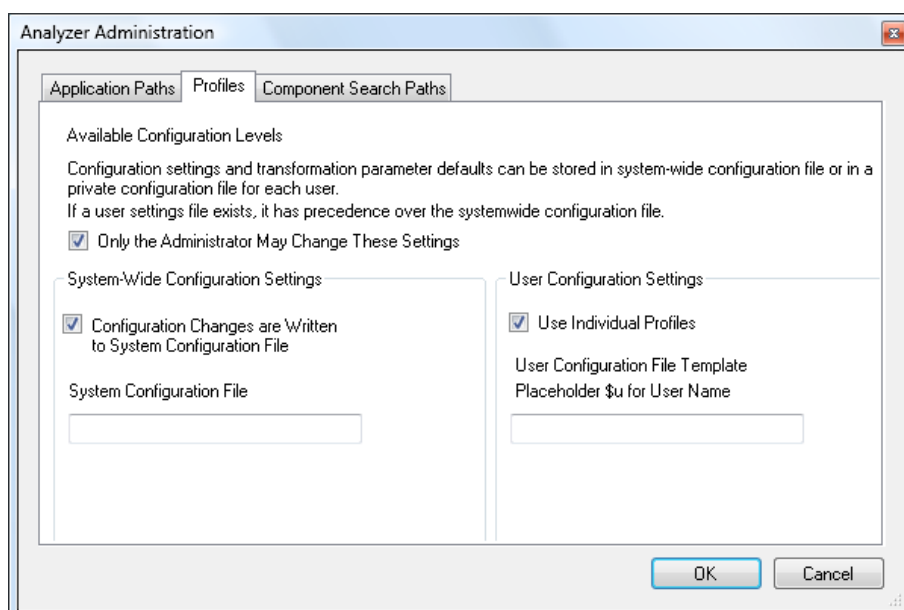


FIGURE 7—51 ANALYZER ADMINISTRATION DIALOG BOX, PROFILES TAB

The user profiles determine where the settings made using **File > Configuration > Preferences** and **File > Configuration > View Settings** are stored. The settings can either be stored separately for each user or in a shared, system-wide file for all users.

If the **Only the Administrator May Change These Settings** check box is selected, the rest of the tab is not accessible to those who are not administrators.

If you select the **Configuration Changes are Written to System Configuration File** check box, when changes are made to the settings they are written to a system-wide file.

SYSTEM-WIDE
CONFIGURATION
SETTINGS GROUP BOX

In the **System Configuration File** text box, you can specify the name of this system-wide file. If you do not specify a name, a default name is used. If you specify only a file name, the file is stored in a location determined by the system. If you specify a full path, the file is stored in the location indicated by this path. Note that you must have read and write access to this path in order to use the file.

If you select the **Use Individual Profiles** check box, when changes are made to the settings they are written to a user-specific file.

USER CONFIGURATION
SETTINGS GROUP BOX

In the **User Configuration File Template** text box, you can specify a name for the template of the user-specific file. If you do not specify a name, a default name is used. In the specified file name the placeholder **\$u** is replaced with the user name.

If you specify only a file name, the user-specific files are stored in a location determined by the system. If you specify a full path, the files are stored in the location indicated by this path. Note that all users must have read and write access to this path in order to use the file.

If the **Configuration Changes are Written to System Configuration File** check box is not selected, the **Use Individual Profiles** check box is selected and cannot be cleared.



If you select settings files on the **Profiles** tab that do not yet exist, the files are created. Default values are used for the settings. If user profiles are selected although there is a system-wide file, users use the system-wide settings unless they have made personal settings that are different from those. In this way, the system-wide configuration file can be used, for example, to determine the settings for a user starting the Analyzer for the first time.

The **Component Search Paths** tab allows additional, modified components or components created by the user to be added to the Analyzer subsequently.

COMPONENT SEARCH
PATHS TAB

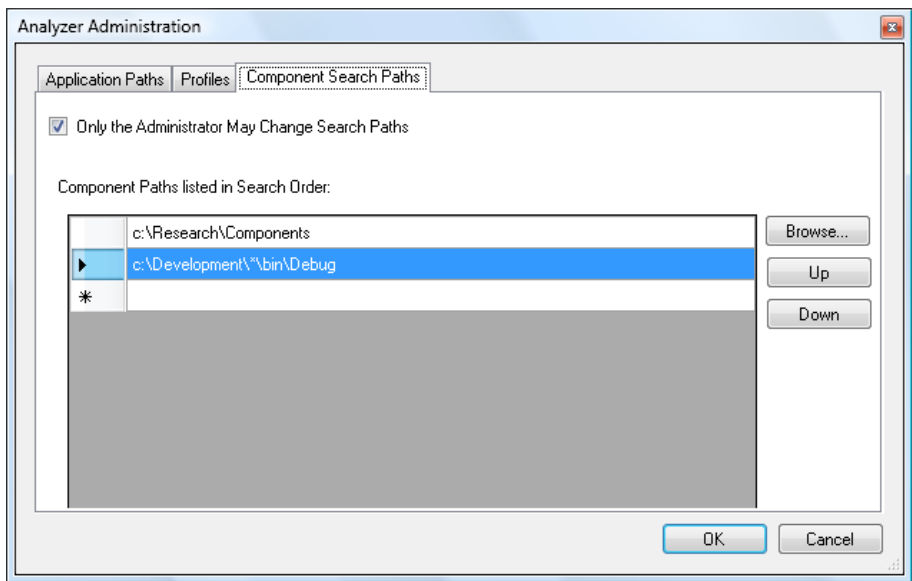


FIGURE 7—52 ANALYZER ADMINISTRATION DIALOG BOX, COMPONENT SEARCH PATHS TAB

If the **Only the Administrator May Change Search Paths** check box is selected, only the administrator has the right to change the path settings.

The table contains a list of the search paths taken into account by the Analyzer when searching for components. The Analyzer searches through all the DLL or VAEM files on these paths. It also always searches through its installation folder.

The asterisk (*) functions as a placeholder in the same way as it does in files. In our example of “c:\Development*\bin\Debug”, the folders “c:\Development\Project_1\bin\Debug” and “c:\Development\Project_2\bin\Debug” would be found.

The **Browse...** button allows you to select the folders.

The **Up** and **Down** buttons allow you to change the order of the rows in the table. The order in which the entries occur in the table is the order in which they are searched. If a component occurs more than once, the component listed first in the table is always used.

Note that the Analyzer installation folder is always searched after the entries in the table.



8 Montages

Montages enable channels to be reconnected on a software basis. In other words, new voltage reference points are assigned to the channels.

SUMMARY

Montages also optimize the display of data by, for example, allowing frontal electrodes to be grouped together in one montage and occipital electrodes in another. When one of these montages is selected, only those channels that have been assigned to it are displayed. The order in which the channels occur can also be changed in a montage. Thus, channels that were originally apart can be shown next to each other. A channel can also appear more than once in a montage.

Another important characteristic of montages is that certain display parameters, such as the position and size of a channel, can be assigned to them in a head view. (A head view is a view in which the channels can be freely positioned in the window. Its size can be adjusted to suit requirements. To find out what can be done in the head view, refer to section 9.2.3.)

A montage is used for visualization purposes only. In other words, the new data only exists temporarily and does not change the original data.



To create a montage, you choose **Create Montage** from the **Display** tab.

CREATING A MONTAGE



ABB. 8—1 DISPLAY TAB, MONTAGES GROUP

The **Create New Montage** dialog box appears.

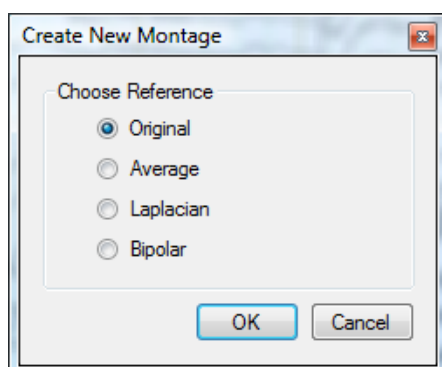


ABB. 8—2 DIALOG BOX FOR CREATING AND EDITING MONTAGES

In the **Choose Reference** group box, you choose the reference type to be used in the new montage. The following radio buttons are available for this:

- **Original:** No new reference is calculated. This type of montage is only used to group channels together or optimize their presentation, as described above.
- **Average:** The average reference is calculated. In other words, the average of all the selected channels is used as the reference.
- **Laplacian:** Source derivation, as described by Hjorth, is carried out. This is a method derived from the Laplace transform in which the reference is calculated from multiple neighboring electrodes of a channel.

In order to work out which are the neighboring electrodes, the program requires information about the position of the electrodes. If you used electrode names on the 10/10 or 10/20 principle when recording the EEG, the program should have this information. However, if you used other channel names, you can use the Edit Channels transform to enter the correct coordinates. You will find detailed information on this in section 12.1.6, “Edit Channels”.

You can also specify a separate file containing default coordinates. You do this on the **Electrodes** tab, which you display by choosing **File > Configuration > Preferences** (see section 7.1, “Configuring preferences”).

- **Bipolar:** Differences between channels are formed.

We advise you to select the simplest reference type (the original reference) initially.



Once you have selected the reference type, click **OK**. The montage editor (the Edit Original Referenced Montage dialog box) appears. The montage editor offers the same basic functions for all four reference types. Some additional controls are displayed for the Laplacian and bipolar reference types.

The montage editor contains the **Head View** and **List View** tabs. The tabs allow you to select the channels contained in the montage. The head view gives you an overview of the arrangement of the channels on the head. The list view allows you to enter new channels not displayed in the head view. You can also activate a grid view of the montage. This view is explained in the subsection entitled “Montage grid”.

The **Head View** tab shows the channels in their position on the head. Channels whose position is not known are displayed to the left of the head. If you click the name of a channel, it is added to the montage. If you click it again, it is removed from the montage.

HEAD VIEW TAB

Channels added to the montage are highlighted in black.

The **Insert current channels** button allows you to add all the existing channels to the montage. **Remove All** removes all channels from the montage.

If you click a point on the head where there is no channel and then drag the mouse, you can select multiple channels.

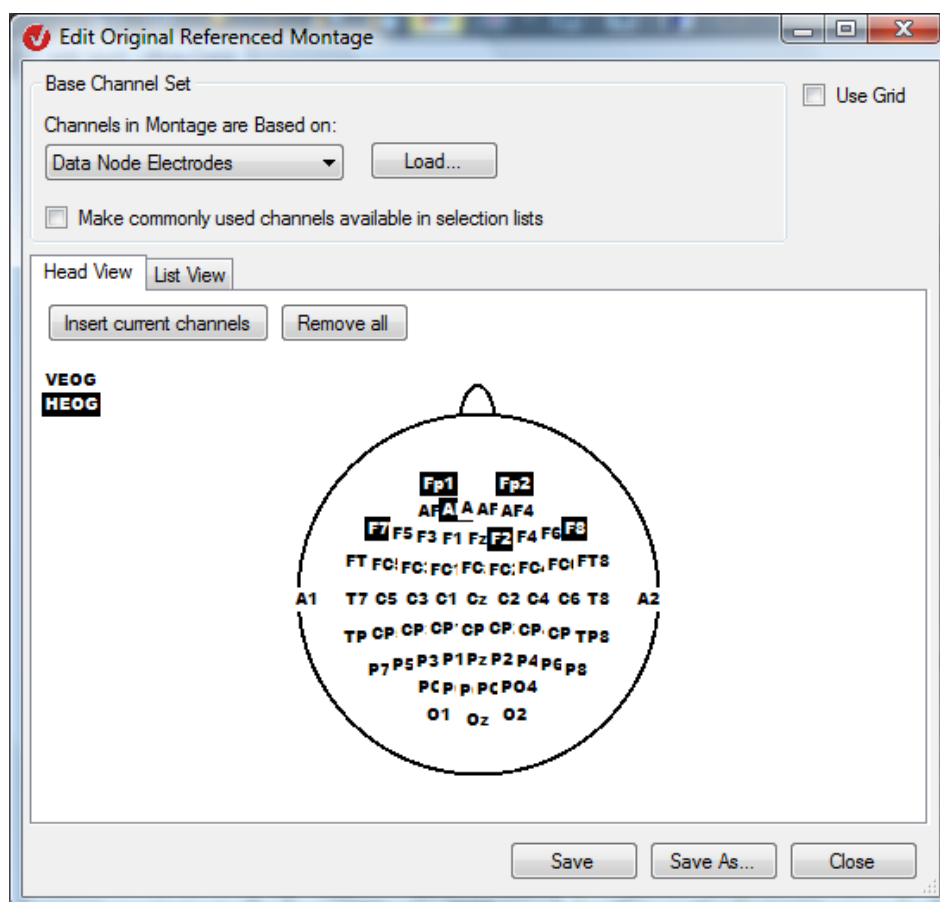


FIGURE 8—3 MONTAGE EDITOR, HEAD VIEW TAB

The **List View** tab displays the list of channels in the order in which they appear in the montage. You can select multiple rows in the list and delete them. In the last row, you add new channels by choosing them from the drop-down list or entering them directly.

LIST VIEW TAB

Channels that you enter manually are added to the drop-down lists in the rows.

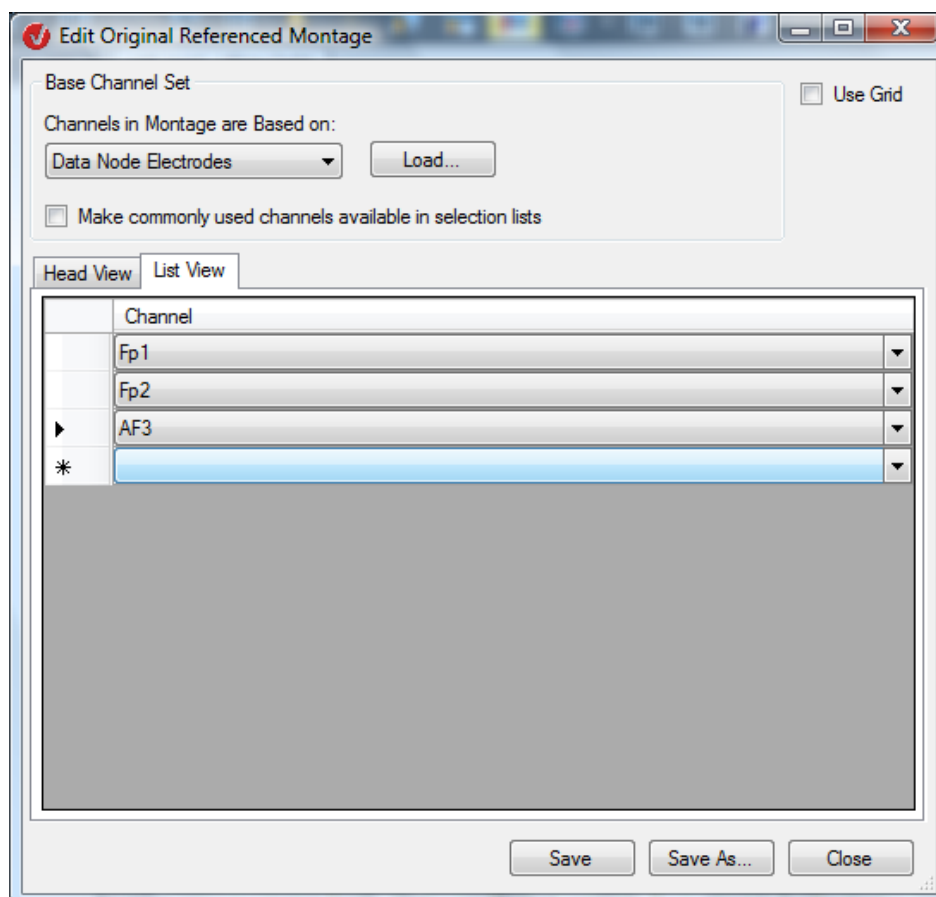


FIGURE 8—4 MONTAGE EDITOR, LIST VIEW TAB

A distinction is drawn between montages with and without grid information. Montages with grid information specify how the channels are displayed when a grid view is used (size of the grid in rows and columns, free cells). Montages without grid information are automatically arranged in a grid view with no cells free.

MONTAGE GRID

You specify whether a montage has grid information by means of the **Use Grid** check box. If you select the check box, an additional section containing a grid appears in the montage editor:

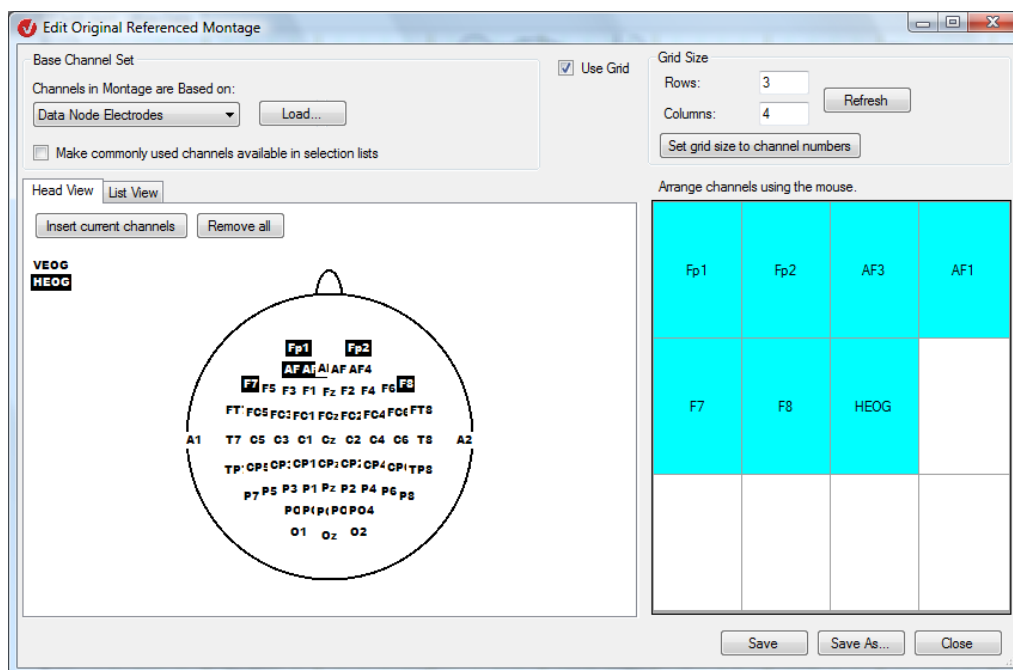


FIGURE 8—5 MONTAGE EDITOR WITH GRID ON THE RIGHT

In the grid, you can use the mouse to add channels and drag them to a different cell. If you drag a channel to a cell occupied by another channel, the channels swap places.

The order in which the channels appear in the list view is always the same as the order in which they occur in the grid on the right. Read from left to right and top to bottom. If you change the position of a channel in the grid on the right, the list is adjusted accordingly.



Even if a montage is not to use any grid information, it can be a good idea to display the grid on the right temporarily to allow you to change the order of the channels slightly.

TIP

In the **Grid Size** group box, you specify the size of the grid in rows (in the **Rows** text box) and columns (in the **Columns** text box). The **Apply** button applies your entries to the grid. If the grid is reduced in size, channels already contained in the grid are rearranged in the new grid, reflecting the original layout as far as possible.

The **Set grid size to channel numbers** button creates an approximately square grid containing the channels of the montage. If you add new channels on the **Head View** or **List View** tab, they are added in free cells. If necessary, the grid is extended.

If the mouse pointer is positioned over a cell in the grid, the corresponding channel is highlighted in color on the **Head View** tab and vice versa.



In addition, you can also drag channels directly from the **Head View** tab to a grid cell.

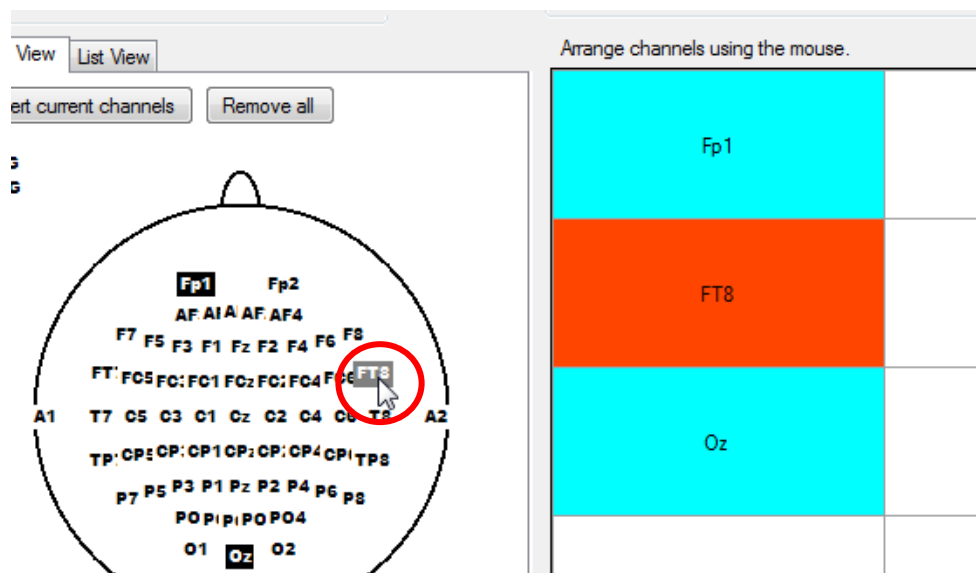


FIGURE 8—6 COLOR HIGHLIGHTING OF CHANNELS

You can use the **Channels in Montage are Based on** drop-down list to select the set of channels on which the head view is based. In the list view, you use the channel drop-down lists. The following options are available for selection:

BASE CHANNEL SET
GROUP BOX

- **Standard 10/20 Electrodes:** The standard set of 10/20 electrodes is used.
- **-NONE-:** With the exception of any existing montage channels, there are no channels available.
- **Data Node Electrodes:** The channels of the open data node are used.

Regardless of the underlying channel set, you can, of course, continue to enter channel names of your choice in the **List View**.

The **Load** button allows you to load a separate electrode configuration file in the BrainVision electrode file format. This XML-based format is explained in Appendix H.

If you select the **Make commonly used channels available in section lists** check box, a selection of frequently used channel names is added to the channel drop-down lists in the list view. If you choose one of these channels from a drop-down list, it appears in the head view with standard coordinates if it is not contained in the selected channel set.

If you select the Laplacian reference type, the **Number of Reference Electrodes** text box appears in the montage editor, thus allowing you to specify the number of reference electrodes.

PECULIARITY OF THE
LAPLACIAN REFERENCE
TYPE

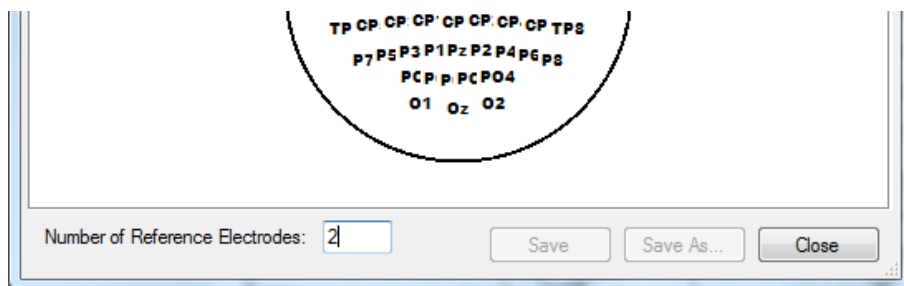


FIGURE 8—7 PART OF THE MONTAGE EDITOR FOR THE LAPLACIAN REFERENCE TYPE

If you select the bipolar reference type, the list view contains two columns: **Channel** and **Reference Channel**.

PECULIARITIES OF THE
BIPOLAR REFERENCE
TYPE

The cells in the grid indicate the difference between the channel and reference channel in each case.

On the **Head View** tab, the channel and reference channel are shown connected by arrows. You can use the mouse to add a channel and drag it to its reference channel.

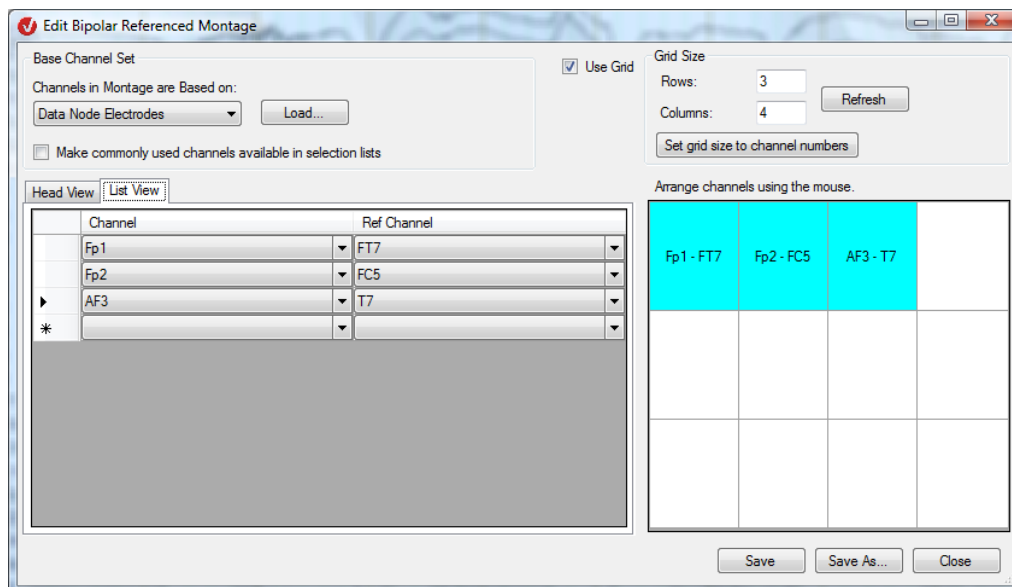


FIGURE 8—8 MONTAGE EDITOR FOR THE BIPOLAR REFERENCE TYPE, LIST VIEW TAB WITH GRID ON THE RIGHT

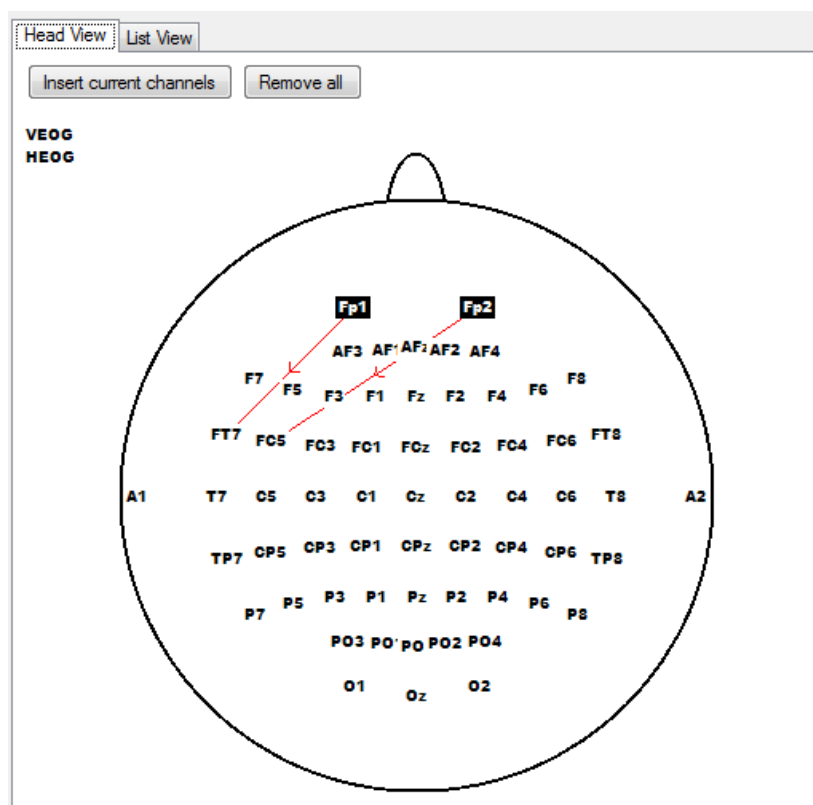


FIGURE 8—9 MONTAGE EDITOR FOR THE BIPOLAR REFERENCE TYPE, HEAD VIEW TAB

The **Save** and **Save As...** buttons are available for saving the montage.

SAVING THE MONTAGE

To modify an existing montage, select the **Edit Montage** radio button in the dialog box. A dialog box appears that allows you to open an existing montage file.

EDITING A MONTAGE

After you have edited the montage, you are again asked for the name under which you want to save the montage. You can enter a new name in order to obtain a new montage from an existing one.

Note that the reference type of an existing montage cannot be changed.



The **Display Montage** menu command allows you to display all your montages easily.

DISPLAYING THE
MONTAGES

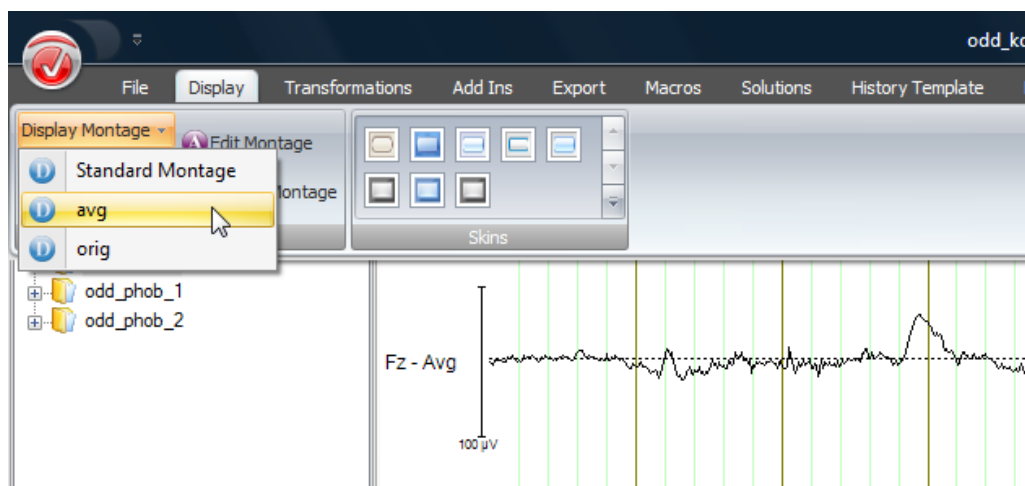


FIGURE 8—10 DISPLAYING MONTAGES

To allow you to switch quickly between different montages, you can assign them keyboard shortcuts. These keyboard shortcuts activate the associated montages. To assign these keyboard shortcuts, you choose **Display > Montages > Options**. The montages are assigned to the keyboard shortcuts **<Ctrl-1>** to **<Ctrl-0>**. **<Ctrl-1>** is reserved for the default montage. You can assign the other keyboard shortcuts to whichever montages you choose.

KEYBOARD SHORTCUTS
FOR MONTAGES

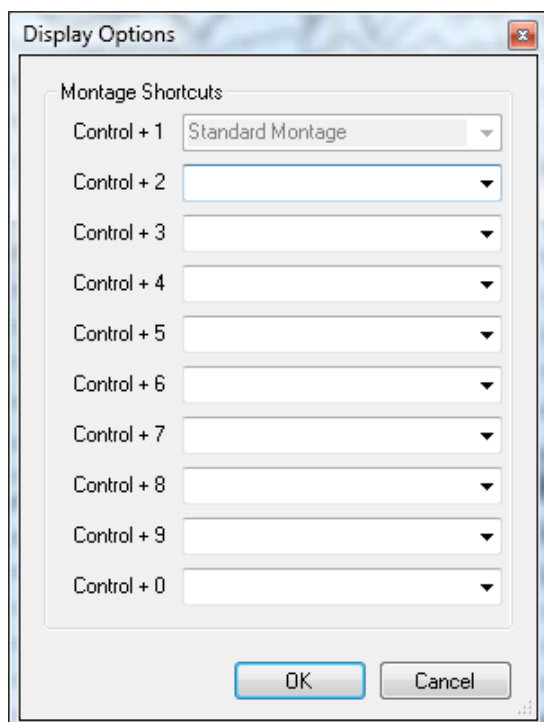


FIGURE 8—11 SELECTING KEYBOARD SHORTCUTS FOR MONTAGES

You can also select a montage to be activated when a new data window is opened. To do this, choose **Configuration > Preferences** and then click the **Views** tab. From the **Default Montage** drop-down list boxes for unsegmented and segmented data sets, you can select the initial (default) montage.

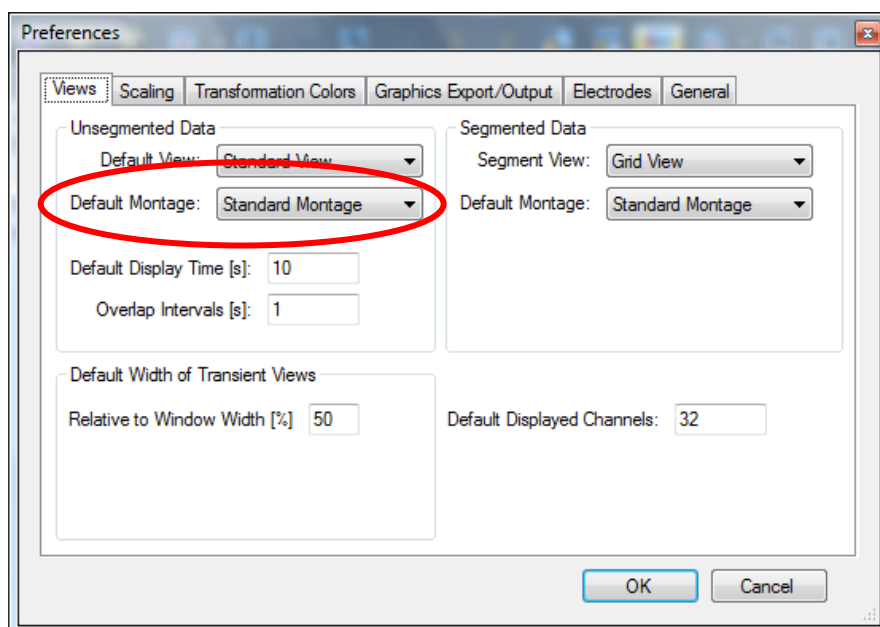


FIGURE 8—12 SELECTING THE INITIAL MONTAGE (DEFAULT MONTAGE)

9 Views (EEG display modes)

9.1 Views: Introduction

Views are ways of displaying the EEG. A view determines how the channels are arranged in the window, for example.

Note that the data displayed was originally digitized. Consequently, the accuracy of the display depends on the digitization rate. Ultimately, there are always limits to the accuracy.



The views available to you include the standard, grid, head and map view. These views display data in both the time and frequency domains. In addition, the Analyzer has numerous specialized views for displaying particular kinds of EEGs.

EEG views are used when you open an EEG data set. Multiple views of an EEG can be displayed simultaneously (see the description of the “Additional View” function).

VIEW FUNCTIONS

The toolbar and navigation bar are used with all views. The open views are displayed in tabs above the EEG. This allows you to switch easily between open view windows (see section 5.1, “The new user interface of the Analyzer”).

Multiple views of an EEG can be displayed simultaneously in an existing window (see the description of the “Switch View” function).

Views can be linked to each other in different ways. For example, in views based on data of the same type, the EEG graphs can be overlaid (see section 9.3, “Overlaying of different data sets”).

In addition, you can also select montage connections of the channels in the EEG for each view (see chapter 8, “Montages”).

You can make general settings for the views, such as the scaling or the area visible when the view or montage is first opened (see section 7.1, “Configuring preferences”).

You can also make detailed settings for the display of each view category (see section 7.3, “Configuring the EEG view settings”). These settings can be saved in individual EEG nodes.

A fundamental function of EEG views is to display EEG channels in the form of a graph. Generally, the views used are handled in a similar way when it comes to channel and range selection, for example. This applies, in particular, to the following frequently used view categories:

INTERACTION OPTIONS

- **Standard view:** The standard view corresponds to the EEG on paper. The curves or EEG channels are shown one after (below) another. The standard view is typically used for spontaneous EEG analyses.
- **Grid view:** The grid view is usually used for the display of segmented data. The data appears in a rectangular grid.
- **Head view:** The head view displays the EEG channels in topographic head positions.

When you move the mouse pointer over the EEG graph in these views, a red cross appears at the nearest point on the graph, and the corresponding details of its position are displayed on the status bar.

CHANNEL HIGHLIGHTING AND SELECTION

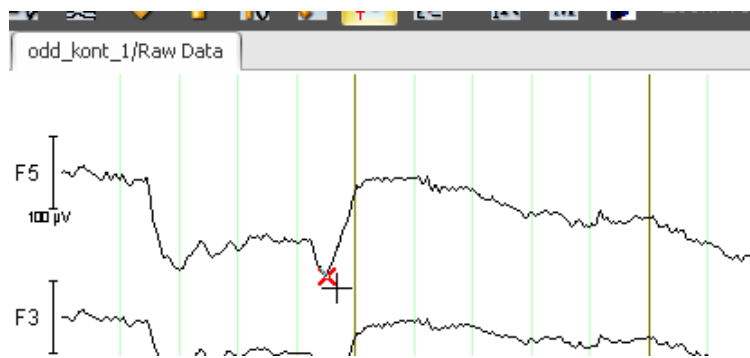


FIGURE 9—1 RED CROSS

You select a channel by clicking the corresponding channel name. The selected channel is highlighted in blue.

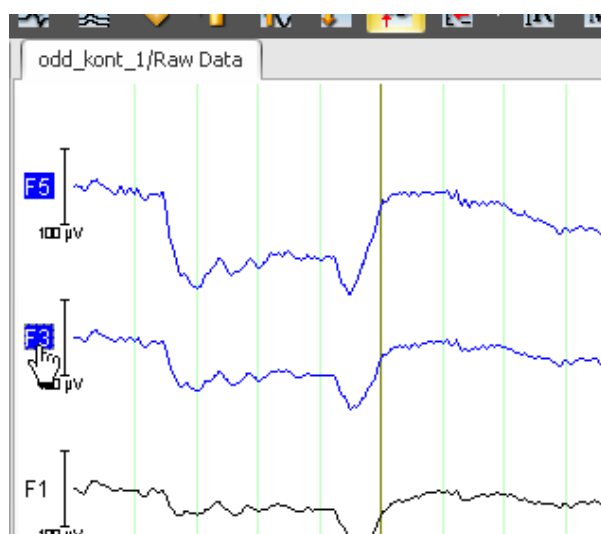


FIGURE 9—2 SELECTED CHANNEL WITH BLUE HIGHLIGHTING

By double-clicking a channel name you can display the corresponding channel separately. If you double-click the channel name again, the display returns to how it was before.

To display a selection of channels, select these channels in the desired sequence by means of a mouse click. If you double-click the channel name selected last, the selected channels are displayed separately. If you double-click the channel name again, the display returns to how it was before.

You deselect a selected channel by clicking the channel name again. To prevent the second mouse click from being interpreted as a double-click, wait about a second before clicking for a second time.

To select a data point or data range, proceed as follows:

SELECTION OF DATA RANGES

Click a channel to highlight a single point. This is a semitransparent blue band with a black line in the middle indicating the exact position of the point.

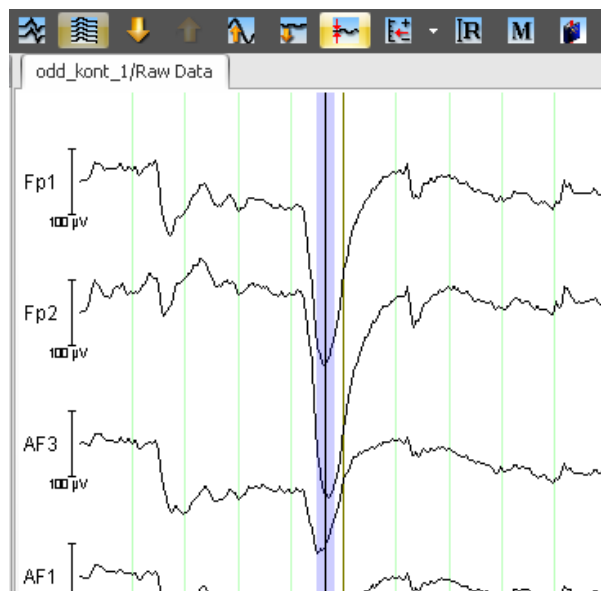


FIGURE 9—3 SINGLE-POINT HIGHLIGHTING

Click the EEG, hold the mouse button down, and drag the mouse pointer to the left or right to mark a range of the EEG. This is a semi-transparent blue band.

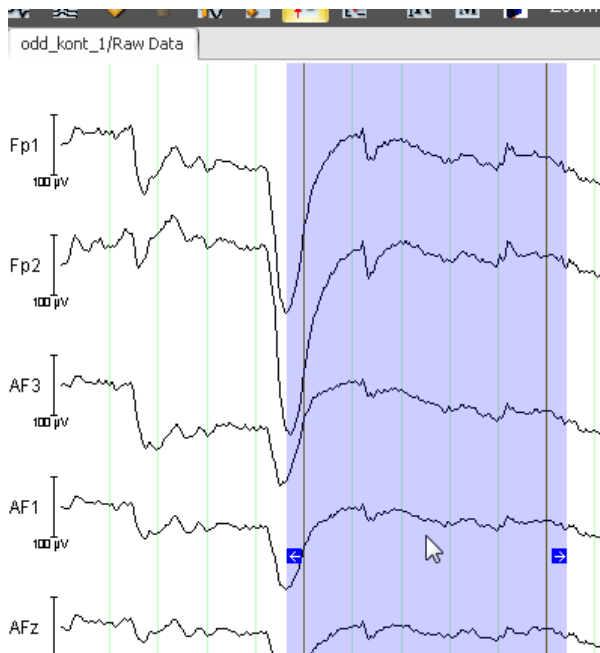


FIGURE 9—4 ARROWS FOR CHANGING THE SIZE OF A HIGHLIGHTED RANGE

To move it, click inside the highlighting, hold the mouse button down, and drag the mouse pointer in the desired direction.

Alternatively, you can use your computer's *left arrow* and *right arrow* keys to move the highlighting.

In the case of the grid view and the head view, the highlighting is only ever displayed for one channel. You can move highlighting across channels to a different channel by clicking it, holding down the mouse button and moving the mouse pointer to the desired channel.

Note that the context menu for selecting transient views appears when you click the EEG and release the mouse button. Click **Cancel** to close the context menu. (You will find detailed information on transient transforms in chapter 14.)

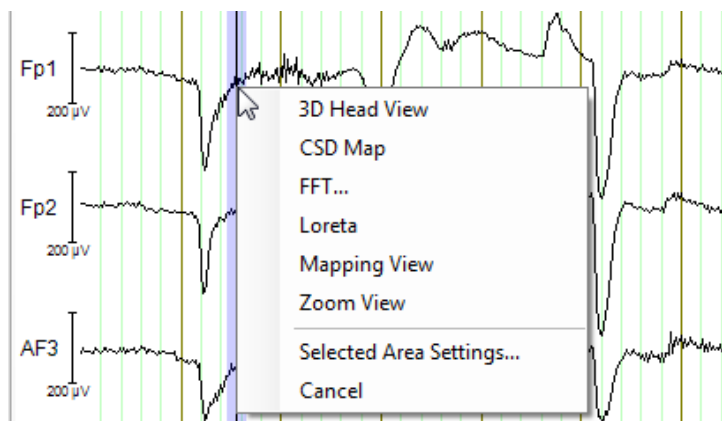


FIGURE 9—5 SINGLE-POINT HIGHLIGHTING INCLUDING THE CONTEXT MENU FOR TRANSIENT TRANSFORMS

You change the width of the highlighting by moving the mouse pointer over it. Two blue arrows appear on its edges. Grab an arrow, and drag the mouse pointer in the required direction.

When you drag the arrows of a single-point highlighting band, it turns into a range highlighting band.

To delete highlighting, items from the **View Toolbox** or similar items from the EEG, press your computer's **Escape** key. Note that this deletes the currently active item.

You can drag items from the **View Toolbox** to the EEG graph by clicking the desired tool, holding down the left mouse button and dragging it to a channel of the EEG. The current target channel is highlighted in orange in the view. You will find detailed information on working with the **View Toolbox** in section 5.1, "The new user interface of the Analyzer".

If you have dragged a tool onto the graph, it is connected to the graph by means of an interactive element. In the case of the mapping tool, for example, this is a small highlighted range. When this highlighting is active, it can be moved and resized in the same way as the semi-transparent bright blue highlighting described above.

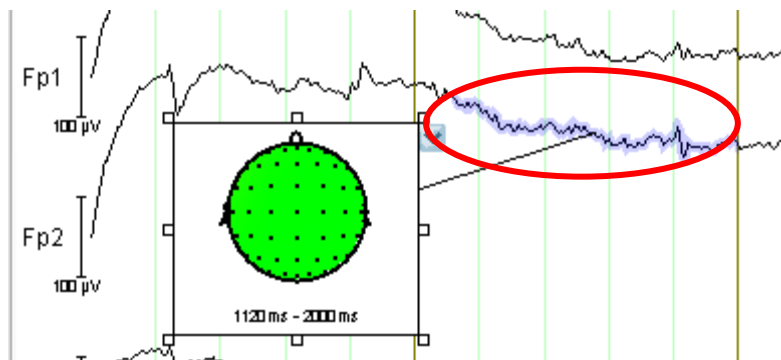


FIGURE 9—6 EEG GRAPH WITH DELTA TOOL AND MAPPING TOOL (INCLUDING RANGE HIGHLIGHTING)

The context menu of the transient transforms also contains the **Selected Area Settings...** command, which allows you to make the following settings:

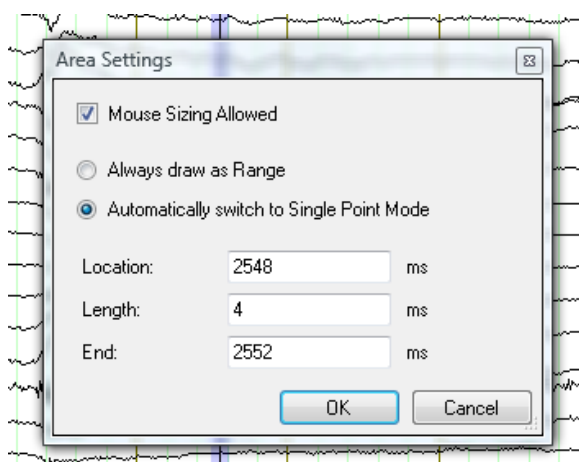


FIGURE 9—7 AREA SETTINGS DIALOG BOX

You can make the following settings:

- If you select the **Mouse Sizing Allowed** check box, you allow the highlighting to be resized using the mouse.
- If you select the **Always Draw as Range** radio button, a range is highlighted.
- If you select the **Automatically switch to Single Point Mode** radio button, a single point is highlighted.
- In the text boxes in the lower part of the dialog box, you can change the position (**Location, End**) and length (**Length**) of the highlighting. Note that the times you specify are rounded to the nearest data point.

9.2 The EEG views in detail

9.2.1 The butterfly view

The butterfly view displays all the EEG channels overlaid over each other. The view allows you, for example, to estimate peaks after data averaging: In this case, the view lets you very easily detect the points in the EEG at which there is activity (figure 9—8).

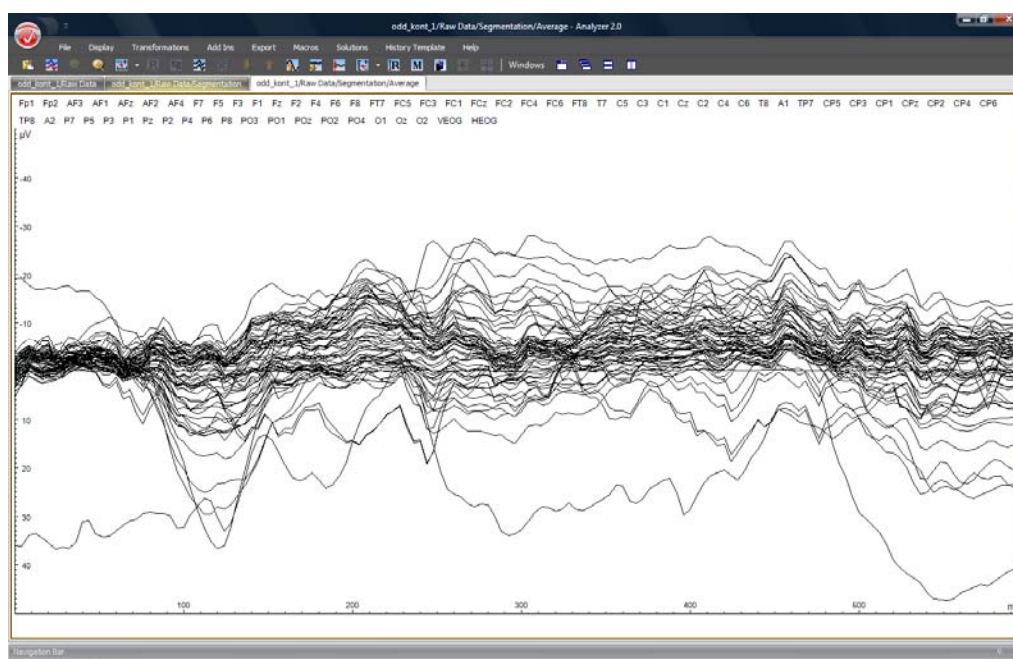


FIGURE 9—8 BUTTERFLY VIEW, AVERAGED EEG

The channel names are listed in the upper part of the view.

If you move the mouse pointer over a channel graph, it is highlighted in orange. At the same time, a small box appears around the channel name at the top of the view to indicate which channel is currently under the mouse pointer. Boxes and orange highlighting also appear when you move the mouse pointer over a channel name in the list.

If you click a channel name, the corresponding channel is deactivated or activated again. Alternatively, you can deactivate the channel currently highlighted by pressing the **Shift** key and the left mouse button. The channel name of a deactivated channel is struck through.

Range highlighting works as described in section 9.1.

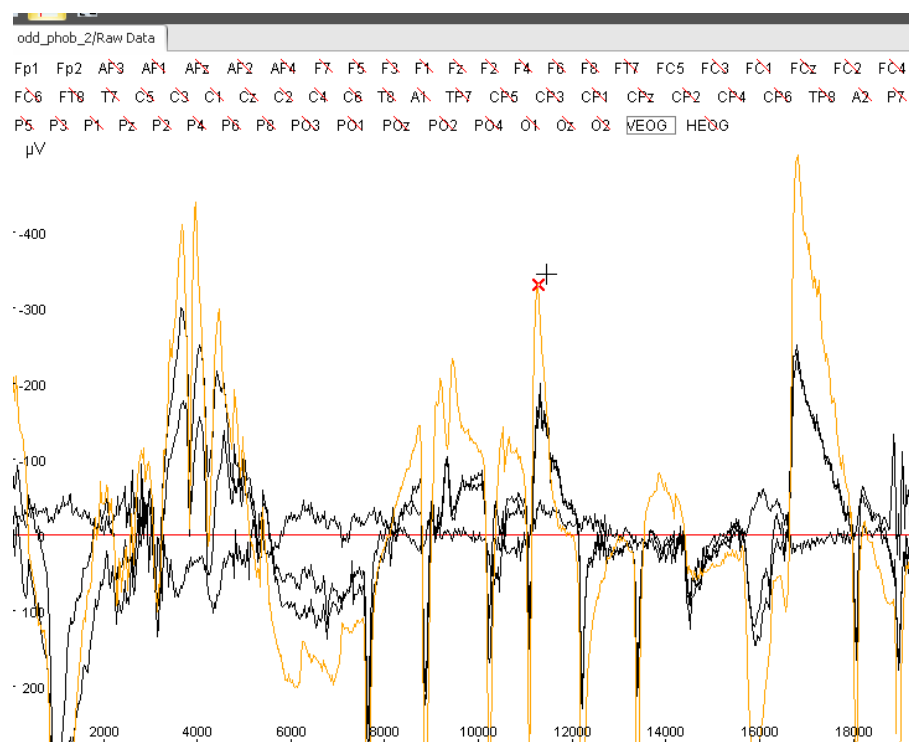


FIGURE 9—9 BUTTERFLY VIEW, CHANNEL SELECTION AND HIGHLIGHTING

You will find a detailed description of the configuration options for the butterfly view in section 7.3.2, “Category-related view settings”.



9.2.2 The grid view

The grid view arranges the channels in a grid.

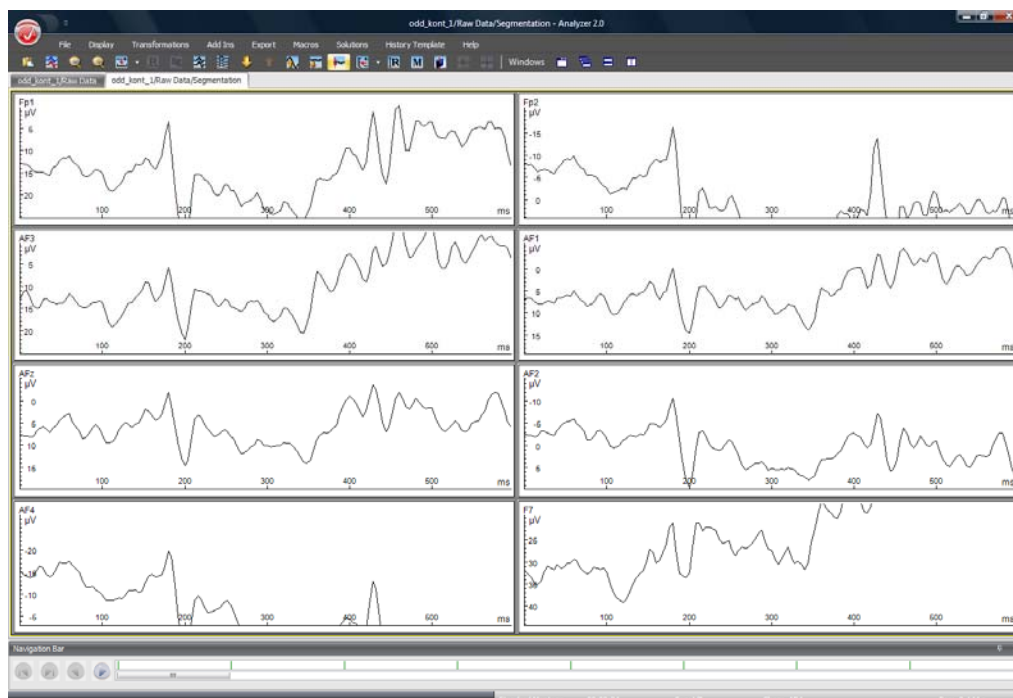


FIGURE 9—10 GRID VIEW

The display of the EEG in the grid view depends on the montage selected. In the case of the standard montage, the channels of the data set are distributed automatically to the rows and columns of the grid. In user-specific montages it is possible to specify which channels are to appear in which grid cells or which grid cells are to remain free.

The grid view also allows overlays to be displayed (overlying of different channels). To do this, you use the mouse to drag a channel to another channel. When a red frame appears, you release the mouse button. You will see two overlaid channels. The moved channel continues to remain in its original position. You can repeat this procedure as often as you like with different channels.

Note that you can get hold of the channels by clicking the channel name or a point in the corresponding grid cell that is sufficiently far away from the graph. The mouse pointer takes the form of a hand or an arrow.

If there are one or more overlays, the **Clear Overlays** button is added to the view. You can use this button to remove the overlays again.

You will find detailed information on the overlaying of data sets in section 9.3, “Overlaying of different data sets”.

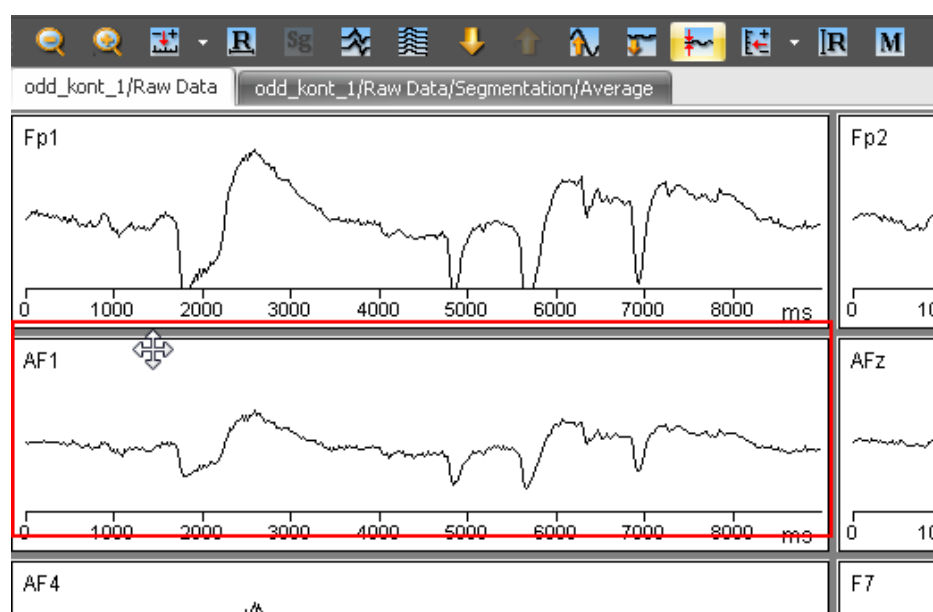


FIGURE 9—11 OVERLAYING OF TWO CHANNELS BY MEANS OF DRAG AND DROP

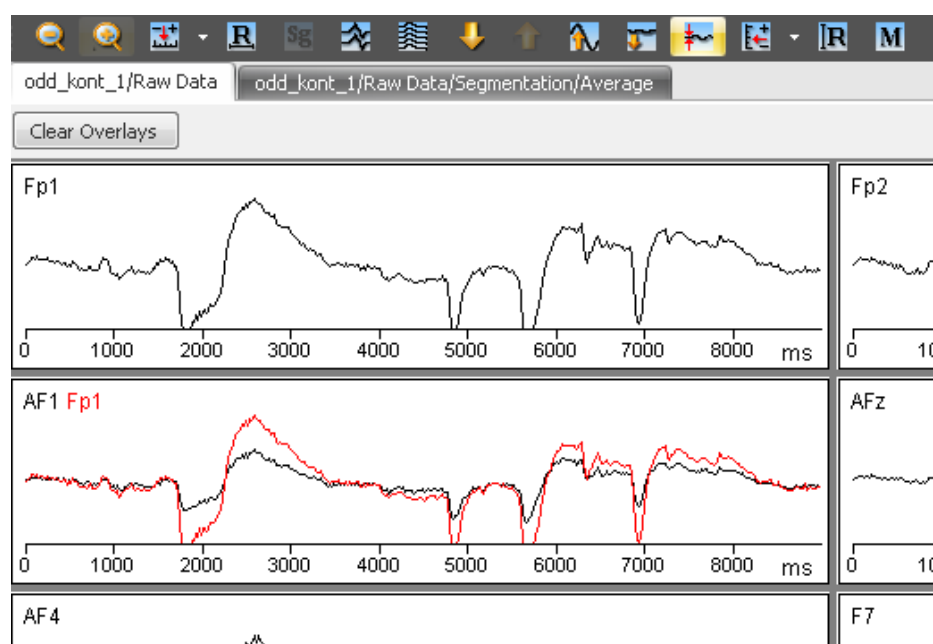


FIGURE 9—12 OVERLAYING OF CHANNELS Fp1 AND AF1

You will find a detailed description of the configuration options for the grid view in section 7.3.2, “Category-related view settings”.



9.2.3 The head view

The head view displays the channels in separate windows arranged in the shape of a head. The windows are positioned at the coordinate position of the associated channel.

Channels that do not have any valid head coordinates, or have coordinates that are not visible on the head, are displayed along the left-hand border of the view. If you used electrode names on the 10/10 or 10/20 principle when recording the EEG, the program should have this information. However, if you used other channel names, you can use the Edit Channels transform to enter the correct coordinates. You will find detailed information on this in section 12.1.6, “Edit Channels”.

You can change the head’s direction of view in the **Default View Settings** dialog box. You do this in the **Direction** group box on the **Maps** tab (see section 7.3.2, “Category-related view settings”).

If you click the channel name or a point in the window that is far enough away from the graph, the desired window is activated. You can move the window by holding down the mouse button.

An active window has a total of 8 handles (small rectangles) on its borders that you can use to resize the window. If you hold down the **Shift** key while you resize a window, the resizing is also applied to the other windows when you release the mouse button.

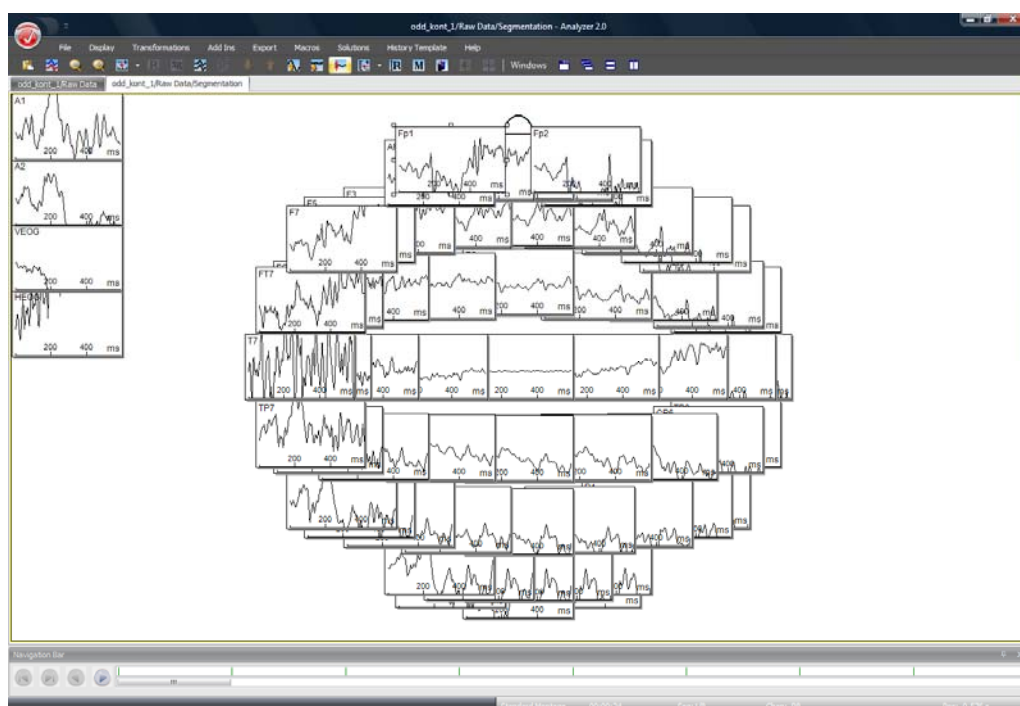


FIGURE 9—13 HEAD VIEW

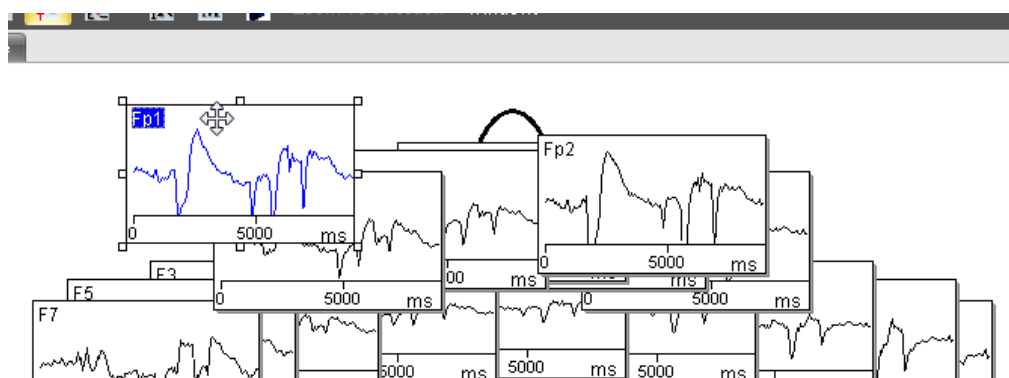


FIGURE 9—14 CHANGING THE POSITION OF AN ACTIVE WINDOW

If you have changed the position of a number of channels and then want to return them to their original positions, right-click any point in the view and choose the **Reset all Channel Positions** command from the context menu that appears. The **Reset Position of Active Channel** command returns only the active channel to its original position.

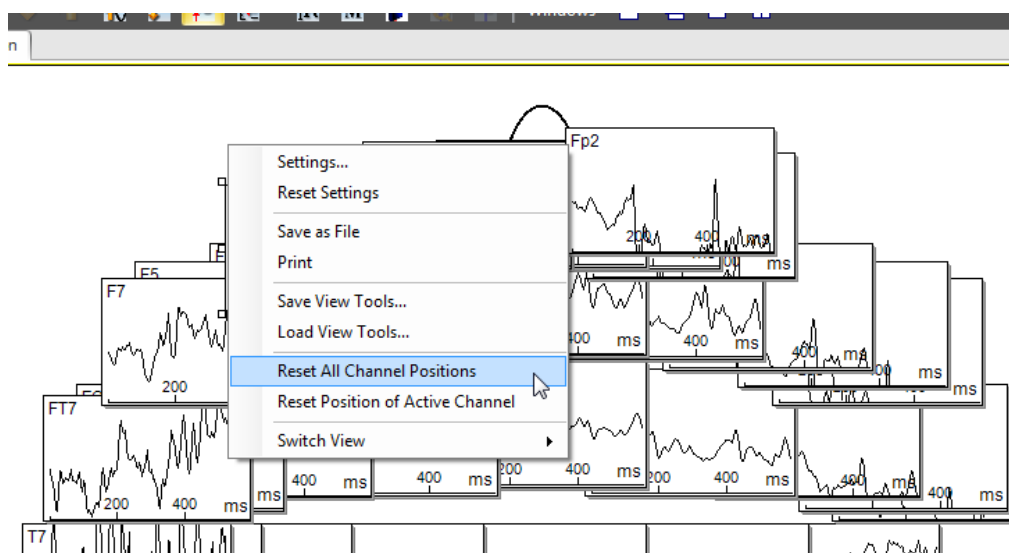


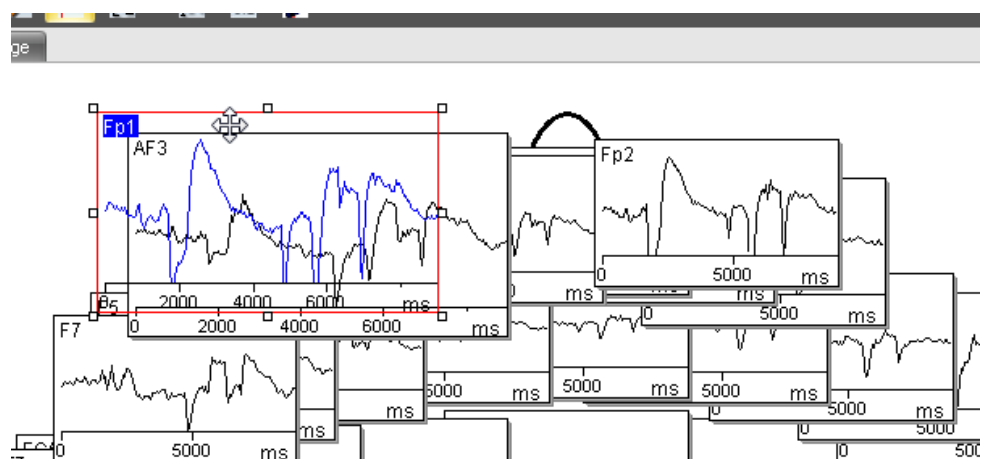
FIGURE 9—15 CONTEXT MENU FOR RESETTING THE CHANNEL POSITIONS

If you have resized the channel windows, the windows will no longer be centered exactly over the associated electrodes. You can also use the **Reset All Channel Positions** command to correct this.

TIP

If you select one or more channels by clicking their names followed by a double-click, these channels are displayed in a grid.

You can create an overlay by dragging one channel to another channel and then releasing the mouse button. The channel you moved becomes transparent and its frame turns red until you release the mouse button.

FIGURE 9—16 OVERLAYING OF CHANNELS Fp1 AND AF₃

You will find a detailed description of the configuration options for the head view in section 7.3.2, “Category-related view settings”.



9.2.4 The mapping view

The mapping view creates topographic maps that display the voltage distribution on the head in the time or frequency domain. The maps are displayed in windows arranged next to each other.

Along the lower border of the view there is a scale that applies to all maps. In addition, the time domain is indicated for each map. For a time domain you can display the head in different directions simultaneously.

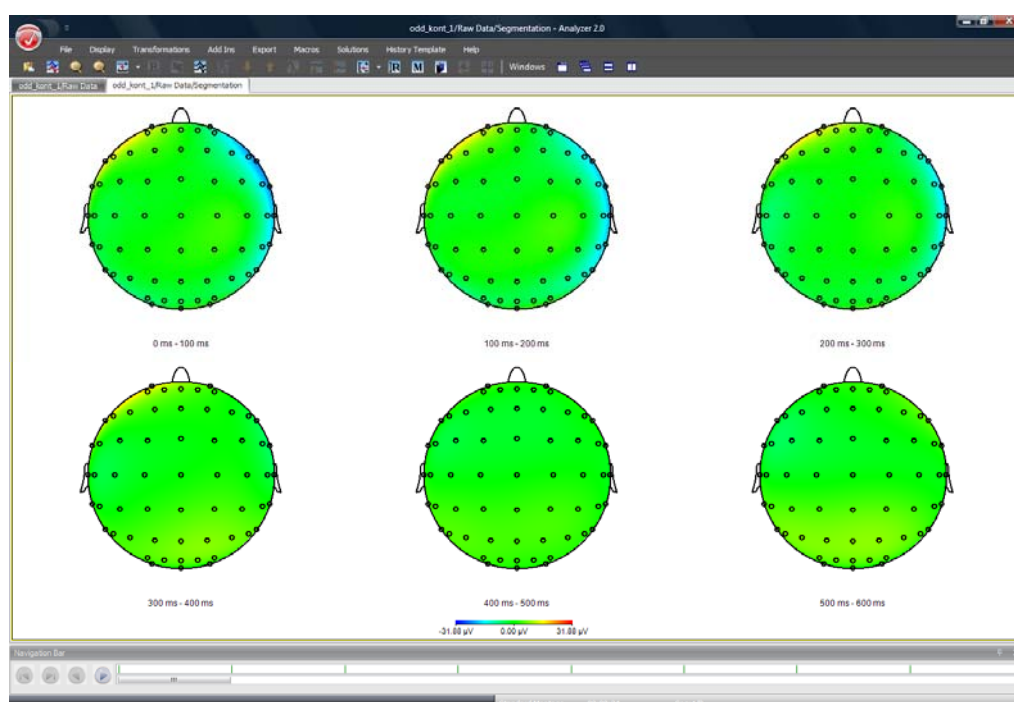


FIGURE 9—17 MAPPING VIEW

In order to generate the map, the program requires information about the position of the electrodes. If you used electrode names on the 10/10 or 10/20 principle when recording the EEG, the program should have this information. However, if you used other channel names, you can use the Edit Channels transform to enter the correct coordinates. You will find detailed information on this in section 12.1.6. You will find information on the coordinate system used in Appendix B.

You will find a detailed description of the configuration options for the mapping view in section 7.3.2, “Category-related view settings”.



You will find detailed information on the methods and algorithms used for mapping in section 12.7.4, “Topographic Interpolation”.

9.2.5 The standard view

The standard view offers you all the standard display options. These include the highlighting and selection of channels, the display of separate channels or a selection of channels, the selection of data ranges (single-point selection and range selection), the resizing and repositioning of highlighting and the use of the tools from the **View Toolbox**.

You will find a more detailed description of these functions in section 9.1.

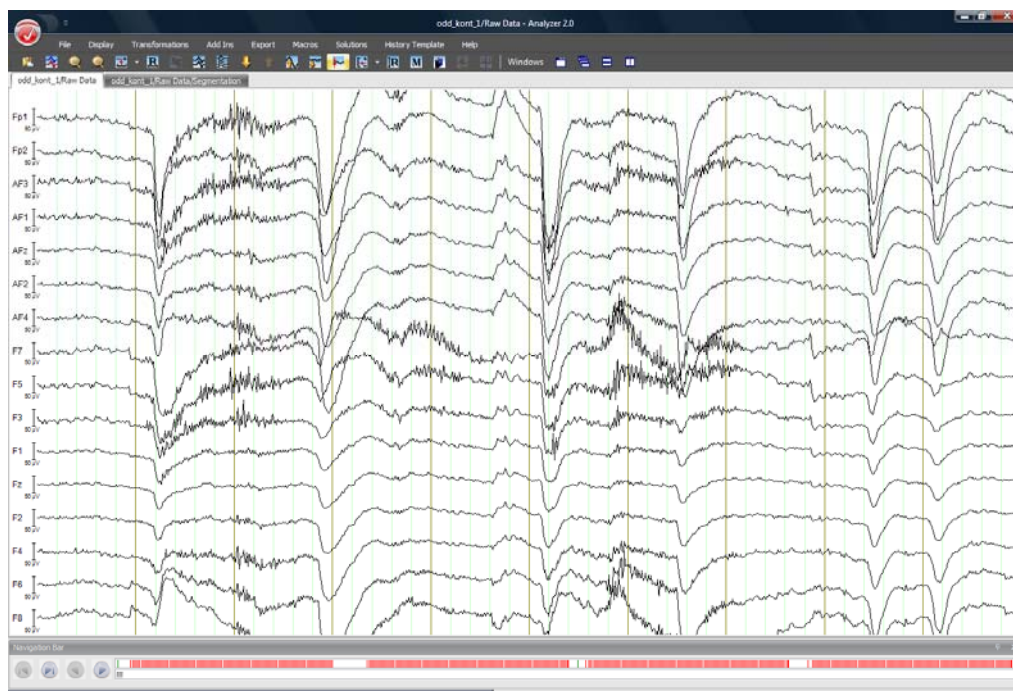


FIGURE 9—18 STANDARD-VIEW

You will find a detailed description of the configuration options for the standard view in section 7.3.2, “Category-related view settings”.



9.2.6 The time-frequency view

The time-frequency view is for displaying data in which a value – typically μV – belongs to a point in time and frequency. This view is available in the form of standard, grid and head views.

The time is on the x-axis, and the frequency on the y-axis. Every point is assigned a color that corresponds to its voltage value, for example.



TIME-FREQUENCY
STANDARD VIEW

At the bottom of the view there is a color scale for displaying the voltage values, for example.

If you select only a few channels to be displayed, line charts appear along the borders of the channel window. The line charts display the values along cross-sections that run parallel to the x- or y-axis. The chart to the right of the channel window displays volts over hertz, for example, while the chart under the channel window displays volts over milliseconds, for example.

The green cross in the channel window indicates the location of the cross-section in the line charts. If you click a point in the window, the cross jumps to the point you click.

If you hold the mouse button down and drag the mouse pointer across the window, the line charts are redrawn accordingly.

The **Scale Up**  and **Scale Down**  buttons change the scaling of the two line charts. The color scale remains unaffected by this. You specify the settings for the color scale in the standard view settings. You will find detailed information on this in section 7.3.2, “Category-related view settings”.

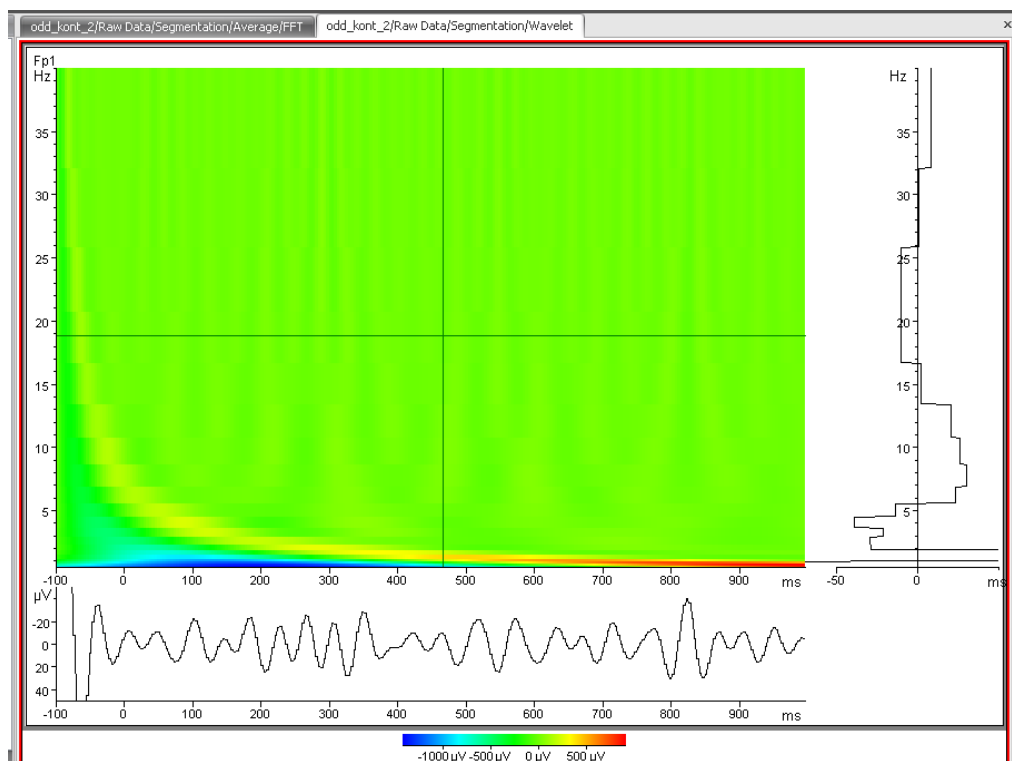


FIGURE 9—19 TIME-FREQUENCY STANDARD VIEW

The display and functions of the time-frequency head view are the same as for the head view.

TIME-FREQUENCY HEAD
VIEW

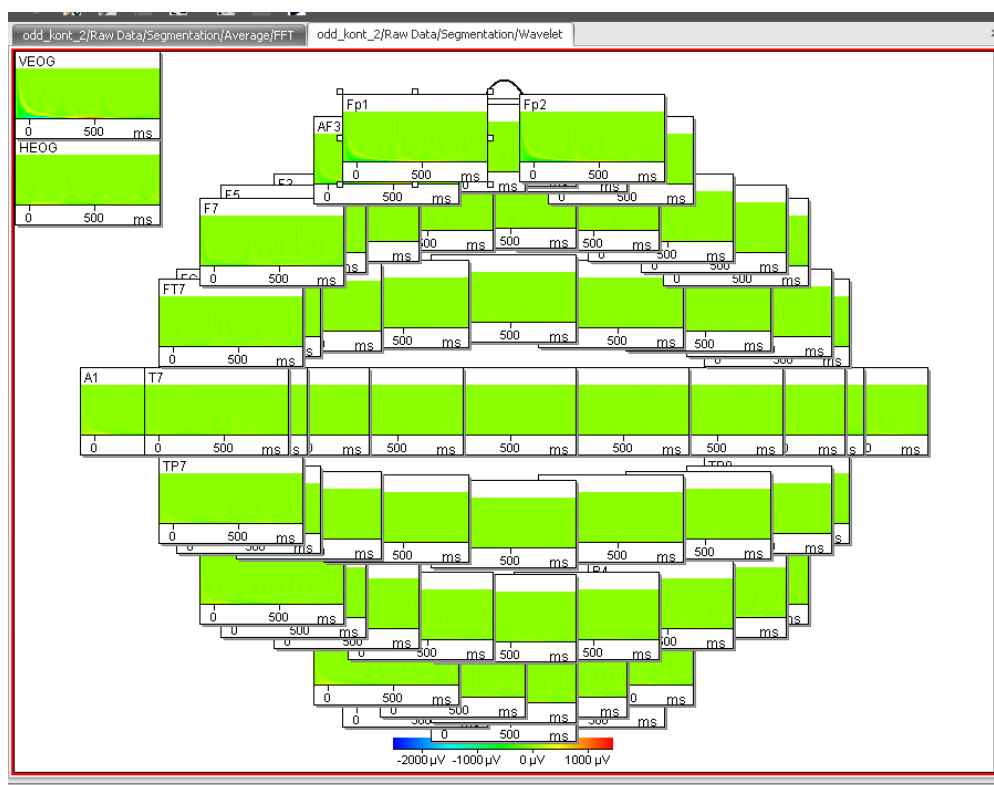


FIGURE 9—20 TIME-FREQUENCY HEAD VIEW

The display and functions of the time-frequency grid view are the same as for the grid view.

TIME-FREQUENCY GRID
VIEW



FIGURE 9—21 TIME-FREQUENCY GRID VIEW

9.2.7 The 3D view

You can use the 3D map view instead of the two-dimensional map. The 3D view projects the map onto a head.

The settings are the same as for the 2D map view. In addition, you can rotate the head displayed and select an alternative head definition file. To do this, move the mouse over the head, hold down the left mouse button, and move the mouse pointer. The head rotates.

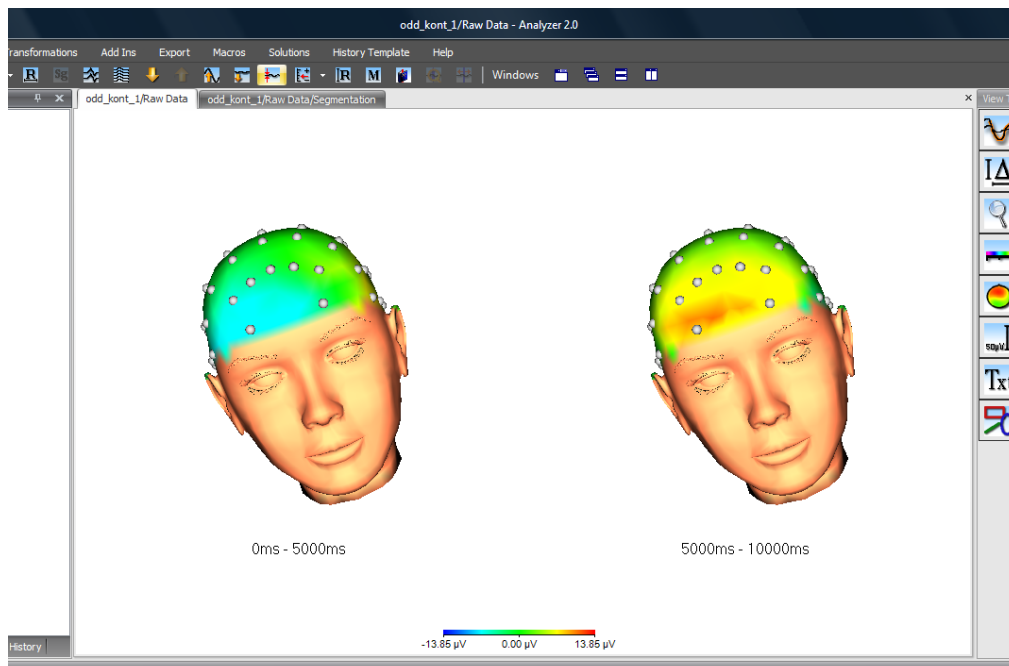



ABB. 9—22 3D VIEW

In the view settings of the 3D view, you can also select the head displayed from several head definitions.

You will find a detailed description of the configuration options for the 3D view in section 7.3.2, “Category-related view settings”.



9.3 Overlaying of different data sets

To overlay multiple complete data sets, click the  **Overlay Data Set** button on the toolbar. The **Overlay** dialog box appears.

Note that this function is only accessible for data sets that have the same sampling rate and duration. The number of channels, on the other hand, does not necessarily have to be identical. The view checks the channel names and only overlays channels with the same name.

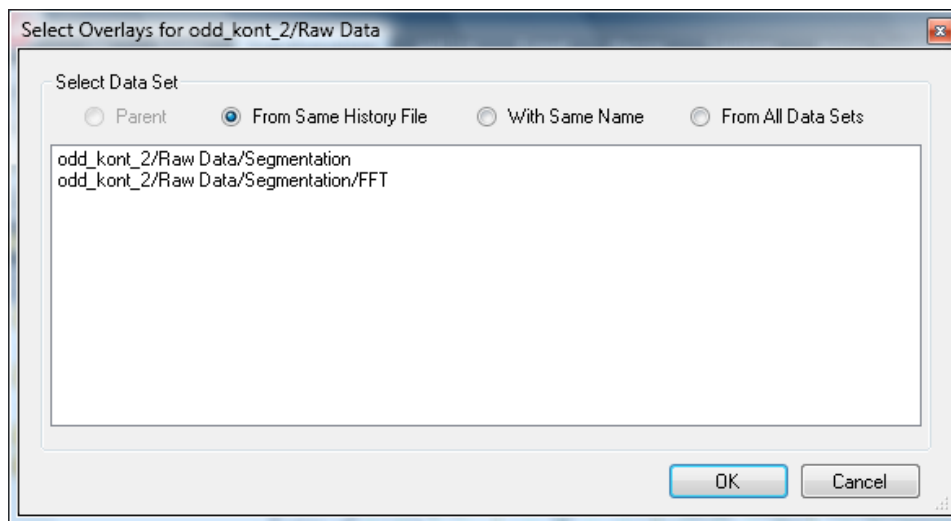


FIGURE 9—23 OVERLAY DIALOG BOX

This dialog box allows you to select one or more data sets from the entire workspace. The selection is made on the basis of the following four criteria:

- **Parent** displays the data set from which the current data set was calculated. If the current data set represents the raw data EEG, this option is not accessible.
- **From Same History File** displays all the data sets in the current history file.
- **With Same Name** lists all the data sets in the workspace that have the same name as the current data set.
- **From All Data Sets** lists all the data sets in the current workspace.

If you select one or more data sets with the same length and sampling rate as the current data set, the channels of the selected data sets are displayed overlaid. If there are one or more overlays, the **Clear Overlays** button is added to the upper-left part of the view. You can use this button to remove the overlays again.

You can also overlay data sets by dragging and dropping them. To do this, use the mouse to select from the History Explorer the required data set, hold down the left mouse button, and drag the data set to the view. Then release the left mouse button. The conditions described in the previous paragraph again have to be met in order to implement the overlay.

9.4 Additional view functions

The **Views** group on the **File** tab contains the following functions:

VIEWS GROUP, FILE TAB

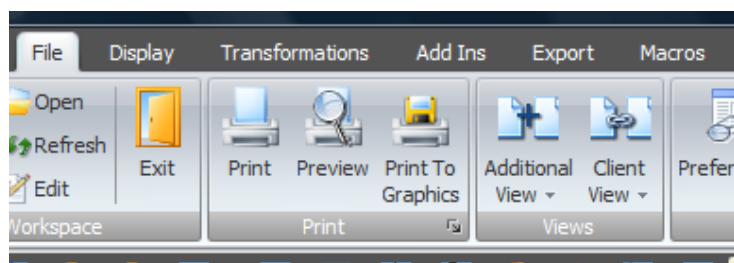


FIGURE 9—24 VIEWS GROUP ON THE FILE TAB

The **Additional View** drop-down list allows you to display additional views for the active history node. The newly selected view appears in an additional window. The same node is thus displayed in multiple view windows.

The **Client View** drop-down list works in the same way as the **Additional View** drop-down list, except that, in this case, navigation of the newly selected view is linked to that of the original view, and navigation is only possible in the original view. In figure 9—25, the mouse pointer is in the newly selected butterfly view. You can see that the toolbar and navigation bar are grayed out (inactive).

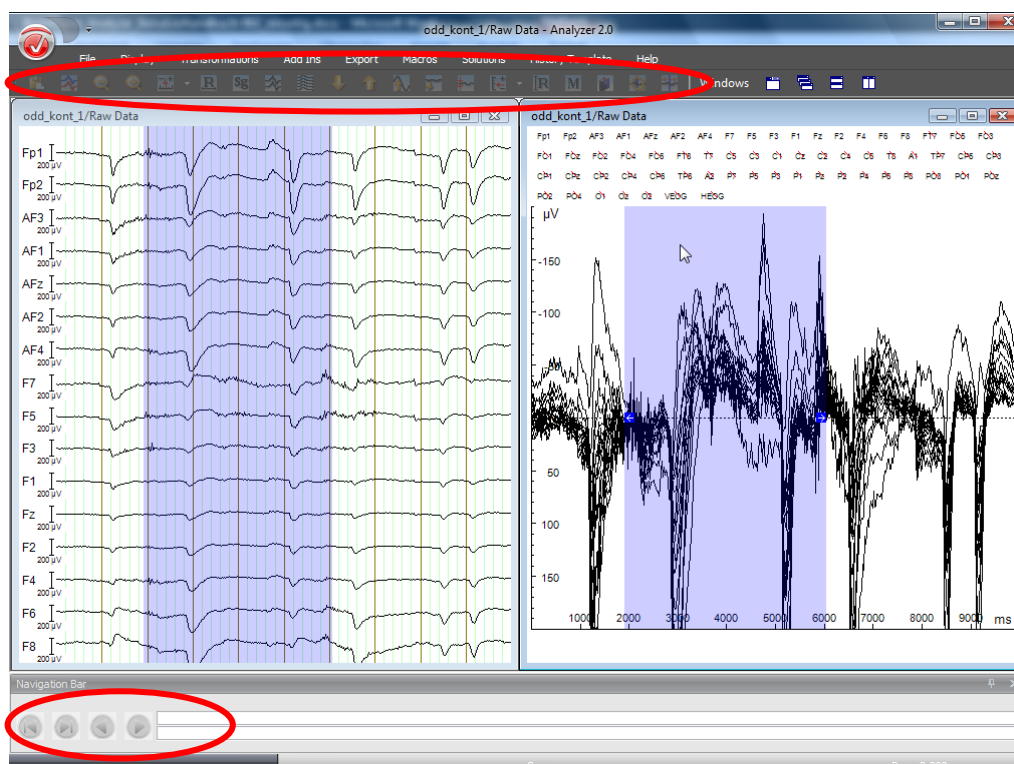


FIGURE 9—25 CLIENT VIEW

To display the view context menu, right-click any point in the view.

VIEW CONTEXT MENU

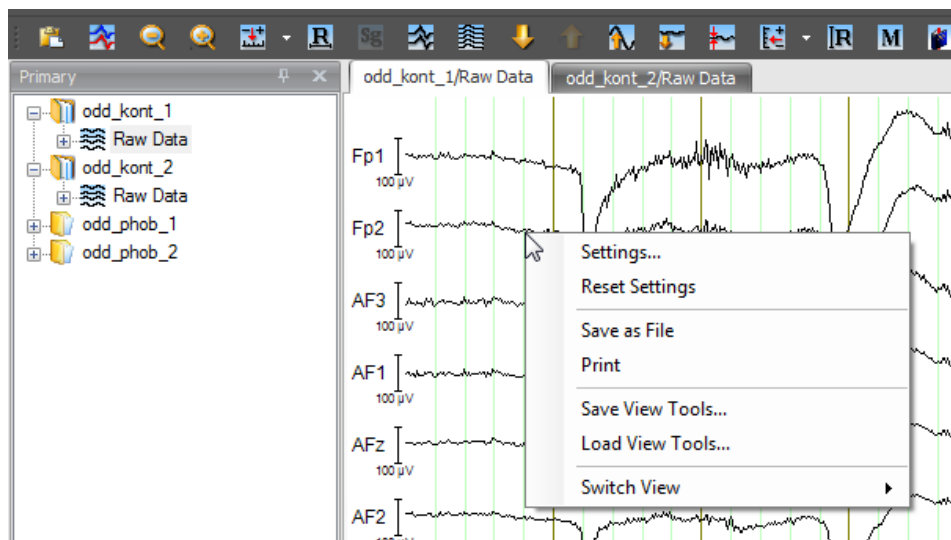


FIGURE 9—26 VIEW CONTEXT MENU

Das Kontextmenü enthält die folgenden Einträge:

- **Settings...** displays the node-specific view settings. You will find detailed information on configuring the view settings in section 7.3, “Configuring the EEG view settings”.
- **Save as File** saves the view as a file. The graphics formats EMF, BMP, PNG and JPEG are available to you.
- **Print** opens the dialog box for printing the open view.
- **Save View Tools...** saves all the view tools in the view in a file.
- **Load View Tools...** loads saved view tools from a file and displays them.
- **Switch View** allows you to switch between different views. Unlike the **Additional View** function, this function opens no additional windows. Instead, the new view replaces the currently open view.

As already mentioned in section 7.3, “Configuring the EEG view settings”, a distinction is drawn between the view settings that apply to the view categories and the settings that apply to the current history node. The former are category-related view settings, while the latter are node-specific view settings.

SWITCHING BETWEEN
VIEW CATEGORIES

There are different view categories, such as the standard view, grid view and head view. To display history nodes with different data types, different views are required. However, in most cases these have uniform design features.

The **Switch View** function switches between view categories. In other words, you use this function to select a view category, and the view that suits the current file type is always displayed.



The **Switch View** menu command opens a context menu from which you can select different views. These include the standard view, grid view and head view. The menu groups together views that display nodes with different data types in the same way – the frequency grid view and time grid view, for example – in the same view category. These view categories are also used for category-related configuration (see section 7.3.2, “Category-related view settings”).

If you select a view category under **Switch View**, the program automatically determines the appropriate view in the category for the data type of the node.

For example, the **Switch View > Head View** command in the standard view for time data (figure A1) displays the head view for time data in figure A2.

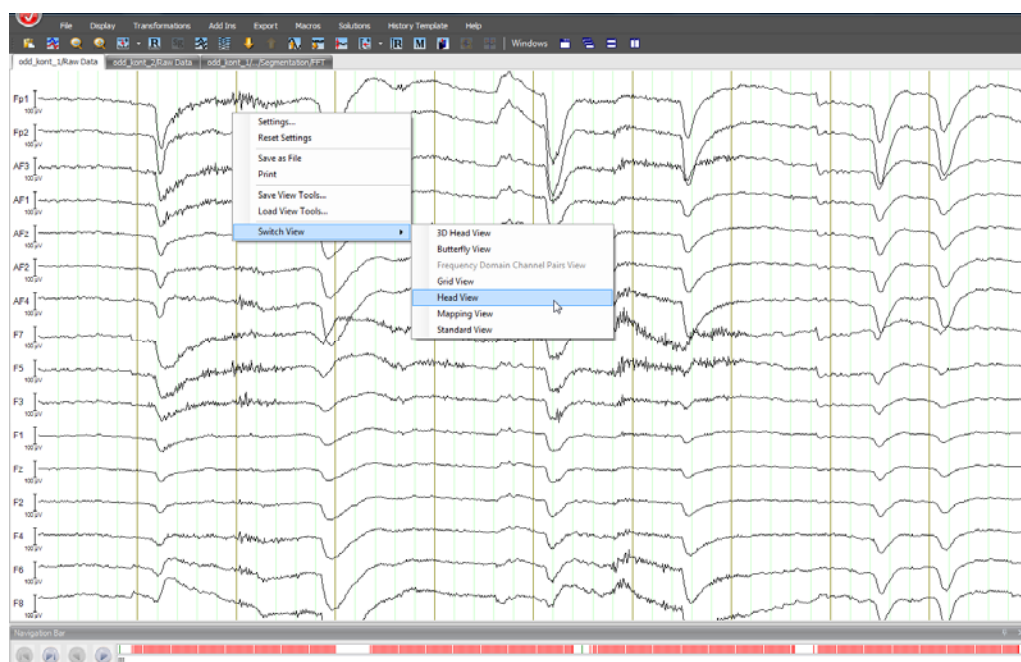


FIGURE 9—27 A1

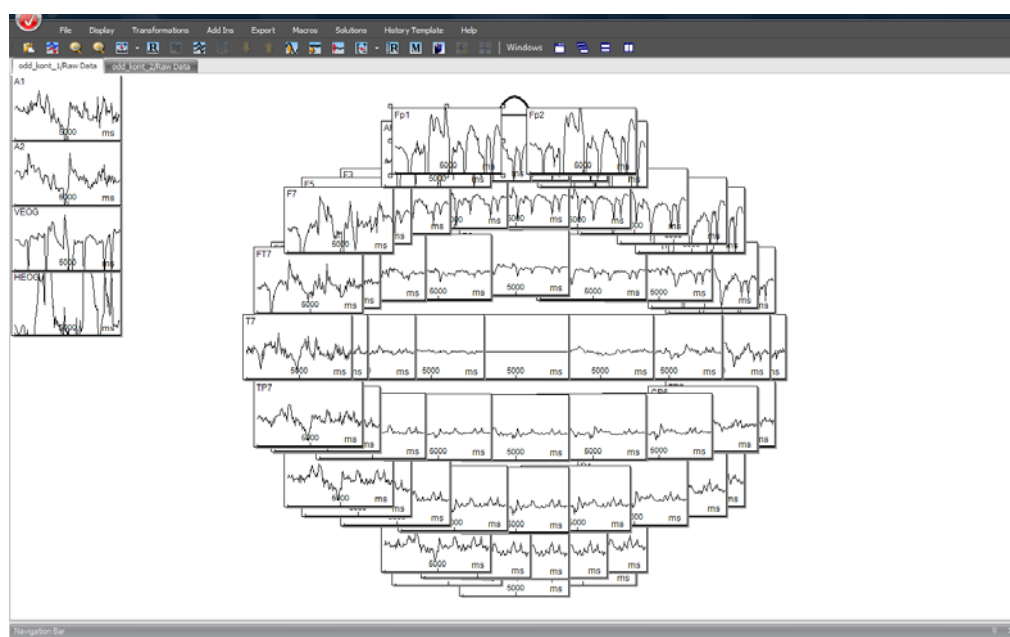


FIGURE 9—28 A2

The **Switch View > Head View** command in the standard view for frequency data (figure B1) displays the head view for frequency data in figure B2.

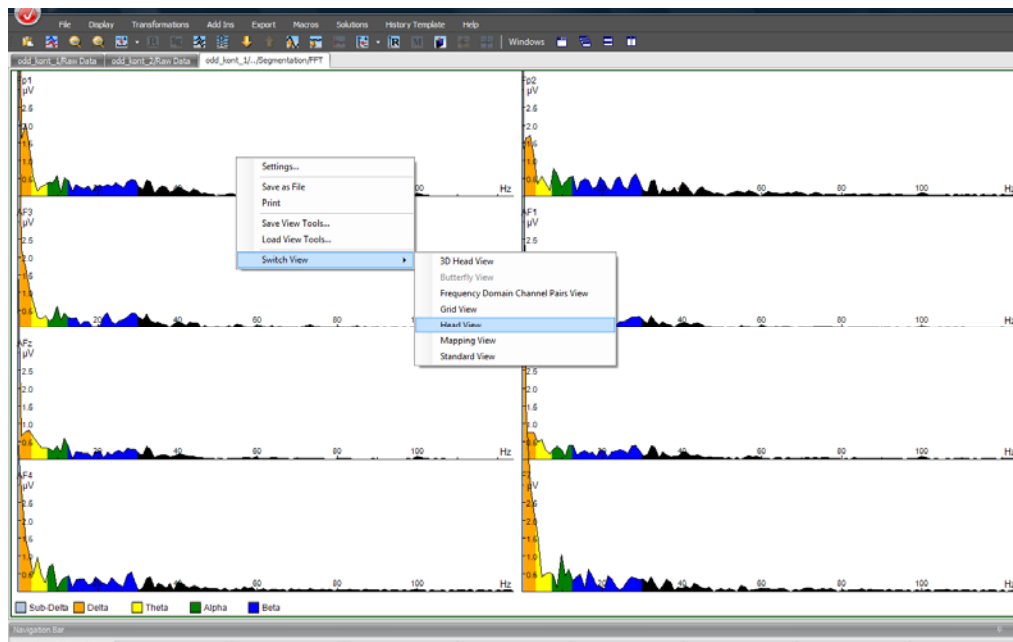


FIGURE 9—29 B1

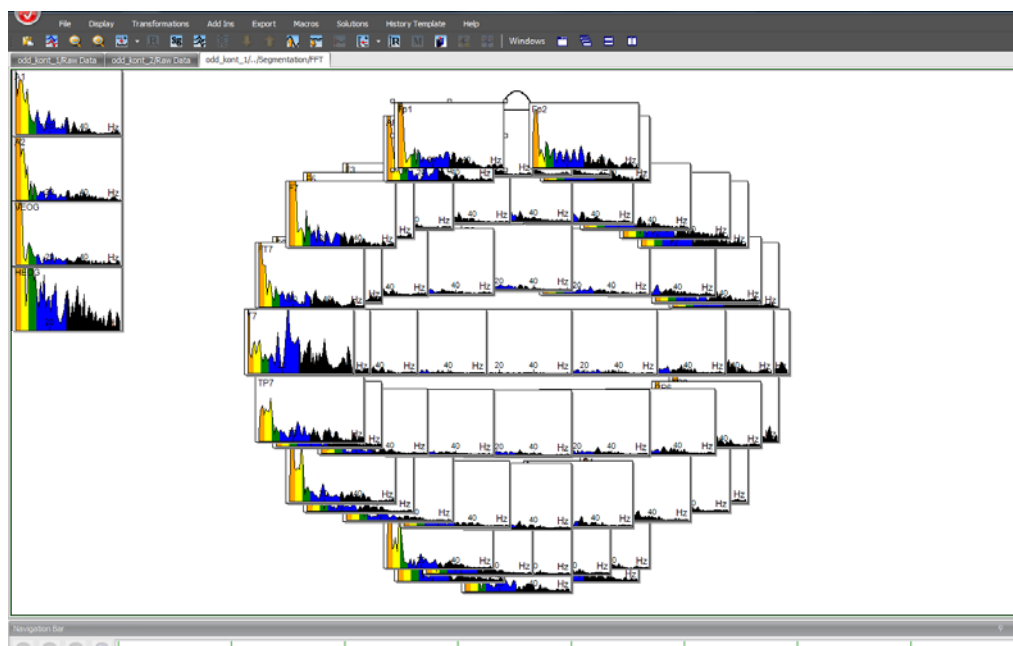


FIGURE 9—30 B2

View categories that do not have a view for the current data type are grayed out on the submenu of the **Switch View** context menu command. This applies, for example, to the butterfly view and frequency data because this view category is available exclusively for data in the time domain (see figure 9—31).

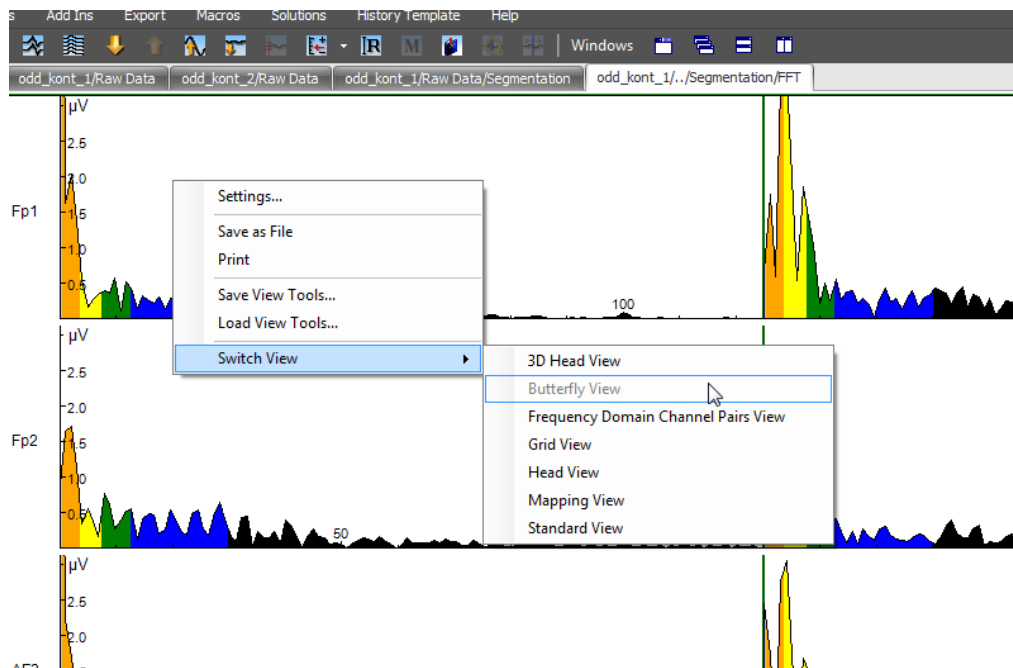


FIGURE 9—31 THE BUTTERFLY VIEW IS NOT AVAILABLE FOR FREQUENCY DATA

10 Automation using history templates

As mentioned in section 5.1, you can transfer an existing processing history from one history file to another. You can also save the processing history in a separate file – known as the history template – and use this template to transfer the processing history automatically to one or more history files.

To create a new history template, choose **New** from the **History Template** group. The **Template Editor** tab appears. This contains the **Root** icon. Open a history file in which you have already executed one or more operations (in our example **odd_kont_1**).

CREATING A HISTORY
TEMPLATE

Use the mouse to drag a data set from the history file to the root node of the history template. This data set and the data sets derived from it are added to the history template. However, it is actually the operation instructions that are transferred to the history template rather than the data itself.

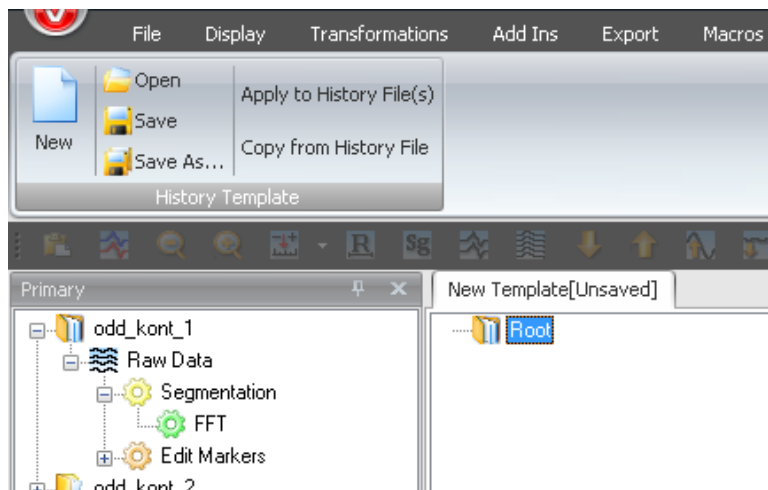


FIGURE 10—1 TEMPLATE EDITOR WITH THE ROOT ICON AND THE COMMAND BUTTONS IN THE HISTORY TEMPLATE GROUP

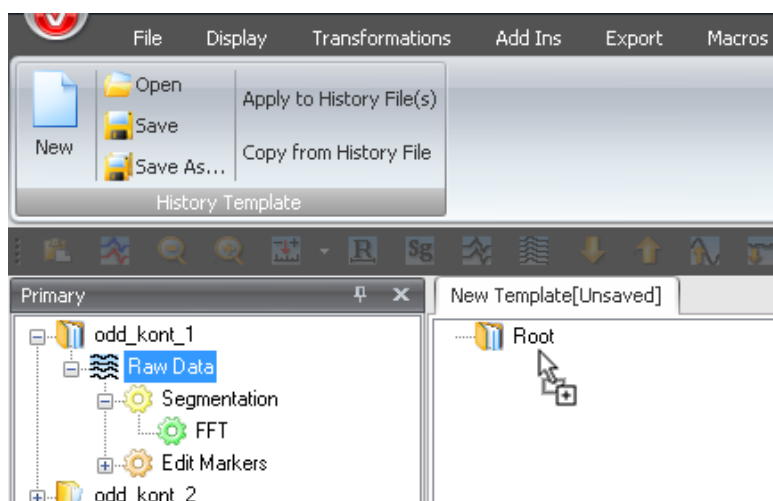


FIGURE 10—2 TRANSFER OF THE DATA BY MEANS OF DRAG AND DROP

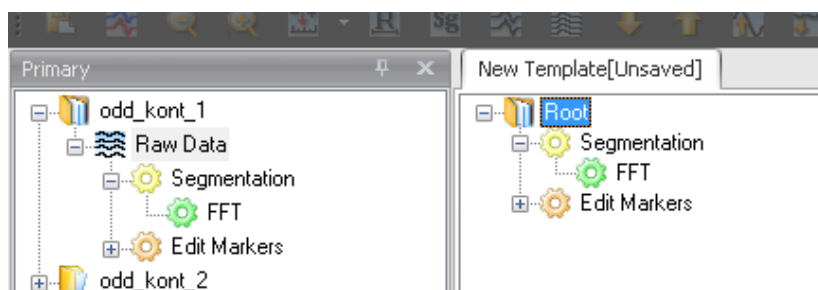


FIGURE 10—3 EXAMPLE OF A HISTORY TEMPLATE

The history structure of the template can be edited in the same way as that of a history file: You can rename or delete nodes, and when a template is open you can use the mouse to drag individual history nodes to history files, thus triggering the corresponding operations.

The **Copy from History File** function copies all the completed nodes of a history file to the template without the need for the history file to be open.

To transfer the history template to an entire set of history files, save the current template as a file by choosing **Save**. Then choose **Apply to History File(s)**. A dialog box appears.

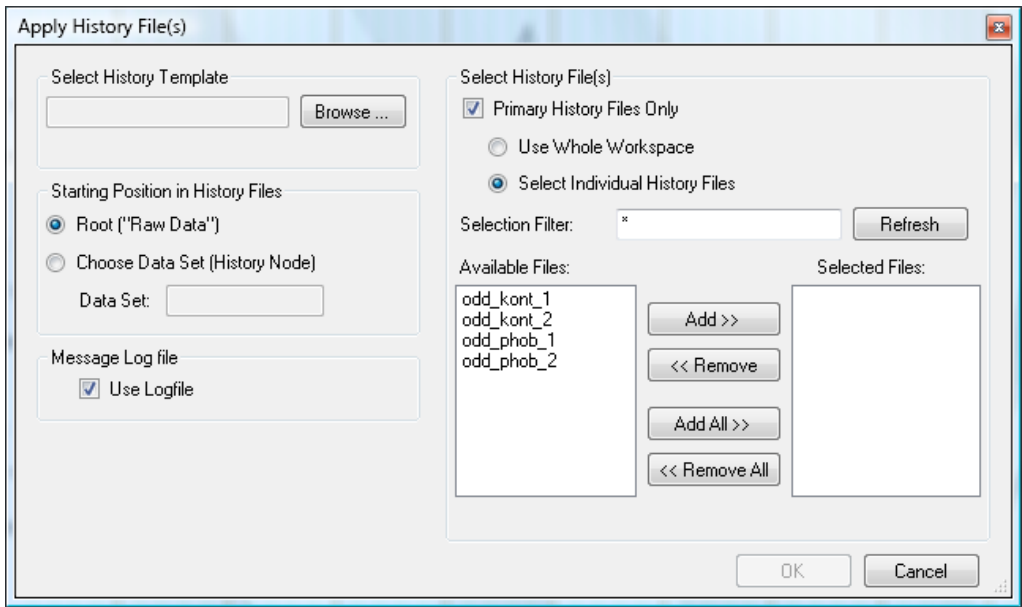


FIGURE 10—4 DIALOG BOX FOR TRANSFERRING HISTORY TEMPLATES

Select a history template under **Select History Template**. If you have not yet closed the window for history templates, the name of the current history template appears in this text box. You can also choose the **Browse** button to select a history template.

SELECT HISTORY
TEMPLATE GROUP BOX

In the **Starting Position in History Files** group box, you specify:

STARTING POSITION IN
HISTORY FILES GROUP
BOX

- Whether the template is to be applied to the initial data set of the history files (**Root ("Raw Data")** radio button)
- Or to a subsequent data set (**Choose Data Set (History Node)** radio button).
- If you select the **Choose Data Set (History Node)** radio button, you specify the name of the data set to which the template is to be transferred in the **Data Set** text box. Note that if there are several data sets with the same name in a history file, only the first one found is taken into account.

If you select the **Use Logfile** check box, all the messages usually output in a dialog are written to a log file. All yes/no questions are automatically answered with “yes” to prevent automatic processing from being interrupted and the program from waiting for input. The log file is displayed on completion of processing.

MESSAGE LOGFILE
GROUP BOX

At this point, you select the history files to which the history template is to be transferred.

SELECT HISTORY FILE(S)
GROUP BOX

- Select the **Primary History Files Only** check box to limit the selection to primary history files.
- Select the **Use Whole Workspace** radio button to include all the files contained in the workspace. If you select the **Select Individual History Files** radio button, on the other hand, you can select specific files.
- In the **Selection Filter** text box, you can then specify a filter. This filters selectable files on the basis of name criteria. An asterisk (*) stands for one or more characters, and a period (.) stands for a single character. If the workspace contains the files "Test1H2", "Test2G" and "Hest5", for example, the string "Test*" filters out the files "Test1H" and "Test2G" (i.e. makes them available). The filter ".est*" accepts all three files. Once you have set the filter, click the **Refresh** button to refresh the selection of available files.
- All the available files are listed in the **Available Files** text box.
- The **Selected Files** text box contains all the selected files.
- To select one or more files or remove them from the list of selected files, you select them and then click the **Add** or **Remove** button. The **Add All** and **Remove All** buttons do the same for all files.

Click **OK** to apply the specified operations to the selected history files. If a history file has already been processed using this template, it is ignored.

Choose **History Template > History Template > Open...** to open an existing history template. To save the history template, choose **Save** or **Save As...**

11 Macros

You can use the Basic interpreter integrated in the Analyzer to create anything from simple automation macros to complex applications. The Basic interpreter accesses the Analyzer via the OLE automation interface.

This interface provides access both to a large number of methods and properties of the ANALYZER and to each data point in each data set (history node) of each history file.

To create a new macro, choose **New...** from the **Macros** group on the **Macros** tab.

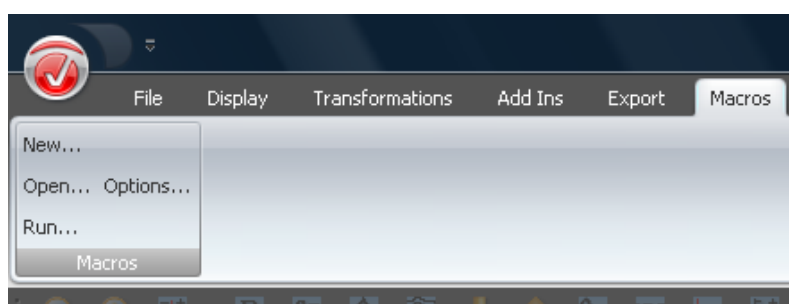


FIGURE 11—1 MACROS TAB WITH COMMAND BUTTONS

The following editing window appears:

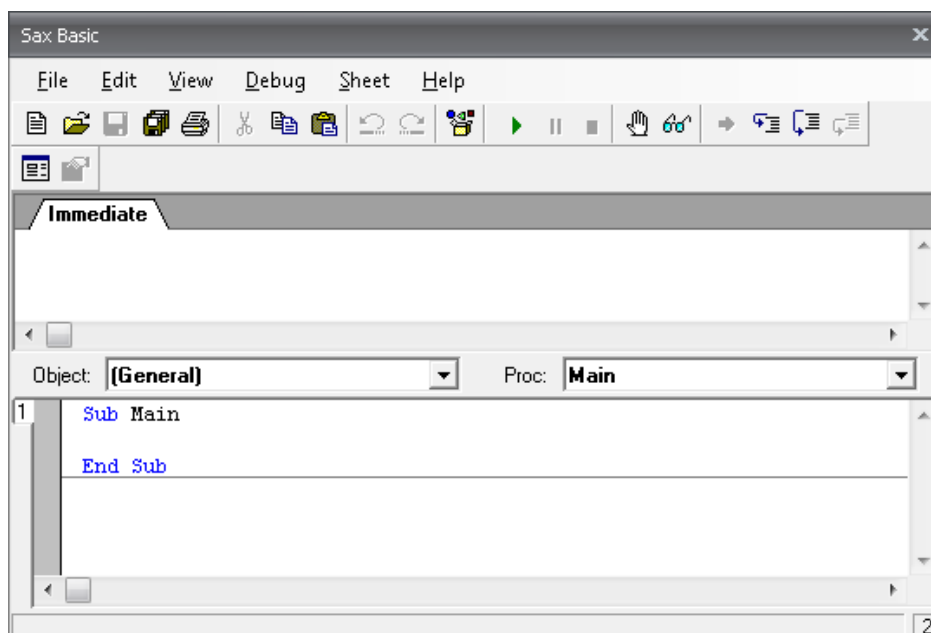


FIGURE 11—2 EDITING WINDOW FOR MACROS

The editing window contains the following two lines:


```
Sub Main
```

```
End Sub
```

You insert the code of the macro between these two lines.

The following small macro opens all the history files and outputs a message before it closes the files again: EXAMPLE OF A MACRO

```
Sub Main
    For Each hf In HistoryFiles
        hf.Open
    Next
    MsgBox "All history files are open"
    For Each hf In HistoryFiles
        hf.Close
    Next
End Sub
```

Enter the code, and then click the **Start/Resume** button . You will get the following intermediate result including the message “All history files are open”:

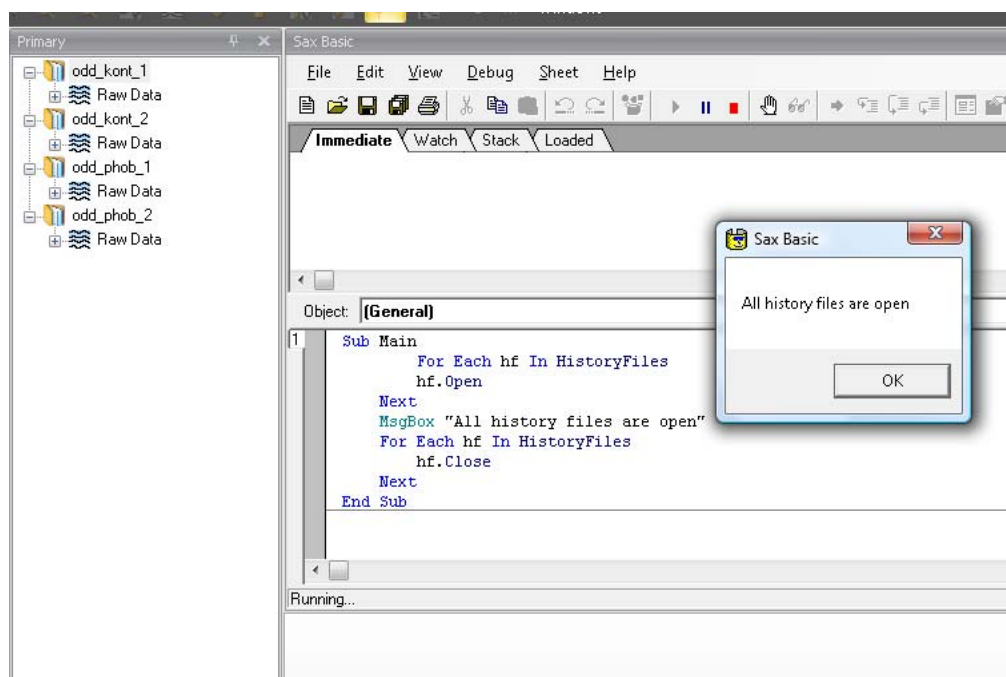



FIGURE 11—3 INTERMEDIATE RESULT OF THE MACRO EXAMPLE

Click the **Save** button  to save the macro and close the editing window.

To open existing macros, choose **Macros > Macros > Open....**

Macros > Macros > Run... allows you to run an existing macro when you are not in the macro editing window. You can then select the macro you want to run.

Alternatively, you can add command buttons for macros to the Ribbon. To do this, choose **Macros > Macros > Options....** The following dialog box appears:

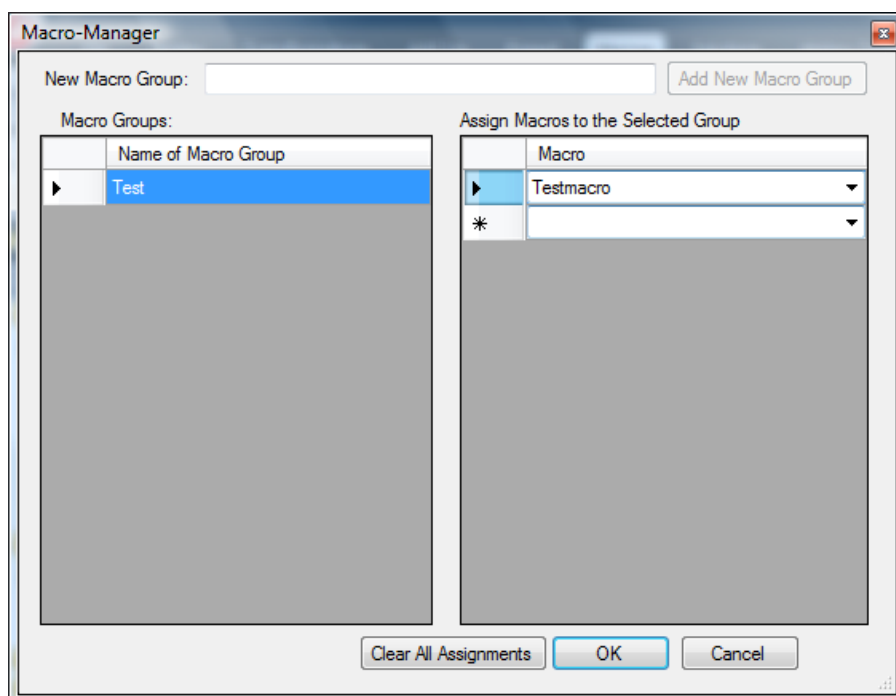


FIGURE 11—4 MACRO-MANAGER DIALOG BOX

In the table on the left (**Name of Macro Group**), specify the name of the macro group. Then choose a macro from the drop-down menu in the table on the right (**Macro**) to be assigned to the group. Once you have done this, you will find the selected macros on the **Macros** tab on the Ribbon (figure 11—5). To delete all the assignments, click **Clear All Assignments**.

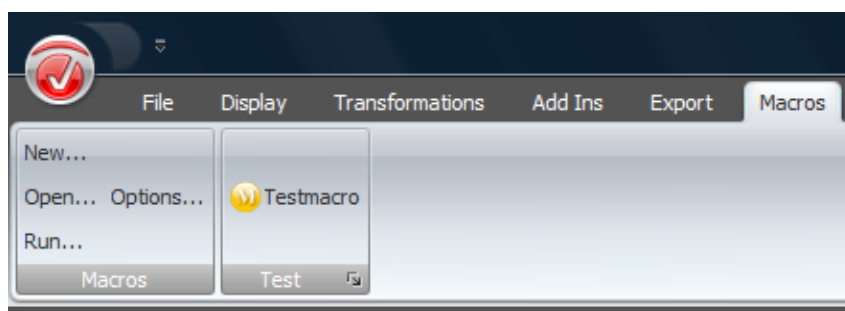


FIGURE 11—5 MACRO ADDED TO THE RIBBON

You can then also call the macros by means of keyboard shortcuts (Alt-M, 1, 2, 3, etc.).

You will find more information on creating macros in the document entitled Vision Analyzer Macro Cookbook and in the Vision Analyzer OLE Automation Reference Manual. You can also get information on the integrated version of Basic by choosing **Sax Basic Help** from the **Help** tab on the toolbar of the editing window.

After changes are made to the OLE components in the Analyzer macro environment, it may be necessary to run the Analyzer once as the administrator so that the system registry can be updated. To do this in Microsoft® Vista, you have to right-click the Analyzer's program icon and choose **Run as administrator** from the context menu.



12 Transforms

There are essentially three types of transform: primary, secondary and transient transforms.

Primary transforms create a history node in a primary history file. Secondary transforms – of which there are only two: the Grand Average transform and the PCA transform – generate secondary history files. Because they only create nodes that cannot be appended to other history nodes, secondary transforms cannot be added to history templates. Transient transforms are for data visualization; their results are only available temporarily.

Chapter 12 describes all the primary and secondary transforms implemented in the Analyzer. The transient transforms are described in chapter 14.

You will find the primary and secondary transforms on the **Transformations** tab.

The structure of this chapter is based on that of the Ribbon: All the transforms in the groups on the **Transformations** tab are described one after the other (going from left to right). Any drop-down lists in a group do not get their own section.



FIGURE 12—1 TRANSFORM GROUPS

12.1 Transforms in the Dataset Preprocessing group

12.1.1 New Reference

The New Reference transform uses the average of selected channels as a new reference.

SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Channel Preprocessing > New Reference**.

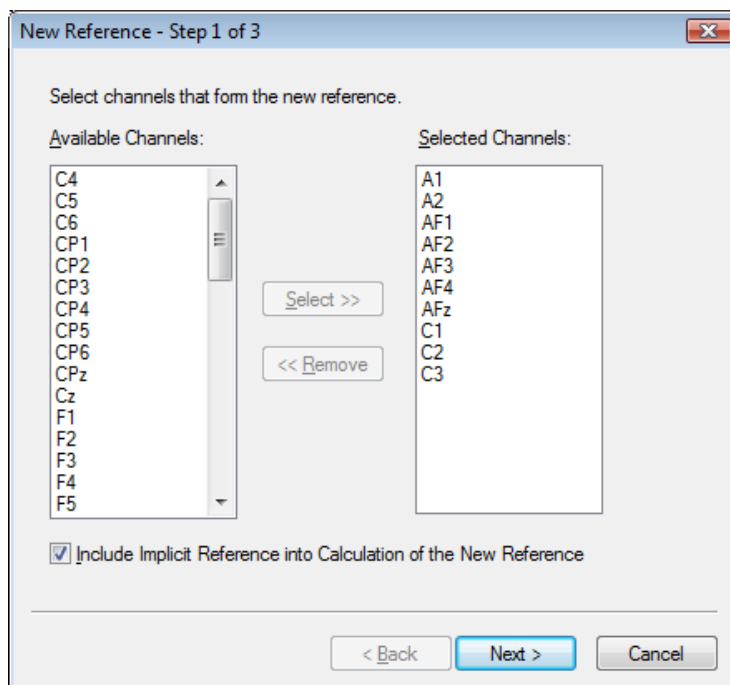


FIGURE 12—2 NEW REFERENCE DIALOG, FIRST PAGE

On the first page of this dialog, you select from the **Available Channels** list box the channels you want to be included in the calculation of the reference. These are transferred to the **Selected Channels** list box.

To select one or more channels or remove them from the list of selected channels, select them and then click the **Select** or **Remove** button.

If you select the **Include Implicit Reference into Calculation of the New Reference** check box, the original reference channel is included in the calculation.

On the second page of the dialog, you select the channels to be referenced (those in the **Selected Channels** list box). In addition, by selecting the **Keep Remaining Channels** check box you can specify that the non-referenced channels are retained.

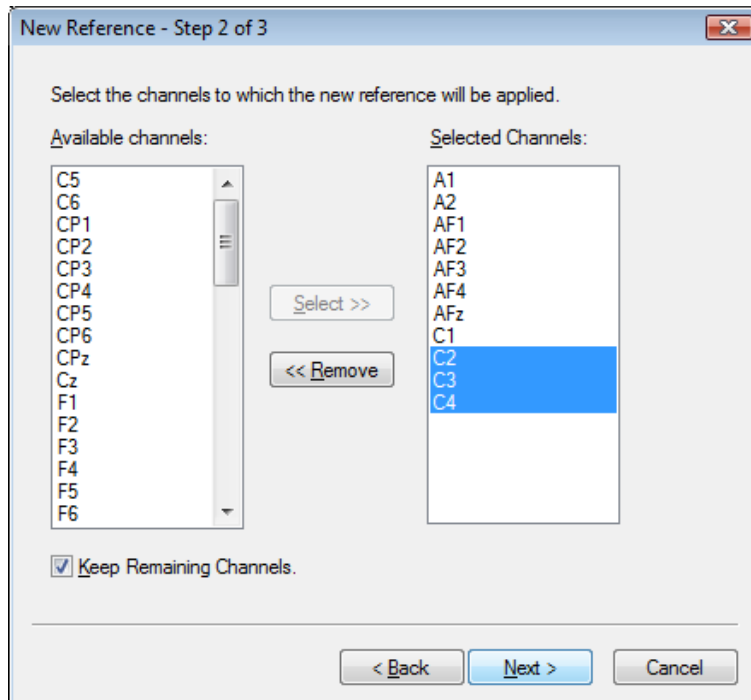


FIGURE 12—3 NEW REFERENCE DIALOG, SECOND PAGE

On the third page of the dialog, you specify the name of the new reference channel in the **Name of New Reference Channel** text box (e.g. “Ears” for A1/A2 reference or “Avg” for averaged reference).

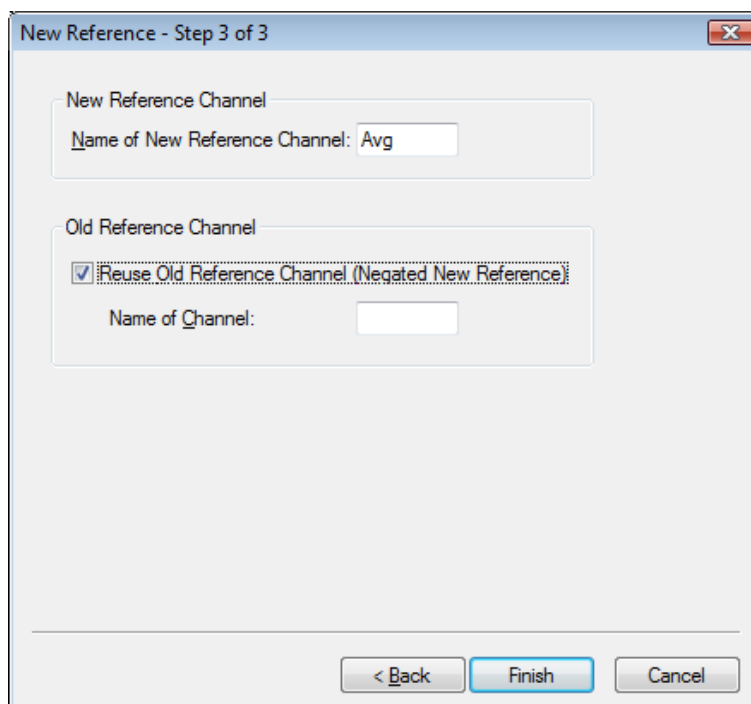


FIGURE 12—4 NEW REFERENCE DIALOG, THIRD PAGE

If you select the **Reuse Old Reference Channel (Negated New Reference)** check box, the old reference channel is reused as a normal data channel. An example of this would be a CZ reference converted to an A1/A2 reference. In this case, the CZ channel can be used for further calculations.

When you click **Finish**, a new view appears, containing the changed channels.

12.1.2 Pooling

The Pooling transform allows you to create new channels by pooling existing channels. The new channels are calculated for each point in time from the average values of the selected channels at this point in time.

SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Channel Preprocessing > Pooling**.

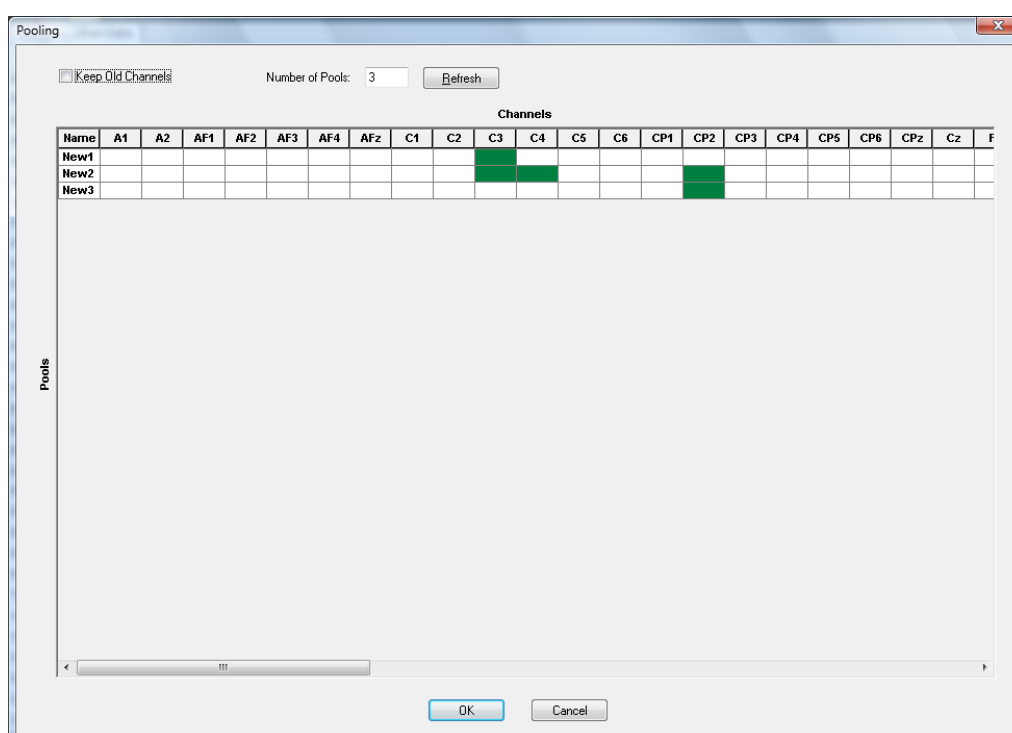


FIGURE 12—5 POOLING DIALOG BOX

You can make the following settings:

- If you select the **Keep Old Channels** check box, the old channels are also included in the new data set; that makes the new channels additional channels. If you do not select the check box, the resulting data set only contains the new channels.
- In the **Number of Pools** text box, you enter the desired number of new channels.
- The **Refresh** button updates the channel matrix.

When you click a cell in the table, its color changes between green and white. Green channels are included in the calculation of the new channel; white channels are not included in the pooling for the new channel.

12.1.3 RMS/GFP (Root Mean Square/Global Field Power)

The RMS/GFP transform allows you to determine the overall activity of certain channels.

SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Data Preprocessing > RMS/GFP**.

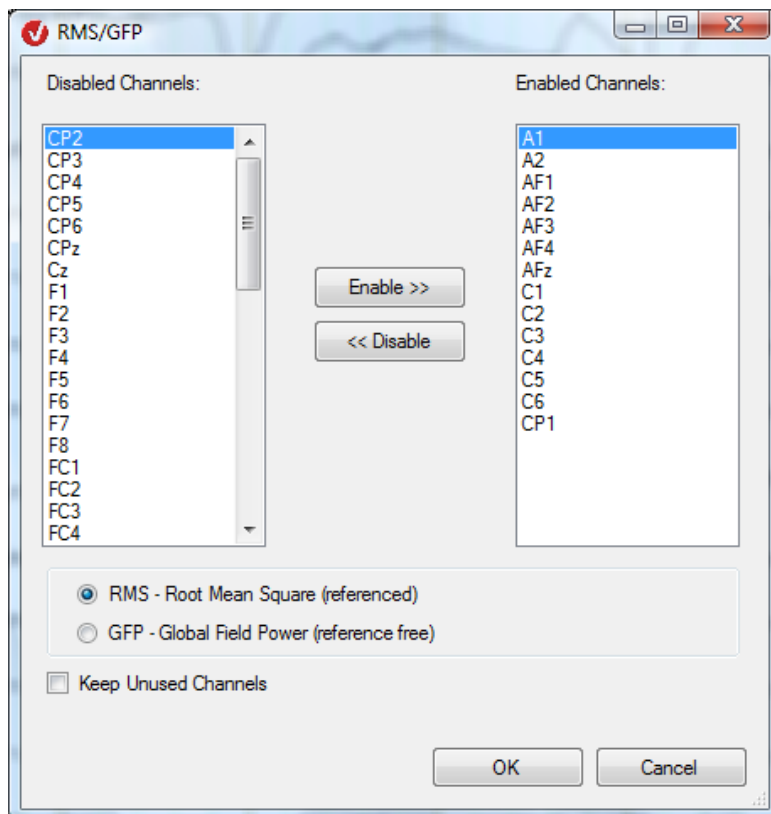


FIGURE 12—6 RMS/GFP DIALOG BOX

You can select the channels for which you want to carry out the calculation (**Enabled Channels**). These channels and the new RMS channel then appear in the new data set.

You can choose between two methods of calculation:

- **RMS – Root Mean Square (referenced):** For each point in time, the root is calculated from the average of the squares of the individual values. The result is contained in an additional channel with the name RMS.
- **GFP – Global Field Power (reference free):** In addition, before the values are squared, the average of all channels at a fixed time is subtracted (average reference). The result is contained in an additional channel with the name GFP.

12.1.4 CSD (Current Source Density) interpolation

The CSD (Current Source Density) transform replaces the voltage values at electrodes that have valid head coordinates with the current source density at these points. Their unit is $\mu\text{V}/\text{m}^2$. The curves created in this way no longer have reference electrodes. The curves can be further processed by means of other transforms.

SUMMARY

The current source density is calculated by applying the spherical Laplace operator to the voltage distribution on the surface of the head at a fixed point in time. Because the voltage distribution is only known at the electrodes, the spherical spline interpolation method is used to calculate the entire voltage distribution. You will find a detailed mathematical description of this method in [Pergo].

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Data Preprocessing > CSD Interpolation**.

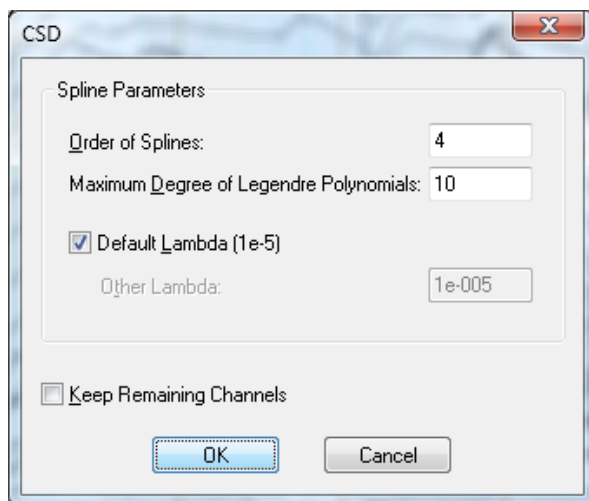


FIGURE 12—7 DIALOG CSD

The following three parameters are required in order to calculate the spherical splines:

- The order of the splines (**Order of Splines** text box), labeled “m” in the above specialist article
- The maximum degree of the Legendre polynomial (**Maximum Degree of Legendre Polynomials**) to be included in the calculation
- The Lambda approximation parameter (**Default Lambda**)

Depending on the values you enter for the order, the interpolation curve displayed will be smoother or wavier: the higher the spline order, the smoother the curve. Basically, the higher the electrode density is, the lower should be the value you specify for the order. Because the calculation of the spherical splines involves an infinite series of polynomials, so this series has to be discontinued at a certain degree. The following rule applies: the higher the spline order, the lower the degree of the polynomial at which the calculation is discontinued.

The Lambda approximation parameter determines the accuracy with which the spherical splines are approximated to the data to be interpolated. A value that is either too high or too low will, for different mathematical reasons, result in an inaccurate representation. Unless you are using unusual methods that require a different value, you should use the default value of “1e-5”.

Regardless of the above rules, you should not accept the results of the transform without checking them. In the CSD method, different parameters can lead to satisfactory or unsatisfactory results for different data sets as a result of approximations and rounding inaccuracies.

We therefore advise you to use the transform as follows:

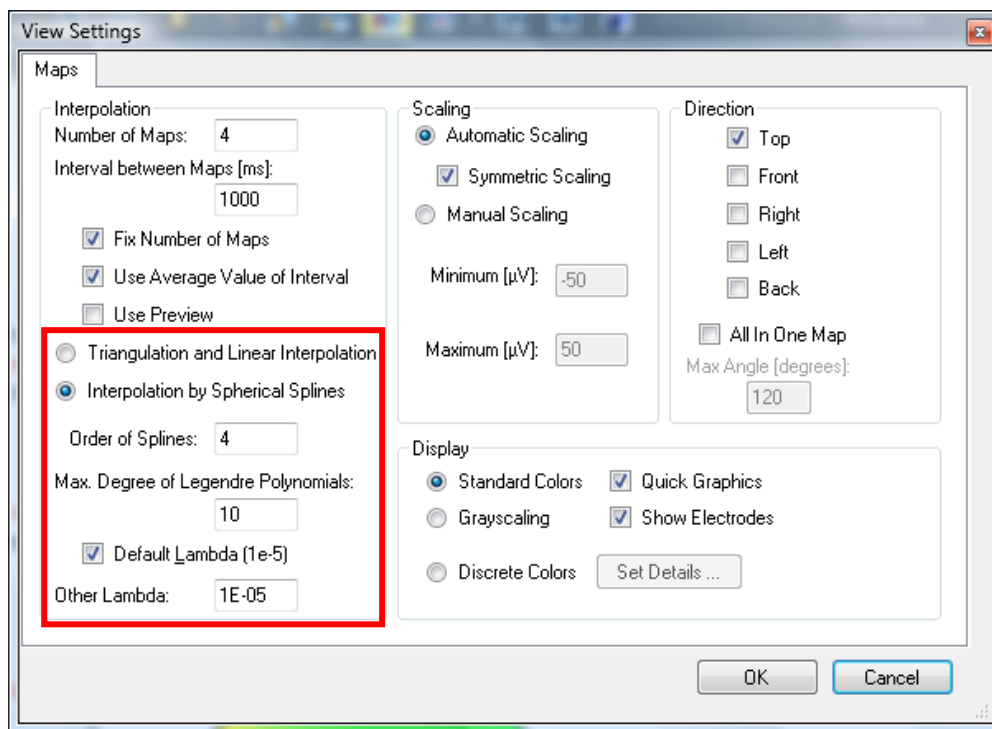


FIGURE 12—8 VIEW SETTINGS DIALOG BOX FOR THE MAP VIEW

- Before the CSD calculation is carried out, check the parameters of the spherical splines using the map view of the current data set. To do this, create a map view for the data set, select the **Interpolation by Spherical Splines** radio button, and enter the values you want to use for the CSD calculation in the **Order of Splines**, **Max. Degree of Legendre Polynomials** and **Lambda** text boxes. (You will find more information on the settings for the map view in section 9.2.4, “The map view”, and section 7.3.2, “Category-related view settings”.)

- Check whether the spherical splines approximate the voltage distribution on the head surface. You could do this by carrying out a comparison with interpolation by triangulation (**Triangulation and Linear Interpolation**). If the splines do not approximate the voltage distribution, change the parameters until they do.
- Carry out the CSD calculation with these parameters, and then use the map view to make sure the result is correct.

[Pergo] F. Perrin et al., Spherical splines for scalp potential and current density mapping. *Electroencephalography and clinical Neurophysiology*, 72 (1990), 184-187, together with the correction in *Electroencephalography and clinical Neurophysiology*, 76 (1990), 565.

REFERENCES

12.1.5 Rectify

The Rectify transform rectifies EEG data. In other words, positive values remain the same, while negative values are converted to positive. SUMMARY

No previous processing steps are required before the transform is used. PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Data Preprocessing > Rectify**.

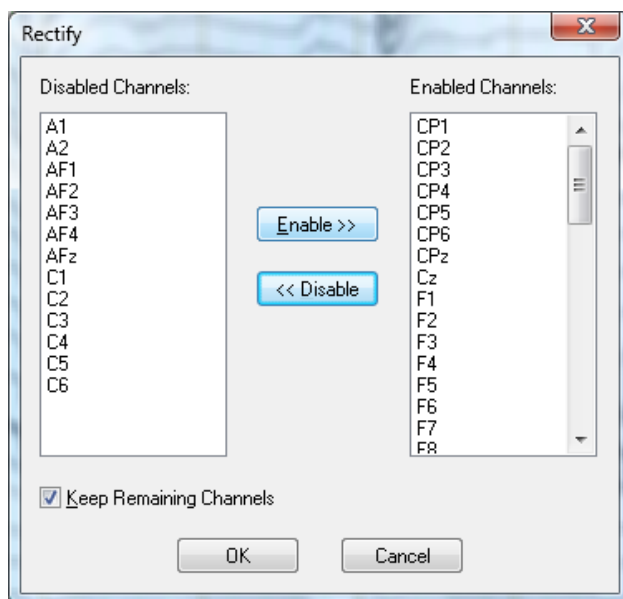


FIGURE 12—9 RECTIFY DIALOG BOX

You can make the following settings:

- You can select the channels to be rectified (**Enabled Channels**).
- If you select the **Keep Remaining Channels** check box, the remaining channels are retained. If you clear the check box, the remaining channels are removed from the data set.

12.1.6 Edit Channels

The Edit Channels transform allows you to edit EEG channel information. You can:

SUMMARY

- Hide channels
- Change channel and reference channel names
- Change position specifications
- Change the unit of measurement for a channel
- Change user-defined channel properties

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Edit Channels**.

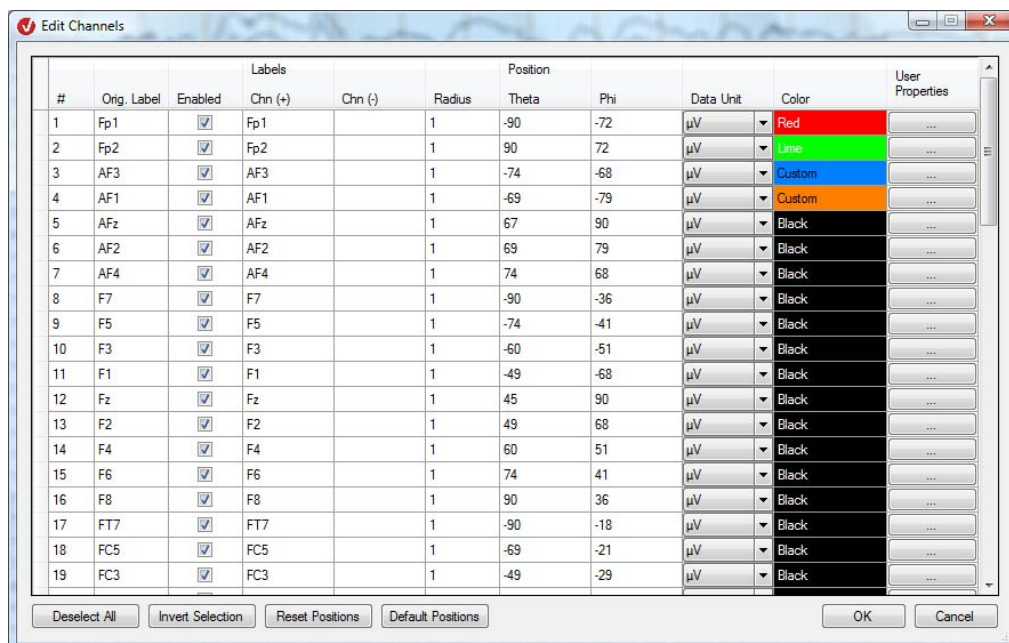


FIGURE 12—10 DIALOG BOX FOR EDITING CHANNEL INFORMATION

The table contains the following cells for each channel:

- **#** (channel number): The channel number is not editable.
- **Orig. Label** (original name of the channel): This is not editable.
- **Enabled** (displayed/hidden): To hide a channel, clear its check box.
- **Chn (+)** (channel name): You can edit this as required.
- **Chn (-)** (reference channel name): You can also edit this as required. Changing the name does not change the referencing. The reference channel name is provided for information purposes only.
- **Radius, Theta, Phi** (position specifications): The Radius cell must always contain either a positive number or 0, the Theta cell a value in the range from -180 to 180 and the Phi cell a value in the range from -360 to 360. See also Appendix B, “Electrode coordinate system”.
- **Data Unit**: The default unit is μV , which you can change by choosing a unit from the drop-down list.
- **Color**: If you click a cell, a color selection dialog box appears, in which you can assign the channel a basic or custom color.
- **User Properties** (user-defined channel properties): If you click the associated button, the following dialog box appears:

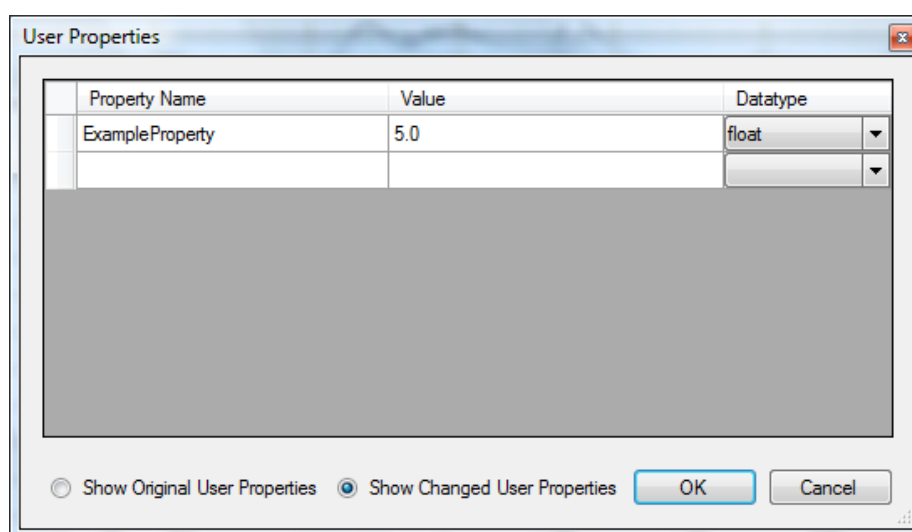


FIGURE 12—11 USER PROPERTIES TAB OF THE EDIT CHANNELS DIALOG BOX

In the **Property Name** cell, enter the name of the property. You can make any entry here. The **Value** cell contains the associated value. This value is assigned a programming data type that you choose from the drop-down list in the **Datatype** column.

The **Show Original User Properties** and **Show Changed User Properties** radio buttons allow you to specify whether the original user properties or the user properties you have edited are to be displayed.

You can delete existing user properties by selecting the row in the grid in the view of the changed user properties and pressing the **⟨Delete⟩** key to delete it. The row turns red, and the data type **NULL** appears in the **Datatype** column. Alternatively, you can specify the data type by choosing **NULL** from the drop-down list. To undo this deletion, you can set one of the other data types for the row at any time.

If you have made changes in a cell, this is indicated by a pencil in the left-hand border of the table. As soon as you exit the cell, your entry is validated. If validation is unsuccessful, an error message appears.

The function and label of the **Select All/Deselect All** button change when it is clicked. You can use it to select or deselect all channels.

To invert the channel selection you have made, click the **Invert Selection** button.

The **Reset Position** button resets the channel positions to the values they had when the dialog box was opened.

You will also find the **Default Position** button on the bottom of the dialog box. Once you confirm that you want to proceed, this button sets all the electrode coordinates to the default positions, depending on the channel names. You will find more information on the default positions for electrodes in section 7.1. All unrecognized channels are set to the position 0,0,0 (invalid).

12.1.7 Level Trigger

The Level Trigger transform allows you to set threshold markers on one or more channels if voltage limits are violated. These markers can be used as a basis for segmentation. SUMMARY

One possible application of the transform would be for muscle activities to be used as a reference for averaging.

Another application would be for when an analog channel is used as a storage location for stimuli in recording systems that do not have digital inputs. Here, different stimuli can be coded as different voltage levels.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Level Trigger**.

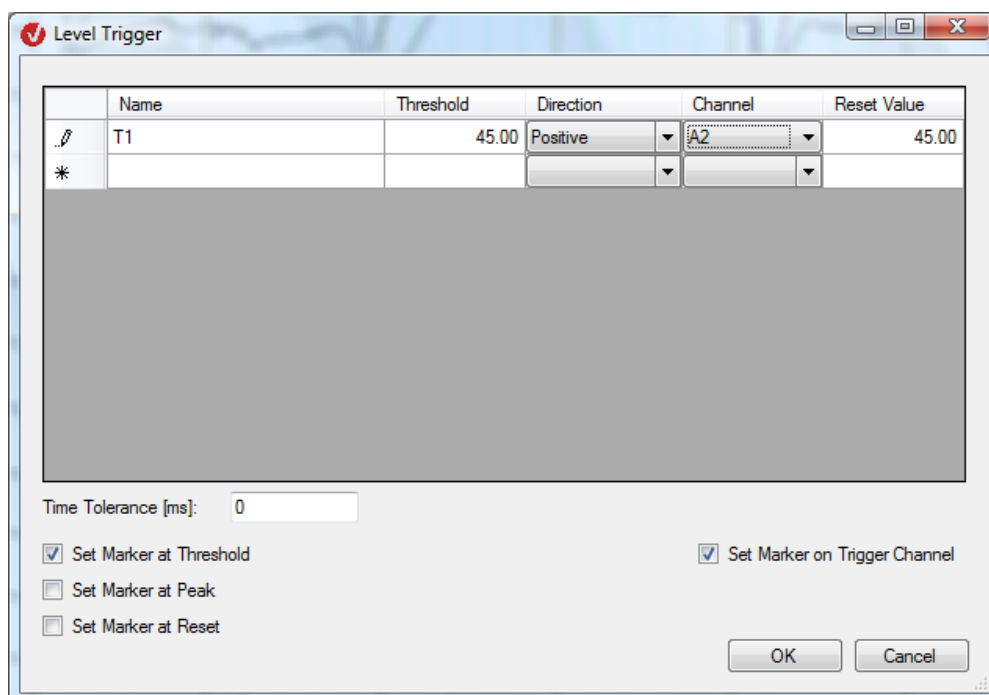


FIGURE 12—12 LEVEL TRIGGER DIALOG BOX

You can make the following settings:

You can specify the following in the table:

- In the **Name** column, you specify a name for the threshold to be searched for.
- In the **Threshold** column, you specify the threshold in μV .
- In the **Direction** column, you choose from the drop-down list the direction of the voltage characteristic that sets the marker when the threshold is reached. Positive means that the marker is set when the voltage is rising and the threshold is reached. Negative sets the marker when the voltage is falling and the threshold is reached.
- In the **Channel** column, you choose from the drop-down list the channel on which the threshold is to be searched for.
- In the **Reset Value** column, you specify the value in μV at which the trigger is to be reset. This value is usually identical to the threshold, but you can set another value for certain purposes. If the direction is positive, the value obtained must be below this one before a new trigger of this kind is found. If the direction is negative, the value obtained must be above this one.

As soon as you make an entry in a field, a new row is added to the table. To delete a row, you select it by clicking its left-hand border and then press the **Delete** key on your keyboard. Note that you must not be in edit mode when you do this.

In the **Time Tolerance [ms]** text box, you can specify an interval within which no distinction is drawn between triggers of the same direction on the same channel. If several thresholds are exceeded within this interval, only the maximum threshold is detected and only one marker is set. The same applies analogously when values fall below several thresholds within the tolerance. You should adjust the size of the interval to the steepness of the edges of the trigger channels.

If you select the **Set Marker on Trigger Channel** check box, the markers are assigned to the channel and displayed. If you do not select the check box, the markers are interpreted as global markers and set independently of the channels.

You can also specify the point at which markers are to be set in relation to the threshold:

- **Set Marker at Threshold** sets a marker at the point at which the threshold is exceeded.
- **Set Marker at Peak** sets a marker at the maximum or minimum value of the channel between the time at which the threshold is exceeded and the time of the reset.
- **Set Marker at Reset** sets a marker at the point at which the trigger is reset.

12.1.8 Linear Derivation

The Linear Derivation transform allows you to create new channels from linear combinations of existing channels. The new channels are calculated from coefficients that are assigned to existing channels based on the following formula:

SUMMARY

$$\text{New channel} = \text{coeff1} * \text{channel1} + \text{coeff2} * \text{channel2} + \dots$$

You can enter these coefficients in a matrix and also save and/or load them.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Linear Derivation**.

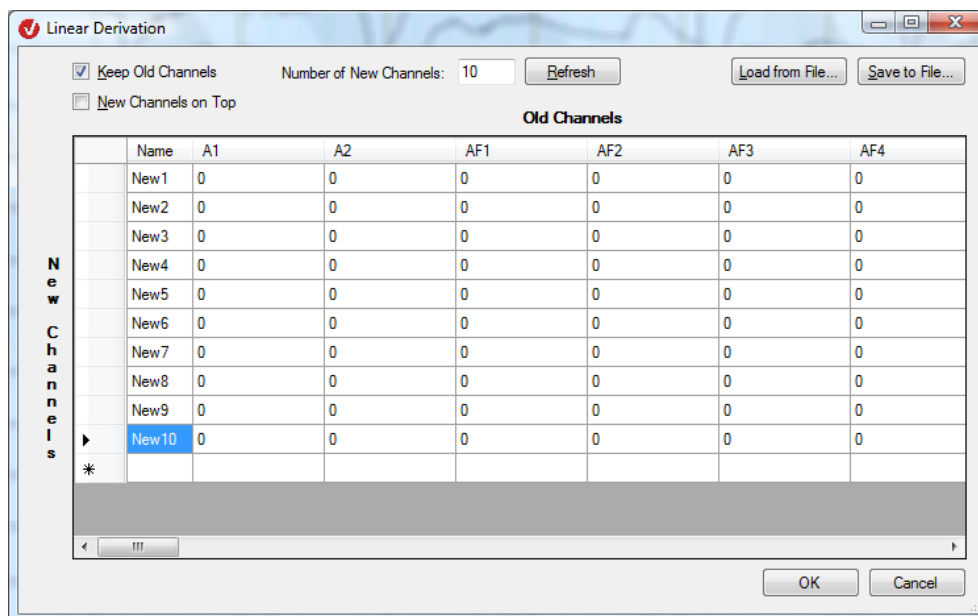


FIGURE 12—13 LINEAR DERIVATION DIALOG BOX

You can make the following settings:

- If you select the **Keep Old Channels** check box, the old channels are included in the new data set; that makes the new channels additional channels. If you do not select the check box, the new data set only contains the new channels.
- If you select the **New Channels on Top** check box, the new channels are listed first.
- In the **Number of New Channels** text box, you specify the number of new channels. The **Refresh** button updates the coefficient matrix or the number of rows in the table in accordance with the value entered in the **Number of New Channels** text box.

- The **Load from File...** button allows you to load a coefficient matrix from a text file.
- Click the **Save to File...** button to save a coefficient matrix you have entered.

If you want to read in a matrix text file you have generated, you must ensure it has the following structure:

	Channel1	Channel2	Channel3 ...
New1	Coeff.	Coeff.	Coeff.
New2	Coeff.	Coeff.	Coeff.

The decimal points of the coefficients must be points rather than commas.

12.1.9 Formula Evaluator

The Formula Evaluator transform allows you to calculate new channels as functions of existing channels. A wide range of mathematical options are available to you for this. SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Formula Evaluator**.

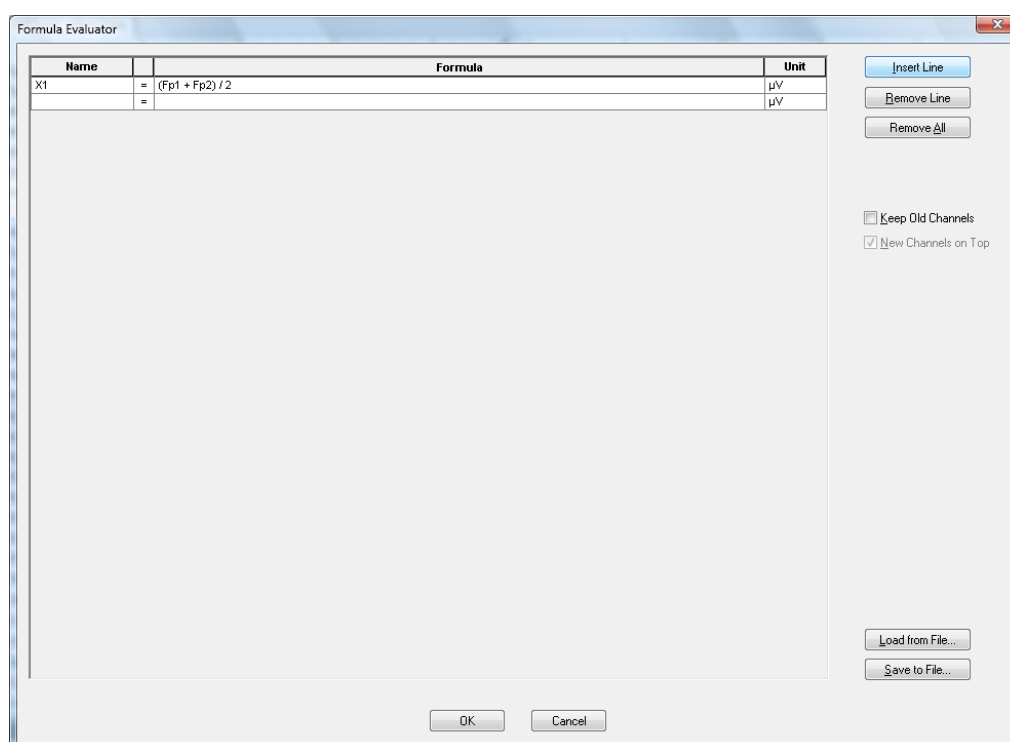


FIGURE 12—14 FORMULA EVALUATOR DIALOG BOX

The formulas are entered in a table.

- In the column on the left (**Name**), you enter the name of the new channel that contains the data for the calculation.
- In the middle column (**Formula**), you enter the formula used to calculate the data. No distinction is drawn between uppercase and lowercase.
- In the column on the right (**Unit**), you enter the unit for the new channel.

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

The **Save to File...** button allows you to save formulas to ASCII files, while the **Load from File...** button lets you add ASCII files containing formulas to the table.

If you want to create the ASCII files using an editor or another program, ensure that each line in the file takes the format “name = formula”.

If you select the **Keep Old Channels** check box, you can accept unchanged all the channels from the previous data set that have not been redefined.

The **New Channels On Top** check box allows you to specify whether new channels are added at the beginning or end of the table. This setting is only relevant if you have selected the **Keep Old Channels** check box.

The following can be used and combined in the formulas:

- The operators +, −, *, and / plus parentheses. Mathematical rules of precedence are observed.
- Channel names. These are interpreted point by point.
- The constants e, pi and i (imaginary unit) as well as numeric entries.
- The mathematical functions sqrt (square root), abs, ln (natural logarithm), log (logarithm to base 10), sin, cos, tan, atan, sinh, cosh, tanh, real (real part), imag (imaginary part), arg (argument of a complex number).
- The shift function

The Formula Evaluator transform processes both real and complex data. Note that the format of the output data must be identical to the format of the input data. Real numbers are automatically converted to complex numbers, if necessary. The mathematical functions are currently available for real arguments only.

Numeric constants are interpreted as a fixed number across the entire time or frequency domain. Channel names are interpreted point by point. The shift function can be applied to channel names. It takes the form “shift(channel, shift index)”.

The shift index can be positive or negative. The function is regarded as a left shift. That means, for example, that shift(Fp1, 1) shifts Fp1 in such a way that the data point that has the index 2 becomes the data point with the index 1. In the same way, shift(Fp1, -2) shifts Fp1 so that the data point with the index 1 becomes the data point with the index 3.

Most of the functions of existing transforms can be calculated using the Formula Evaluator:

EXAMPLES

- Linear derivation can be calculated using a formula of the following type:

$$\text{channel} = a * \text{channel 1} + b * \text{channel 2} + \dots$$
- RMS (Root Mean Square) of Fp1, Fp2 and Fz can be calculated using the following formula:

$$\text{RMS} = \sqrt{(\text{Fp1} * \text{Fp1} + \text{Fp2} * \text{Fp2} + \text{Fz} * \text{Fz}) / 3}$$

Other measures can also be defined here in a similar way:

- Rectify can be defined by means of:

$\text{channel} = \text{abs}(\text{channel})$

It is also possible to use the shift function to implement simple filters such as sliding averages:

- $\text{Fp1} = (\text{shift}(\text{Fp1}, -1) + \text{Fp1} + \text{shift}(\text{Fp1}, 1)) / 3$

or

- $\text{Fp1} = \text{shift}(\text{Fp1}, -1) * 0.25 + \text{Fp1} * 0.5 + \text{shift}(\text{Fp1}, 1) * 0.25$

If you use numeric channel names, enclose them in quotes in the formula. For example:

- $1 = (\text{shift}("1", -1) + "1" + \text{shift}("1", 1)) / 3.$

12.1.10 Change Sampling Rate

This transform allows you to change the sampling rate of a data set.

SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Dataset Preprocessing > Change Sampling Rate**.

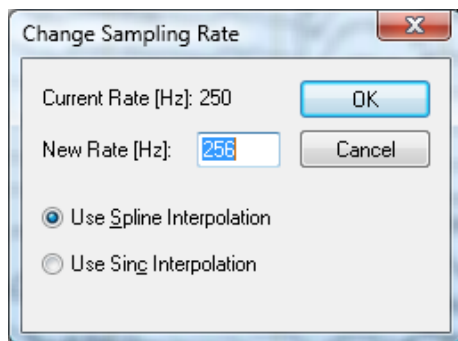


FIGURE 12—15 CHANGE SAMPLING RATE DIALOG BOX

The dialog box displays the current sampling rate (**Current Rate [Hz]**). In the **New Rate [Hz]** text box, you enter a new rate.

You can also specify whether data conversion is to be carried out by means of cubic spline interpolation (by selecting **Use Spline Interpolation**) or sinc interpolation (by selecting **Use Sinc Interpolation**).

The data is converted by means of cubic spline interpolation (third-degree polynomial). Note that in cubic spline interpolation (third-degree polynomial) the length of the EEG is generally reduced by a number of milliseconds because the polynomial cannot be calculated right up to the limits of the original data set. You should therefore carry out the conversion in the raw EEG.

ADDITIONAL
INFORMATION

12.2 Transforms in the Artifact Rejection/Reduction group

12.2.1 Complex Demodulation

The Complex Demodulation transform works on the principle of complex demodulation. The EEG signal is continuously transformed by means of mathematical methods in such a way that the resulting signal consists only of frequencies that lie in the defined range.

SUMMARY

Unlike the Fast Fourier transform, only a specific frequency band can be extracted. The advantage of this transform is that it also works at high speed on non-segmented EEGs and that the output of each channel is also a continuous channel.

The transform should not be confused with bandpass filtering. The resulting signal is not the filtered input signal; it describes the power or phase of the selected frequency range at each point in time.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Data Filtering > Complex Demodulation**.

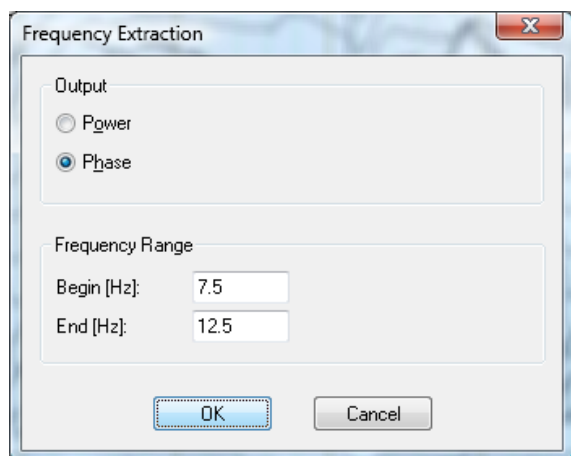


FIGURE 12—16 FREQUENCY EXTRACTION DIALOG BOX

You can make the following settings:

- Under **Output**, you specify whether the power (**Power**) or phase (**Phase**) is to be output.
- Under **Frequency Range**, you specify the beginning (**Begin [Hz]**) and end (**End [Hz]**) of the frequency band to be extracted.

If you specify that the power is to be output, the average power in the specified frequency band is calculated for each data point.

If you specify that the phase is to be output, the phase of the signal in the specified frequency band is calculated. This number is only unambiguous for multiples of 2π . When different intervals are selected, the output values can therefore differ by multiples of this value. On the basis of the phase, you can obtain the dominant frequency in the calculated frequency range. A rising phase indicates that the dominant frequency lies under the middle of the selected interval, while a falling phase indicates that it lies above the middle of the interval.

12.2.2 IIR Filters

The IIR Filters transform allows you to filter the EEG data by means of three different types of filter: SUMMARY

- High-pass filtering with a selectable cutoff frequency or time constant
- Low-pass filtering with a selectable cutoff frequency
- Band-rejection filtering for 50 Hz or 60 Hz (notch filter) to eliminate interference from the electricity network. The notch filter has a bandwidth of 5 Hz, which is symmetrical around the set notch frequency (i.e. 50 Hz +/- 2.5 Hz or 60 Hz +/- 2.5 Hz). The edge rise is always 24 dB/octave.

The cutoff frequency or time constant specifies the frequency at which the signal is 3 dB lower than the input signal (i.e. the input signal is reduced by approx. 70%). The filters are implemented as phase shift-free Butterworth filters. It is also possible to choose the slope of the filter for high- and low-pass filters. It can be 12 dB/octave, 24 dB/octave or 48 dB/octave.

We recommend that you use the filter before segmentation in order to minimize as far as possible the effect of discontinuities on the filter and transient phenomena. PREREQUISITE FOR USE

To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Data Filtering > IIR Filters**. PROCEDURE

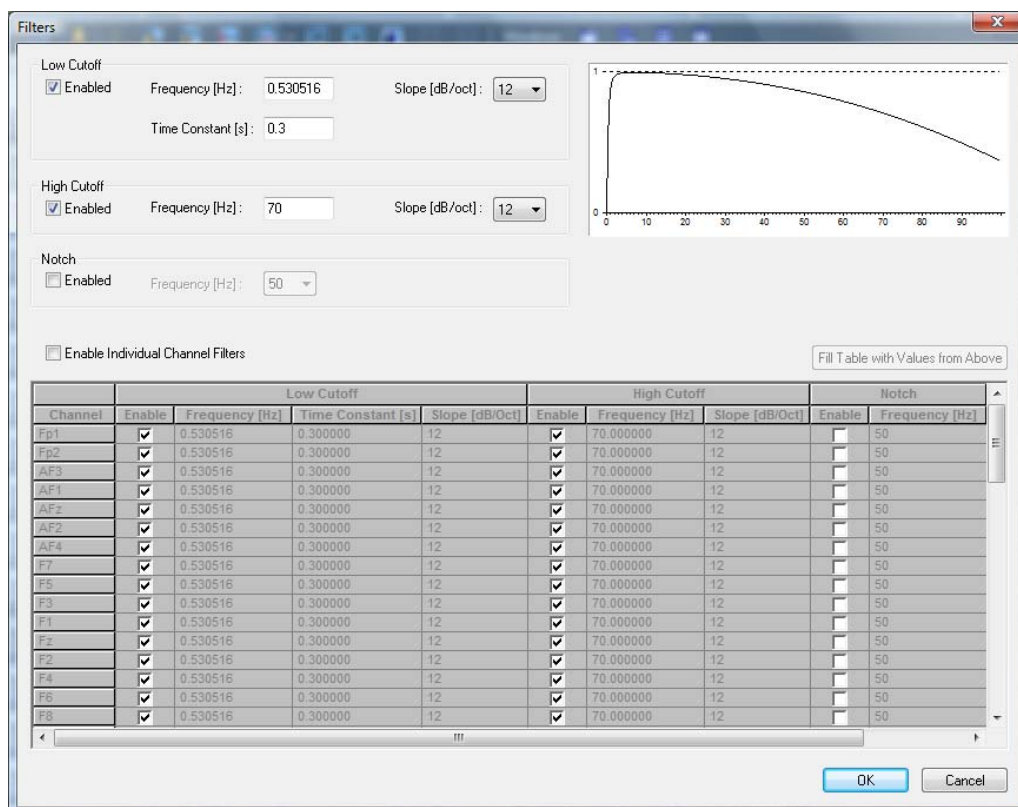


FIGURE 12—17 FILTERS DIALOG BOX

You can make the following settings in the **Low Cutoff** (for high-pass filtering) and **High Cutoff** (for low-pass filtering) group boxes:

LOW CUTOFF AND HIGH
CUTOFF GROUP BOXES

- The **Enable** check box allows you to switch the associated filter on/off.
- In the **Frequency [Hz]** text box, you specify the cutoff frequency of the associated filter.
- For the high-pass filter, you can specify the time constant in the **Time Constant [s]** text box instead of the cutoff frequency.
- The **Slope [dB/oct]** drop-down list allows you to specify the slope of the filter.

In the Notch group box (for band-rejection filtering), you can make the following settings:

NOTCH GROUP BOX

- The **Enable** check box allows you to switch the filter on/off.
- The **Frequency [Hz]** drop-down list allows you to specify the stop (rejection) frequency. You can choose between 50 and 60 Hertz.

If you select the **Enable Individual Channel Filters** check box, you can make separate filter settings for each channel in the table.

If you click the **Fill Table with Values From Above** button, the values entered in the upper part of the dialog box are applied to the table. You can then change the channels to be filtered based on different criteria.

12.2.3 Band-Rejection Filters

Band-rejection filters are used to filter interference signals of a constant frequency.

SUMMARY

Interference signals like this can come from the electricity network or from poorly shielded monitors. Whereas these sources of interference can be eliminated by improved shielding, other sources of interference when EEGs are recorded are unavoidable. These include interference signals that come from magnetic-field changes when an EEG is recorded during an MRI scan in an MRI scanner.

Such interference signals have typical frequencies, and consequently they can be largely eliminated by means of a combination of low-pass and band-rejection filters.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box required for the transform, you choose **Transformations > Artifact Rejection/Reduction > Data Filtering > Band Rejection**.

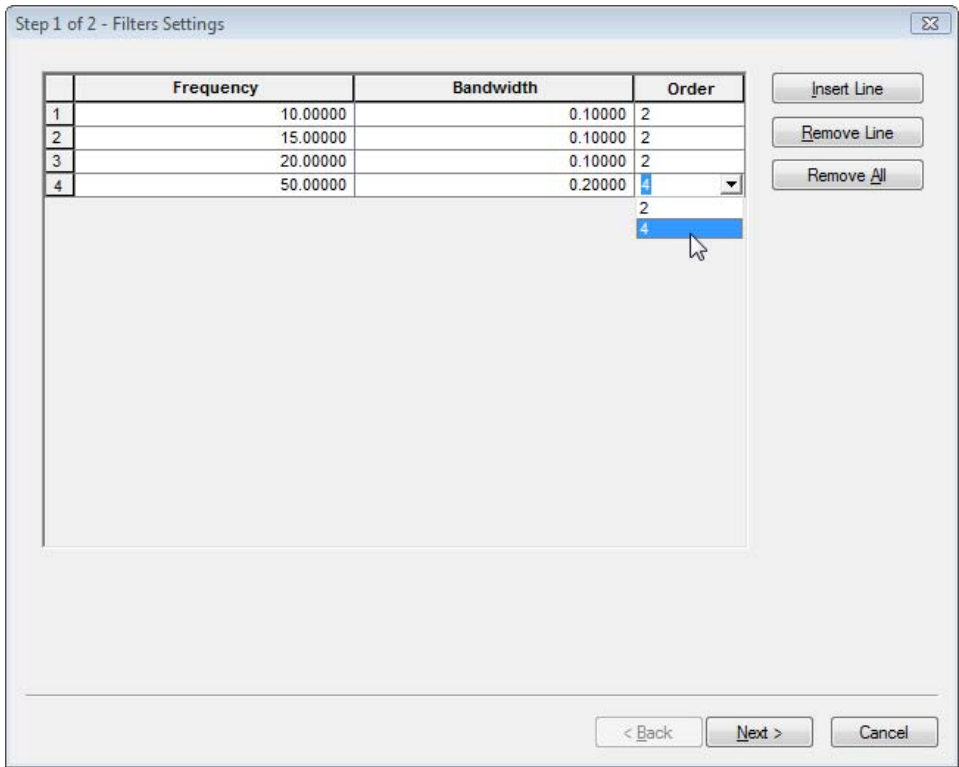


FIGURE 12—18 DIALOG FOR BAND-REJECTION FILTERS, FIRST PAGE

In the table, you can specify as many band-rejection filters as you like to be applied to the EEG. The filter is determined by frequency (in the **Frequency** column), bandwidth (in the **Bandwidth** column) and order (in the **Order** column).

The signal is reduced to half of its amplitude at the limiting frequencies (frequency \pm bandwidth / 2). The order determines the slope of the filter. You can choose between an order of 2 or 4 from a drop-down list. A higher order results in stronger filtering in the interval between the two limiting frequencies.

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

When you have finished making your entries, you click **Next** to go to the second page of the dialog.

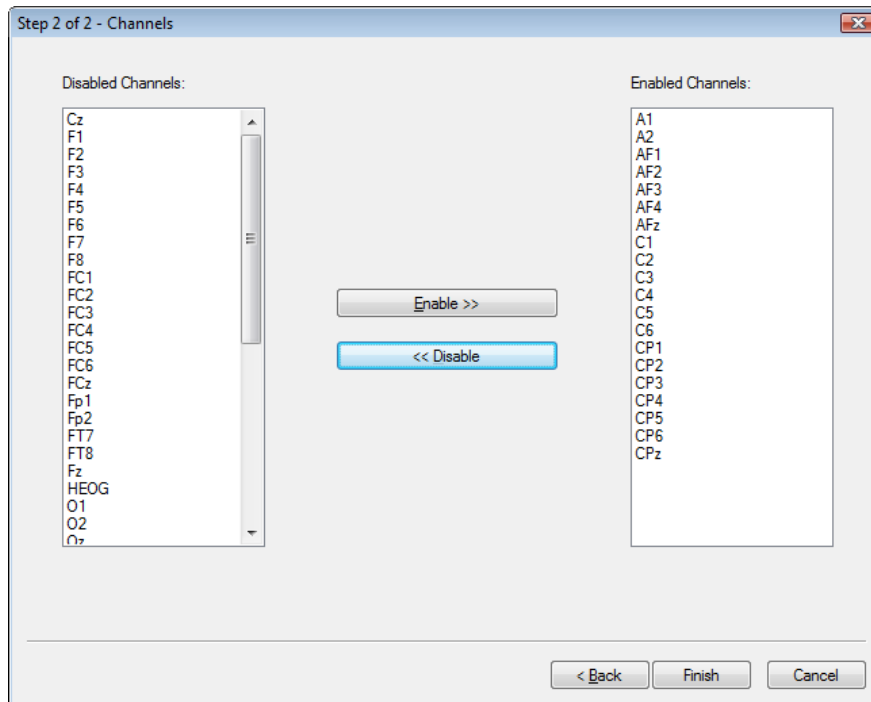


FIGURE 12—19 DIALOG FOR BAND-REJECTION FILTERS, SECOND PAGE

On the second page of the dialog, you select the channels to which the filters are to be applied (those in the **Enabled Channels** list box). In this way, you can exclude from filtering those channels, such as control signal channels, that are not affected by interference signals (in the **Disabled Channels** list box).

You can use this transform several times to apply different band-rejection filters to different channels.

12.2.4 Artifact Rejection

The Artifact Rejection transform allows you to search the data set for physical artifacts following segmentation and to remove or mark segments with artifacts.

SUMMARY

To mark artifacts before segmentation, you use the Data Inspector transform. You will find detailed information on this in section 12.2.5, "Data Inspector".



The Artifact Rejection transform is typically used after:

PREREQUISITE FOR USE

- Segmentation

To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Artifact Rejection**.

PROCEDURE

On the **Inspection Method** tab, you can choose between the following three segment selection methods:

INSPECTION METHOD
TAB

- Manual (**Manual Segment Selection** radio button)
- Semiautomatic (**Semiautomatic Segment Selection** radio button)
- Automatic (**Automatic Segment Selection** radio button)

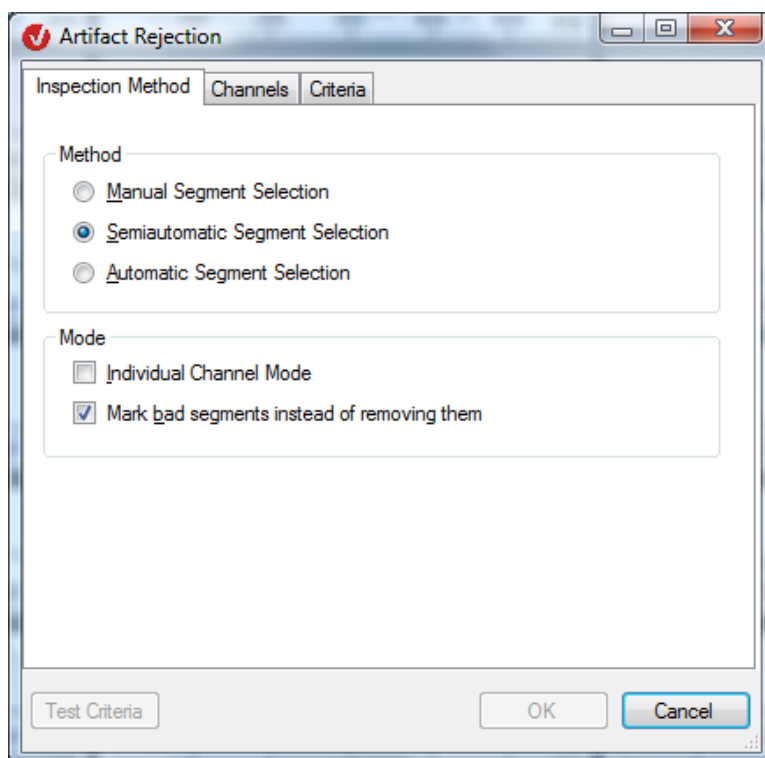


FIGURE 12—20 INSPECTION METHOD TAB IN THE ARTIFACT REJECTION DIALOG BOX

If you select the **Individual Channel Mode** check box, you activate individual channel mode, which allows bad intervals to be taken into account channel by channel. The Average transform can then be used in a subsequent step to search for as many segments as possible separately for each channel.

You will find detailed information on the Average transform in section 12.4.6.

If you select the **Mark bad segments instead of removing them** check box, segments with artifacts are merely marked rather than removed. If you do not select the check box, the new data set only contains the remaining segments.

The three segment selection methods are explained in detail below:

If you select the **Manual Segment Selection** radio button and click the **OK** button, a temporary semiautomatic view dialog box appears on the right.

MANUAL SEGMENT
SELECTION WITHOUT
INDIVIDUAL CHANNEL
MODE

You can use the mouse to mark intervals found in the various channels as artifacts.

To delete a marker, press the **Shift** key and click the marker. If you have not activated individual channel mode, you can use this temporary semiautomatic view dialog box to remove individual segments containing artifacts.

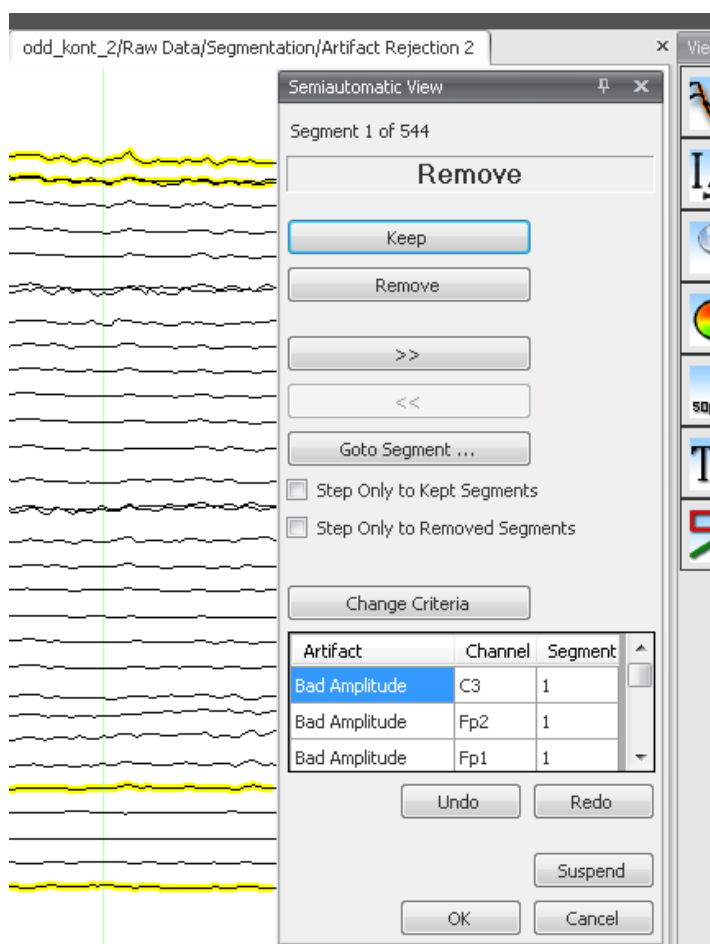








FIGURE 12—21 ARTIFACT REJECTION WITH MANUAL SEGMENT SELECTION AFTER THE “MARK BAD SEGMENTS...” CHECK BOX IS CLEARED

The temporary semiautomatic view dialog box contains the following information and functions:

- The current segment number is displayed (**Segment 1 of 544** in figure 12—21).
- The group below this contains one of the following headings: **Remove** or **Keep**.
- The heading indicates whether the current segment is to be removed or kept.
- The **Keep** button removes the current segment from the list of channels to be removed and switches to the next segment.
- The **Remove** button adds the current segment to the list of segments to be removed and switches to the next segment.
- The buttons  and  take you to the previous and next segment, respectively.
- The **Goto Segment...** button allows you to select a segment you want to go to.
- If you select the **Step Only to Kept Segments** check box, when you click the button  you are taken to the nearest previous segment that is not listed in the table of segments to be removed. A similar principle applies to subsequent segments when you click the button .
- If you select the **Step Only to Removed Segments** check box, when you click the button  you are taken to the nearest previous segment that is listed in the table of segments to be removed. A similar principle applies to subsequent segments when you click the button .
- The **Change Criteria** button allows you to change parameters and channels subsequently in semiautomatic mode.
- The table below this contains all the artifacts to be removed, together with the channel and segment affected in each case. If you double-click an entry, the program jumps directly to the corresponding artifact.

The **Undo** and **Redo** buttons allow you to undo and redo changes, respectively.

If you want to interrupt what you are doing and resume later, click the **Suspend** button. The Artifact Rejection transform is highlighted in red in the list of history nodes, and all the processing steps carried out continue to apply.

You click the **OK** button to conclude your entries.

If you have selected the **Mark bad segments instead of removing them** check box, the temporary semiautomatic view dialog box marks any bad segments.

In addition, you can use the mouse to mark intervals found in the various channels as artifacts.

To delete a marker, press the **«Shift»** key and click the marker.

MANUAL SEGMENT
SELECTION WITH
INDIVIDUAL CHANNEL
MODE

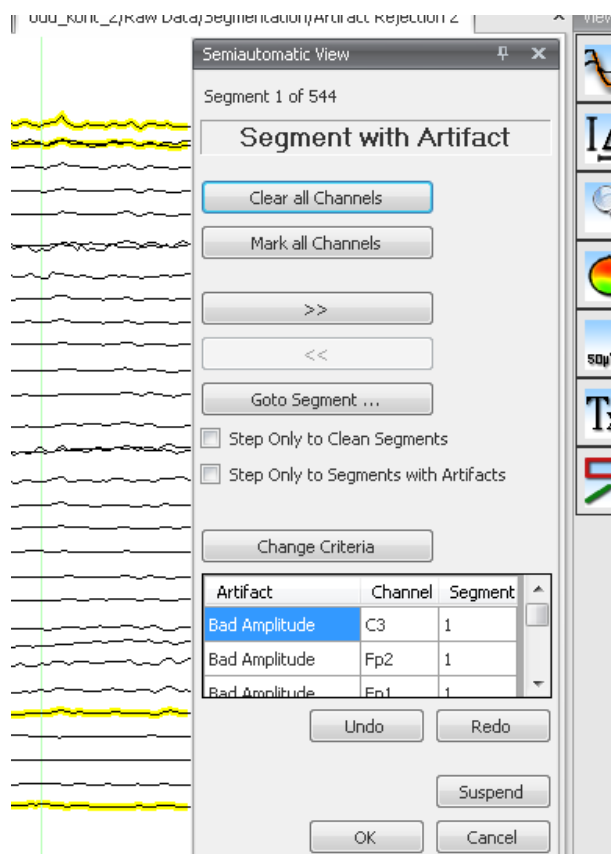


FIGURE 12—22 ARTIFACT REJECTION WITH MANUAL SEGMENT SELECTION AFTER THE “MARK BAD SEGMENTS...” CHECK BOX IS SELECTED

The temporary semiautomatic view dialog box contains the following information and functions:

- The current segment number is displayed (**Segment 1 of 544** in figure 12—22).
- The group below this contains one of the following headings: **Segment with Artifacts** or **No Artifact**.
- This heading indicates whether an artifact has been marked at any point in the current segment.
- The **Mark all Channels** button highlights in color all channels, indicating that they contain artifacts, and switches to the next segment. The **Clear all Channels** button clears all “bad channel” markers for the current segment and switches to the next segment.
- The buttons **>>** and **<<** take you to the next and previous segment, respectively.
- The **Goto Segment...** button allows you to select a segment you want to go to.

- If you select the **Step Only to Clean Segments** check box, when you click the button **<<** you are taken to the nearest previous segment that does not contain an artifact and is therefore not listed in the table of segments to be removed. A similar principle applies to subsequent segments when you click the button **>>**.
- If you select the **Step Only to Segments with Artifacts** check box, when you click the button **<<** you are taken to the nearest previous segment that contains artifacts and is therefore listed in the table of segments to be removed. A similar principle applies to subsequent segments when you click the button **>>**.
- The **Change Criteria** button allows you to change parameters and channels subsequently in semiautomatic mode.
- The table below this contains all the marked artifacts, together with the channel and segment affected in each case. If you double-click an entry, the program jumps directly to the corresponding artifact.

The **Undo** and **Redo** buttons allow you to undo and redo changes, respectively. If you want to interrupt what you are doing and resume later, click the **Suspend** button. The Artifact Rejection transform is highlighted in red in the list of history nodes, and all the processing steps carried out continue to apply. You click the **OK** button to conclude your entries.

Select the **Semiautomatic Segment Selection** radio button, and then make the settings you require on the **Channels** and **Criteria** tabs.

SEMIAUTOMATIC
SEGMENT SELECTION

On the Channels tab, you can select the channels to be searched for artifacts (**Enabled Channels**) and exclude channels from the search for artifacts (**Disabled Channels**).

CHANNELS TAB

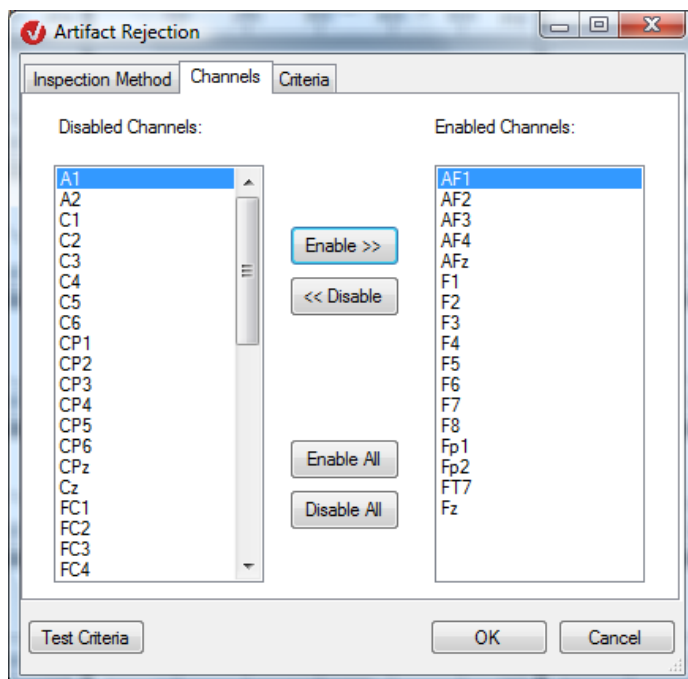


FIGURE 12—23 CHANNELS TAB IN THE ARTIFACT REJECTION DIALOG BOX

On the **Criteria** tab, you specify the criteria for marking channels (individual channel mode enabled) or for excluding segments (individual channel mode disabled). CRITERIA TAB

To do this, you make settings on the following tabs: Gradient, Max-Min, Amplitude and Low Activity. Each tab contains the settings for an artifact criterion.

When the gradient criterion is applied, the absolute difference between two neighboring sampling points must not exceed a specific value. GRADIENT CRITERION

On the **Gradient** tab, you can make the following settings:

- If you select the **Check Gradient** check box, the gradient criterion is applied.
- In the **Maximal allowed voltage step** text box, you specify the maximum permissible difference between two data points.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

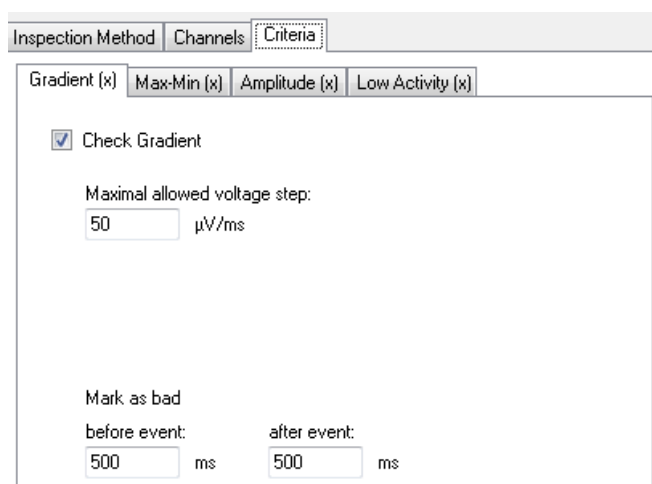


FIGURE 12—24 GRADIENT TAB ON THE CRITERIA TAB IN THE ARTIFACT REJECTION DIALOG BOX

When the max-min criterion is applied, the difference between the maximum and minimum in a segment must not exceed a specific value. MAX-MIN CRITERION

On the **Max-Min** tab, you can make the following settings:

- If you select the **Check maximum difference of values in the segment** check box, the max-min criterion is applied.
- In the **Maximal Allowed Absolute Difference** text box, you specify the maximum difference in voltage.
- In the **Interval Length** text box, you specify the length of the interval in ms or the period within which the difference in voltage must not exceed the specified value.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Inspection Method Channels Criteria

Gradient (x) Max-Min (x) Amplitude () Low Activity (x)

☒ Check maximal difference of values in intervals

Maximal allowed absolute difference:
200 µV

Interval length:
200 ms

Mark as bad

before event: 200 ms after event: 200 ms

FIGURE 12—25 MAX-MIN TAB ON THE CRITERIA TAB IN THE ARTIFACT REJECTION DIALOG BOX

When the amplitude criterion is applied, the amplitude must not violate specified maximum and minimum values. **AMPLITUDE CRITERION**

On the **Amplitude** tab, you can make the following settings:

- If you select the **Check maximal and minimal amplitude** check box, the amplitude criterion is applied.
- In the **Minimal allowed amplitude** text box, you specify the minimum permissible value for the voltage.
- In the **Maximal allowed amplitude** text box, you specify the maximum permissible value for the voltage.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Inspection Method Channels Criteria

Gradient (x) Max-Min (x) Amplitude (x) Low Activity (x)

☒ Check maximal and minimal amplitude

Minimal allowed amplitude:
0 µV

Maximal allowed amplitude:
0 µV

Mark as bad

before event: 0 ms after event: 0 ms

FIGURE 12—26 AMPLITUDE TAB ON THE CRITERIA TAB IN THE ARTIFACT REJECTION DIALOG BOX

When the low activity criterion is applied, the difference between the maximum and minimum in an interval of a selectable length must not exceed a specific value. **LOW ACTIVITY CRITERION**

On the **Low Activity** tab, you can make the following settings:

- If you select the **Check low activity in intervals** check box, the criterion for low activity is applied.
- In the **Lowest allowed activity (Max-Min)** text box, you specify the minimum level of activity.
- In the **Interval Length** text box, you specify the length of the interval within which the specified minimum level of activity cannot be violated.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Inspection Method Channels Criteria

Gradient (x) Max-Min (x) Amplitude (x) **Low Activity (x)**

☒ Check low activity in intervals

Lowest allowed activity (Max - Min):
0.5 µV

Interval length:
100 ms

Mark as bad
before event: 500 ms after event: 500 ms

FIGURE 12—27 LOW ACTIVITY TAB ON THE CRITERIA TAB IN THE ARTIFACT REJECTION DIALOG BOX

You can combine the different criteria. As an aid to clarity, the title of each tab indicates whether the criterion is currently applied. **(x)** (parentheses with a cross) indicate that the criterion is currently applied. **()** (parentheses without a cross) indicate that the criterion is not currently applied.

The **Test Criteria** button allows you to test the criteria.

Once you have completed all your settings, click the **OK** button on one of the tabs. A temporary dialog box appears on the right of the window. This temporary dialog box contains a table of the marked artifacts. You can adjust the results of your settings subsequently in the same way as for manual segment selection.

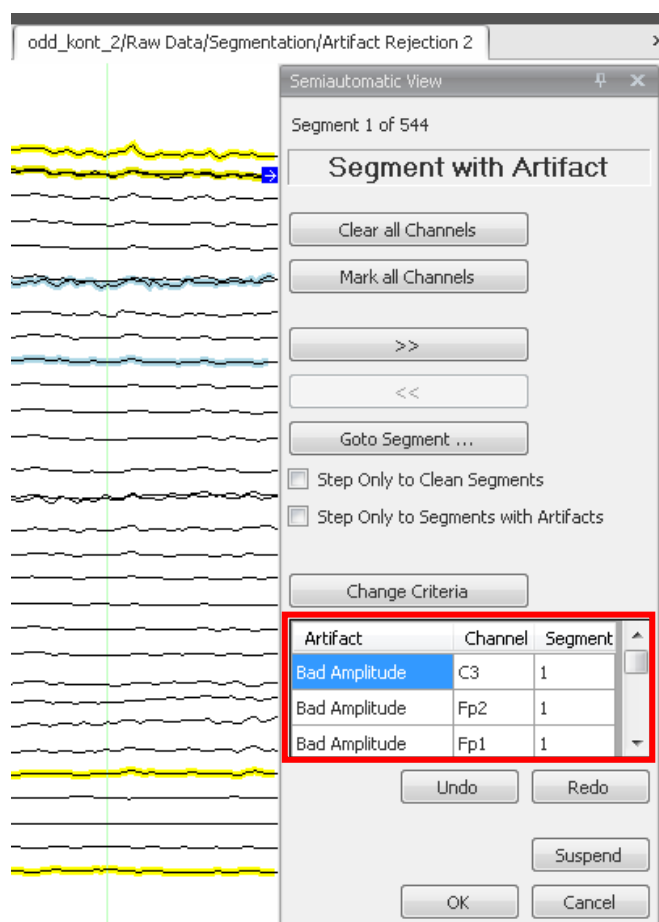


FIGURE 12—28 ARTIFACT REJECTION, SEMIAUTOMATIC SEGMENT SELECTION, TEMPORARY DIALOG BOX

In automatic segment selection you make all your settings in the same way as for semiautomatic segment selection. The only difference is that you are not able to make corrections interactively as you can in the semiautomatic view.

AUTOMATIC SEGMENT
SELECTION

12.2.5 Data Inspector

The Data Inspector transform allows you to check the raw EEG data set for physical artifacts. The inspection can be carried out manually, semiautomatically or automatically. In a semiautomatic or automatic inspection, you can specify criteria for the artifacts and ranges before and after the artifact that are to be marked as bad. In a manual or semiautomatic inspection, you can change or delete the intervals subsequently. You can also add new intervals.

SUMMARY

To remove artifacts after segmentation, you use the Artifact Rejection transform. You will find detailed information on this in section 12.2.4.



No previous processing steps are required before the transform is used. To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Data Inspector**.

PROCEDURE

On the Inspection Method tab, you can choose between the following three inspection methods:

INSPECTION METHOD TAB

- Manual (**Manual Inspection** radio button)
- Semiautomatic (**Semiautomatic Inspection** radio button)
- Automatic (**Automatic Inspection** radio button)

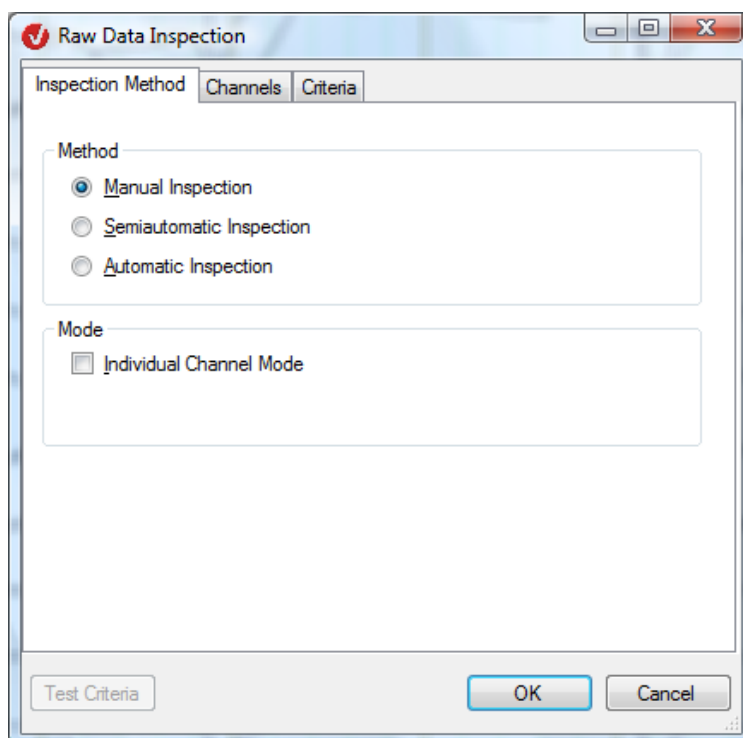


FIGURE 12—29 INSPECTION METHOD TAB IN THE RAW DATA INSPECTION DIALOG BOX

If you select the **Individual Channel Mode** check box, you activate individual channel mode, which allows you to identify the marked channels as bad individually even after completion of the inspection. The Average transform can then be used in a subsequent step to search for as many segments as possible separately for each channel. If you do not select the check box, on completion of the inspection the entire interval in which one or more channels has been marked is declared as a bad interval.

You will find detailed information on the Average transform in section 12.4.6.

The three inspection methods are explained in detail below:

If you select the **Manual Inspection** radio button and click the **OK** button, a temporary semiautomatic view dialog box appears on the right. MANUAL INSPECTION

You can use the mouse to mark intervals found in the various channels as artifacts.

To delete a marker, press the **⌘Shift** key and click the marker.

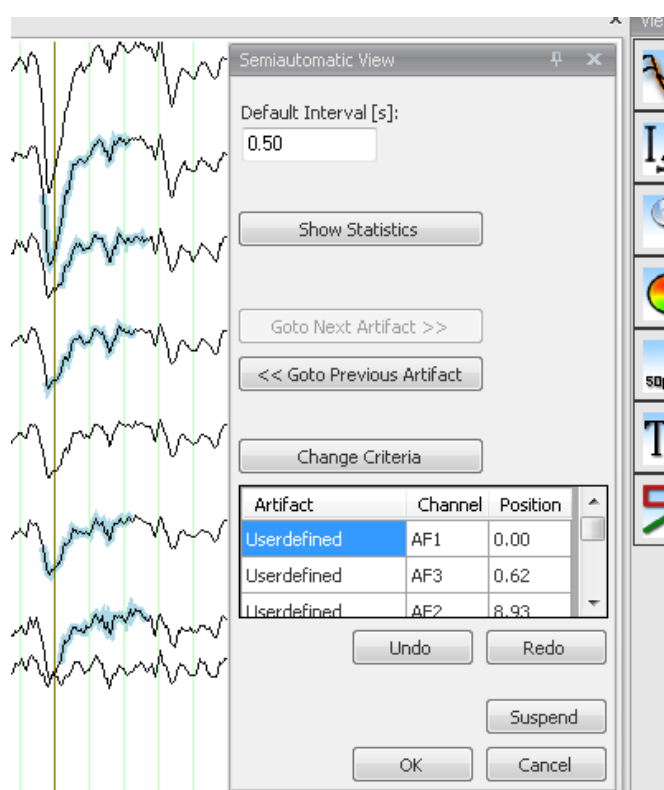


FIGURE 12—30 RDI, MANUAL INSPECTION, TEMPORARY SEMIAUTOMATIC VIEW DIALOG BOX

The temporary semiautomatic view dialog box contains the following information and functions:

- The minimum interval length set during manual artifact detection is displayed (**Default Interval [s]**).
- The Show Statistics button displays the **Artifact Statistics** dialog box, which lists the artifacts by type and channel.
- The **Go to Next Artifact >>** and **<< Go to Previous Artifact** buttons take you to the next and previous artifacts, respectively.
- The **Change Criteria** button allows you to change parameters and channels subsequently in semiautomatic mode.
- The table below this contains all the artifacts found, together with their channel and position. If you double-click an entry, the program jumps directly to the corresponding artifact.

The **Undo** and **Redo** buttons allow you to undo and redo changes, respectively. If you want to interrupt what you are doing and resume later, click the **Suspend** button. The Artifact Rejection transform is highlighted in red in the list of history nodes, and all the processing steps carried out continue to apply. You click the **OK** button to conclude your entries.

Select the **Semiautomatic Inspection** radio button, and then make the settings you require on the **Channels** and **Criteria** tabs.

SEMIAUTOMATIC
INSPECTION

On the **Channels** tab, you can select the channels to be included in the search for artifacts (**Enabled Channels**) and exclude channels from the search (**Disabled Channels**).

CHANNELS TAB

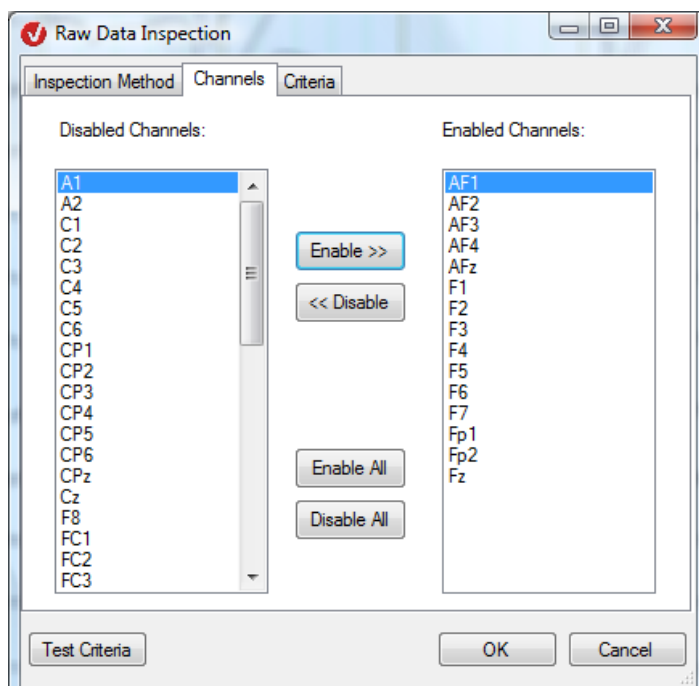


FIGURE 12—31 CHANNELS TAB IN THE RAW DATA INSPECTION DIALOG BOX

On the **Criteria** tab, you specify the criteria for marking channels (individual channel mode enabled) or excluding segments (individual channel mode disabled). CRITERIA TAB

To do this, you make settings on the following tabs: Gradient, Max-Min, Amplitude and Low Activity. Each tab contains the settings for an artifact criterion.

When the gradient criterion is applied, the absolute difference between two neighboring sampling points must not exceed a specific value. GRADIENT CRITERION

On the **Gradient** tab, you can make the following settings:

- If you select the **Check Gradient** check box, the gradient criterion is applied.
- In the **Maximal allowed voltage step** text box, you specify the maximum permissible difference in voltage between two data points.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Gradient (x) Max-Min (x) Amplitude (x) Low Activity (x)

☒ Check Gradient

Maximal allowed voltage step:
50 µV/ms

Mark as bad
before event: 500 ms after event: 500 ms

FIGURE 12—32 GRADIENT TAB ON THE CRITERIA TAB IN THE RAW DATA INSPECTION DIALOG BOX

When the max-min criterion is applied, the difference between the maximum and minimum in a segment must not exceed a specific value. MAX-MIN CRITERION

On the **Max-Min** tab, you can make the following settings:

- If you select the **Check maximal difference of values in intervals** check box, the max-min criterion is applied.
- In the **Maximal Allowed Absolute Difference** text box, you specify the maximum difference in voltage.
- In the **Interval Length** text box, you specify the length of the interval in ms or the period within which the difference in voltage must not exceed the specified value.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Inspection Method Channels Criteria

Gradient (x) **Max-Min (x)** Amplitude () Low Activity (x)

☒ Check maximal difference of values in intervals

Maximal allowed absolute difference:
200 µV

Interval length:
200 ms

Mark as bad
before event: 200 ms after event: 200 ms

FIGURE 12—33 MAX-MIN TAB ON THE CRITERIA TAB IN THE RAW DATA INSPECTION DIALOG BOX

When the amplitude criterion is applied, the amplitude must not violate specified maximum and minimum values. **AMPLITUDE CRITERION**

On the **Amplitude** tab, you can make the following settings:

- If you select the **Check maximal and minimal amplitude** check box, the amplitude criterion is applied.
- In the **Minimal allowed amplitude** text box, you specify the minimum permissible value for the voltage.
- In the **Maximal allowed amplitude** text box, you specify the maximum permissible value for the voltage.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Gradient (x) Max-Min (x) **Amplitude (x)** Low Activity (x)

☒ Check maximal and minimal amplitude

Minimal allowed amplitude:
5 µV

Maximal allowed amplitude:
50 µV

Mark as bad
before event: 500 ms after event: 500 ms

FIGURE 12—34 AMPLITUDE TAB ON THE CRITERIA TAB IN THE RAW DATA INSPECTION DIALOG BOX

When the low activity criterion is applied, the difference between the maximum and minimum in an interval of a selectable length must not exceed a specific value.

LOW ACTIVITY CRITERION

On the **Low Activity** tab, you can make the following settings:

- If you select the **Check low activity in intervals** check box, the criterion for low activity is applied.
- In the **Lowest allowed activity (Max-Min)** text box, you specify the minimum level of activity.
- In the **Interval Length** text box, you specify the length of the interval within which the specified minimum level of activity cannot be violated.
- In the **Mark as bad before event** and **Mark as bad after event** text boxes, you specify the period before and after the actual occurrence of the criterion that is to be marked as an artifact.

Inspection Method Channels Criteria

Gradient (x) Max-Min (x) Amplitude (x) Low Activity (x)

☒ Check low activity in intervals

Lowest allowed activity (Max - Min):
0.5 µV

Interval length:
100 ms

Mark as bad
before event: 500 ms after event: 500 ms

FIGURE 12—35 LOW ACTIVITY TAB ON THE CRITERIA TAB IN THE RAW DATA INSPECTION DIALOG BOX

You can combine the different criteria. As an aid to clarity, the title of each tab indicates whether the criterion is currently applied. **(x)** (parentheses with a cross) indicate that the criterion is currently applied. **()** (parentheses without a cross) indicate that the criterion is not currently applied.

The **Test Criteria** button allows you to test the criteria.

Once you have completed all your settings, click the **OK** button on one of the tabs. A temporary semiautomatic view dialog box appears on the right of the window. This contains a table of the marked artifacts. You can adjust the results of your settings subsequently in the same way as for manual segment selection. Click the **OK** button when the inspection of the EEG is completed.

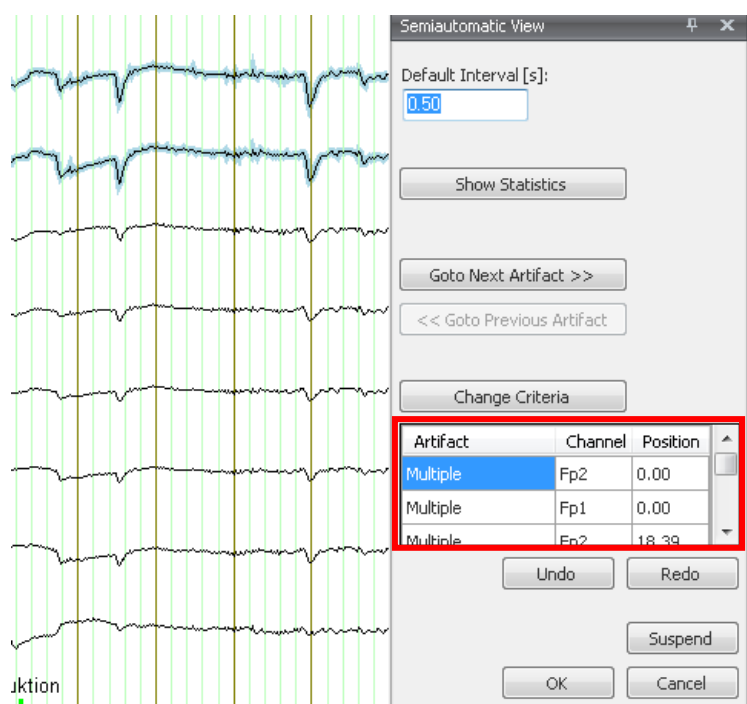


FIGURE 12—36 RDI, SEMIAUTOMATIC INSPECTION, TEMPORARY SEMIAUTOMATIC VIEW DIALOG BOX

The automatic inspection method is the same as the semiautomatic inspection method except that it is not possible to make corrections manually. AUTOMATIC INSPECTION

12.2.6 Ocular Correction ICA

The Ocular Correction ICA transform allows ocular artifacts in the EEG to be corrected. This is an ICA-based correction process using a simplified version of ICA. Ocular artifacts could also be corrected using the ICA transform in semiautomatic mode. Compared with ICA, however, the Ocular Correction transform has the advantage that it offers more comprehensive methods of detecting artifact-related ICA components.

SUMMARY

Since this is an ICA-based correction process, we recommend that you do not work with data containing noise. This is because, in most cases, ocular correction significantly increases noise. We therefore advise you to apply the transform to filtered data.

PREREQUISITE FOR USE

To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Ocular Correction ICA**.

PROCEDURE

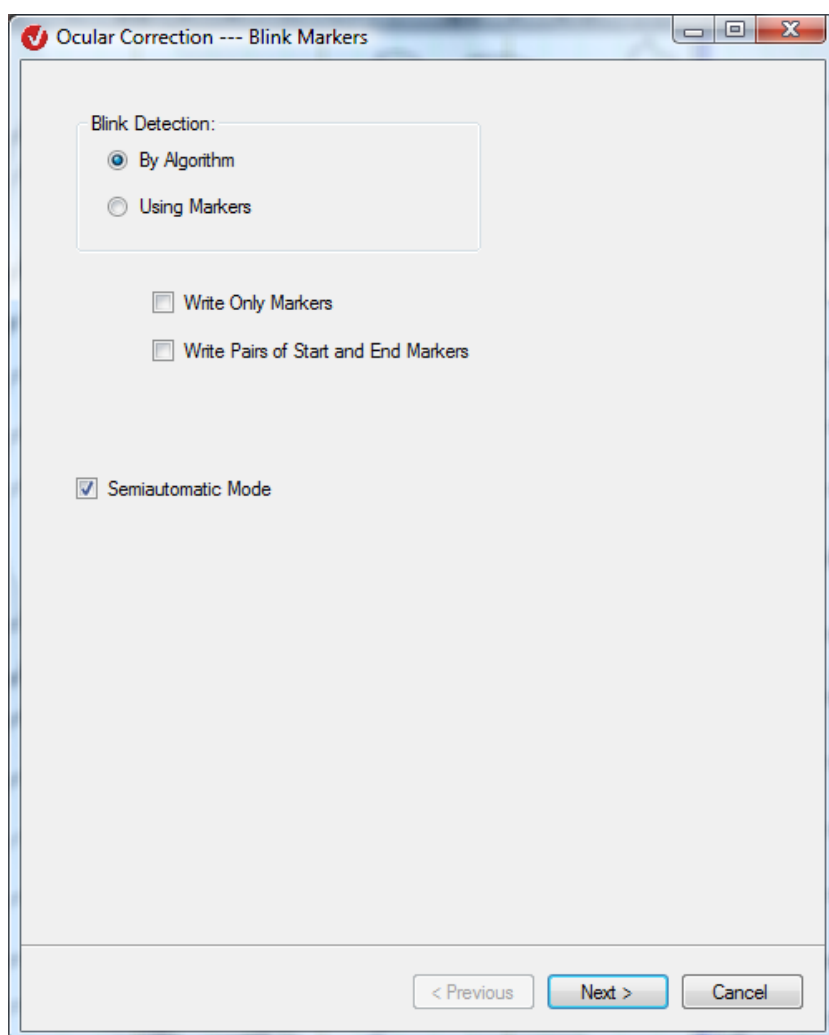


FIGURE 12—37 OCULAR CORRECTION ICA DIALOG, PAGE 1

On the first page of the dialog, you specify how blinks are to be detected.

- If you select the **Using Markers** radio button, blinks that are already marked are used in blink detection.
- If you select the **By Algorithm** radio button, on the other hand, the blinks are detected by means of an algorithm.

If you select the **Write Only Markers** check box, markers are set, but no correction is carried out.

If you select the **Write Pairs of Start and End Markers** check box, the blinks are marked by pairs of markers: one at the start of the blink and one at the end. This check box is independent of the **Write Only Markers** check box.

If you select the **Semiautomatic Mode** check box, semiautomatic mode is activated. This allows you to correct the data set subsequently. If you select the **Write Only Markers** check box and use semiautomatic mode, markers are edited, but no correction is carried out.

The parameters that appear on the second page of the dialog depend on whether you select **By Algorithm** or **Using Markers**:

In the **Detection Algorithm** group box, you select the algorithm to be used to detect blinks.

SECOND PAGE OF THE
DIALOG: "BY
ALGORITHM"

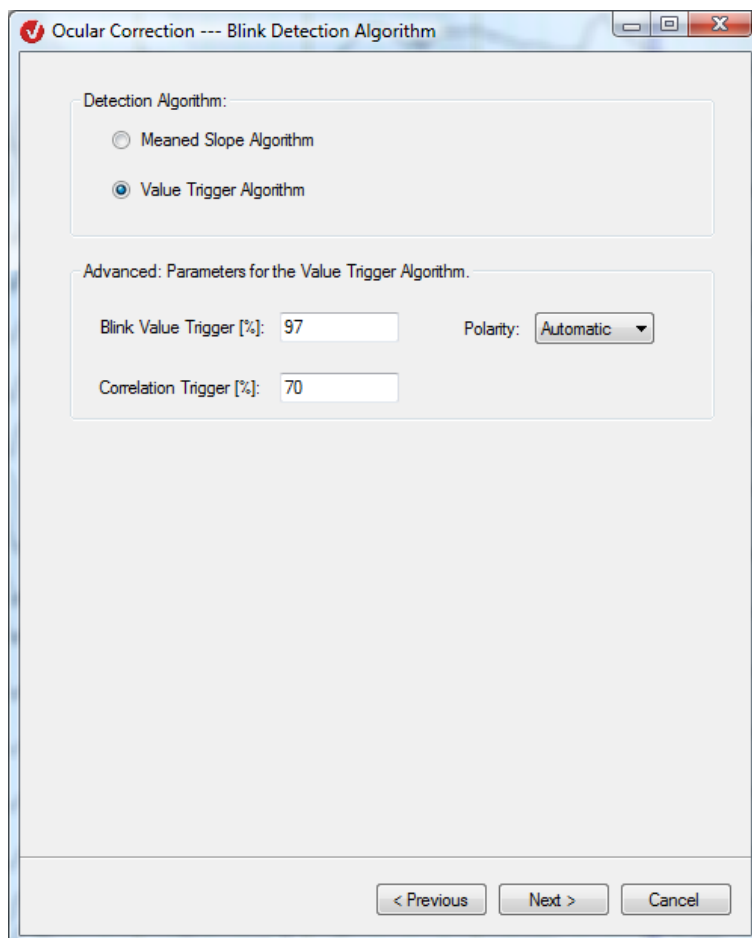


FIGURE 12—38 OCULAR CORRECTION ICA DIALOG, SECOND PAGE IF YOU SELECT "BY ALGORITHM"

You can select one of the following radio buttons:

- **Meaned Slope Algorithm:** This algorithm is the same as the one in BrainVision Analyzer 1.0. No further settings are required. Those sections of the selected VEOG channel with strong variations in gradient are detected. Experience shows that these are the blinks.
- or
- **Value Trigger Algorithm:** Blinks are detected on the basis of their absolute values. The definitive blinks are ascertained by means of a correlation method.

If you select the **Value Trigger Algorithm** radio button, the **Advanced: Parameters for the Value Trigger Algorithm** group box is activated, thus allowing you to make settings in it.

The value in the **Blink Value Trigger [%]** text box specifies the threshold above which blinks are recognized as being blinks. The **Polarity** drop-down list box allows you to specify the polarity of the VEOG recording (positive or negative). If you choose **Automatic**, the polarity is determined automatically.

In the **Correlation Trigger [%]** text box, you enter the minimum correlation required. The possible blinks are correlated with a blink sample, and only when their correlation is higher than the value in this text box are they recognized definitively as blinks.

On this page, you select the markers to be used in blink detection.

SECOND PAGE OF THE
DIALOG: "USING
MARKERS"

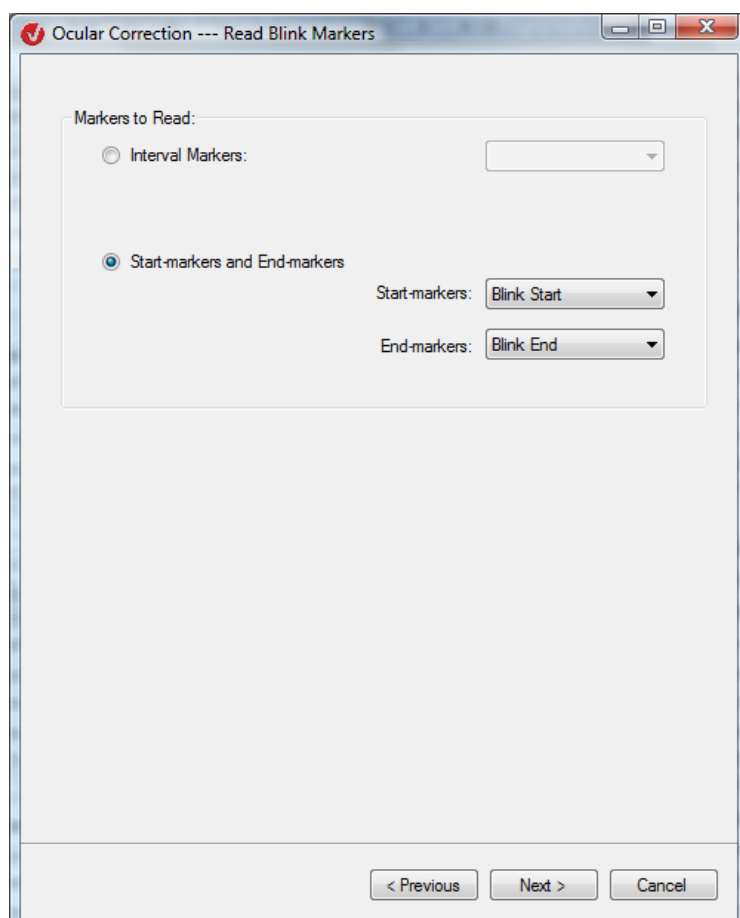


FIGURE 12—39 OCULAR CORRECTION ICA DIALOG, SECOND PAGE IF YOU SELECT "USING MARKERS"

To use an interval marker, you select the **Interval Markers** radio button and choose a marker name from the associated drop-down list box.

To use start and end markers, you select the **Start-markers and End-markers** radio button and choose the markers you want to use from the drop-down list boxes.

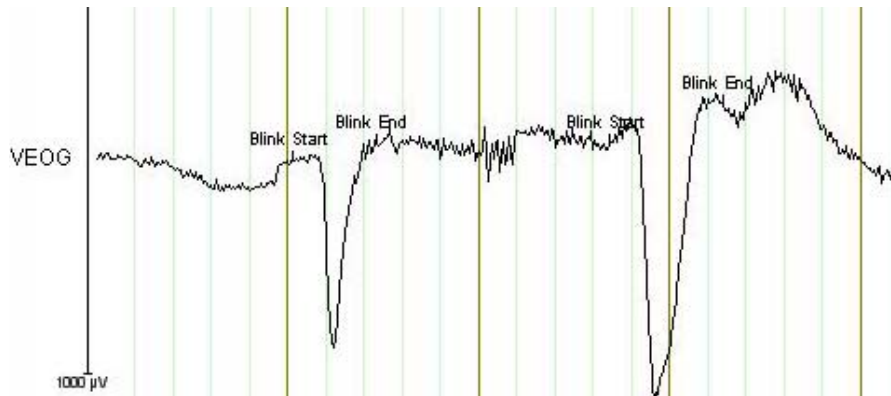


FIGURE 12—40 OCULAR CORRECTION ICA, START AND END MARKERS

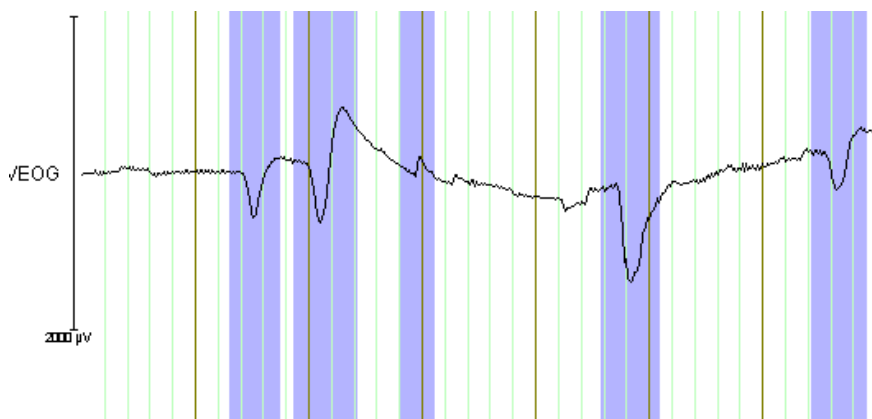


FIGURE 12—41 OCULAR CORRECTION ICA DIALOG, INTERVAL MARKERS

If you do not select the **Write Only Markers** check box, the **Next** button takes you to the next page.

FIGURE 12—42 OCULAR CORRECTION ICA DIALOG, THIRD PAGE IF YOU DO NOT SELECT “WRITE ONLY MARKERS”

On this page, you specify the channels in which the eye activity occurs. You also select the criteria for determining the relevant ICA components for the eye activity. Finally, you specify the percentage of the energy of the ICA components to be removed from the EEG. Energy in this case means global field power or VEOG or HEOG variance.

The following description applies to the components of vertical eye movements.

VERTICAL ACTIVITY
GROUP BOX

Select the **VEOG Channel** check box to set the VEOG channel, and then choose a channel from the associated drop-down list box.

If vertical eye activity was measured with only one electrode during the recording of the EEG, or if it was measured with two electrodes and the difference between the measured values already exists in a separate channel, select the **Use Common Reference** radio button.

On the other hand, if vertical eye activity was measured with two electrodes and the measured values are in two different channels, select the **Use Reference Channel** radio button and then choose the reference channel from the associated drop-down list box.

To find the relevant ICA components for the vertical eye movements, you can choose between two criteria: global field power and relative VEOG variance.

FIND VEOG
COMPONENTS GROUP
BOX

If you select the **Use the Global Field Power** radio button, the components are found by means of global field power. The components with the highest values for global field power, the sum of which exceeds the percentage specified in the **Global Field Power to Delete [%]** text box, are deleted from the EEG.

If you select the **Use Relative VEOG Variance** radio button, the components are found by means of relative VEOG variance. The components with the highest values for relative VEOG variance, the sum of which exceeds the percentage specified in the **VEOG Variance to Delete [%]** text box, are deleted from the EEG.

The following description applies to the components of horizontal eye movements.

HORIZONTAL ACTIVITY
GROUP BOX

Select the **HEOG Channel** check box to set the HEOG channel, and then choose a channel from the associated drop-down list box.

You select the common reference or the reference channel as described above for the **Vertical Activity** group box.

The search for the ICA components relevant to the horizontal eye activity takes place exclusively on the basis of the criterion of the relative HEOG variance in the interval. The components with the highest values for relative HEOG variance, the sum of which exceeds the percentage specified in the **HEOG Variance to Delete [%]** text box, are deleted from the EEG.

FIND HEOG
COMPONENTS GROUP
BOX

Click **Next** to proceed to the fourth page of the dialog, where you make the ICA settings.

The screenshot shows the 'Ocular Correction --- ICA Procedure' dialog box, page 4. The dialog is titled 'Ocular Correction --- ICA Procedure' and has a standard Windows window frame. It contains the following settings:

- ICA Domain:**
 - ☐ Whole Data
 - ☒ Interval:
 - Start [s]: 0
 - Length [s]: 20
 - ☐ Around Blinks
- ICA:**
 - ☒ Infomax.
 - ☐ Fast ICA
 - ☐ Biased Infomax
- ☒ Restricted
- ☐ Extended
- ☐ Bound Number of Blinks: 60
- Number of ICA Steps: 512

At the bottom right, there are three buttons: '< Previous', 'Next >', and 'Cancel'.

FIGURE 12—43 OCULAR CORRECTION ICA DIALOG, PAGE 4

If you select the **Whole Data** radio button, the entire data set is included in the calculation of the ICA matrix. Note that calculating the matrix is very time-consuming when you use the **Whole Data** option. An alternative is to select a large interval (e.g. 2 minutes).

ICA DOMAIN GROUP
BOX

If you select the **Around Blinks** radio button, only intervals defined around blinks are included in the ICA calculation. The middle of each of these intervals is the beginning of a blink, and the interval is twice as long as the blink.

If you want to define an interval to be included in the calculation, select the Interval radio button and enter the beginning and length of the interval in the **Start (s)** and **Length (s)** text boxes.

If you select the **Bound Number of Blinks** check box, you can enter in the associated text box the maximum number of blinks to be included in the calculation. If you do not select the check box, all blinks are included in the ICA calculation. This function is always accessible, regardless of what you select under **ICA Domain**. If you use the **ICA Domain > Whole Data** or **ICA Domain > Interval** function and limit the number of blinks, this only affects blinks used to obtain the relevant VEOG components.

For example, if you select the **Interval** radio button and enter a value of 60 in the **Bound Number of Blinks** text box, the first 60 blinks that occur in this interval are used to obtain the relevant VEOG components. The same applies if you select the **Whole Data** radio button, although in this case the interval is the entire data set.

The radio buttons in the **ICA** group box allow you to choose between the four available ICA methods: **Restricted Infomax**, **Extended Infomax**, **Restricted Fast ICA** and **Extended Fast ICA**.

If you select an infomax method, the **Biased Infomax** check box is available to you. If you select this check box, at each ICA calculation step an additional method [MBJGS97] is used in order to improve the quality of the ICA separation by highlighting particular characteristics of individual components.

In the **Number of Steps** text box, you specify the maximum number of steps to be taken in order to get to the separating matrix (the matrix calculated for component separation). The default value for fast ICA methods is 150. The default value for infomax methods is 512. You can change these default values.

The **Next** button takes you to the fifth page of the dialog.

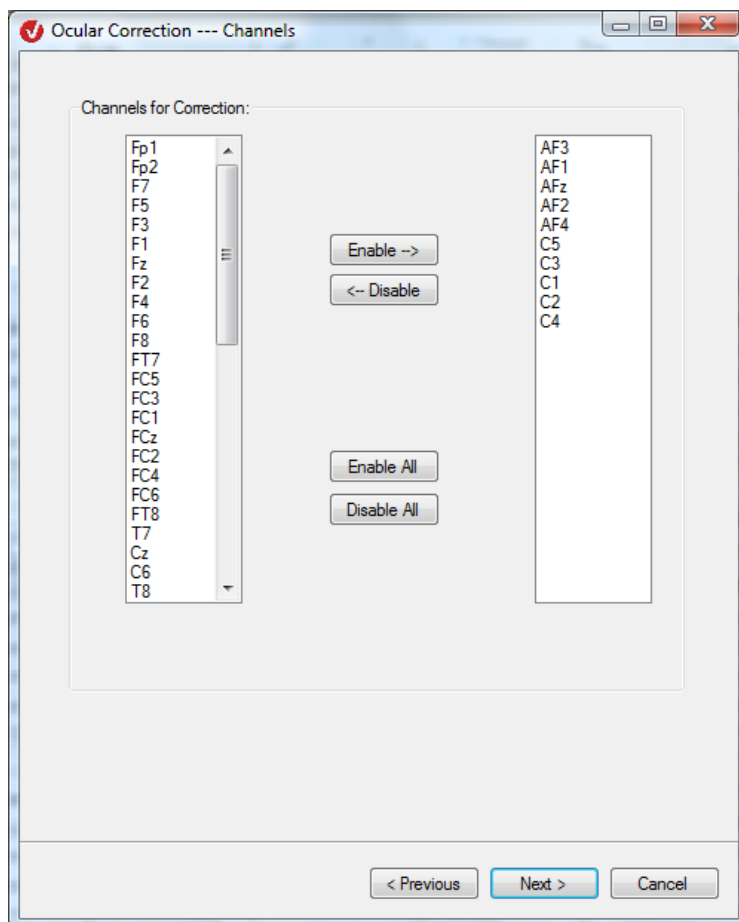


FIGURE 12—44 OCULAR CORRECTION ICA DIALOG, PAGE 5

On the fifth page of the dialog, you select the channels to be included in the ICA calculation and ocular artifact correction.

The **Next** button takes you to the sixth page of the dialog.

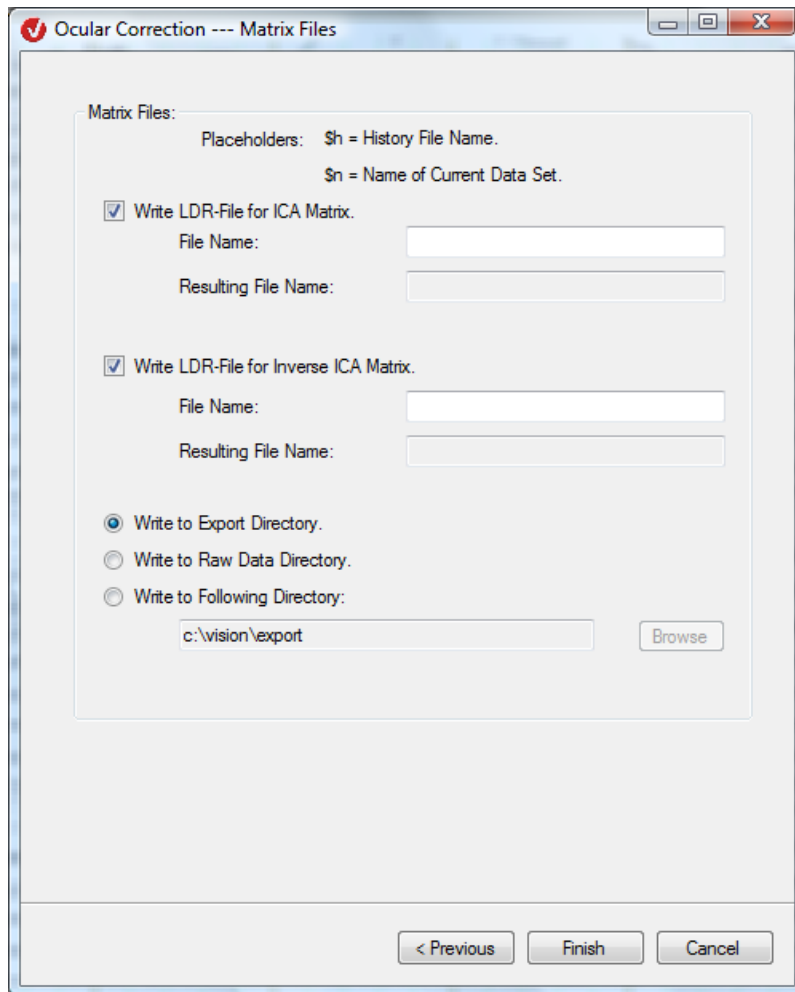


FIGURE 12—45 OCULAR CORRECTION ICA DIALOG, PAGE 6

On this page of the dialog, you specify the LDR-compatible files in which the ICA matrix and the inverse of the matrix are to be saved. The matrix and its inverse in the LDR files can then be used by the linear derivation transform.

If you select the **Write LDR-File for ICA Matrix** check box, the calculated ICA matrix is written to an LDR file. In the **File Name** text box, you enter the name of the associated file. The placeholders \$h (for the name of the history file) and \$n (for the name of the current data set) are available to you. The **Resulting File Name** text box displays the full name of the file.

If you select the **Write LDR-File for Inverse ICA Matrix** check box, the inverse of the ICA matrix is written to an LDR file. The **File Name** and **Resulting File Name** text boxes are available to you again in the same way as those above for the ICA matrix.

There are also three options available to you for exporting the LDR files:

- **Write to Export Directory:** The LDR files are written to the export folder.
- **Write to Raw Data Directory:** The LDR files are written to the raw data folder.
- **Write to Following Directory:** The LDR files are written to the folder you select by clicking the Browse button.

If you selected the **Write Only Markers** check box on the first page of the dialog, the following dialog box is the second – and last – page of the dialog to appear:

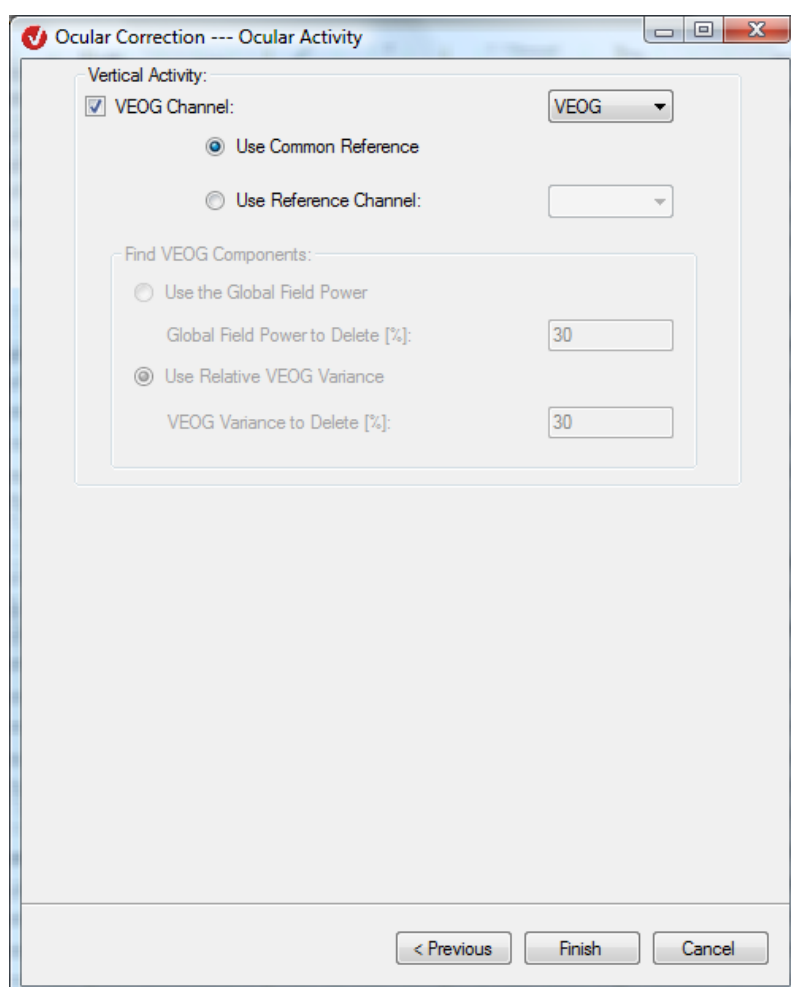


FIGURE 12—46 OCULAR CORRECTION ICA DIALOG, THIRD PAGE IF YOU SELECT “WRITE ONLY MARKERS”

In this case, you simply set the VEOG channel by selecting the **VEOG Channel** check box and then choosing a channel from the associated drop-down list box.

The **Common Reference** and **Use Reference Channel** radio buttons are used as described above (“Vertical Activity” group box without having selected the “Write Only Markers” check box).

If you selected the **Semiautomatic Mode** check box on the first page of the dialog, a semiautomatic view opens after you enter the parameters:

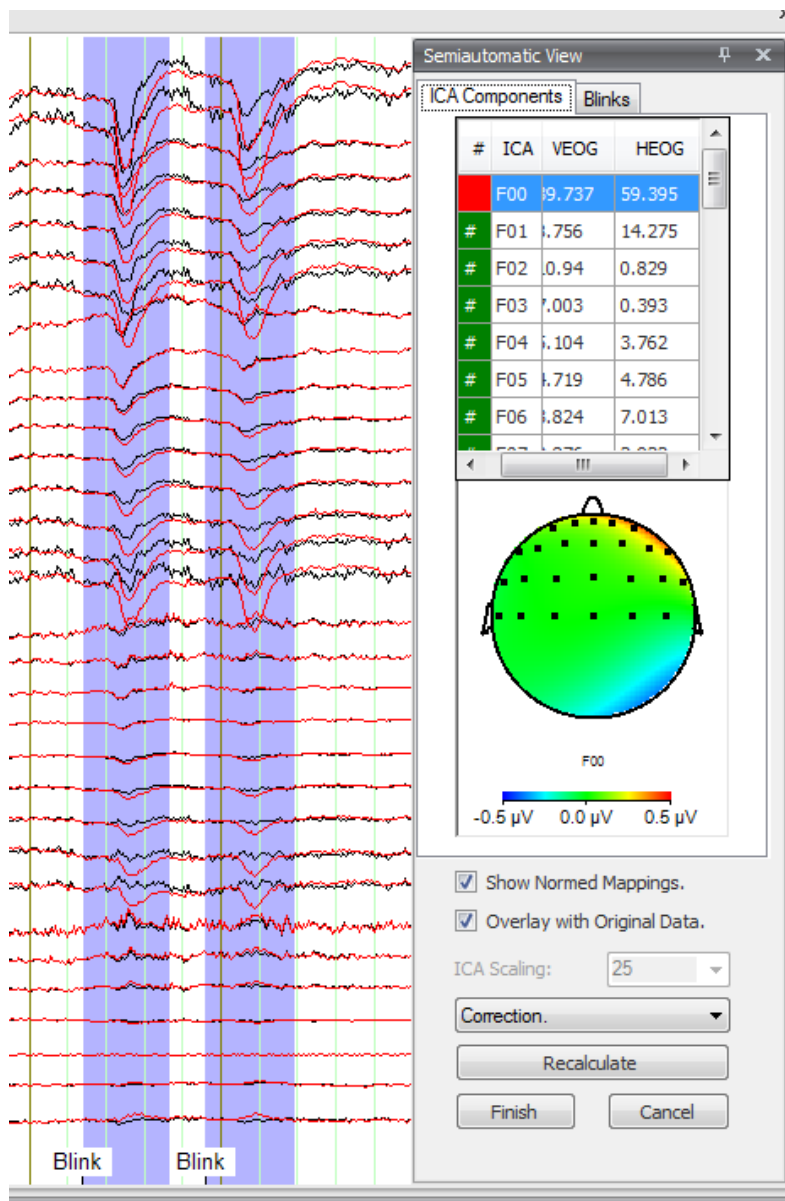


FIGURE 12—47 OCULAR CORRECTION DIALOG, SEMIAUTOMATIC MODE, ICA COMPONENTS TAB

The semiautomatic view contains mobile blink markers. These can be edited in the same way as in semiautomatic mode when using the Edit Markers transform.

The drop-down list box in the temporary semiautomatic view under the map view contains the following four items: **ICA-Components**, **Correction**, **Subtracted** and **Topographies**:

- If you choose **ICA Components**, the components are displayed first, followed by the unselected channels.
- If you choose **Correction**, the corrected data set is displayed without the components highlighted in red.
- If you choose **Subtracted**, the sum of the excluded components (those highlighted in red) is displayed.
- If you choose **Topographies**, the associated map view is displayed next to the components.

If you select the **Show Normed Mappings** check box, the maps and topographies are replaced with standardized maps and topographies.

If you select the **Overlay with Original Data** check box, the current data is overlaid with the original data. This option is important, above all, when you have chosen **Correction** or **Subtracted** from the drop-down list box.

If you want to view unselected channels and calculated ICA components simultaneously, it is difficult to find a scaling factor that suits them both. To increase the size of the ICA components independently of the channels, choose from the **ICA Scaling** drop-down list box the scaling factor or coefficient by which the ICA components are to be multiplied to optimize the display.

You can select one of the four values provided or enter a user-specific value. Note that the **ICA Scaling** list box is only available if you choose **ICA Components** from the drop-down list box above it.

The **Recalculate** button allows you to modify all the settings made. A wizard appears in which you can make your changes. Except for its first page, the wizard is the same as the original dialog.

In the upper part of the temporary semiautomatic view, there are two tabs that allow you to switch between ICA components and blinks.

The table contains the energy values of all the ICA components, depending on the criterion selected on the second page of the dialog (global field power, VEOG variance, HEOG variance).

ICA COMPONENTS TAB

The column on the left has either a green or red background. Green means that the corresponding component has been selected; red means it has not. If you double-click the row, the color switches from green to red.

If you click a row, it turns blue, and the map view (under the table) displays the head topography of the highlighted row (i.e. the selected component).

On this tab, you can carry out a blink inspection. You can accept or reject blinks.

BLINKS TAB

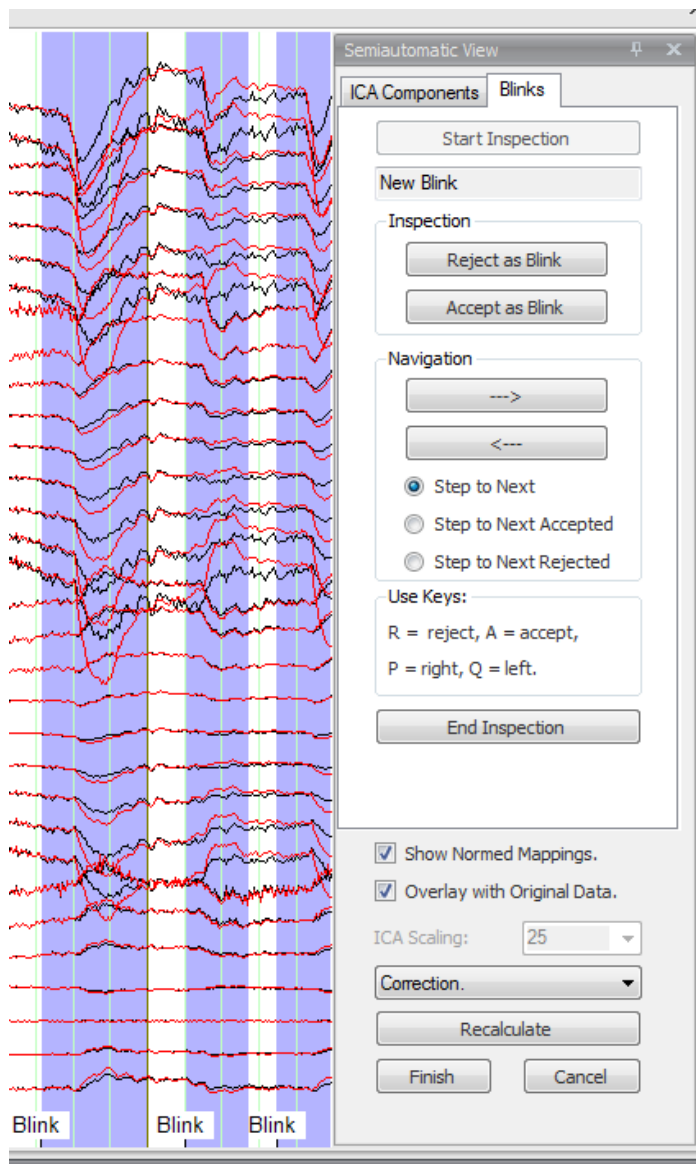


FIGURE 12—48 OCULAR CORRECTION ICA DIALOG, SEMIAUTOMATIC MODE, BLINKS TAB

The **Start Inspection** button activates inspection mode. The first blink in the data set appears in yellow, and the system navigates automatically to this blink.

Color legend (blink statuses):

- Blue: possible blink
- Yellow: currently selected blink
- Green: accepted blink
- Red: rejected blink

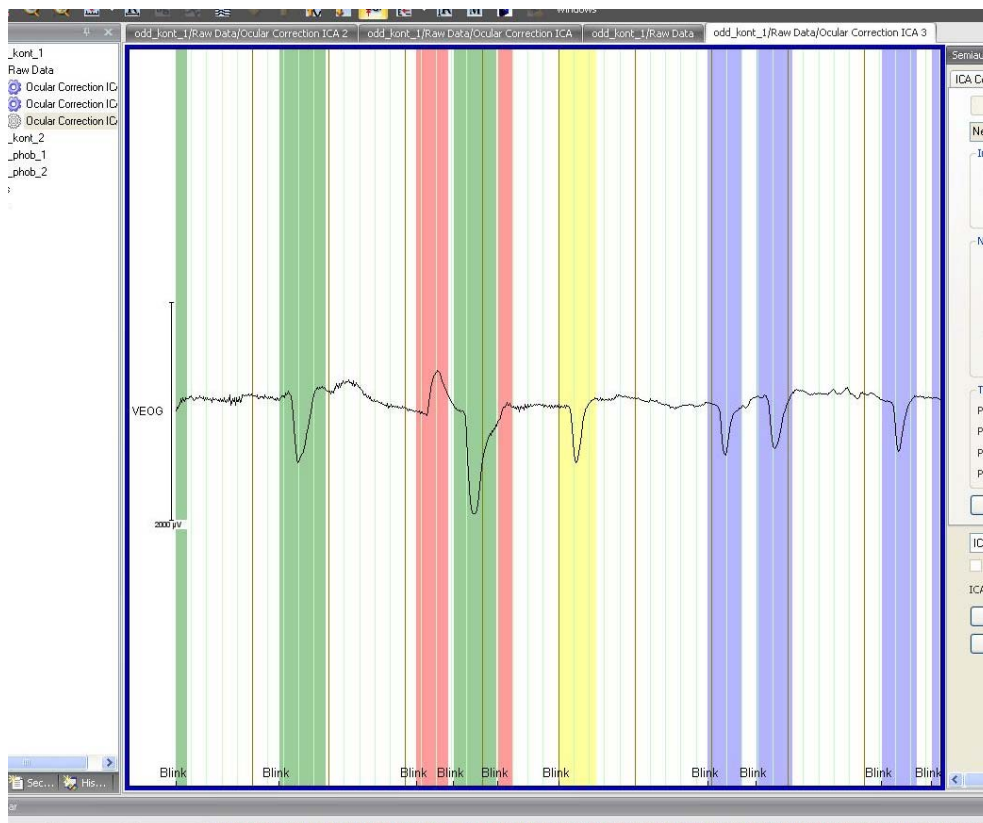


FIGURE 12—49 OCULAR CORRECTION ICA DIALOG, BLINKS IN DIFFERENT COLORS

The status of the currently selected blink appears in the text box under the **Start Inspection** button.

You can use the **Reject as Blink** and **Accept as Blink** buttons to reject and accept blinks. When you click one of these buttons, the focus switches to the next blink.

The **Navigation** group box allows you to navigate around the data set. The buttons **-->** and **<--** take you to the next and previous blinks that meet one of the criteria **Step to Next** (next marker), **Step to Next Accepted** (next accepted marker) or **Step to Next Rejected** (next rejected marker).

The **To Use Keys** group box explains how to use the keys on the PC keyboard to navigate:

- You press the “R” key to reject the blink.
- You press the “A” key to accept the blink.
- You press the “P” key to navigate to the right.
- You press the “Q” key to navigate to the left.

Note that you can only use these keys when the semiautomatic view is active.



The **End Inspection** button terminates inspection mode.

If you interrupt the inspection by clicking **Recalculate** or terminate it with **Finish**, only red markers are rejected. All other markers (blue, yellow and green) are accepted.



If you select the **Write Only Markers** check box, the temporary semiautomatic view contains only the control elements for the blink inspection.

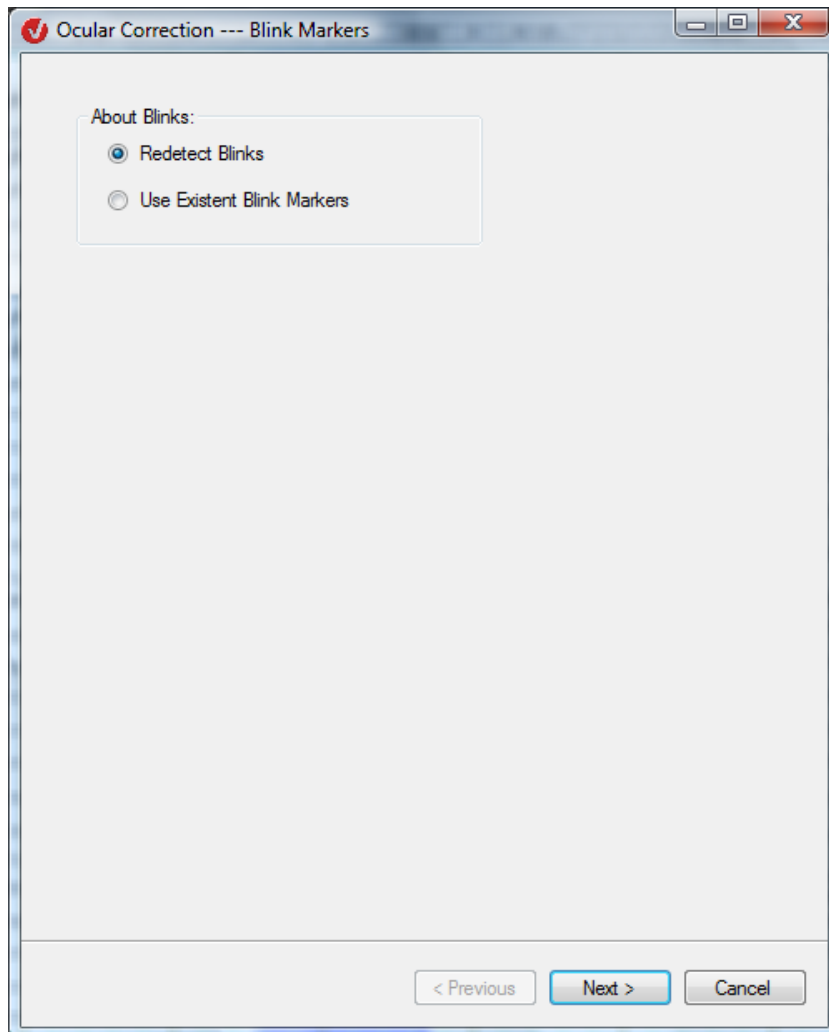


FIGURE 12—50 OCULAR CORRECTION ICA DIALOG, FIRST PAGE IF YOU CLICK THE “RECALCULATE” BUTTON

On the alternative first page, you can make entries relating to the blinks:

If you select the **Redetect Blinks** radio button, the blinks are detected again.

If you select the **Use Existent Blink Markers** radio button, the blink markers that have not been rejected by the user are used in the subsequent calculation.

Ocular artifact correction is ICA-based. It runs analogously to the correction carried out by the ICA transform: Those ICA components that are relevant to the feature to be corrected are subtracted from the EEG. In comparison to the ICA transform, the Ocular Correction transform offers two functions for the specific task of correcting ocular artifacts: automatic and manual detection of blinks and automatic detection of ICA components that are relevant to the eye activity. The blink markers are determined by means of the same method used for non-ISA-based ocular correction in Version 1.0 of the Analyzer. Moreover, they can be edited in semiautomatic mode.

METHOD

The relevant ICA components are selected by means of the following methods:

- 1) The global field power method calculates the share of each ICA component in the global field power of the data set using only the intervals containing blinks. It is not important to this method which values the VEOG channel assumes. In other words, the VEOG channel is required exclusively for the detection of blinks.
- 2) The method of relative VEOG variance calculates the share of each ICA component in the variance of the selected VEOG channel using only the intervals containing blinks. If the VEOG channel itself is not included in the ICA calculation, this calculation is replaced by a correlation calculation.
- 3) The HEOG variance method calculates the share of each ICA component in the variance of the selected HEOG channel across the whole ICA range. If the HEOG channel itself is not included in the ICA calculation, this calculation is replaced by a correlation calculation.

The advantage of semiautomatic mode is that the user can use the transparent blink markers to assess the relevance of the ICA components and exclude the relevant components.

[MBJGS97] S. Makeig, A.J. Bell, T.-P. Jung, D. Ghahremani, T.J. Sejnowski, Blind separation of auditory event-related brain responses into independent components. Proc. Natl. Acad. Sci. USA, 94 (1997), 10979-10984.

REFERENCES

12.2.7 Ocular Correction

The Ocular Correction transform eliminates or at least reduces the effect of eye movements on the EEG. The Gratton & Coles method [GCD83] is used for this. SUMMARY

To display the dialog box for the transform, you choose **Transformations > Artifact Rejection/Reduction > Ocular Correction**. PROCEDURE

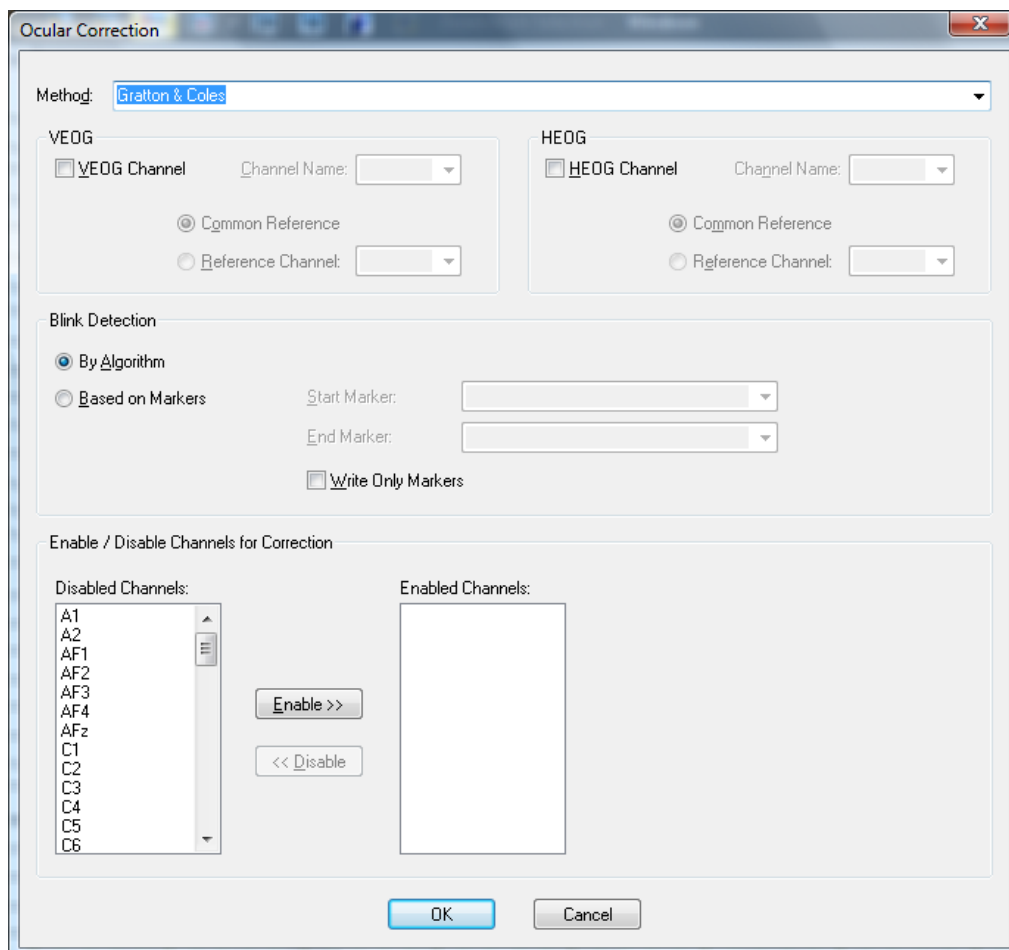


FIGURE 12—51 OCULAR CORRECTION DIALOG BOX

You can make the following settings:

The method used appears in the **Method** drop-down list box. The Gratton & Coles algorithm and a slightly modified version of it, “Gratton & Coles without Raw Average Subtraction”, are available for selection. These algorithms and their differences are described below.

Select the **VEOG Channel** check box if there is a VEOG channel in the EEG.

VEOG GROUP BOX

Choose the channel's name from the **Channel Name** drop-down list.

If you select the **Common Reference** radio button, it is assumed that the reference electrode of the VEOG channel is shorted to the common reference.

If, on the other hand, you select the **Reference Channel** radio button, it is assumed that the reference electrode of the VEOG channel is not identical to the common reference.

The following principle applies: If your VEOG signal takes the form of a single channel, you should select **Common Reference**, because, as far as the program is concerned, the signal is a unipolar signal and thus shorted to the common reference. However, if your VEOG signal takes the form of two individual channels, such as "VEOG Upper" and "VEOG Lower", select **Reference Channel** and then the second channel from the list of available channels. In blink detection, the program will then treat these two channels as a bipolar channel pair.

The functions of the **HEOG** group box for the HEOG channel correspond to the functions of the **VEOG** group box for the VEOG channel.

HEOG GROUP BOX

You can specify:

BLINK DETECTION
GROUP BOX

- Whether the blinks are to be searched for in the VEOG channel selected above (**By Algorithm** radio button)
- Or whether you have detected the blinks that are relevant to you without using the Ocular Correction transform (using a macro based on your own algorithm, for example) and have marked them with a "Blink Start" and "Blink End" marker (**Based on Markers** radio button)

To do this, specify the names of the desired markers in the **Start Marker** and **End Marker** drop-down list boxes.

If you select the **By Algorithm** radio button, you can also select the **Write Only Markers** check box to specify that no data correction is carried out in this analysis step and that the blinks found are merely marked in the data set. If you want to change these markers subsequently, you use the relevant functions in the semiautomatic view of the Ocular Correction ICA transform.

Please note that on the first page of the dialog for the Ocular Correction ICA transform, the **Write Only Markers** and **Write Pairs of Start and End Markers** check boxes must be selected.



You can carry out the actual ocular correction in a subsequent step by selecting the **Based on Markers** radio button.

In this group box, you select the channels for which correction is to be carried out (**Enabled Channels**).

ENABLE / DISABLE
CHANNELS FOR
CORRECTION GROUP
BOX

The VEOG and HEOG channels can be used for correction. This is not advisable, however, since the information contained in these channels is largely lost.

The information loss is as follows: If you use an ocular channel with the **Common Reference** radio button selected, this channel has a constant signal after the correction. On the other hand, if you use an ocular channel with the **Reference Channel** radio button selected, both the ocular channel and the reference channel have the same signal after the correction. It is essential to take this into account when reusing the channels as pure data channels.

The Gratton & Coles algorithm corrects ocular artifacts by subtracting the voltages of the ocular channels, multiplied by a channel-independent correction factor, from the EEG channels.

METHOD

The correction factors are calculated in several steps.

In the first step, a blink detection method is applied to the vertical ocular channel in order to calculate separate factors within and outside blinks.

In the next step, after the subtraction of the average, an average of the various events (i.e. of the different segmentation markers) is obtained for each channel.

To calculate the correction factors, in the third step this average is subtracted from the channel in each segment in order to prevent the event-correlated data from being included in the calculation. This step is not included if you selected the "Gratton & Coles without Raw Average Subtraction" method.

In the final step, the correction factors are calculated by linear regression.

[GCD83] G. Gratton, M.G.H. Coles, E. Donchin, A new method for off-line removal of ocular artifact. *Electroencephalography and Clinical Neurophysiology*, 55 (1983), 468-484.

REFERENCES

12.3 Transforms in the Frequency and Component Analysis group

12.3.1 ICA (Independent Component Analysis)

The ICA transform is used to split the EEG signals up into independent components using information theory methods. It is assumed here that EEG signals are a linear combination of independent components (independent as defined in information theory). The ICA transform separates the independent virtual components from the complex signals and analyzes them.

SUMMARY

The purpose of the ICA transform in what is known as “blind source separation” is to reconstruct source signals from a combination of these signals. Both the source signals and the combination are unknown, so assumptions are made about the signals and how they are combined. It is assumed that the signals to be reconstructed are statistically independent of each other. You will find detailed information on the theory used in [BS95], [Car98] and [MBJS96]. At this point, it is enough to say that the ICA transform is a purely statistical (i.e. mathematical) method. It is based on the above assumptions and does not use any additional physiological information. It is up to you, the user of the transform, to check that the assumptions are correct and that they correspond to the physiological conditions. This is critical to the meaningfulness of the results generated by the ICA transform.

The result of the ICA transform is a set of components that are defined analogously to EEG channels in the time domain. In addition, the ICA transform provides a transformation matrix by means of which the components can be calculated from the channels. The infomax algorithm or the fast ICA algorithm is used to determine this weight matrix. The infomax algorithm is an iterative gradient method used to estimate maximum likelihood and is described in [MBJS97], for example. The fast ICA algorithm is an iterative fixed-point method used to minimize negentropy and is described in [HKO01], for example.

Please note that the term “fast” has a slightly different meaning when it is used in the name of the fast ICA algorithm from when it is used in the Fast Fourier transform (FFT), for example. The Fast Fourier transform is an accelerated method that returns the same results as a conventional Fourier analysis. ICA with infomax and fast ICA are two different methods of calculating independent components. Only in an ideal case do they return the same results. Fast ICA has stricter requirements in terms of the separability of components. If these requirements are met, it calculates more quickly than conventional methods, hence its name. If the requirements for good component separability are not met, calculation with fast ICA is generally slower than with other methods. In this case, the suitability of the initial data for an ICA analysis should be examined.



To display the dialog box for the transform, you choose **Transformations > Frequency and Component Analysis > ICA**.

PROCEDURE

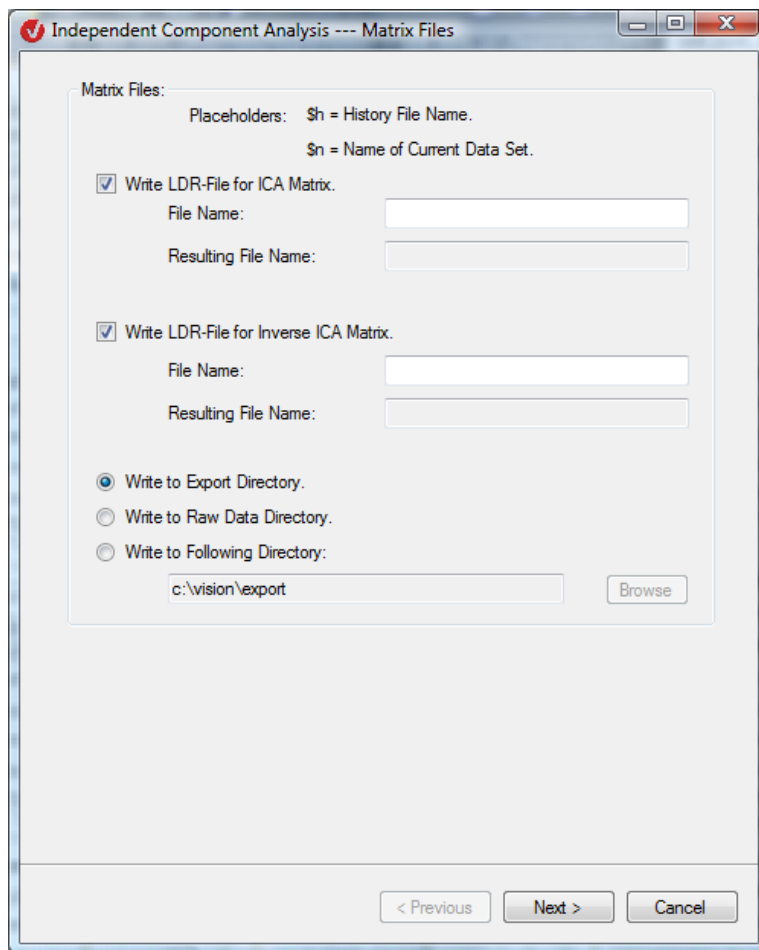


FIGURE 12—52 ICA DIALOG, PAGE 1

On the first page of the ICA dialog, you specify the LDR-compatible files in which the ICA matrix and the inverse of the matrix are to be saved. The matrix and its inverse in the LDR files can then be used by the linear derivation transform.

If you select the **Write LDR-File for ICA Matrix** check box, the calculated ICA matrix is written to an LDR file. In the **File Name** text box, you enter the name of the associated file. The placeholders \$h (for the name of the history file) and \$n (for the name of the current data set) are available to you. The **Resulting File Name** text box displays the full name of the file.

If you select the **Write LDR-File for Inverse ICA Matrix** check box, the inverse of the ICA matrix is written to an LDR file. The **File Name** and **Resulting File Name** text boxes are available to you again in the same way as those above for the ICA matrix.

There are also three options available to you for exporting the LDR files:

- **Write to Export Directory:** The LDR files are written to the export folder.
- **Write to Raw Data Directory:** The LDR files are written to the raw data folder.
- **Write to Following Directory:** The LDR files are written to the folder you select by clicking the **Browse** button.

Click **Next** to go to the second page of the dialog.

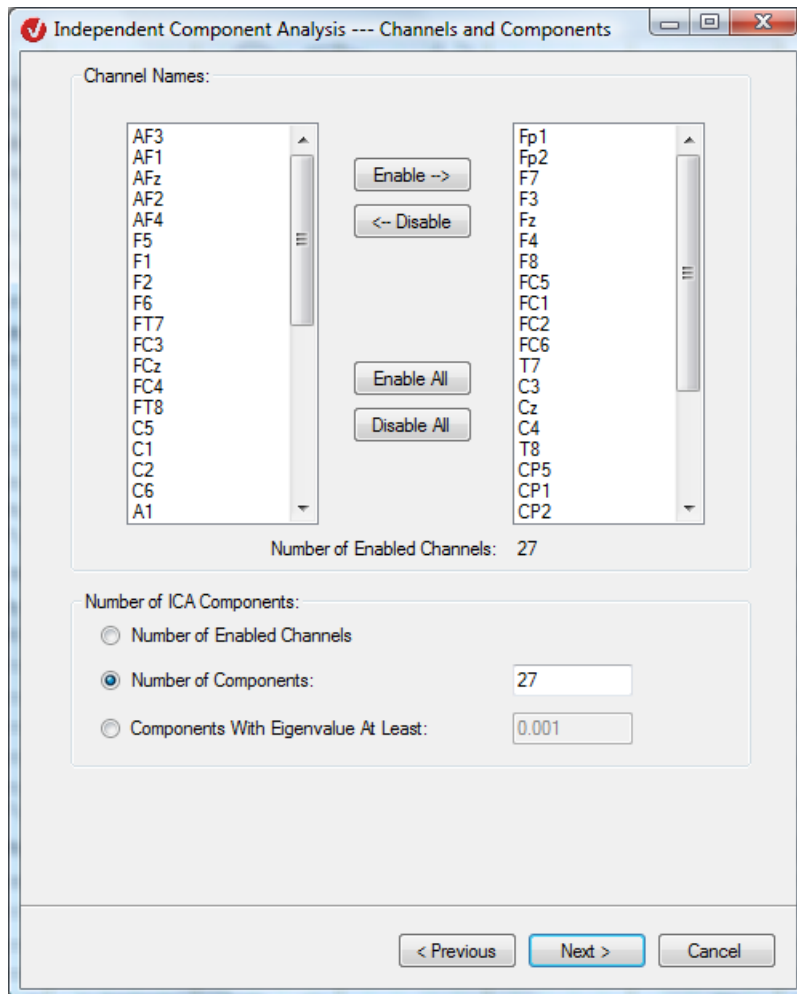


FIGURE 12—53 ICA DIALOG, PAGE 2

On the second page, you specify the size of the ICA matrix. The width of the matrix is the number of channels selected, and its height is the number of components to be calculated.

In the **Channel Names** group box, you specify which channels are to be included in the ICA calculation. The number of selected channels is displayed below the two list boxes (**Number of Enabled Channels**).

In the **Number of ICA Components** group box, you specify how many ICA components are to be calculated:

- By default, the number of components calculated is equal to the number of channels selected (the **Number of Enabled Channels** radio button is selected).
- You can also specify that a lower number of components is calculated. To do this, you select the **Number of Components** radio button and enter the number of components to be calculated in the associated text box.

If you erroneously enter a value in this text box that is higher than the number of selected channels, this entry is ignored and the maximum possible number of components (i.e. number of selected channels) is calculated.



- You can also specify that the number of components to be calculated is determined automatically by selecting the **Components With Eigenvalue At Least** radio button.
- If you select this radio button, the covariance matrix of the signals is diagonalized (PCA method). The resulting values are referred to as eigenvalues.

Those ICA components that correspond to the smallest eigenvalues provide little information. In most cases, they consist of noise and can therefore interfere with the calculation of the ICA matrix. They should therefore not be included in the calculation of the ICA matrix. To this end, you enter a limit value in the **Components With Eigenvalue At Least** text box (default value: 0.001). The components whose eigenvalues are under this limit value are not included in the calculation of the ICA matrix.

Click **Next** to go to the third page of the dialog.

Independent Component Analysis --- ICA Domain

☐ Use Whole Data ☒ Use Interval:

Range:

Start [s]: 0 Length [s]: 10

☐ Use Equal Intervals Around Markers:

Marker and Range:

Name:

Start [ms]: -100 End [ms]: 1000

☐ Use Interval Markers:

Interval Marker:

Name:

☐ Between Start and End Markers:

Start and End Markers:

Start: End:

< Previous Next > Cancel

FIGURE 12—54 ICA DIALOG, PAGE 3

Because the ICA transform is a statistical method, it is not essential to use the whole length of the data set in the calculation. Specific ranges of the EEG signal are often more meaningful than the whole data set as far as the components are concerned. This is why the third page of the dialog allows you to limit the range of the EEG that is used in order to both limit the calculation to statistically significant ranges and improve performance.

You can define the range of the EEG by means of five different methods. For methods 3, 4 and 5, the ICA range is composed of the separately defined intervals by means of markers.

- (1) **Use Whole Data:** The entire data set is used for the calculation.
- (2) **Use Interval:** The calculation applies only to a specific interval, the beginning and length of which you specify in the **Start [s]** and **Length [s]** text boxes in the **Range** group box.
- (3) **Use Equal Intervals Around Markers:** Intervals of equal size around the markers are used.

From the **Name** drop-down list box in the **Marker and Range** group box, you choose the name of a marker. You then specify the beginning and end of the interval in relation to the selected marker in the **Start [ms]** and **End [ms]** text boxes. Example: If you enter a value of -100 in the **Start [ms]** text box and a value of 500 in the **End [ms]** text box, the interval begins 100 ms before the selected marker and has a length of 600 ms.

If the selected marker is an interval marker, the interval is defined in relation to the starting point of this marker.



- (4) **Use Interval Markers:** Intervals defined exclusively by interval markers are used.

From the **Name** drop-down list box in the **Interval Marker** group box, you choose the name of the marker to be used.

- (5) **Between Start and End Markers:** Intervals defined by start and end markers are used.

From the drop-down list boxes in the **Start and End Markers** group box, you choose the names of the start and end markers to be used.

If either or both of the selected markers are interval markers, the interval is defined in relation to the starting point of the marker. In other words, the end of the interval is defined by the starting point of the end marker.



If an end marker occurs after several successive start markers, the interval starts at the first start marker in the series and ends at the end marker. If this end marker is followed by further end markers, these are ignored. The next interval starts at the next start marker.

An interval is not recognized as an interval unless it is concluded by an end marker.

Click **Next** to go to the fourth page of the dialog.

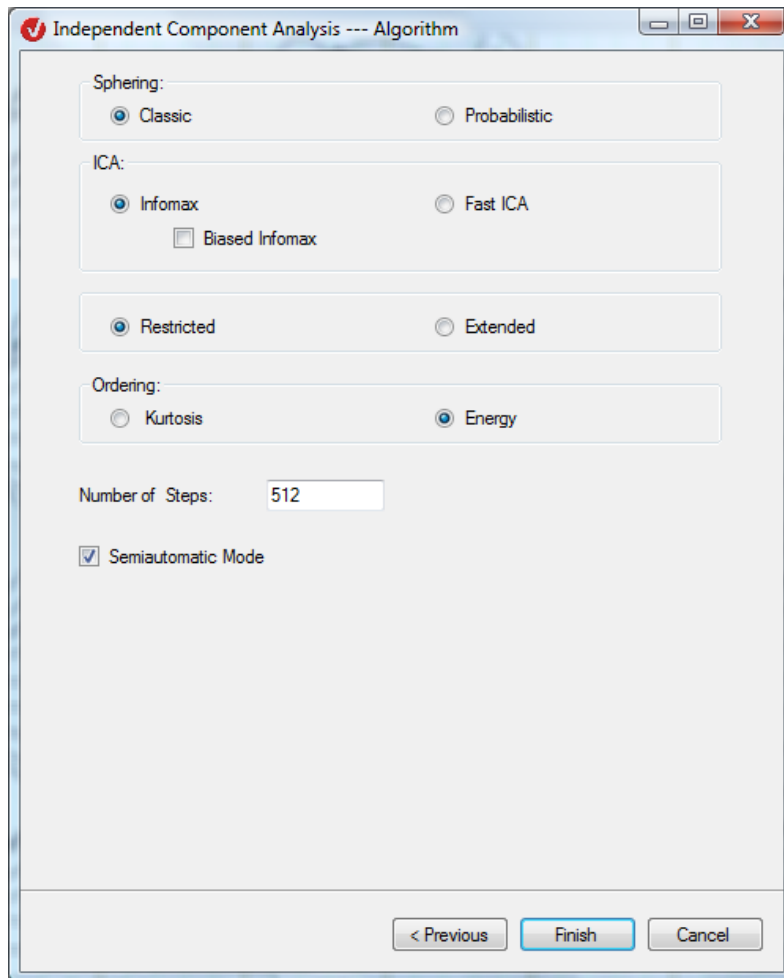


FIGURE 12—55 ICA DIALOG, PAGE 4

In the **Sphering** group box, you can choose between two sphering methods. Sphering is for the preliminary processing of the EEG signals:

- **Classic** (conventional sphering): The conventional method treats all components equally.
- **Probabilistic** (probabilistic sphering): The combination of probabilistic sphering and any ICA method is referred to in the literature as probabilistic ICA (PICA). The noise is filtered out of the EEG data set using the probabilistic method.

If you are uncertain about the correct number of components, we recommend that you use this method. The reason for this is that, if the ICA transform is used with an incorrect number of components, it causes noise or exacerbates existing noise, thus contaminating components. This is because the noise has a Gaussian structure, and the Gaussian components can only be separated with great difficulty using the ICA method.

The radio buttons in the **ICA** group box allow you to choose between the four available ICA methods: **Restricted Infomax**, **Extended Infomax**, **Restricted Fast ICA** and **Extended Fast ICA**.

If you select an infomax method, the **Biased Infomax** check box is available to you. If you select this check box, at each ICA calculation step an additional method ([MBJGS97]) is used in order to improve the quality of the ICA separation by highlighting particular characteristics of individual components.

In the **Number of Steps** text box, you specify the maximum number of steps to be taken in order to get to the separating matrix (the matrix calculated for component separation). The default value for fast ICA methods is 150. The default value for infomax methods is 512. You can change these default values.

In the **Ordering** group box, you select one of the following sort criteria for the components:

- **Kurtosis** (in descending order)
- **Energy** (in descending order)

Kurtosis (K) is a numerical estimate of the peakedness of a curve (graph). The following distinctions are drawn:

- $K = 0$ means normal peak, Gaussian or mesokurtic.
- $K > 0$ means steep peak, super-Gaussian or leptokurtic.
- $K < 0$ means flat peak, sub-Gaussian or platykurtic.

Note that the restricted infomax method, unlike the extended infomax method, can only separate components with positive kurtosis ($K > 0$).

Semiautomatic mode allows you to experiment with the result of the exclusion of certain components and the reconstruction of the data set from the other components. To do this, you select the **Semiautomatic Mode** check box. After you enter the parameters, a semiautomatic view appears.

Click **OK** to start the ICA calculation.

Please note the following points about the display:

- The names of the components consist of the letter “F” followed by a number – in accordance with the selected sort criterion (kurtosis or energy).
- If you include all the channels in the ICA calculation, only the components are displayed.

On the other hand, if you do not select all the channels, the components are displayed at the top. The unselected channels are displayed below these in the order in which they occur in the original EEG.

- Channel markers that were originally on a selected channel automatically turn into global markers.

Channel markers that were originally on an unselected channel remain in position on that channel.

Markers that were originally global remain global.

- If the ICA components are displayed with unselected channels, their amplitude is considerably lower than that of the channels. To obtain a better display, select one, several or all components and view them separately.

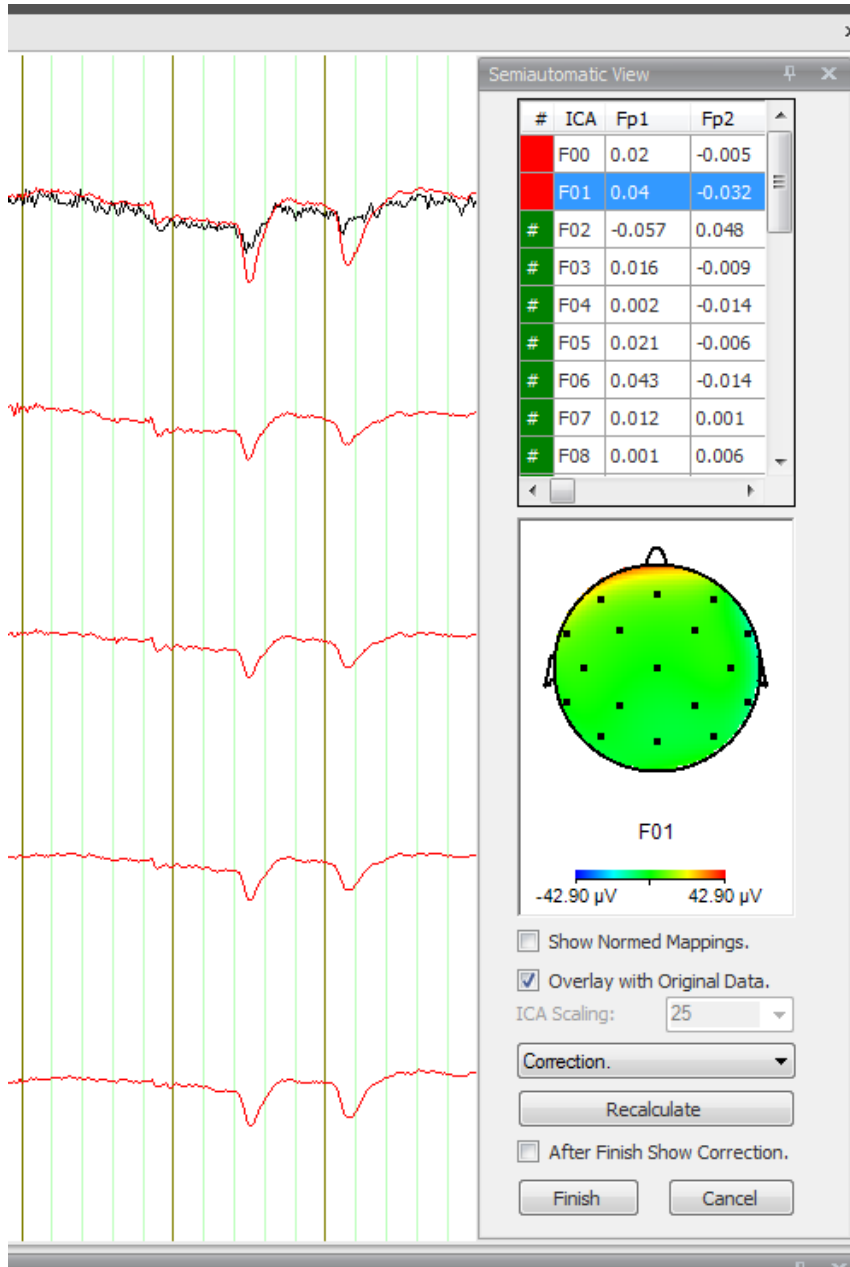


FIGURE 12—56 SEMIAUTOMATIC MODE WITH THE TEMPORARY SEMIAUTOMATIC VIEW DIALOG BOX

The table in the upper part of the semiautomatic view contains the components and the names of the selected channels. The values in the columns represent the separating matrix.

The column on the left has either a green or red background. Green means that the corresponding component has been selected for the reconstruction process, and red means it has not. If you double-click the row, the color switches from green to red.

If you click a row, it turns blue, and the map view (under the table) displays the head topography of the highlighted row (i.e. the selected component).

The drop-down list box under the mapping view contains the following four items: **ICA-Components**, **Correction**, **Subtracted** and **Topographies**.

- If you choose **ICA Components**, the components are displayed first, followed by the unselected channels, as in semiautomatic mode.
- If you choose **Correction**, the reconstructed data set is displayed without the components highlighted in red.
- If you choose **Subtracted**, the reconstructed data set is displayed using only the components highlighted in red.
- If you choose **Topographies**, the associated map view is displayed next to the components.

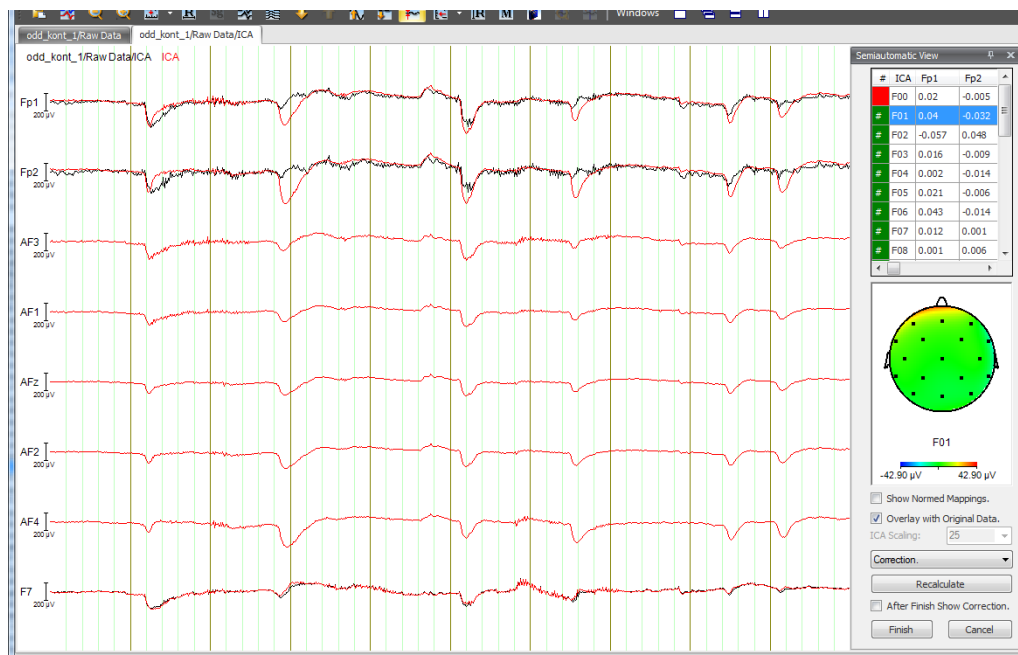


FIGURE 12—57 “CORRECTION” OPTION, COMPONENT F00 NOT SELECTED (RED)

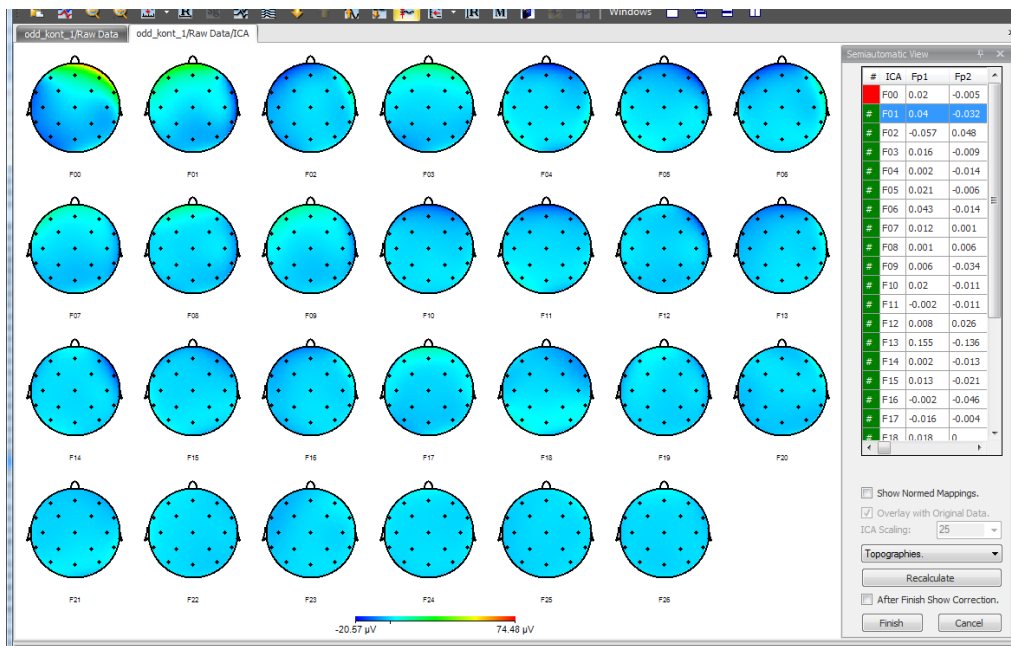


FIGURE 12—58 “TOPOGRAPHIES” OPTION

If you select the **Show Normed Mappings** check box, the maps and topographies are replaced with standardized maps and topographies.

If you select the **Overlay with Original Data** check box, the current data is overlaid with the original data. This option is important, above all, when you have chosen **Correction** or **Subtracted** from the drop-down list box.

If you want to view unselected channels and calculated ICA components simultaneously, it is difficult to find a scaling factor that suits them both. To increase the size of the ICA components independently of the channels, choose from the **ICA Scaling** drop-down list box the scaling factor or coefficient by which the ICA components are to be multiplied to optimize the display.

You can select one of the four values provided or enter a user-specific value. Note that the **ICA Scaling** list box is only available if you choose **ICA Components** from the drop-down list box above it.

The **Recalculate** button allows you to modify all the settings made. The **ICA** dialog appears again to allow you to make your changes.

If you select the **After Finish Show Correction** check box, when you click the **Finish** button, the reconstructed data set is displayed without the components highlighted in red. If you do not select the check box, the ICA components are displayed first, followed by the unselected channels:

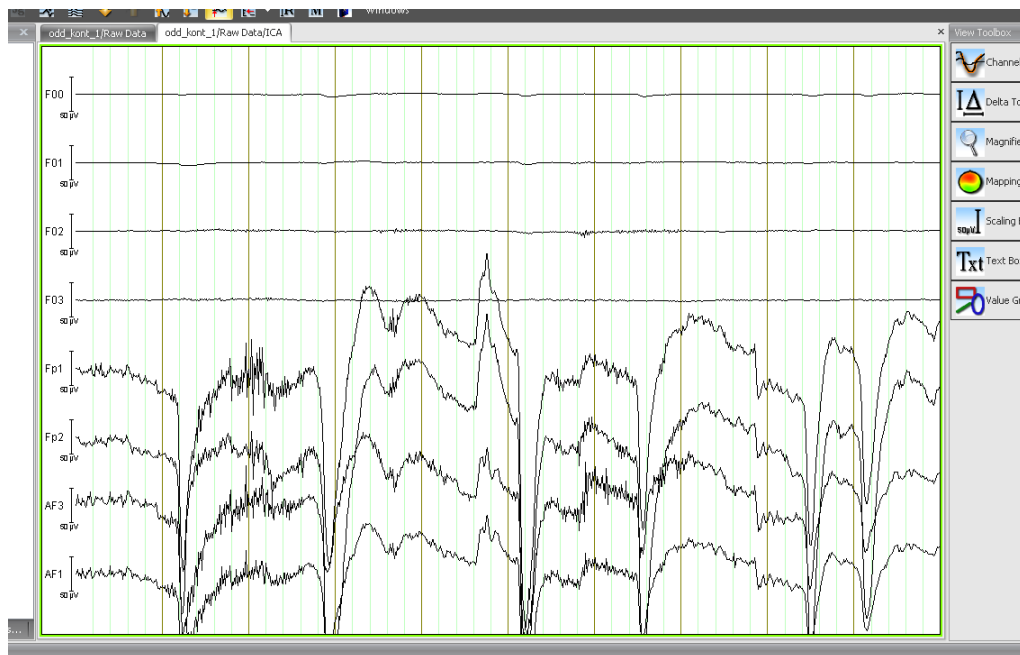


FIGURE 12—59 DISPLAY OF THE ICA COMPONENTS FIRST, FOLLOWED BY THE UNSELECTED CHANNELS

If you have not selected semiautomatic mode, or if you have not selected the **After Finish Show Correction** check box in semiautomatic mode, the following user properties are automatically saved in the node created: MeanValue, ICAMatrix, InverseMatrix, NumberComponents:

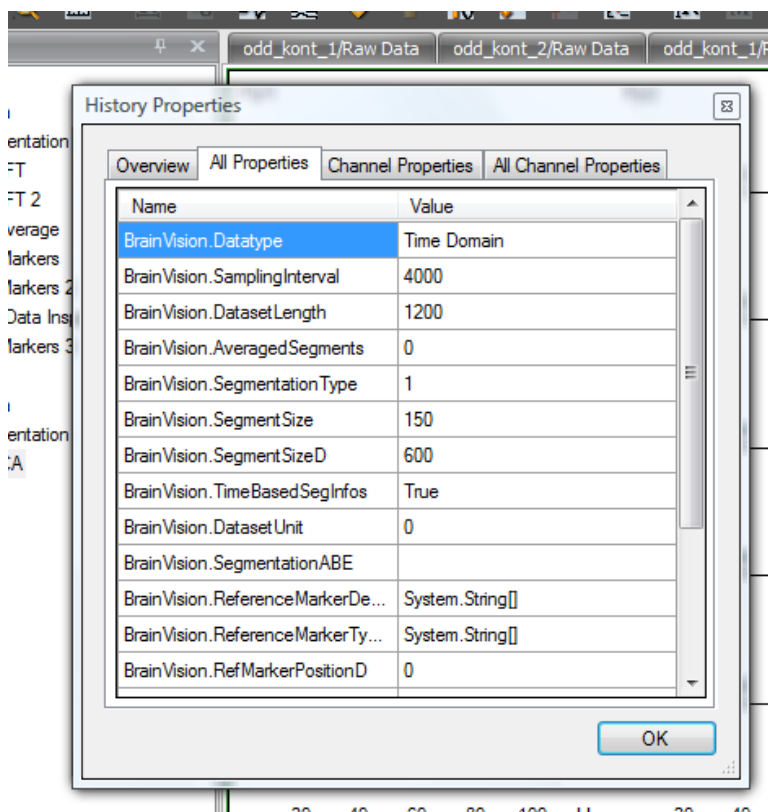


FIGURE 12—60 USER PROPERTIES, ICA

The user properties can be read by means of OLE Automation and used by other solutions.

When using the ICA transform, you choose a sphering method and a method of ICA training.

THE ICA METHOD

The data in the selected interval is stored in the main memory of the PC for further processing. If the volume of data in the interval is greater than the available main memory, as much data as possible is stored and processed. Consequently, the more memory the computer has available, the better the ICA transform works. We also recommend that you close other applications to make more memory available.

The ICA transform consists of the following steps:

- The mean values of the channels are subtracted from the data set.
- The sphering matrix is calculated and applied to the data set (PCA).
- ICA training: The resulting data is inspected repeatedly until the ICA matrix has been calculated with sufficient precision.
- The ICA components are determined by applying the ICA matrix to the data set.
- The arrangement of the components in the newly created data set is adjusted depending on which sort criterion is selected.

The calculation and application of the sphering matrix to the data is also referred to as preprocessing.

In contrast to conventional sphering, probabilistic sphering is designed to reduce noise in the EEG.

The infomax methods, which are also known as gradient methods, are generally slower than the fast ICA methods when component separability is good. However, there are exceptions with fast ICA methods in which calculation is interrupted and new parameters have to be selected. In such cases, it is possible for a fast ICA method to be slower.

The Infomax/Fast-ICA and Restricted/Extended options provide you with a total of four methods of ICA training. The restricted methods repeat the same training method for each component. The extended methods adapt the training method to suit the component depending on the kurtosis of the partially calculated component.

Note that the restricted infomax method can only calculate components with positive kurtosis.

[BS95] A.J. Bell, T.J. Sejnowski, An information-maximization approach to blind separation and blind deconvolution. *Neural Computation* 7 (1995), 1129-1159.

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[MBJGS97] S. Makeig, A.J. Bell, T.-P. Jung, D. Ghahremani, T.J. Sejnowski, Blind separation of auditory event-related brain responses into independent components. *Proc. Natl. Acad. Sci. USA*, 94 (1997), 10979-10984.

[HKO01] A. Hyvärinen, J. Karhunen, E. Oja, *Independent Component Analysis*, John Wiley & Sons, New York, 2001.

12.3.2 FFT (Fast Fourier transform)

The Fourier transform converts data from the time domain to the frequency domain. In other words, the resulting data indicates the extent to which the individual frequencies between 0 Hz and up to half of the sampling rate are represented in the EEG.

SUMMARY

In principle, no previous processing steps are required before the transform is used. We nevertheless recommend that you carry out the FFT after:

PREREQUISITE FOR USE

- Segmentation

To display the dialog box for the transform, you choose **Transformations > Frequency and Component Analysis > FFT Analysis**.

PROCEDURE

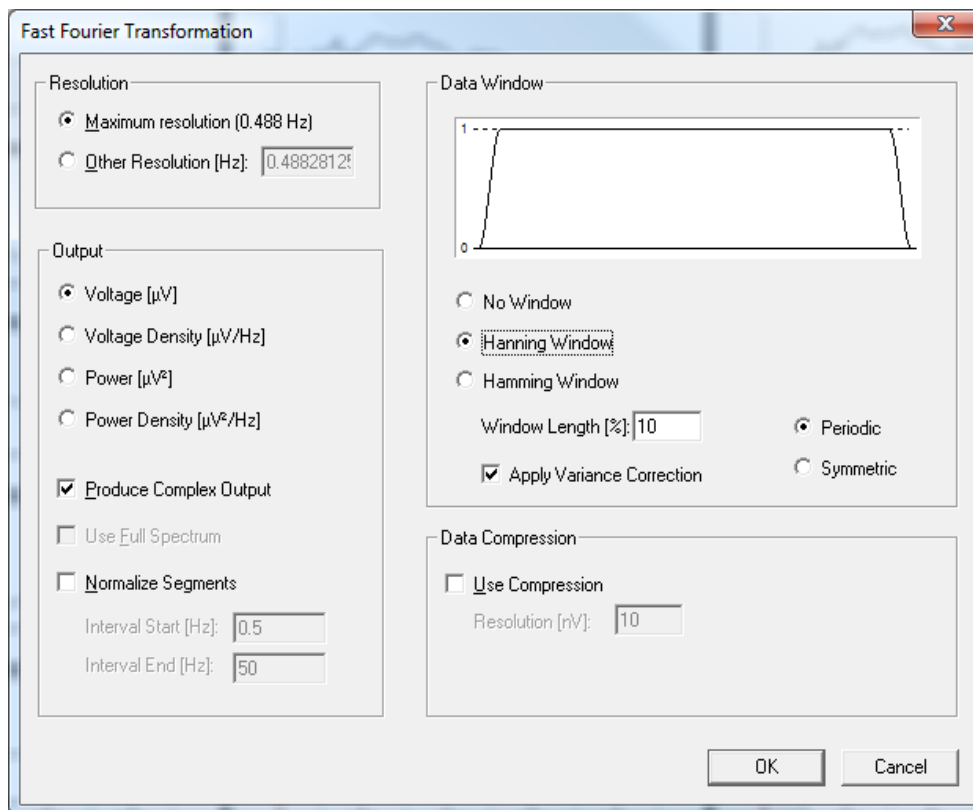


FIGURE 12—61 FAST FOURIER TRANSFORMATION DIALOG BOX

You can make the following settings:

In the **Resolution** group box, you specify the resolution of the new data set in hertz. You can choose between the maximum resolution, which is obtained from the number of points in the segments and the sampling rate (**Maximum resolution**), and a user-defined resolution (**Other Resolution [Hz]**). The maximum resolution is calculated as follows: sampling rate ÷ segment length.

RESOLUTION GROUP BOX

In the **Output** group box, you can make the following settings:

OUTPUT GROUP BOX

- You specify the type of the resulting data and the unit in which it is calculated. You can choose between the following data types: voltage (**Voltage [μV]** radio button), voltage density (**Voltage Density [$\mu\text{V}/\text{Hz}$]** radio button), power (**Power [μV^2]** radio button) and power density (**Power Density [$\mu\text{V}^2/\text{Hz}$]** radio button).

In the case of the voltage density and power density functions, the spectral line values are scaled as if they were calculated with spectral line spacing of 1 Hz. This permits comparisons between FFT analyses that have been carried out with different spectral resolutions. To this end, the spectral line values are multiplied by a constant factor b , which corresponds to the reciprocal value of the spectral line spacing ($b=1/fb$).

- By selecting the **Produce Complex Output** check box, you specify that the FFT transform is to create complex data. You should do this whenever you want to further process the data resulting from the FFT with transforms that have to process not only the values of the spectral lines but also their phase information and consequently require complex data. Coherence analysis is an example of this.
- The **Use Full Spectrum** check box allows you to specify whether you want only one or both halves of the spectrum to be used to calculate the spectral line values. When both halves are used, the spectral line values are effectively doubled. This is of particular significance when power spectra are calculated, since this check box allows both of the definitions of spectral power (μV^2 or as $\mu\text{V}^2/2$) used with EEGs to be taken into account. If you select the **Use Full Spectrum** check box, the resulting FFT power spectra behave in accordance with the Parseval theorem, which states that the total power in the power spectrum should always be equal to the total variance in the time signal.
- If you select the **Normalize Segments** check box, the FFT data becomes comparable in a different way. It is sometimes important in EEG research to be able to make relative comparisons by changing the spectral composition of the EEG signal. Since the total power of the EEG varies from segment to segment, such comparisons generally cannot be carried out. However, the **Normalize Segments** function allows you to normalize the total area in the EEG spectrum or part of the EEG spectrum and thus render it comparable.

If you do not select this check box, the transform creates the data in the frequency domain. If you do select the check box, the data is multiplied after the Fourier transform by a factor that makes the normalization area under every channel and in every segment identical. In this case, it is not the absolute data that is output but the relative distribution of the activity to the individual spectral lines.

- In the Interval **Start [Hz]** and Interval **End [Hz]** text boxes, you can specify the lower and upper limits of the normalization range. The minimum lower limit is set at 0.5 Hz, since it is generally assumed that frequencies under 0.5 Hz are not electrocortical in origin and, moreover, that these frequencies are extremely unstable from segment to segment. The area of this frequency range is calculated and an area value of 100 is set by multiplying it by a normalization factor that differs from segment to segment and channel to channel. In the same way, all of the spectral line values that are not within the normalization range are multiplied by this factor and thus also normalized.

Band comparisons, such as the relative alpha share of the EEG or the alpha slow wave index, can thus be calculated easily using this function. Normalization also makes it much easier to calculate the spectral corner frequency, for example.

In the **Data Window** group box, you can specify the type of the FFT data window. The following three radio buttons allow you to choose between different window types: **No Window**, **Hanning Window** and **Hamming Window**.

DATA WINDOW GROUP
BOX

In the **Window Length [%]** text box, you enter the window length as a percentage of the segment length.

The window function is displayed graphically.

If you select the **Apply Variance Correction** check box, the power in the EEG signal is identical before and after the application of the FFT, even when a window function is used.

The **Periodic** and **Symmetric** radio buttons allow you to configure the right-hand margin of the data window. **Periodic** configures the right-hand margin of the window in such a way as to optimize the analytical characteristics of the window for the periodic continuation of the window. **Symmetric** configures the right-hand margin of the window to be exactly symmetrical to the left-hand margin.

The **Use Compression** check box allows you to specify whether you want to store the data compressed or uncompressed. Compressed data saves storage space in the history file but is not as accurate as uncompressed data.

DATA COMPRESSION
GROUP BOX

If you select the **Use Compression** check box, you can specify the resolution of the data in nanovolts ($1000 \text{ nV} = 1 \text{ }\mu\text{V}$) in the **Resolution [nV]** text box. The lower the resolution of the data (higher values), the greater the compression effect. Consequently, less storage space is required.

Strictly speaking, a Fourier transform extends from 0 Hz to the maximum sampling rate. However, the data in the high frequency range results from conjugate-complex values from the data in the lower frequency range is therefore not calculated explicitly.

ADDITIONAL
INFORMATION
PROCESS

The data values are scaled in such a way that a sine wave of 1 Hz and an amplitude of 100 μV generate a value of 50 μV at 1 Hz when the output format is **Voltage**, calculation takes place without a data window (**No Window**) and the **Use Full Spectrum** check box is not selected. Together with the corresponding data value in the high frequency range (i.e. when the **Use Full Spectrum** check box is selected), this results in the original value of 100 μV at 1 Hz. This approach corresponds to the calculation of a Fourier transform with subsequent division by the number of data points used.

Although the Fourier transform can in principle be used at any point in the process, it is recommended for segmented EEG data to save time.

INTERPOLATION

The transform is executed separately for each segment. It is not essential for the number of data points in a segment to be a power of 2. If the number is not a power of 2, the segments are automatically extended to the next higher power of 2, and the corresponding number of zeros is added to the existing data.

This process, which is also known as padding, corresponds to the interpolation of the data in the frequency spectrum of the original data set. As a result, a frequency spectrum is obtained that has a higher resolution than the original data set. No data is lost here, and the resulting data does not contain any artifacts.

On account of the interpolations, however, it cannot be expected that using this process on data with any segment length and sampling frequency will always produce comparable results, since the FFTs calculated in this way differ in terms of the total number of data points and thus also in terms of the information content of the original input data. This inevitably leads to differences in the resulting spectra. Interpolated FFT spectra are thus suitable, above all, for visual data inspection.

To prevent the interpolation of the FFT data at all resolutions, you should thus ensure that the number of data points in the segments is a power of two and select the **Maximum resolution** radio button in the **Resolution** group box.

If you select a different resolution from the maximum spectral resolution determined by the segment length and data rate, the resulting FFT spectra are also either interpolated or both interpolated and integrated, depending on the selected resolution. As mentioned above, interpolation like this always produces correct FFT spectra without creating any artifacts. Note, however, that an FFT analysis like this is not necessarily comparable with an FFT analysis using a data set that has the resolution selected here as the maximum spectral resolution.

This can be illustrated by an example in which an EEG has a sampling rate of 1024 Hz and segments of 4096 points. The maximum spectral resolution is thus 0.25 Hz ($1024/4096=0.25$). If you select the **Other Resolution** radio button and enter a resolution of 1.0 Hz, instead of 1024 data points being included in the analysis, as would be the case given a maximum resolution of 1.0 Hz (segments of 1024 data points and a sampling rate of 1024 Hz), four times that number of data points are included. The resolution of 1.0 Hz is established by integrating four spectral line values. If the resolution ratios are not exactly divisible, the overlaps of the values at the spectral line edges are interpolated. However, since the original segments are four times longer and thus inevitably contain different information from the short segments, in spite of the FFT resolution theoretically being identical, the results can by no means be expected to be the same.

Note that this is not a problem caused by the method used; it is an inevitable result of the differences in the quantity and contents of the information included in the FFT analysis when there are different spectral resolutions.

This problem, which is inherent in interpolation, applies particularly to the calculation of complex FFT values when a resolution other than the maximum spectral resolution is selected. This is because it is not just the values of the spectral lines but also their phase information that have to be interpolated and/or integrated. This can impair the flow of the phase information, which is actually rather constant, and, for example, make the result of a subsequent coherence analysis appear questionable.

It is worth repeating that spectra interpolated like this are suitable above all for the visual inspection of data and should not form the basis for subsequent calculations.

In the Fourier transform, it is assumed that the output signal is repeated periodically. Since this requirement is generally not met when EEG sections are transformed, the difference between the voltage level at the beginning and end of the segment is a point of discontinuity in Fourier transform calculations and causes the data to be corrupted.

DIGRESSION: FUNCTION
OF THE DATA WINDOW

To reduce this effect, it is possible to place a data window over the segment to be transformed. This data window damps the EEG data at its margins. When the data window is applied, the voltage level at the beginning and end of the segment is 0, rising to the original measured value in the middle of the segment.

The range in which the data window is used can be specified as a percentage. 100% means that only the value in the middle of the segment matches the original data value, and all other values are damped by the data window. The lower the percentage specified, the smaller the range changed by the data window. This principle is represented graphically and very clearly in the FFT module.

The Hanning window is calculated using the following equation:

$$W_p = 0.5(1 - \cos(2\pi x/P)).$$

The Hamming window is calculated using the following equation:

$$W_p = 0.54 - 0.46 \cos(2\pi x/P).$$

P is the percentage specified in the **Window Length [%]** text box. Corresponding symmetric equations apply to the end of the segment.

It follows from the way in which the data window works, as described above, that the overall signal and thus the total variance of the EEG signal are weakened by the window, particularly toward the margins. Accordingly, the use of a data window also results in the damping of the data produced by the Fourier transform.

For this reason, before the Fourier transform is applied, a correction factor is calculated for the data window and window width used. This factor is used to multiply the data on completion of the Fourier transform. This correction ensures that the total variance of the transformed signal matches the total variance of the original signal.

12.3.3 Wavelets

Like the Fourier transform, the wavelet transform is a method of analyzing the frequency of a signal. The essential difference between the two methods is that the Fourier transform uses the trigonometric functions as basic functions. In other words, the values are calculated by means of sine/cosine functions. The Wavelet transform, on the other hand, uses wavelets (i.e. functions whose properties can be adjusted to suit particular problems). In contrast to the FFT, it is possible with the Wavelet transform to analyze local frequency properties as well.

SUMMARY

The following example illustrates the difference between the Wavelet transform and the FFT:

The frequency resolution (i.e. the accuracy with which statements can be made about the signal content at specific frequencies) in the case of the FFT is, at $1/T$ (T = segment length in data points), directly dependent on the length of the EEG sections included in the FFT analysis. In order to obtain frequency resolution accuracy of 1 Hz, you therefore require EEG sections of exactly a second (regardless of the sampling frequency).

This is precisely where the analytical problem begins. The cortical activation that is actually of interest often takes place within quite a narrow time range around the time of stimulation. An example of this would be the examination of changes in the delta range directly after electrical pain stimulation. In this case, the changes that are of interest take place in the first 250 ms after stimulation. To carry out an FFT analysis with a frequency resolution of 1 Hz, 1000 ms must be included in the FFT analysis. Thus, four times as much data as is necessary is included in the analysis. In addition, the power in the delta band is also calculated for this data, which is actually superfluous, and this inevitably corrupts the results.

Another result of this is that in our example the frequency content of the frequency range that is actually of interest here (e.g. the delta range) obviously does **not** exist to the same extent over the entire section analyzed using the FFT. The same applies to all the other signal components that occur in the EEG. A signal in which the frequency components vary over time is referred to as **non-stationary**.

However, since the frequency resolution in the case of the FFT is directly linked to the number of data points included, it is simply not possible to make a statement about the changes to the spectral composition of the signal within intervals that are shorter than specified by the frequency resolution. Moreover, if the signal in the segments analyzed is not stationary, this variation in the signal over time cannot be represented with the FFT either.

This is where wavelet analysis comes into play. The Wavelet transform compares the EEG signal with the wavelet used over the entire duration of the EEG signal and for different frequency ranges. It is critical here that after the wavelet transform for each point of time in the time domain there is also a wavelet value for each point of time and frequency range. In the above example, this would mean that after the Wavelet transform there would also be a curve for the activity over time for the delta band.

The Wavelet transform also permits changes in the spectral content of EEG signals to be examined over time. This is a key difference between it and the FFT.

A distinction can be drawn here between the discrete Wavelet transform and the continuous Wavelet transform.

Discrete Wavelet transform (DWT)

DISCRETE WAVELET TRANSFORM

The discrete Wavelet transform is actually a special case of the continuous Wavelet transform (CWT), but it is nevertheless dealt with here first since, on account of its simple algorithm and associated high analysis speed, it is already widely used in EEG research.

The discrete Wavelet transform is based essentially on a method known as “subband coding”. In this method, the signal of interest is filtered by means of two semiband filters that are as perfect as possible. One filter (the low-pass filter) filters the frequency components above the halfway point of the available frequency band (the Nyquist frequency), and the other filters the frequency components below the Nyquist frequency symmetrically.

Since the resulting signal of the low-pass filter only contains frequencies up to the Nyquist frequency but still retains its full segment length, half of the data is inevitably redundant (Nyquist’s law) and is eliminated by subsampling (i.e. by simply deleting every second data point). As a result of this processing step, the time resolution of the signal is halved, since the entire signal is now characterized by half the data points. At the same time, however, half of the data points represent the entire frequency content of the signal, and the frequency resolution is thus doubled. This process of constant halving of the time resolution and doubling of the frequency resolution is referred to as subband coding.

This subband coding is repeated for as long as frequency components of interest are to be extracted, and each step results in wavelet data that corresponds to the time-related composition of the frequency components in the original data.

Ultimately, a set of coefficients is obtained that contains the time-frequency curve for all the required subcoding steps (i.e. for all the desired frequency ranges).

An obvious limitation of this method is that it is impossible to examine the time-frequency behavior of a signal at a specific frequency, since in the DWT the original signal is repeatedly divided into half-frequency ranges, beginning at the Nyquist frequency. It is thus clear that a time-frequency analysis specifically for 32 Hz, for example, cannot be implemented.

Given a signal with a sampling rate of 256 Hz, however, accurate time-frequency statements can be made for the frequency ranges 64-128 Hz, 32-64 Hz, 16-32 Hz, 8-16 Hz, 4-8 Hz, 2-4 Hz and 1-2 Hz. Cumulation of the result values is also possible so that, for example, the analysis of the delta band can be carried out on the time-frequency curve.

A further advantage that often makes the DWT rather than the CWT the method of choice in the EEG field is the simplicity with which the wavelet coefficients can be converted back to the time domain. This is possible because the filters used represent orthonormal bases, and reverse conversion can thus be implemented easily. The discrete Wavelet transform can thus also be used for wavelet-based filtering of the data.

Continuous Wavelet transform (CWT)

CONTINUOUS WAVELET TRANSFORM

The continuous Wavelet transform provides considerably more scope at those very points where the DWT, which is actually very elegant, has its limitations. It permits specification of the frequency bands to be examined and of their resolution, and it offers more options when it comes to selecting the underlying filters (mother wavelets, see below).

Unlike the DWT, the CWT does not work with semiband filters; it works with mother wavelets instead. These are short signal sections shaped on the basis of underlying functions in such a way that, when filters are applied to the raw data, they represent particular signal characteristics in the time-frequency domain as accurately as possible. Here, too, filtering or folding thus takes place, but with a specific filter characteristic for the signal of interest.

The two mother wavelets used most frequently in the CWT are the “Mexican hat” and “Morlet” wavelets, which are shown below.

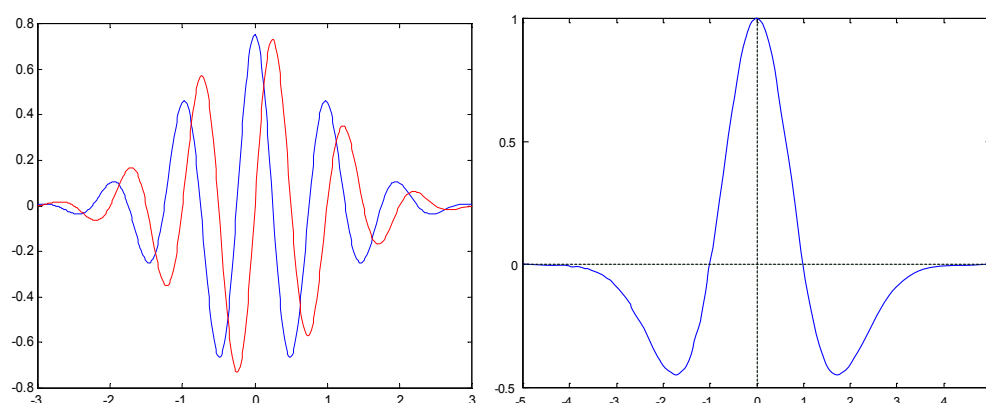


FIGURE 12—62 THE GRAPHS OF THE COMPLEX MORLET WAVELET (LEFT) AND THE MEXICAN HAT WAVELET (RIGHT)

The complex Morlet wavelet, which is also known as the modulated Gauss function, is defined by the following formula:

$$\psi(t) = A e^{-t^2/2} e^{i2\pi ct}$$

The factor A is used for normalization. The parameter c is a special property of the Morlet wavelet. It enables the number of oscillations of the wavelet – and thus the filter width in the frequency range – to be varied.

The real Morlet wavelet consists of the real part of the complex function.

The formula for the Mexican hat wavelet is:

$$\psi(t) = A(1 - t^2)e^{-t^2/2}$$

The Mexican hat wavelet looks rather like a sombrero, as you can see in the figure above.

How do the two wavelets filter the raw data? To begin with, the mother wavelet is successively translated via the raw data, and for each point in the raw data a scalar product with all the points is calculated in the wavelet. As a result, the data is filtered with the wavelet or – depending on how it is viewed – a correlation function of the wavelet is calculated with the data in the time domain. The resulting wavelet vector thus represents a kind of point-for-point correlation of the raw data with the wavelet.

It becomes clear here why the selection of a suitable mother wavelet is important for the desired analysis in this approach. Both of the wavelets shown above will show a high correlation at precisely those raw data points or segments that correspond to the time-frequency characteristic of the wavelet (thus, in this case, at local, steep rises with a particular time-voltage characteristic).

But how can different frequency ranges be analyzed in this way? This is where it becomes evident that the CWT is closely related to the DWT. After the initial analysis step of the wavelet with all the points in the raw data set, the wavelet is widened by a small amount or “scaled”. Consequently, we talk about “scales” rather than frequencies in connection with the CWT, and the mother wavelet has a scale of $s=1$. However, widening the wavelet also means that when the data is filtered again with the wavelet, other, slower frequency components result in a higher correlation of the raw data with the wavelet.

This is then carried out for the entire frequency band required and for the required number of scales. For each scale, a vector of wavelet coefficients is calculated that contains the time-frequency behavior of the raw signal for the corresponding scale.

Because the change to the wavelet in the case of the CWT is referred to as a change to the wavelet scale rather than to the wavelet frequency, the representation of the time-based section of data against the successively slowed frequency content is referred to as a “scalogram”. The scales of the wavelet calculation can, of course, be converted into corresponding frequency ranges again. Consequently, the wavelet results in the Analyzer can be displayed in a time-frequency chart again.

On account of the scaling of the mother wavelet, it is important that there is an interaction between the time resolution and frequency resolution in the case of the CWT, just as there is with the DWT. At lower scale values (i.e. in the analysis of higher frequencies), the resulting wavelet coefficients have a good time resolution but a poor frequency resolution. At higher scales (i.e. in the analysis of lower frequencies), on the other hand, wavelet coefficients with a good frequency resolution but a poor time resolution are obtained.

You will find more information on wavelet analysis in [LMR98], for example, from which the algorithm used for the discrete Wavelet transform was obtained.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Frequency and Component Analysis > Wavelets**.

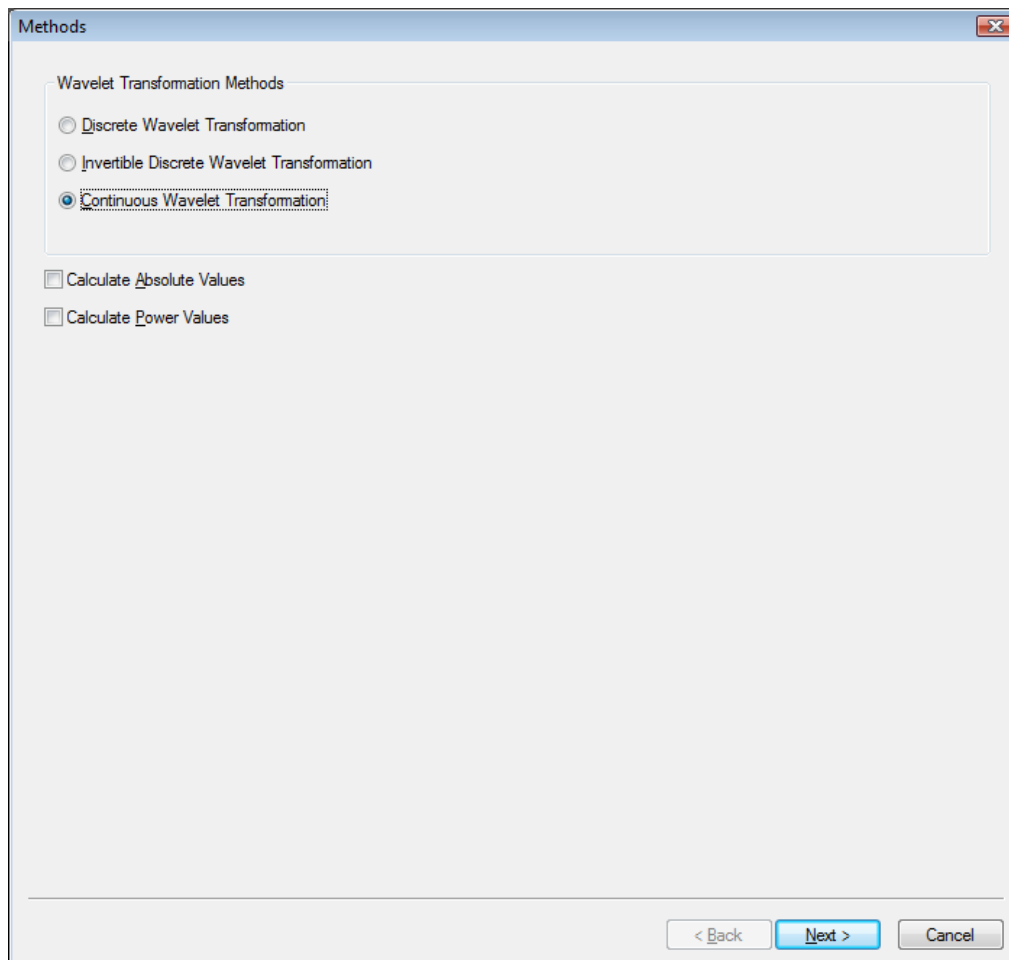


FIGURE 12—63 INITIAL DIALOG BOX FOR THE WAVELET TRANSFORM

In the **Wavelet Transformation Methods** group box, you can choose a discrete Wavelet transform (**Discrete Wavelet Transformation**), an invertible discrete Wavelet transform (**Invertible Discrete Wavelet Transformation**) or a continuous Wavelet transform (**Continuous Wavelet Transformation**).

WAVELET
TRANSFORMATION
METHODS GROUP BOX

Moreover, you can specify for the discrete and continuous Wavelet transform which of the following are output:

- The Wavelet coefficients (if you clear the check boxes)
- Their absolute values (if you select the **Calculate Absolute Values** check box)
- The power values, the square of the absolute values (if you select the **Calculate Power Values** check box)

The calculation of absolute coefficient values makes sense, for example, if you want to average the wavelet coefficients calculated from segmented data and are not interested in the polarity of the original signal, only in its spectral composition.

A striking example of this involves investigating the EEG for induced versus evoked activity in a frequency range. The only factor of interest in terms of the induced activity is the absolute extent of the frequency activity. Its time (phase) position, on the other hand, is not of interest. However, it is precisely these phase differences in the presence of induced activity that are eliminated by averaging the data for an evoked potential. This means the Wavelet transform of the evoked signal only contains the evoked wavelet activity. The behavior is the same when calculating power values.

If you select the discrete Wavelet transform, the **Next** button takes you to the **Discrete Wavelet Transformation** dialog box.

DISCRETE WAVELET
TRANSFORM

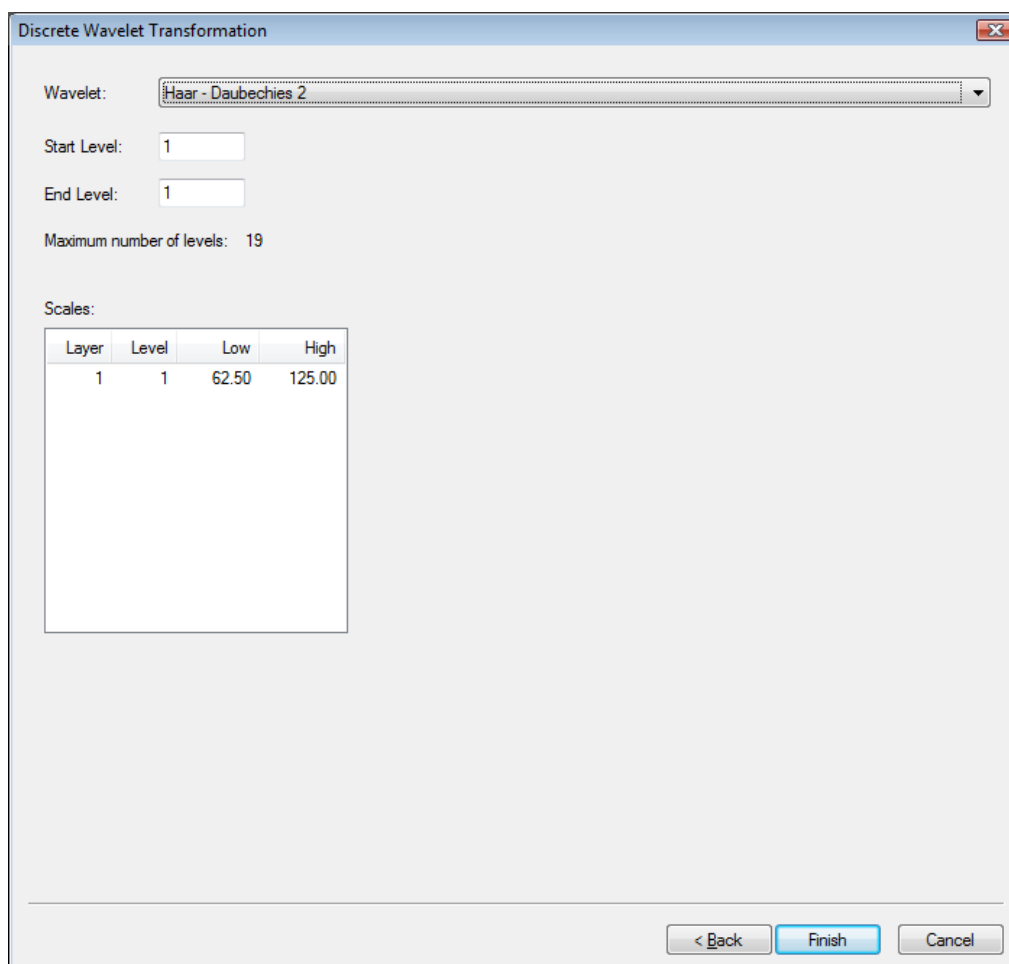


FIGURE 12—64 DISCRETE WAVELET TRANSFORMATION DIALOG BOX

The **Wavelet** drop-down list allows you to specify the wavelet type for the discrete transform. You currently have the choice between the Haar wavelet and Daubechies wavelets of various filter lengths.

In the **Start Level** and **End Level** text boxes, you specify the frequency ranges (or transform levels) to be analyzed. A level 1 transform generates high frequency components (between half and a quarter of the sampling rate) at a high resolution. Higher levels generate lower-frequency components at a lower resolution. The frequency is halved from level to level.

Like the continuous Wavelet transform, the discrete Wavelet transform also creates the transformed data in the form of a two-dimensional data field, where one dimension represents the time domain and the other dimension represents the logarithmically scaled frequency domain. The data values are displayed color-coded in a rectangular area in the Analyzer.

Note that the specified limits are only guidelines. Because the discrete Wavelet transform works with filter methods, the components of a frequency of the EEG do not fall 100% into a single scale (frequency step); they also occur in neighboring scales in a very weakened form.

If you select the invertible discrete Wavelet transform, the **Next** button takes you to the **Discrete Wavelet Transformation** dialog box.

INVERTIBLE DISCRETE
WAVELET TRANSFORM

If the data to be processed is segmented data, you are taken to the **Window Function** dialog box in a second step.

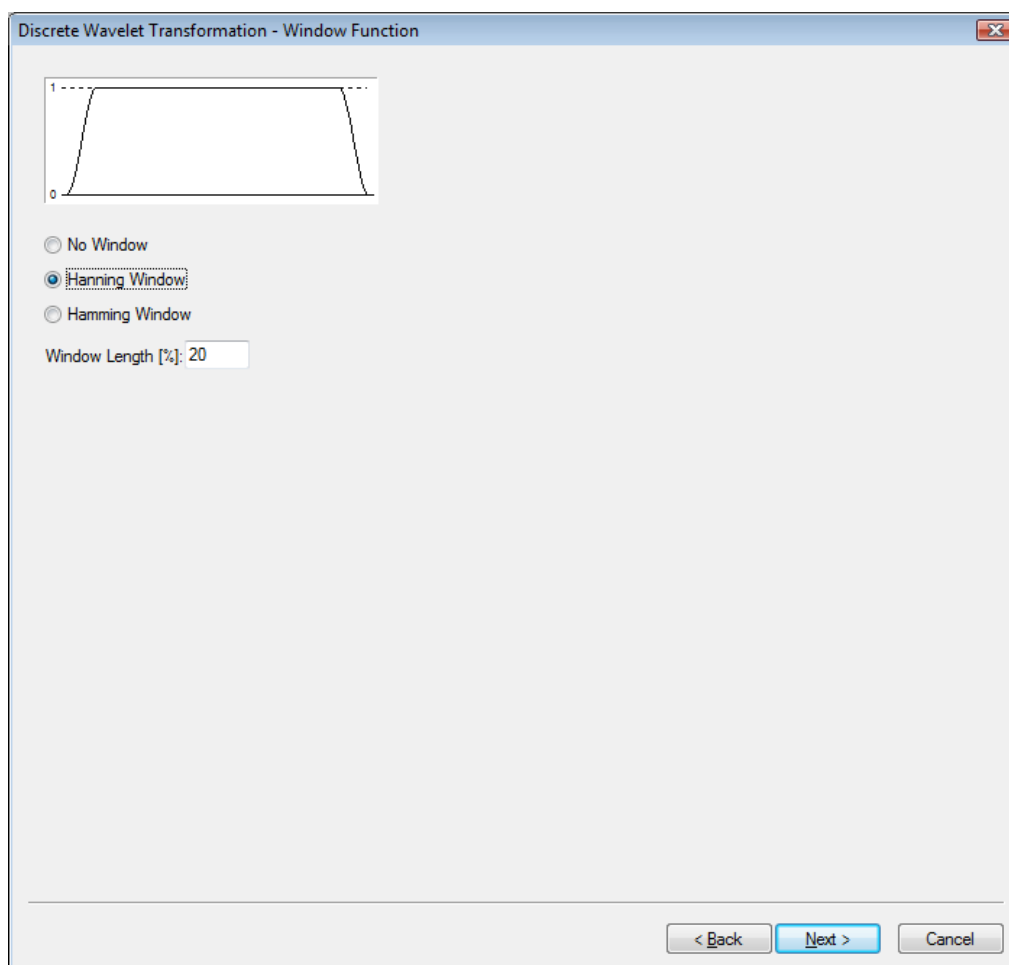


FIGURE 12—65 DISCRETE WAVELET TRANSFORMATION – WINDOW FUNCTION DIALOG BOX

Select a radio button (**No Window**, **Hanning Window** or **Hamming Window**), and specify the window width in the **Window Length [%]** text box. The window function is applied to the data before the Wavelet transform is executed.

The window function processing step must be carried for the invertible discrete Wavelet transform for the same reason as for normal spectral analysis. In both cases, data ranges of a finite length are used in wavelet analysis. In the case of the transform, this would lead to discontinuities that would make it impossible to perform a complete reverse transform of the signal.

If you select the continuous Wavelet transform, the **Next** button takes you to the **Continuous Wavelet Transformation** dialog box.

CONTINUOUS WAVELET
TRANSFORM

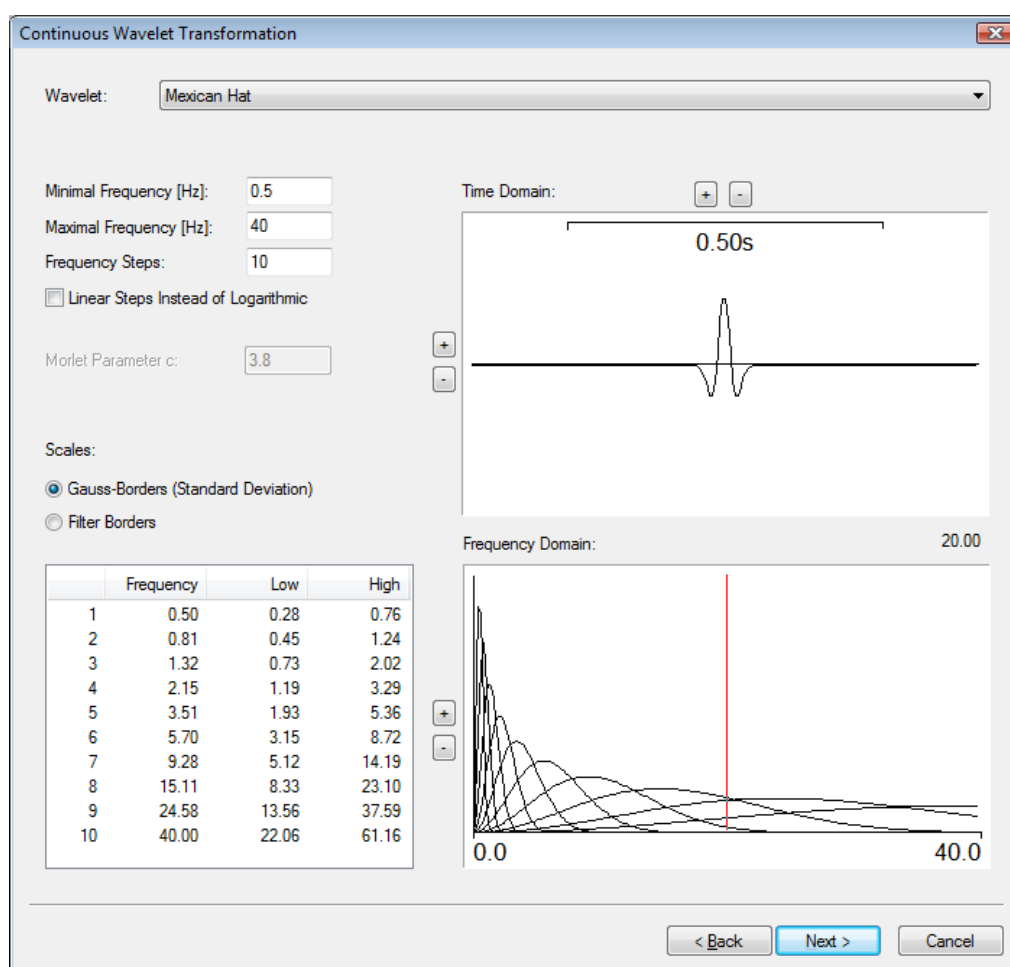


FIGURE 12—66 CONTINUOUS WAVELET TRANSFORMATION DIALOG BOX

From the **Wavelet** drop-down list box, you choose the real Morlet wavelet, the complex Morlet wavelet or the Mexican hat wavelet as the basic wavelet.

In the **Minimal Frequency [Hz]** and **Maximal Frequency [Hz]** text boxes, you specify the lower and upper frequency limits for the calculation. In the **Frequency Steps** text box, you specify the number of frequency steps for which the wavelet function is to be calculated.



40 frequency steps have proved to be practical for the usual representations of the entire EEG spectrum. As the number of frequency steps rises, however, the processing time becomes longer because the wavelet function is calculated separately for each frequency step.

If you select the **Linear Steps Instead of Logarithmic** check box, the scaling shown in the frequency domain is linear.

In the **Morlet Parameter c** text box, you specify the Morlet parameter c. This parameter affects the width of the envelope of the Morlet wavelet.

Under **Scales**, you specify whether the scale limits are interpreted statistically (**Gauss Borders (Standard Derivation)**) or in a signal processing sense (**Filter Borders**). Consequently, the **Low** and **High** columns in the table are updated automatically. These specifications have no effect on the calculation of the wavelets.

The **Time Domain** and **Frequency Domain** boxes display the wavelets in the time and frequency domains.

The buttons  and  allow you to adjust the display of the graphs.

The frequency ranges covered by the scales (frequency steps) cannot always be easily worked out in the case of the continuous Wavelet transform. Consequently, they are listed in the table to provide orientation. If you change the frequency range to be analyzed or the number of frequency steps, this table is automatically updated.

As with the discrete Wavelet transform, the limits of the scales should be viewed only as guidelines. The Wavelet transform actually distributes a given frequency over the frequency range in the form of a more or less bell-shaped curve. The actual shape of the curve depends on the wavelet used. As with filters, the information in the dialog box therefore applies to the range in which the effect of the frequencies is strongest. Consequently, the overlapping of the boundaries shown in figure 12—62 is normal. If the ranges do not overlap, you have to expect a loss of information. In this case, you should select more scales.

The frequency distribution of the wavelet function is nearly Gaussian in shape. The frequency limits in figure 12—62 are therefore shown as Gaussian or filter limits (68% or 71% of the signal amplitude at the wavelet's central frequency). Figure 12—67 below shows examples of these limits for the Morlet and the Mexican hat wavelet.

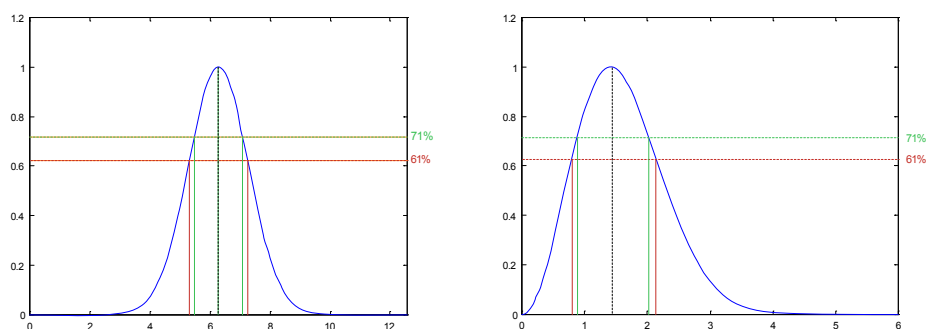


FIGURE 12—67 FILTER LIMITS OF THE MORLET WAVELET (LEFT) AND MEXICAN HAT WAVELET (RIGHT)

The filter limits of the Morlet wavelet run symmetrically on either side of the central frequency, whereas the filter limits of the Mexican hat wavelet are slightly asymmetrical and offset to the left. The standard deviation of this function for the Morlet wavelet for a parameter c is $1/c$. Consequently, the ratio of the frequency to the standard deviation is exactly c . The ratio of the filter frequency to half the filter width c' for the Morlet wavelet is calculated with $c' = 1,2c$.

Unfortunately, the Morlet wavelet is not a wavelet in the sense of the actual wavelet definition. This explains why in many articles a value for c of at least 5 is required for the Morlet wavelet so as to guarantee at least an approximation to that of the Wavelet definition and to ensure further regularity properties. Alternatively, a correction term is also sometimes added to the underlying e function. In practical usage, the exact value of c is less important due to the numeric calculation. However, it can be used to make accurate statements about the frequency bands used:

Take, for example, a Morlet wavelet with $c = 5$. At the filter frequency of 20 Hz, this results in a drop in the signal to 61% at the limits 16 Hz and 24 Hz (standard deviation) and a drop to 71% at the limits 23.3 Hz and 16.7 Hz (filter width). However, this does not mean that other frequencies are no longer contained in the wavelet-transformed signal. They are merely weakened, as can be seen in the figure above.

If you change the value of the parameter c in the dialog, the width of the wavelet frequency functions displayed inevitably changes as well. As a general rule, a steeper frequency function of a wavelet at the same central frequency (i.e. with the parameter c getting higher) is associated with a poorer time resolution. You can easily reproduce this in the dialog by changing the parameter.

It also follows from the above that a wavelet scale with a lower central frequency has, in absolute terms, a smaller standard deviation in the frequency distribution. On the other hand, the time resolution is comparatively poor. This can be illustrated very effectively by moving the vertical red line in the frequency distribution chart in the lower right part of the dialog box. As the frequency falls, the wavelet shown in the box in the upper right part of the dialog box becomes longer.

This display is extremely useful for analyzing EEG data using wavelets, since the task, after all, is to find the optimum ratio between frequency and time resolution for the scales of interest. This can be achieved easily using the parameter c and the two boxes in the dialog box with the frequency and the time resolution of the resulting wavelets.

The “natural” arrangement of the central frequencies of the scales between the upper and lower ends of the frequency band for wavelet analyses using frequency ranges is logarithmic and thus corresponds to the dyadic function of the discretized continuous wavelet function used here.

However, what is often required is even, linear sampling of the spectrum rather than complete coverage of the frequency band between the upper and lower ends of the band. This can be achieved using the “Linear Steps instead of Logarithmic” option. A frequency band from 20 to 50 hertz, sampled in 7 steps, would thus result in six wavelet functions with central frequencies of 20, 25, 30, 35, 40, 45 and 50 hertz instead of the central frequencies of 20.0, 23.3, 27.1, 31.6, 36.8, 42.9 and 50 hertz applicable in the logarithmic arrangement.

If the data to be processed is segmented, the **Normalize and Baseline Correction** dialog box appears.

CONTINUOUS WAVELET
TRANSFORM:
NORMALIZATION AND
BASELINE CORRECTION

FIGURE 12—68 NORMALIZATION AND BASELINE CORRECTION OF THE WAVELET TRANSFORM

Prior to convolution, the Wavelet function can be normalized with one of three normalization methods implemented in the Wavelet Transformation in order to select the type of data the wavelet function is meant to return during convolution with the data.

You can specify whether the wavelet data is to be normalized (**Enable Normalize**) or whether baseline correction of the wavelet coefficients is to be carried out (**Enable Baseline Correction**).

For both normalization and baseline correction, you can specify the time interval or data point interval for which the operation is to be carried out (**Based on Time / Based on Data Points**). You specify the beginning, end and length of the interval in milliseconds or data points.

Under **Wavelet Normalization**, you choose which method is used to normalize the wavelet function by selecting one of the following radio buttons:

- **Instantaneous Amplitude (Gabor Normalization):** In close analogy to the Gabor Transform, the Wavelet Transformation directly returns the instantaneous amplitude of the wavelet analyzed signal if the wavelet function is normalized with the Gabor Normalization factor A_w . The formula used for this normalization is: $A(\omega) = \text{Sqrt}(2/\pi) / \sigma_T$

- **Uniform Scale Power (Unit Energy Normalization):** This method normalizes the wavelet function to have the same energy of 1.0 at all scales (unit scale energy). In this case, the wavelet power spectra of an analyzed signal are then directly comparable to each other across all scales. The formula used for this normalization is: $A(\omega) = 1 / (\text{Sqrt}(\sigma_T) * \pi^{(1/4)})$
- **Relative Wavelet Power (Unit Scale Power to Sample Rate):** This normalization method was the default method implemented in BrainVision Analyzer since Analyzer version 1.04. It is equivalent to the above Uniform Scale Power, except for an additional normalization with the square root of the sample frequency. With this normalization Wavelet scales thus have unit scale power across all scales and the resulting wavelet amplitude or power values will be reported relative to the sample rate. The formula used for this normalization is: $A(\omega) = 1 / (\text{Sqrt}(\sigma_T) * \pi^{(1/4)}) * \text{Sqrt}(\text{SampleFreq})$

If you select normalization, the wavelet coefficients are normalized to a total of 100 in the selected range for each scale (frequency step). This permits relative comparisons of the activities between conditions or test groups to be carried out.

If you select baseline correction, the average value of the wavelet coefficients in the specified time range is calculated for each scale and deducted from all the wavelet coefficients in the entire time range. In this way, as with the analysis of time-based data, existing baseline activities can be obtained from the data before the experimental stimulation in order to get stimulus-induced changes to the frequency content.

Note that the normalization and baseline functions can be used at the same time, but not over the same time ranges. This is because, by definition, a baseline function sets the total of the values in the defined time range to 0. If a normalization function were to be carried out at the same time, it would attempt to define this total of 0 as 100%. Purely due to the finite accuracy of the numeric results of the baseline function, completely nonsensical values would be calculated, although no errors would occur. The module therefore issues a warning when the same time ranges are entered for the normalization and baseline functions. The normalization and baseline ranges can, of course, overlap. Indeed, there may be very good reasons for making them overlap.

[LMR98] A.K. Louis, P. Maaß, A. Rieder, Wavelets: Theorie und Anwendungen, Teubner, Stuttgart, 1998.

REFERENCES

12.3.4 Inverse FFT

The inverse FFT allows data to be converted back from the frequency domain to the time domain. This is generally desirable when artifacts or parts of the EEG that are not required can be removed more easily from the frequency-transformed data, but further processing is to take place in the time domain. A typical example of this is the use of user-specific filters, which is considerably easier and clearer in the frequency domain.

SUMMARY

The inverse FFT is typically used after:

PREREQUISITE FOR USE

- Segmentation
- The FFT

To enable a Fast Fourier transform to be inverted accurately, you have to make certain parameter settings in the FFT dialog box:

SETTINGS IN THE FFT DIALOG BOX

- Select the **Voltage** radio button.
- Select the **Produce Complex Output** check box.
- Do not select the **Normalize Segments** check box.

We also recommend that you do the following things:

- You should select the **No Window** radio button. If you do not do this, the output data of the inverse FFT is multiplied with the window function.
- You should not select the **Use Compression** check box. This is because the data can no longer be recovered in its entirety following compression; only an approximation is possible.
- You should not select the **Other Resolution** radio button. If you do, the inverse FFT can only restore the data converted by an interpolation process at a different sampling rate.

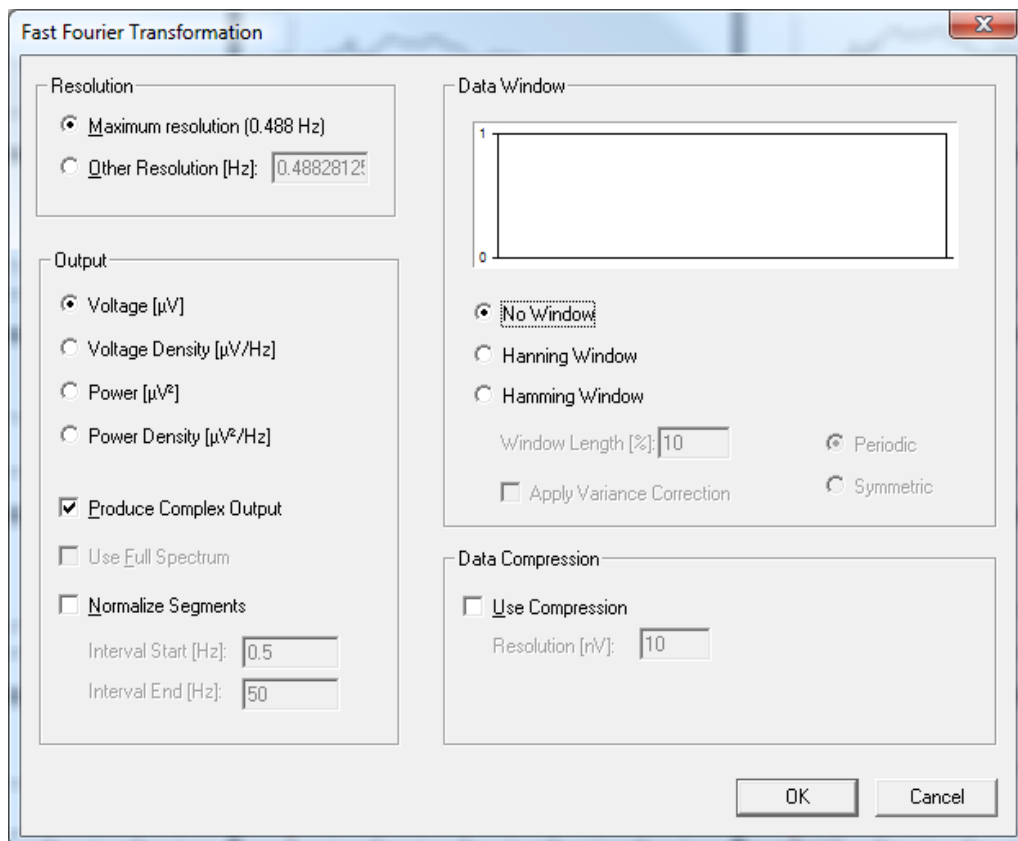


FIGURE 12—69 FAST FOURIER TRANSFORMATION DIALOG BOX, PARAMETER SETTINGS FOR THE INVERSE FFT

Once you have made the required settings in the Fast Fourier Transformation dialog box, you display the dialog box for the inverse FFT by choosing **Transformations > Frequency and Component Analyses > FFT inverse**.

PROCEDURE

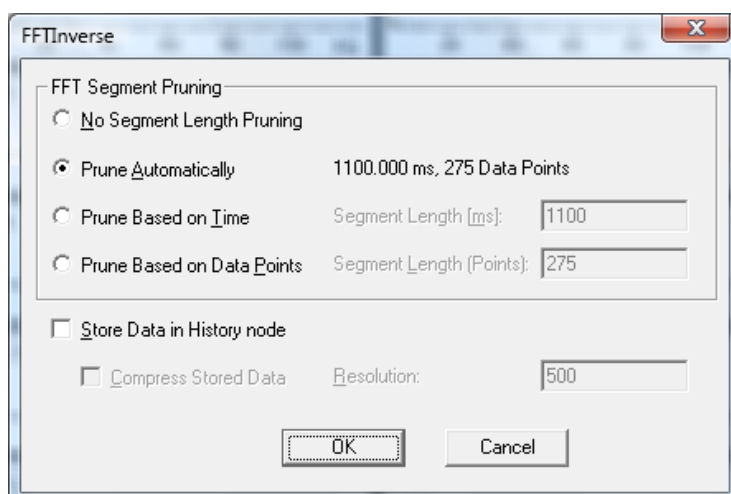


FIGURE 12—70 INVERSE FFT DIALOG BOX

You can make the following settings:

Because the Analyzer's FFT adds the value 0 to segments whose length is not a power of 2, you can specify a pruning parameter in the **FFT Segment Pruning** group box. This value determines the length to which the segment is truncated in the time domain.

There are four radio buttons for the pruning parameter:

- **No Segment Length Pruning:** The segment is not truncated, and any zeros added are retained.
- **Prune Based on Time:** You can enter a value for this.
- **Prune Based on Data Points:** You can enter a value for this.
- **Prune Automatically:** The invertable FFT stores the invisible information about the original length of the segments (i.e. before zeros were added to the data set) in the data set node.

For each channel and segment, the FFT stores in the data set node a value that is required for the execution of the inverse FFT. For this reason, the number of segments, the number of channels and the channel sequence must not be changed by the transforms executed between the FFT and the inverse FFT. Otherwise, it is no longer possible to assign the value to the appropriate channel or segment.

By default, the required data is calculated at runtime without any intermediate storage. However, if you select the **Store Data in History node** check box, the data is saved in a history node in order to optimize the performance of subsequent modules.

In addition, if you select the **Compress Stored Data** check box, the data can be compressed with the specified resolution. You can specify the resolution in the **Resolution** text box.

12.3.5 Wavelet Extraction

The Wavelet Layer Extraction transform allows you to extract a frequency range (layer) from a wavelet data set in order to further process it separately. The data set obtained as a result of this transform is a pure time domain data set (contrasting with the time/frequency domain of the wavelets).

SUMMARY

The transform is used after:

PREREQUISITE FOR USE

- The Wavelet transform

To display the dialog box for the transform, you choose **Transformations > Frequency and Component Analysis > Wavelet Extraction**.

PROCEDURE

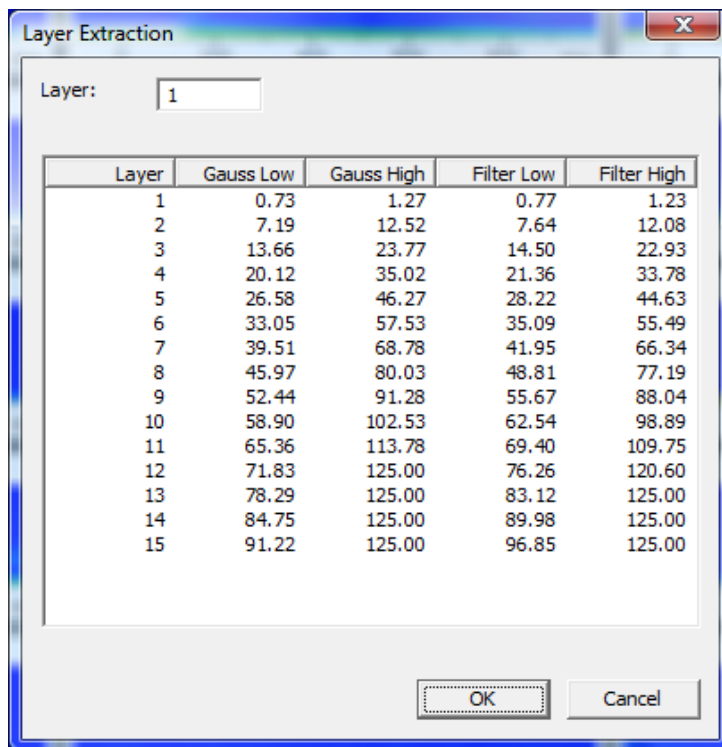


FIGURE 12—71 EXTRACTION DIALOG BOX FOR SELECTING A LAYER

In the **Layer** text box, you specify the layer to be extracted from the data set for further processing.

The table lists the layers with their filter limits.

12.3.6 PCA (Principle Component Analysis)

This is a secondary transform. In other words, it stores its results in the current workspace as secondary history files.

The Principal Component Analysis transform is used, on the one hand, to reduce the volume of data and, on the other, to extract hypothetical variables that permit a data set to be characterized. It groups together covariant variables of a data set that can be interpreted as a single factor.

SUMMARY

You can use BrainVision Analyzer 1.0 to open PCA nodes created using BrainVision Analyzer 2.0 without problems. However, this is not possible unless at least one of the data nodes on which the PCA calculation is based are in the workspace. In contrast, the PCA nodes created using Analyzer 2.0 supply data after their generation regardless of the existence of other nodes.

DOWNWARD
COMPATIBILITY

In addition, the behavior of Analyzer 1.0 PCA nodes differs from that of Analyzer 2.0 PCA nodes with regard to the data forwarded to child nodes. The Analyzer 2.0 nodes forward the PCA components segment by segment. The Analyzer 1.0 forwards only the loadings as standard data (i.e. as graphs).

If you are using segmented, averaged, ... data, you can only apply the transform when all the segments – even those from different data sets – have the same length.

PREREQUISITE FOR USE

If you are using non-segmented data, the data must be of a uniform length (in this case, each data set is viewed as a single segment).

To display the dialog box for the transform, you choose **Transformations > Frequency and Component Analysis > PCA**. PROCEDURE

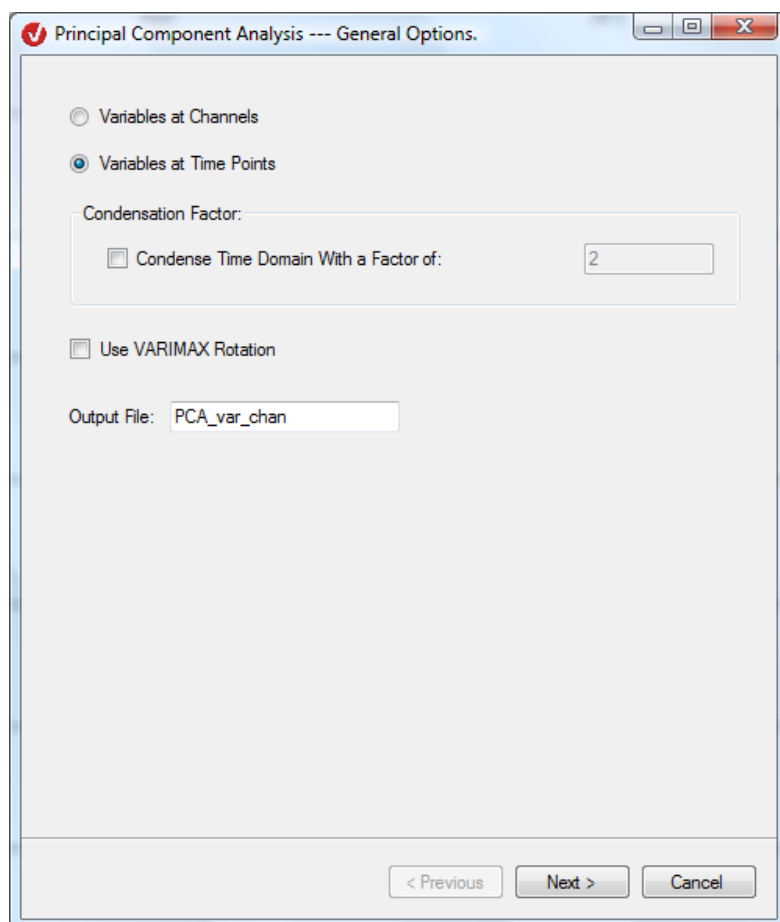


FIGURE 12—72 PCA DIALOG, PAGE 1

If you select the **Variables at Channels** radio button, the channels are interpreted as variables. If you select the **Variables at Time Points** radio button, the points in time are interpreted as variables.

If you have selected the **Variables at Time Points** radio button, the **Condense Time Domain With a Factor of:** check box and associated text box have a special significance. If you select this check box, the time domain is subdivided into groups of points of equal length. The length of each group corresponds exactly to the value in the **Condense Time Domain With a Factor of:** text box (the value in the text box is always in the range 1 to 1000). Consequently, the length of the time domain in points is reduced by this factor, and the sampling interval is increased by this factor. The use of a condensing factor thus reduces the volume of data and accelerates processing.

If you select the **Use VARIMAX Rotation** check box, an optional method is used to rotate the inverse of the covariance matrix in its space. The purpose of this rotation is to make the differences between PCA components clearer.

In the **Output File** text box, you can specify the name of the node in the secondary history files that contains the result.

Click the **Next** button to go to the second page of the dialog:

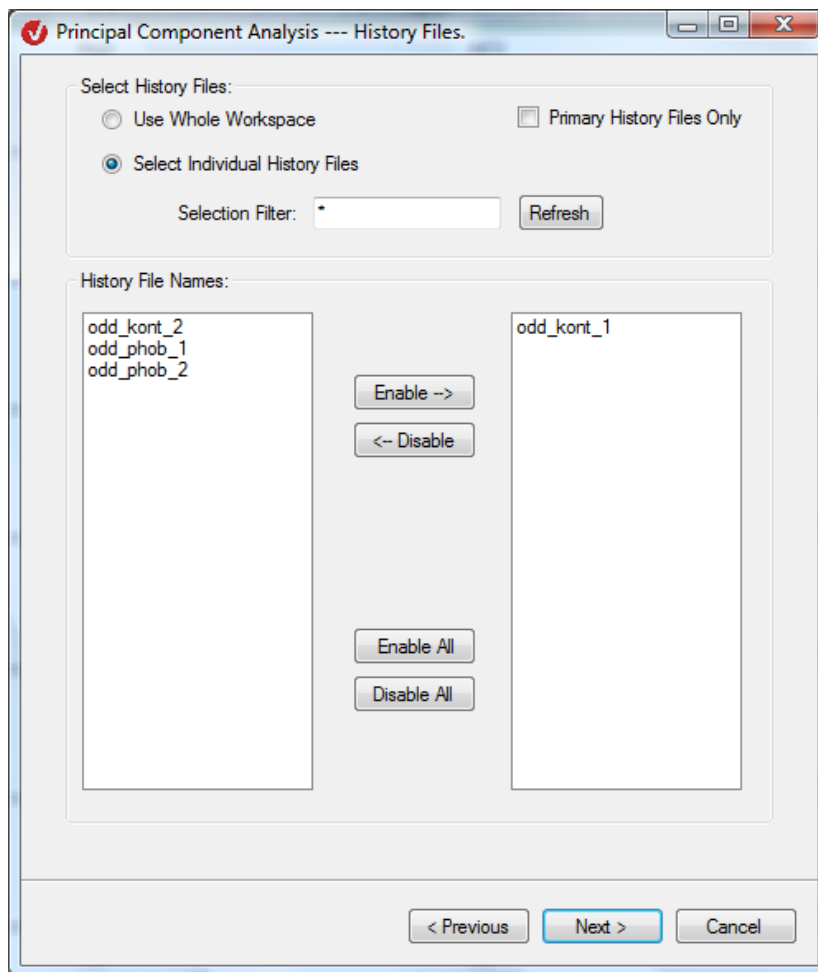


FIGURE 12—73 PCA DIALOG, PAGE 2

The **Select History Files** group box allows you to select the history files included in the PCA. If you select the **Use Whole Workspace** radio button, the history nodes are searched for in both primary and secondary history files. If you select the **Select Individual History Files** radio button, on the other hand, you can select specific history files.

SELECT HISTORY FILES
GROUP BOX

If you select the **Primary History Files Only** check box, the list of selected node names contains only the node names of primary history files.

In the **Selection Filter** text box, you can specify a filter to be used to search through the history file names. The placeholders “?” (for an unknown letter) and “*” (for an unknown part of a word) are available to you for this. If you click the **Refresh** button, the filter is applied to the list on the left, which contains the names of the history files.

You then make a selection from the history file names contained in the list on the left. The **Enable**, **Disable**, **Enable All** and **Disable All** buttons allow you to change your selection.

HISTORY FILE NAMES
GROUP BOX

Click the **Next** button to go to the third page of the dialog.

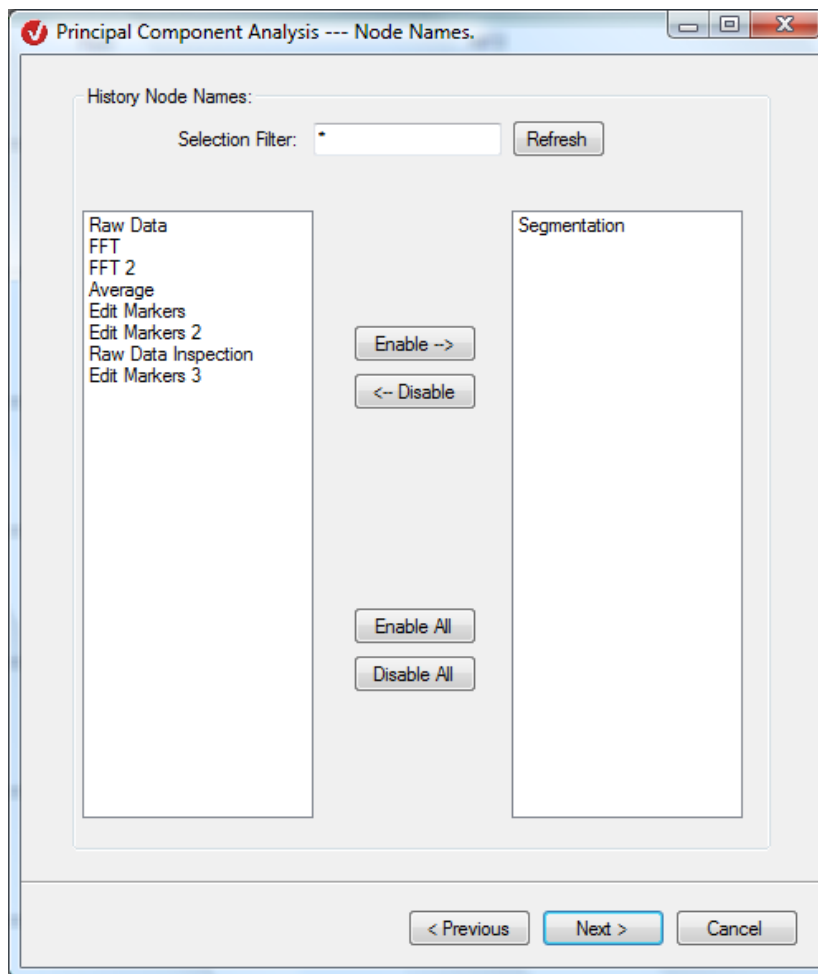


FIGURE 12—74 PCA DIALOG, PAGE 3

On the third page of the dialog, you select the names of the history nodes.

In the **Selection Filter** text box, you can specify a filter to be used to search through the history file names. The placeholders “?” (for an unknown letter) and “*” (for an unknown part of a word) are available to you for this. If you click the Refresh button, the filter is applied to the list on the left, which contains the names of the history nodes.

The **Enable**, **Disable**, **Enable All** and **Disable All** buttons allow you to change your selection.

Click the **Next** button to go to the fourth page of the dialog.

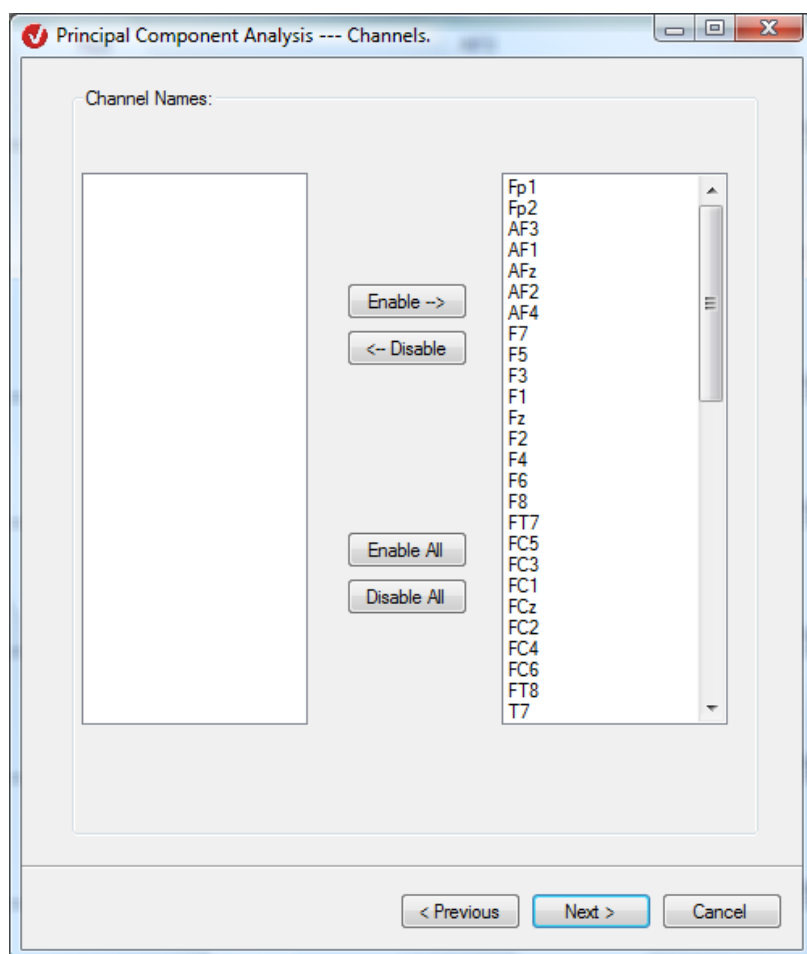


FIGURE 12—75 PCA DIALOG, PAGE 4

The **Channel Names** group box contains a list of the channel names of the first node found and a list of the selected channel names. The **Enable**, **Disable**, **Enable All** and **Disable All** buttons allow you to change your selection.

CHANNEL NAMES
GROUP BOX

Click the **Next** button to go to the fifth page of the dialog.

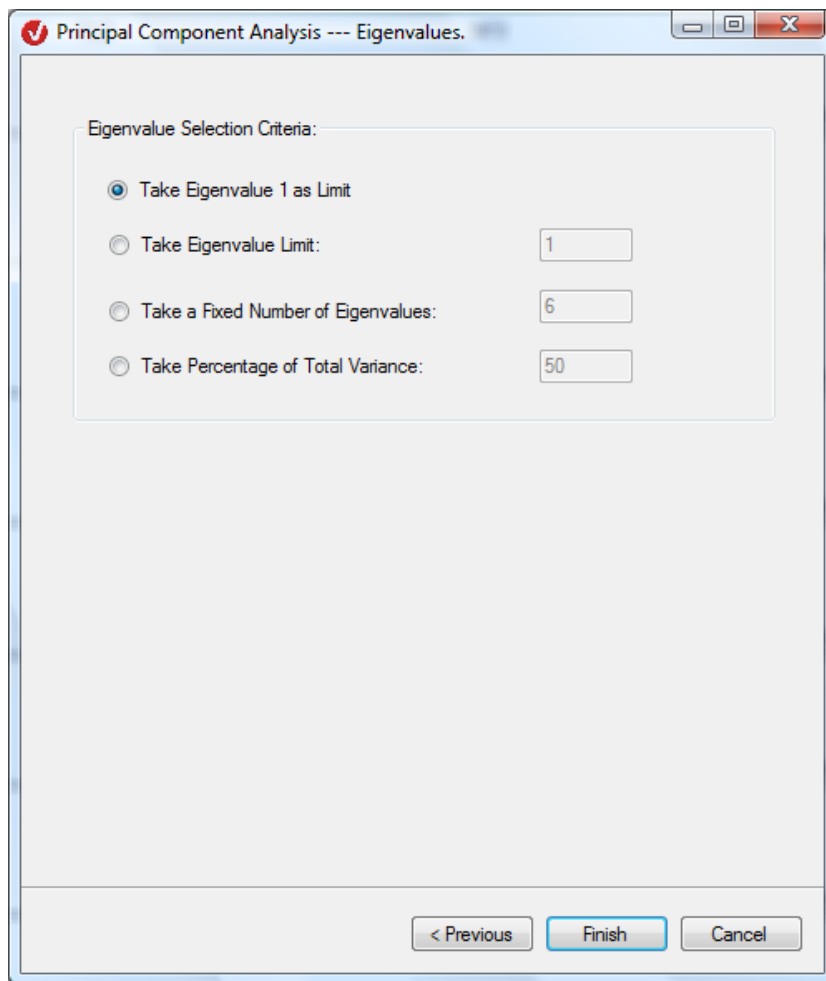


FIGURE 12—76 PCA DIALOG, PAGE 5

In the **Eigenvalue Selection Criteria** group box, you select the criterion to be used to calculate the eigenvalue:

EIGENVALUE SELECTION
CRITERIA GROUP BOX

- **Take Eigenvalue 1 as Limit** includes all eigenvalues greater than 1.
- **Take Eigenvalue Limit** includes all eigenvalues greater than the value entered in the associated text box.
- **Take a Fixed Number of Eigenvalues** selects the n largest eigenvalues, where n is the value in the associated text box.
- **Take Percentage of Total Variance** includes the largest components in terms of variance (eigenvalues), whose sum exceeds the percentage entered in the associated text box (the text box can contain any value from 1 to 1000).

When you have finished, click **Finish**.

A new history file with the corresponding name appears on the **Secondary** tab of the History Explorer. If the **Secondary** tab already contains a file with an identical name, it is replaced with the new file.

A specific view appears with a Semiautomatic View dialog box on the right.

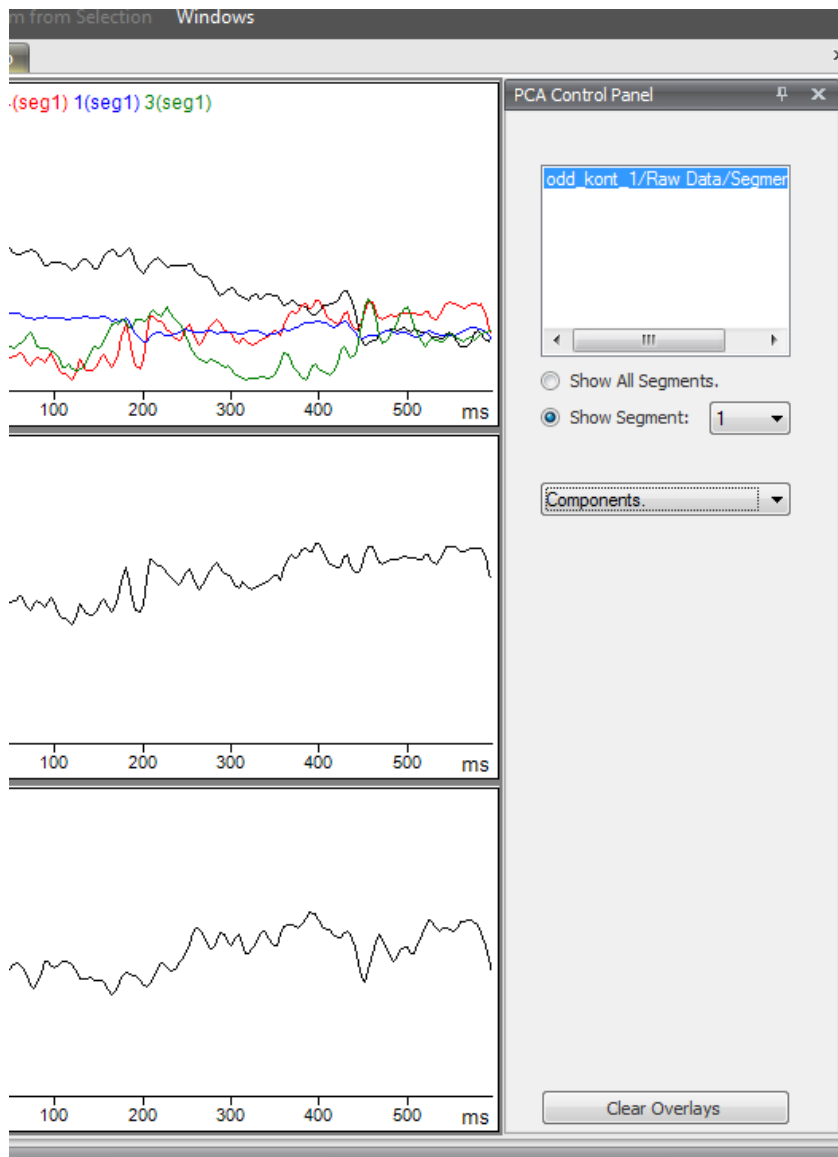


FIGURE 12—77 SPECIFIC PCA VIEW

In secondary history files calculated with the “Variables at Channels” radio button selected, the components are displayed as graphs and the loadings as head topographies.

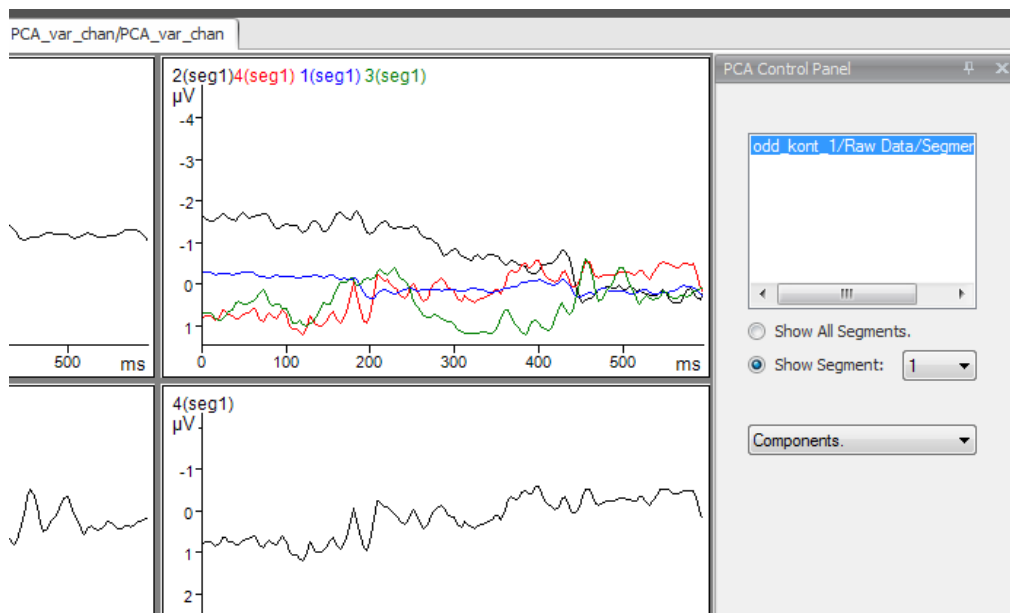


FIGURE 12—78 DISPLAY OF THE COMPONENTS AS GRAPHS WHEN “VARIABLES AT CHANNELS” IS SELECTED

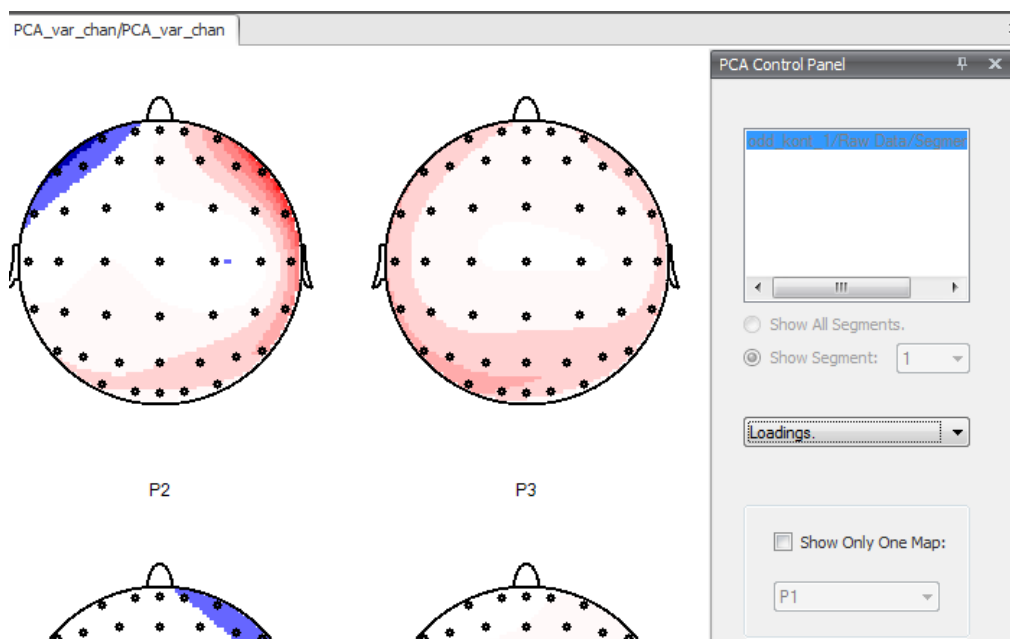


FIGURE 12—79 DISPLAY OF THE LOADINGS AS HEAD TOPOGRAPHIES WHEN “VARIABLES AT CHANNELS” IS SELECTED

In the corresponding secondary history files calculated with the “Variables at Time Points” radio button selected, the components are displayed as head topographies and the loadings as graphs.

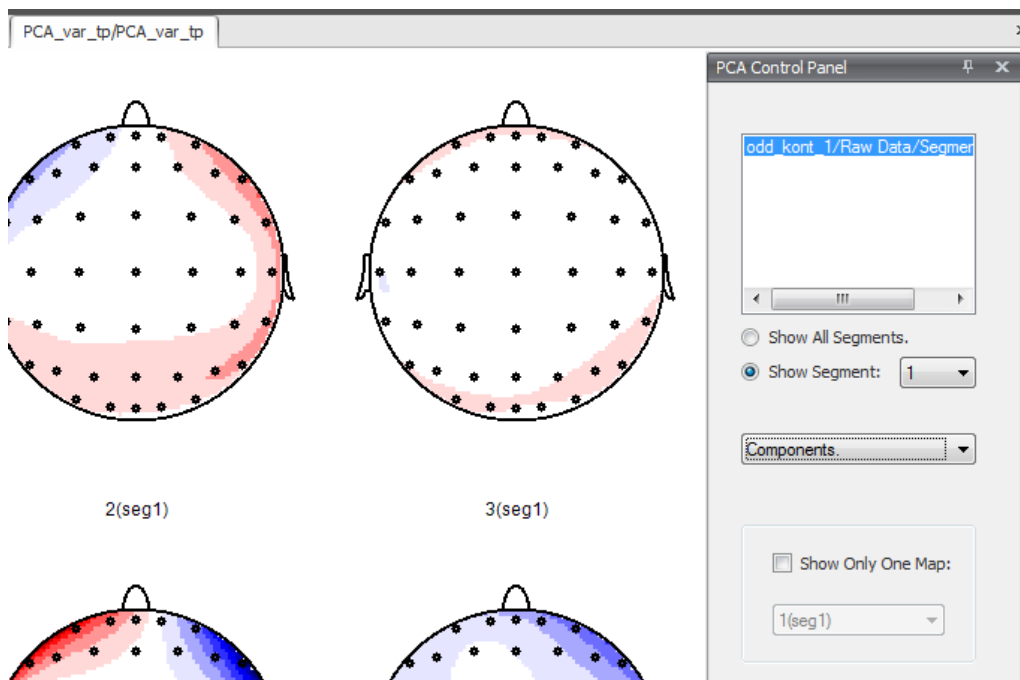


FIGURE 12—80 DISPLAY OF THE COMPONENTS AS HEAD TOPOGRAPHIES WHEN “VARIABLES AT TIME POINTS” IS SELECTED

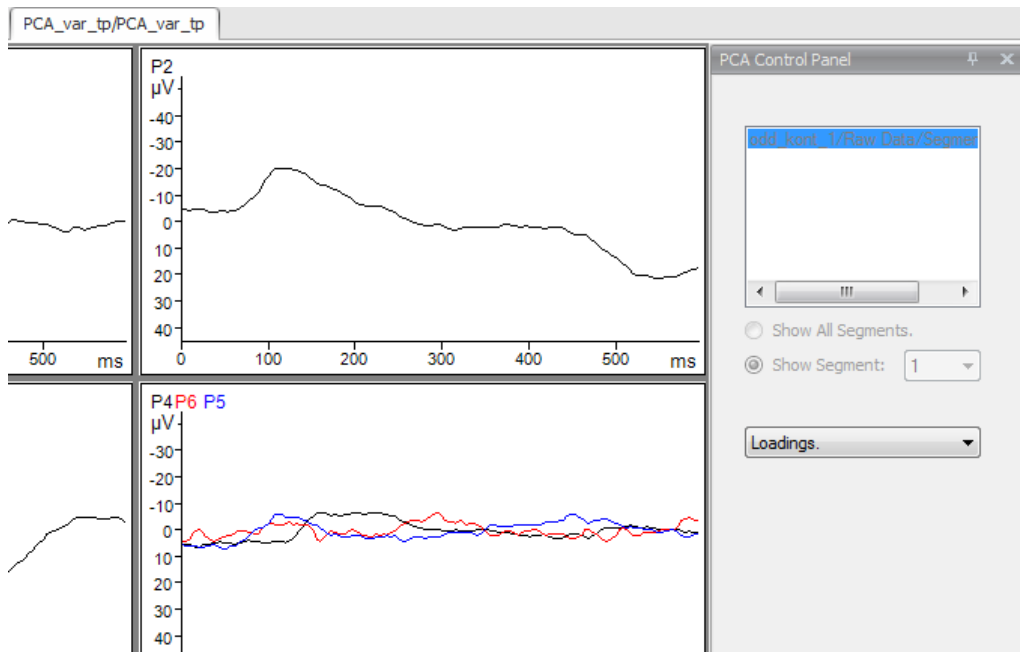


FIGURE 12—81 DISPLAY OF THE LOADINGS AS GRAPHS WHEN “VARIABLES AT TIME POINTS” IS SELECTED

The box in the upper part of the Semiautomatic View dialog box contains all the history nodes used. You can switch between these nodes with ease in order to switch between different views of the components.

If you select the **Show All Segments** radio button, all the segments of the history node selected in the box above are displayed. If you select the **Show Segment** radio button, you can use the associated drop-down list to select a segment to be displayed.

In the drop-down list, you can specify what is to be displayed by choosing **Components** or **Loadings**.

If you choose **Loadings**, the controls above the drop-down list become unavailable. This is because the loadings correspond to the lines of a square root of the inverse of the shared covariance matrix. Consequently, these loadings are identical for all segments and all selected data sets.

If graphs are displayed, the **Clear Overlays** button is also available to you for removing any overlays that have been created. Note that overlays can only be created with the channels in the grid view.

If topographic heads are displayed, an additional group box appears. This contains the **Show Only One Map** check box, which allows you to limit the display to only one map. The associated drop-down list always contains the names of the head topographies that are currently being displayed:

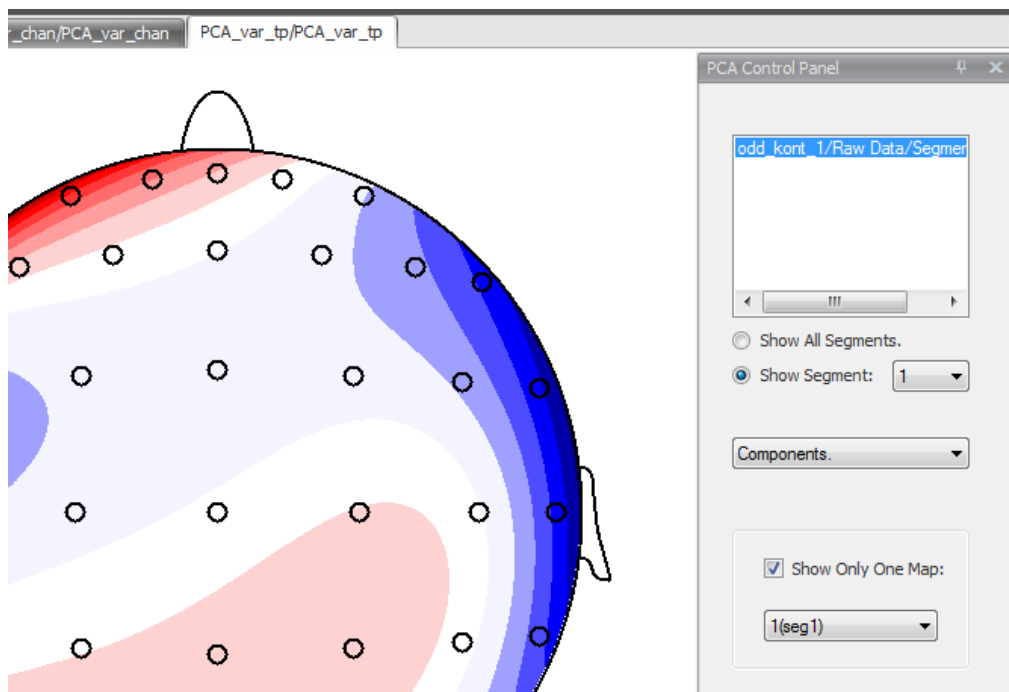


FIGURE 12—82 ADDITIONAL FUNCTION: “SHOW ONLY ONE MAP”

A data set created by means of the “Variables at Channels” radio button is referred to as a data set of the type “Components”. A data set created by means of the “Variables at Time Points” radio button is referred to as a data set of the type “Loadings”.

REMARKS

Each history node created by the PCA transform consists of two interlinked data sets: one of the type “Components” and one of the type “Loadings”. In a history node of the type “Components”, the underlying data set is of the type “Components”. The additional data set of the type “Loadings” takes the form of a set of inserted user properties:

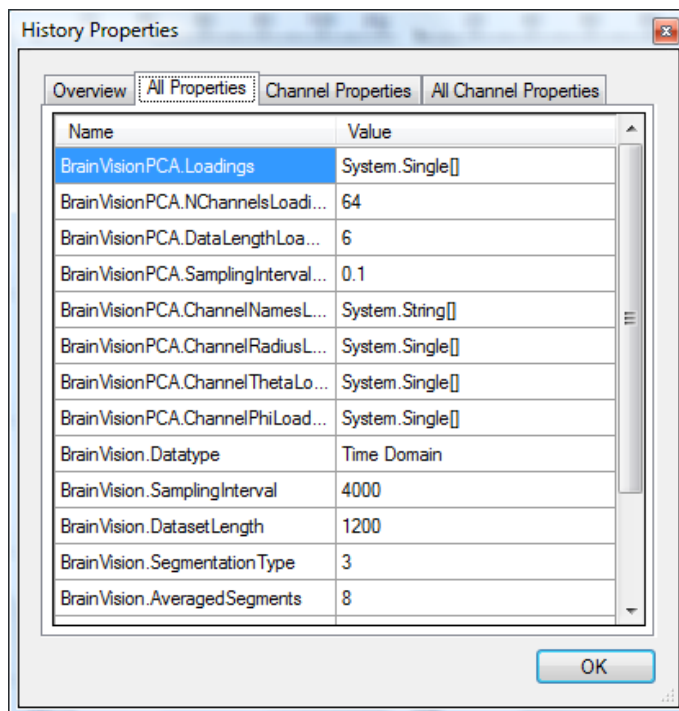


FIGURE 12—83 PROPERTIES OF A NODE OF THE TYPE “COMPONENTS” (CONTAINING THE DATA SET OF THE TYPE “LOADINGS” IN THE FORM OF USER PROPERTIES)

In history nodes of the type “Loadings”, the reverse applies:

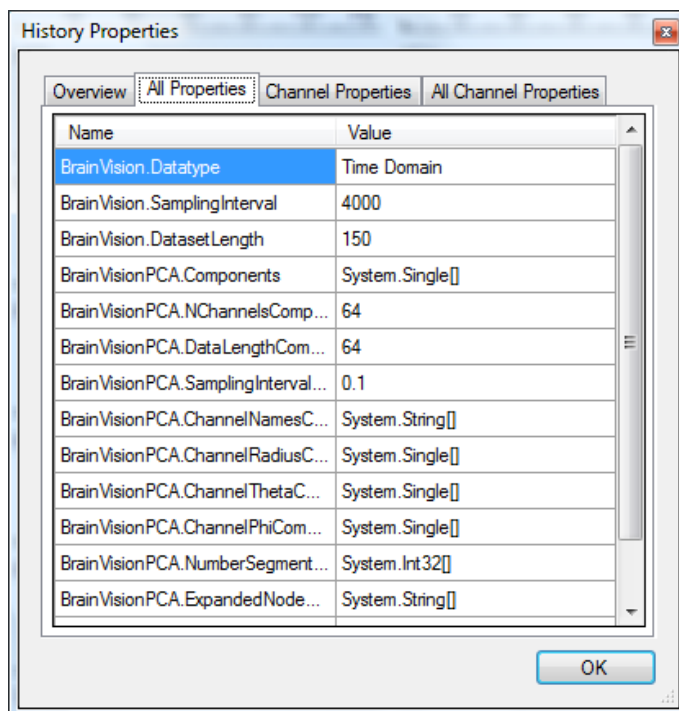
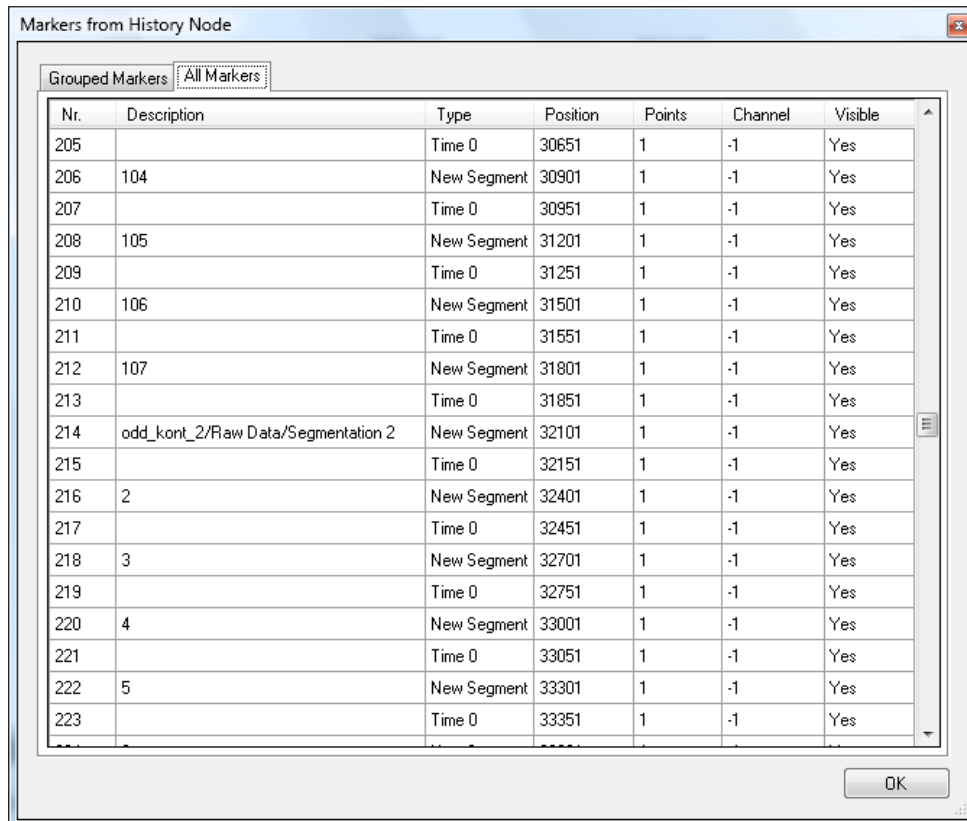


FIGURE 12—84 PROPERTIES OF A NODE OF THE TYPE “LOADINGS” (CONTAINING THE DATA SET OF THE TYPE “COMPONENTS” IN THE FORM OF USER PROPERTIES)

The child nodes of a history node created by the PCA transform are displayed in conventional views rather than in the specific PCA view. It is necessary to understand their structure in order to be able to navigate in them effectively. The data displayed corresponds to the PCA segments in their natural arrangement within a selected node. The segment packages, which correspond to different selected nodes, are arranged one after the other in the order in which the selected nodes occur. The markers of the type “New Segment”, which define these segments, have meaningful names that take the following form: The first “New Segment” marker of a segment packet has the expanded name of the original node. All subsequent markers of the type “New Segment” have the ordinals 2, 3, 4 and so on as their names. These markers also contain the following user properties: “Original Node” and “Original Segment”:



Nr.	Description	Type	Position	Points	Channel	Visible
205		Time 0	30651	1	-1	Yes
206	104	New Segment	30901	1	-1	Yes
207		Time 0	30951	1	-1	Yes
208	105	New Segment	31201	1	-1	Yes
209		Time 0	31251	1	-1	Yes
210	106	New Segment	31501	1	-1	Yes
211		Time 0	31551	1	-1	Yes
212	107	New Segment	31801	1	-1	Yes
213		Time 0	31851	1	-1	Yes
214	odd_kont_2/Raw Data/Segmentation 2	New Segment	32101	1	-1	Yes
215		Time 0	32151	1	-1	Yes
216	2	New Segment	32401	1	-1	Yes
217		Time 0	32451	1	-1	Yes
218	3	New Segment	32701	1	-1	Yes
219		Time 0	32751	1	-1	Yes
220	4	New Segment	33001	1	-1	Yes
221		Time 0	33051	1	-1	Yes
222	5	New Segment	33301	1	-1	Yes
223		Time 0	33351	1	-1	Yes

FIGURE 12—85 MARKER NAMES

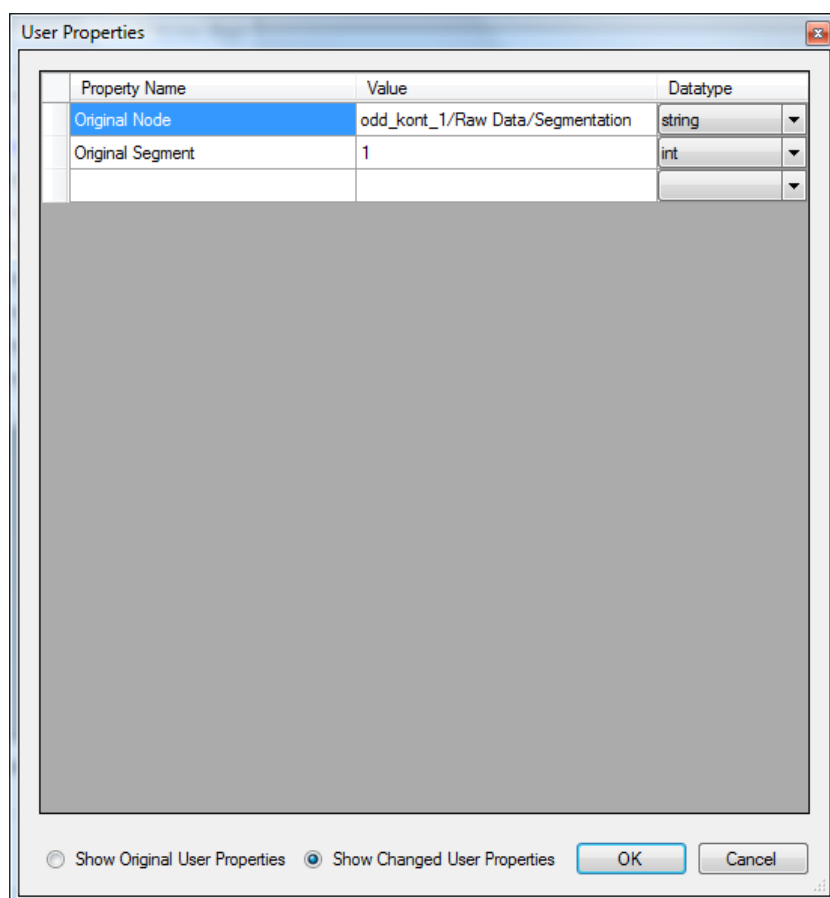


FIGURE 12—86 USER PROPERTIES OF THE MARKERS (EDIT MARKERS TRANSFORM)

If you use the PCA transform on non-segmented data, the original data sets become segments.

In all cases, however, the number of channels of the child nodes corresponds exactly to the number of components found by the PCA transform. These have the names P₁ to P_n.

In contrast to the channels of child nodes, the channels are named as follows in the PCA view: In data of the type “Components”, the names of the channels take the form k(segn), and the loadings are named P₁ to P_n. In data of the type “Loadings”, the channels are named P₁ to P_n, and the names of the head topographies take the form k(segn).

If you use segmented data containing a time zero marker, these kinds of markers are also inserted in PCA components or PCA loadings.

The entire set of data (from all the selected segments and nodes) is used to calculate a covariance matrix that corresponds to the selected criterion. METHOD

In principal component analysis, the covariance matrix of all the variables is calculated first. If there are n variables, this results in an $n \times n$ matrix from which n factors can theoretically be extracted. In practice, however, you limit yourself to a number whose variance is greater than a specific limit in order to eliminate effects such as those caused by noise from the calculation.

If the number of desired factors is m , the m largest eigenvalues and the associated eigenvectors are calculated from the covariance matrix.

The factor loadings are obtained from the product of the root of the eigenvalue and the eigenvector. From the factor loadings, the associated component is calculated for each value of a variable in such a way that the sum of the products of the component and factor loading approximate the value of the variable to optimum effect.

The covariance matrix is a square matrix whose size corresponds to the number of channels when the “Variables at Channels” radio button is selected or to the number of points when the “Variables at Time Points” radio button is selected. Consequently, the user must select channels that are present in all the selected data or have carried out segmentation and calculated averages using the same segment length each time. (Otherwise, error messages are displayed.)

When variables are selected as points in time, the variables take on different values depending on the channel, the segment and the EEG file. When variables are selected as channels, the values depend on the point in time, the segment and the EEG file.

The covariance matrix, which is always a symmetrical, real, positive-definite matrix, is diagonalized using the Lagrange method. The diagonal elements are referred to as the eigenvalues of the matrix. The largest eigenvalues are selected using the selection criterion selected in the dialog, and the part of the covariance matrix that meets this criterion is retained.

Using the theory of symmetrical, real, positive-definite matrices, a square root of the inverse (of the relevant part) of the covariance matrix is calculated. The columns of this matrix are known as loadings. However, this method of breaking down the variables is just one of many. A direct result of the construction of the loadings is that they are orthogonal, although this is not required on physiological grounds. For this reason, the results of the Principal Component Analysis transform are often rotated subsequently in the hope of obtaining data that better corresponds to the physiological facts. The results of the Principal Component Analysis transform with or without rotation should never be accepted uncritically; you should always subject them to a scientific examination.

If the “Variables at Channels” radio button is selected, the loadings are vectors whose length corresponds to the number of channels, and they are displayed as head topographies. If the “Variables at Time Points” radio button is selected, the loadings are vectors whose length corresponds to the number of points, and they are displayed as EEG graphs.

The loadings matrix is multiplied out individually with each EEG segment as a matrix. The result of this multiplication is referred to as a PCA component. If the “Variables at Channels” radio button is selected, the PCA components are vectors whose length corresponds to the number of points, and they are displayed accordingly as EEG curves. If the “Variables at Time Points” radio button is selected, the PCA components are vectors whose length corresponds to the number of channels, and they are displayed as head topographies.

[RM81] F. Rösler, D. Manzey, Principal Components and VARIMAX-Rotated Components in Event-Related Potential Research: Some Remarks on Their Interpretation. *Biological Psychology* 13 (1981), 3-26.

REFERENCES

12.4 Transforms in the Segment Analysis Functions group

12.4.1 Peak Detection

The Peak Detection transform is for detecting and marking peaks. Peaks are local minimum or maximum values in an averaged EEG.

SUMMARY

The transform allows you to specify peaks in a table, together with their name and range. You also have to specify whether the peak is positive or negative. You can select specific channels where the peaks are to be marked.

The Peak Detection transform is typically used after:

PREREQUISITE FOR USE

- Average

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Result Evaluation > Peak Detection**.

PROCEDURE

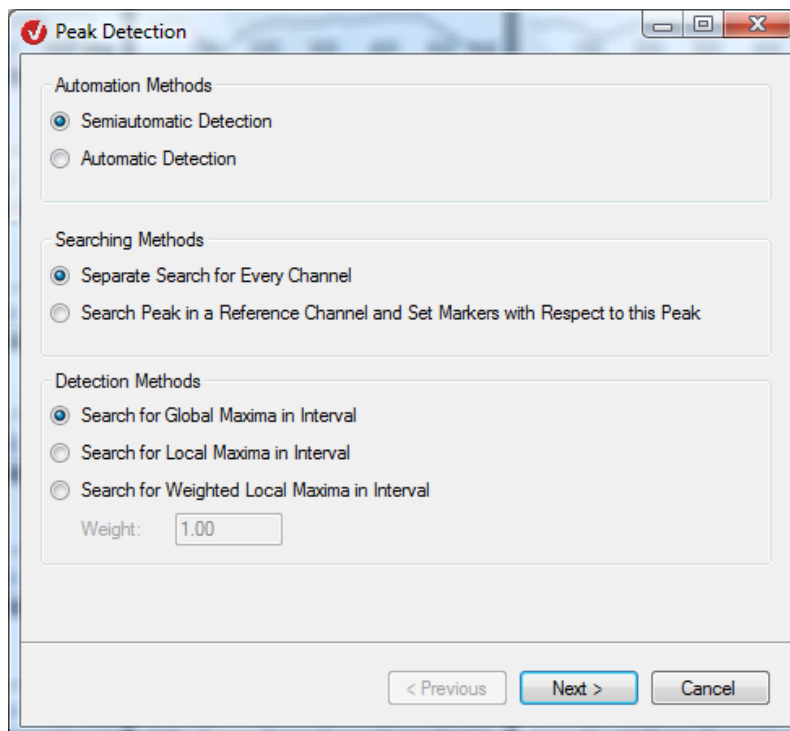


FIGURE 12—87 PEAK DETECTION DIALOG, FIRST PAGE

In the **Automation Methods** group box, you specify whether peak detection is to be carried out in semiautomatic mode (**Semiautomatic Detection** radio button) or automatic mode (**Automatic Detection** radio button).

AUTOMATION METHODS
GROUP BOX

In semiautomatic detection, a cursor appears at the point at which the algorithm finds a peak. You can use this cursor to change the position of the peak manually.

In the **Detection Methods** group box, you select the peak search method.

DETECTION METHODS
GROUP BOX

- If you select the **Search for Global Maxima in Interval** radio button, a search is carried out for the global maximum (or minimum) in a set interval.
- If you select the **Search for Local Maxima in Interval** radio button, a search is carried out for a local maximum.
- If you select the **Search for Weighted Local Maxima in Interval** radio button, a search is carried out for a weighted local maximum.

The difference between a local and global maximum is that, in the search for a global maximum, the edge points of the intervals are found as peaks if the value there is greater (or less) than all the values within the interval.

In the search for local maxima, extreme values are searched for within the interval. The edge values are only included if this initial search is unsuccessful.

Since several local maxima can occur in an interval in certain circumstances, it is possible to weight them during selection. When this method is used, all maxima that are found are multiplied by the weighting factor $1 - a \cdot t^2$, and the highest value is then searched for. The value “t” is from the interval [-1, 1] and describes the variance of the position of the data point from the middle of the search interval. The value “a” can be entered in the **Weight** text box. The value can be in the range from 0 to 1.

If the weighting is 0, the weighted method is identical to the unweighted method. If the weighting is greater than 0, peaks that are closer to the middle of the interval have a higher weighting than peaks at the edges of the interval. However, the peaks found are still all local maxima of the voltage distribution. The weighting function only has an impact on the selection of peaks when there are several possible local maxima, not on their position or size.

In the **Searching Methods** group box, you can choose between two different methods for settings markers:

SEARCHING METHODS
GROUP BOX

- If you select the **Separate Search for Every Channel** radio button, the search for peaks and the setting of markers is carried out separately for each channel selected.
- If you select the **Search Peak in a Reference Channel and Set Markers with Respect to this Peak** radio button, the search for peaks is carried out only in a specified channel. In all the selected channels, the peaks are marked at the position at which they are found in the specified channel.

The detected peaks are output as markers of the type “Peak”.

On the second page of the dialog, you enter the peaks you want to search for.

SEPARATE SEARCH FOR
EVERY CHANNEL RADIO
BUTTON

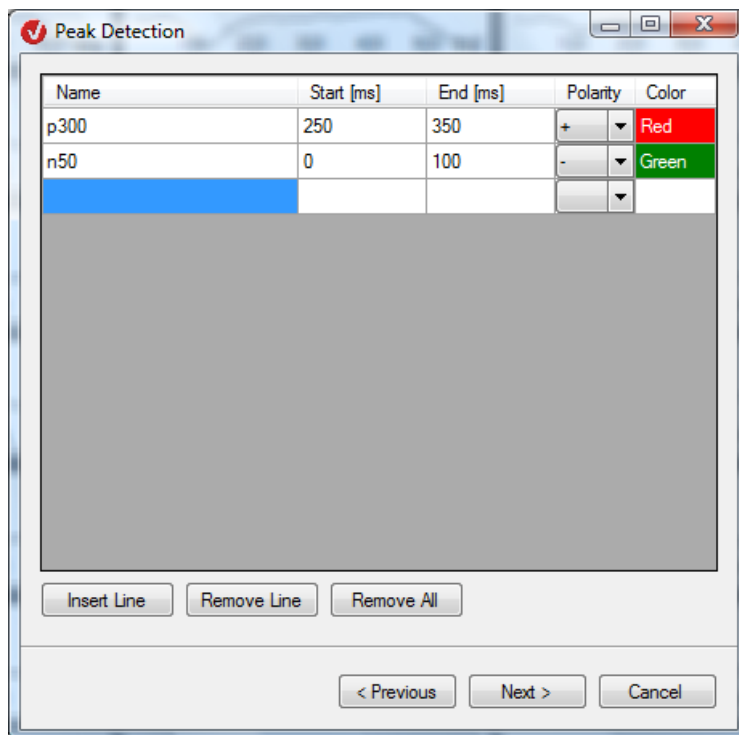


FIGURE 12—88 PEAK DETECTION DIALOG, SECOND PAGE, SEPARATE SEARCH FOR EVERY CHANNEL RADIO BUTTON SELECTED

You can make the following settings:

- In the **Name** cell, you enter the name of the peak (“p300” and “n50” in our example).
- In the **Start [ms]** and **End [ms]** text boxes, you specify the length (i.e. the beginning and end) of the interval in which you want to search for peaks.
- The **Polarity** drop-down list allows you to specify the polarity (positive or negative) of the peak.
- If you selected the **Search Peak in a Reference Channel and Set Markers with Respect to this Peak** radio button on the first page of the dialog, you can use the **Reference Channel** drop-down list to specify the reference channel to be searched for.
- The **Color** cell indicates the color in which the peak indicator is displayed in the semiautomatic search. To assign a color to a peak or change the color selected, click the relevant cell. A color selection dialog box appears.
- The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

On the third page of the dialog, you select the channels in which the peak marker is to be set.

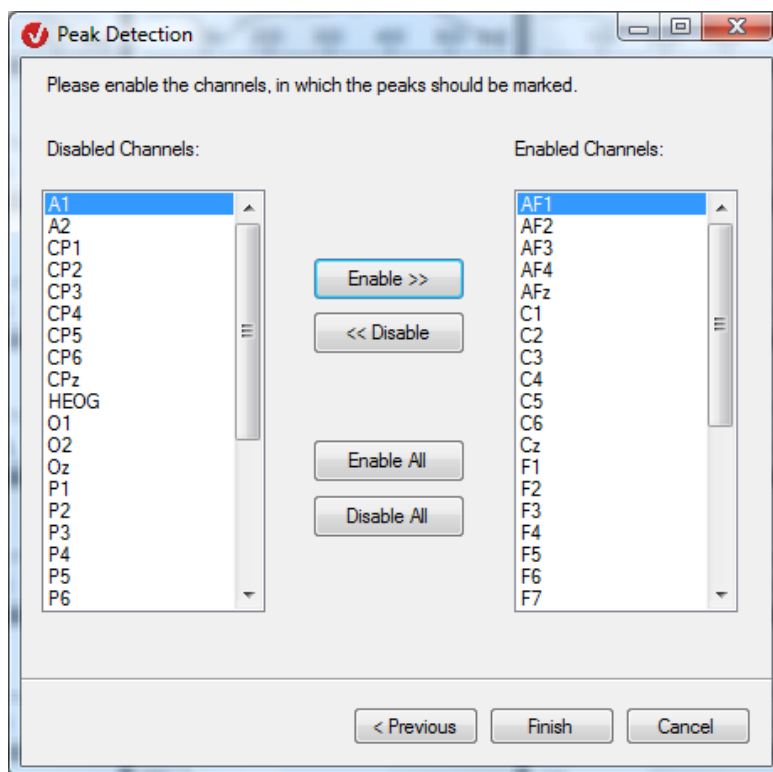


FIGURE 12—89 PEAK DETECTION DIALOG, THIRD PAGE, SEPARATE SEARCH FOR EVERY CHANNEL RADIO BUTTON SELECTED

If you selected semiautomatic peak detection, the semiautomatic view appears. This permits fine adjustment of the peaks detected.

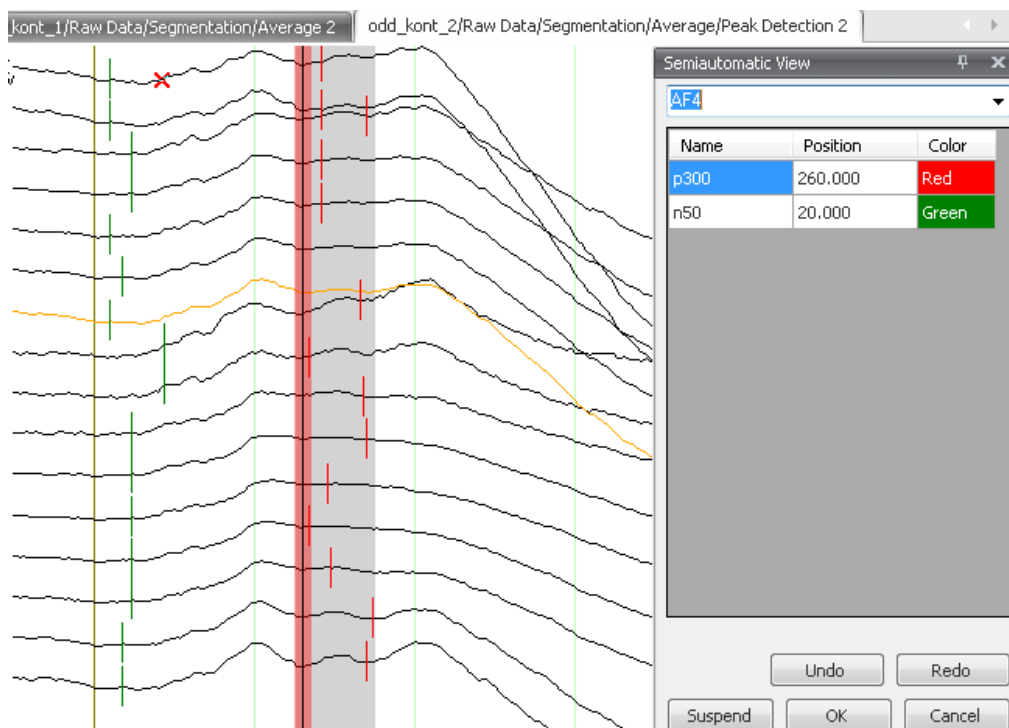


FIGURE 12—90 EXTRACT FROM A SEMIAUTOMATIC PEAK DETECTION DIALOG, SECOND PAGE, SEPARATE SEARCH FOR EVERY CHANNEL RADIO BUTTON SELECTED

The drop-down list box at the top of the temporary semiautomatic view dialog box allows you to select the active channel. An active channel is highlighted in orange (like the channel “AF2” in our example).

If you click the corresponding row of the table, a section highlighted in gray appears that indicates the search interval set for the peak.

If you double-click a row, the associated peak cursor turns into a movable slider. You can use the mouse to move this slider into the ideal position. You can cancel the operation by pressing the **Escape** key. The slider turns back into the peak cursor.

Alternatively, you can display the gray highlighting and the slider by clicking the peak cursor. This also activates the corresponding channel.

The **Undo** and **Redo** buttons allow you to undo and redo changes, respectively.

If you want to interrupt what you are doing and resume later, you click the **Suspend** button. The Data Inspector transform is highlighted in red in the list of history nodes, and all the processing steps carried out continue to apply.

You click the **OK** button to conclude your entries.

If you search a fixed reference channel for peaks, the table on the second page of the dialog also contains the **Reference** dialog box. You can select the reference channel from the associated drop-down list.

SEARCH PEAK IN A
REFERENCE CHANNEL
RADIO BUTTON

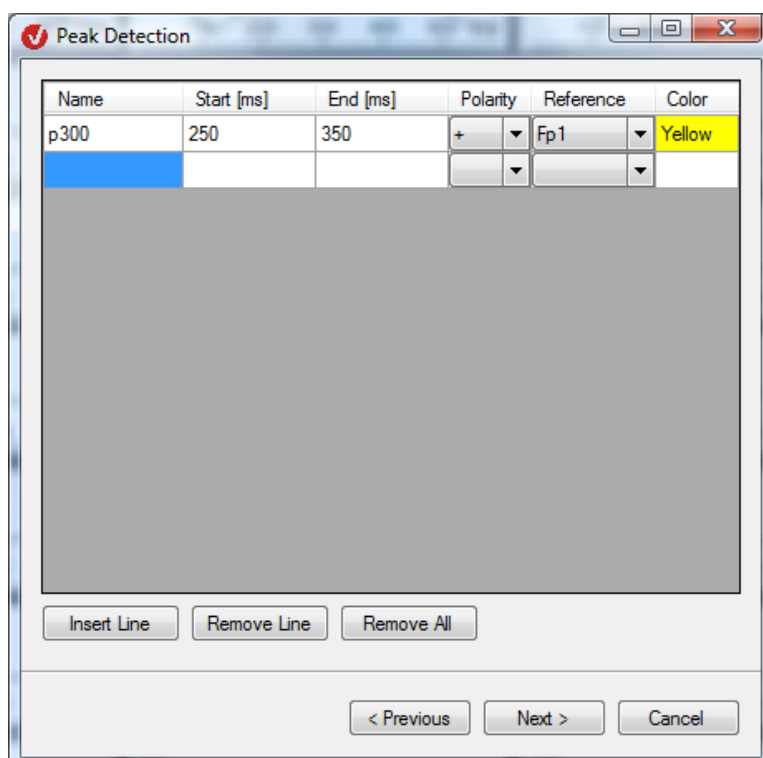


FIGURE 12—91 PEAK DETECTION DIALOG, SECOND PAGE, SEARCH PEAK IN A REFERENCE CHANNEL RADIO BUTTON SELECTED

On the third page of the dialog, you select the channels in which the peak marker is to be set (as for the **Separate Search for Every Channel** radio button).

If you selected semiautomatic peak detection, the semiautomatic view dialog box appears. This permits fine adjustment of the peaks detected.

Note that there is no drop-down list allowing you to select a channel in the semiautomatic view.

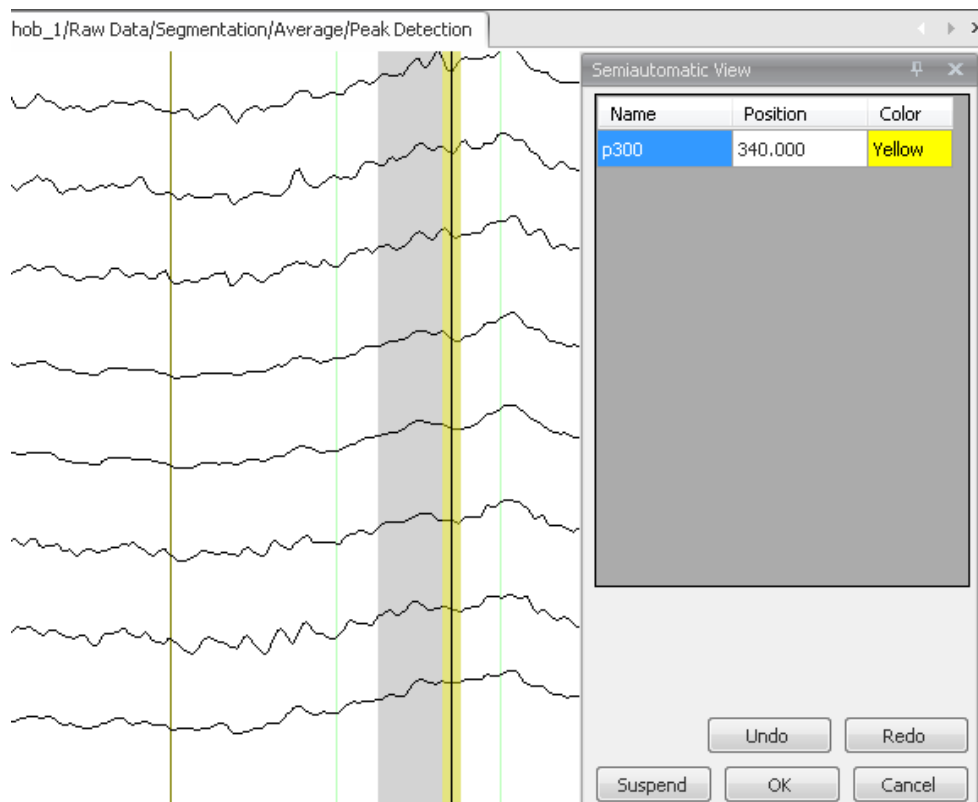


FIGURE 12—92 EXTRACT FROM A SEMIAUTOMATIC PEAK DETECTION DIALOG, SEARCH PEAK IN A REFERENCE CHANNEL RADIO BUTTON SELECTED

12.4.2 LRP (Lateralized Readiness Potential)

The LRP transform calculates the lateralized readiness potential (LRP) from two data sets (e.g. movements of the left and right hands). SUMMARY

No previous processing steps are required before the transform is used. PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Result Evaluation > LRP**.

The first step is to create two data nodes. You should segment the first node based on the first condition (e.g. movement of the left hand) and the second node based on the second condition (e.g. movement of the right hand). In the second step, you obtain an average for both nodes.

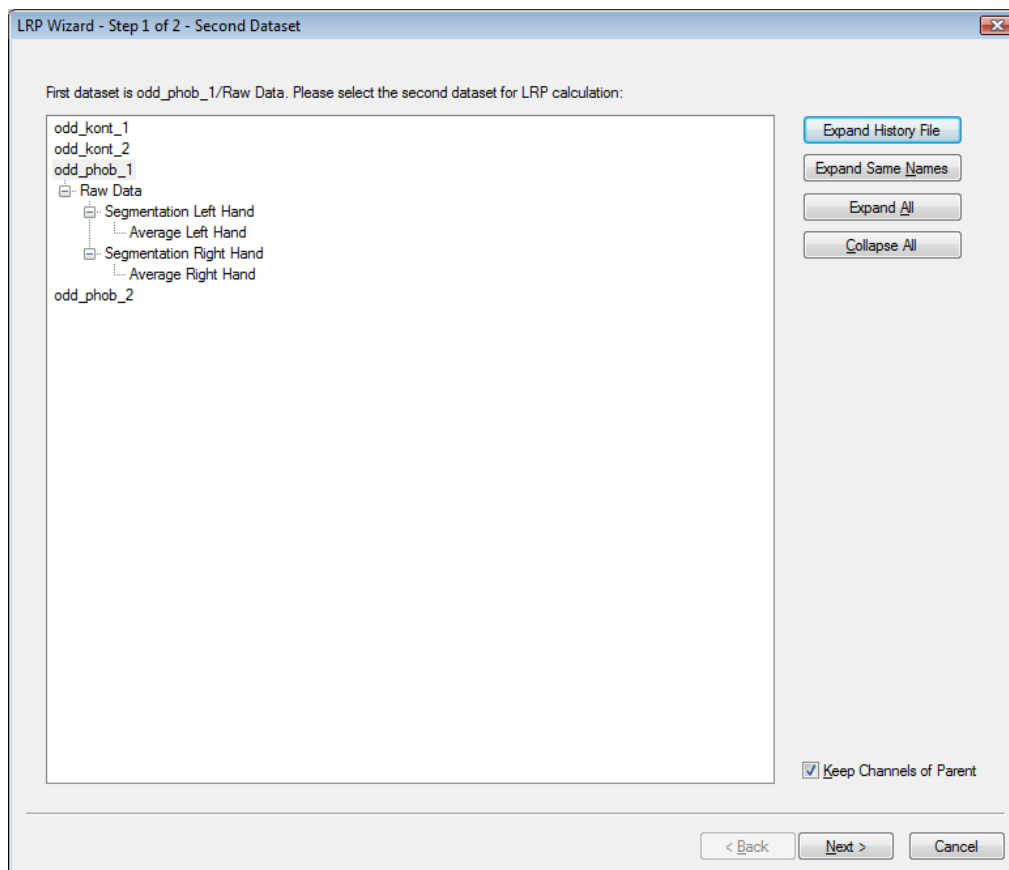


FIGURE 12—93 LRP, SELECTION DIALOG FOR THE SECOND DATA SET

The LRP transform then calculates the lateralized readiness potential and writes the result to new channels whose names take the following form: LRP(., .). To run this calculation, you begin by selecting the path of the second data set in the dialog.

The structure of the selection tree in the dialog is like the Analyzer's history tree. You select the path by clicking the node. You can search for the node by expanding certain parts of the tree using the buttons on the right-hand side of the dialog box.

In addition, you can use the **Keep Channels of Parent** check box to specify whether the channels of the parent node are to be included in the new data set or whether the new data set is to consist of LRP data only. If you double-click the selected node or click the **Next** button, the second page of the dialog appears, in which you can select the channels for the LRP.

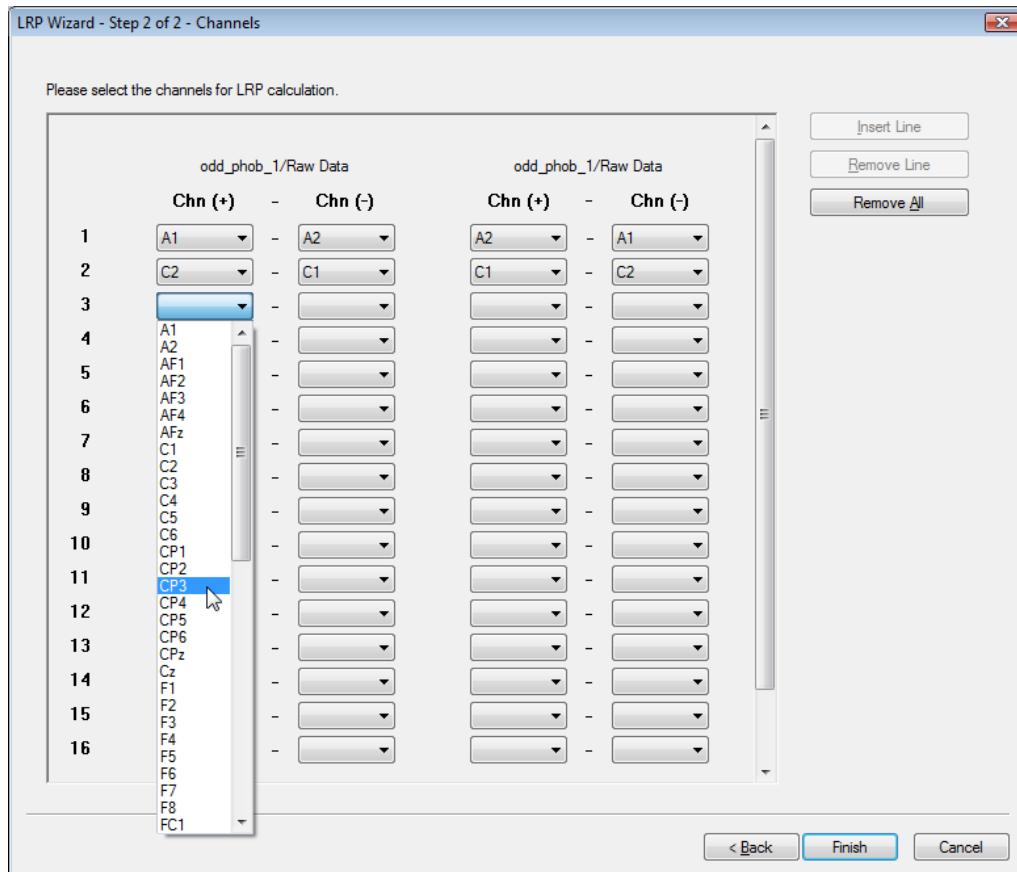


FIGURE 12—94 LRP, SELECTION DIALOG FOR THE CHANNELS

When the LRP is calculated, the difference between contralateral and ipsilateral electrodes in the parent node and the corresponding reverse difference in the second node are formed, and the average of these two differences is calculated. The two left-hand columns of the channel list are therefore assigned to the first data node (parent), and the two right-hand columns are assigned to the second data node.

It is generally sufficient to fill the two left-hand or two right-hand columns. The dialog then searches for the corresponding channels in the other data set and fills the other columns accordingly when suitable channels are found. You can also modify these entries. If no suitable channels are found, you have to fill all columns manually.

When all the columns of the required rows are filled correctly, you conclude your entries by clicking the **Finish** button. The LRP is calculated. The structure of the LRP channels is also described in the operation information.

The following example illustrates how entries are made:

EXAMPLE

In an experiment, a warning stimulus tells the subject which hand to use in response to a subsequent imperative stimulus. The warning stimulus, imperative stimulus and response (left hand, right hand) are stored as markers in the raw EEG. The Segmentation transform and advanced Boolean expressions are used to create two segmented data sets (nodes). One node corresponds to the response with the left hand, and the other to the response with the right hand. You will find more information on this in section 12.4.5, "Segmentation".

An average is calculated for the two nodes, and the average nodes are given meaningful names (e.g. Avg left, Avg right). The LRP data is to be created as subnodes of the "Avg left" node. Consequently, the LRP module is applied to this node. The "Avg right" node is selected as the second data set. The LRP is to be calculated, for example, for channels C3 and C4 (i.e. C4 - C3 is calculated for "Avg left" and C3 - C4 for "Avg right"). These differences are then averaged. Thus, C4 is entered in the first column and C3 in the second column. The channel names C3 and C4 appear in the third and fourth columns. After the calculation, a channel named LRP(C4,C3) appears. This is the result of the formula $(C4(\text{left}) - C3(\text{left}) + C3(\text{right}) - C4(\text{right})) / 2$.

You will find further information on lateralized readiness potential in:

REFERENCES

[SUL96] W. Sommer, R. Ulrich, H. Leuthold, Das Lateralisierte Bereitschaftspotential als psychophysiologischer Zugang bei der Untersuchung kognitiver Prozesse. Psychologische Rundschau, 47 (1996) 1-14.

12.4.3 ERS/ERD (Event-Related Synchronization/Desynchronization)

The ERS/ERD transform is for the analysis of the event-related course of individual frequency bands of the EEG. SUMMARY

This transform is typically executed after:

PREREQUISITE FOR USE

- Segmentation
- Baseline correction (optional)
- Bandpass filtering (optional)

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Result Evaluation > ERS/ERD**. PROCEDURE

The screenshot shows the 'ERS/ERD' dialog box with the following settings:

- Filter Settings:**
 - ☒ Use Filter
 - Filter Frequency [Hz]: 10
 - Filter Bandwidth [Hz]: 5
- ERS / ERD Method:**
 - ☐ Instantaneous Power
 - ☒ Intertrial Variance
- Comparison Settings:**
 - ☒ Show Change Compared to Reference Interval
 - ☒ Create a Data Set for Significance
 - ☒ Show significance for ERD
 - ☐ Show significance for ERS
- Reference Interval Settings:**
 - ☒ Based on Time
 - Allowed Range: 100 to 1000
 - Start [ms]: -100 End [ms]: 4 Duration [ms]: 104
 - ☐ Based on Data Points
 - Allowed Range: -25 to 249
 - Start: -25 End: 0 Duration: 26
 - ☐ Reference Uses Median
 - ☒ Reference Uses Mean
- Segment / Channel Selection:**
 - Available Segments: 544
 - ☒ Use Full Range
 - ☐ Specify Range of Segments From: 1 To: 1
 - ☐ Calculate with Odd - Even Segments
 - ☐ Use only Odd Segments
 - ☒ Use only Even Segments
 - ☐ Enable Individual Channel Mode

FIGURE 12—95 ERS/ERD DIALOG BOX

You make the following settings before running the ERS/ERD transform:

If you select the **Use Filter** check box, filters are used. In the **Filter Frequency [Hz]** and **Filter Bandwidth [Hz]** text boxes, you specify the filter frequency and bandwidth.

FILTER SETTINGS GROUP BOX

If you have already carried out bandpass filtering, it is not necessary to select the **Use Filter** check box.



In the **ERS/ERD Method** group box, you select the method for the processing of the EEG. The methods – **Instantaneous Power** and **Intertrial Variance** – differ in terms of what happens before averaging (see [KP95]). In the case of the **Instantaneous Power** method, the voltage measured is squared before averaging, while the **Intertrial Variance** involves calculating the variance of the signal.

ERS/ERD METHOD GROUP BOX

If you select the **Show Change Compared to Reference Interval** check box, the data is specified as a percentage change based on the comparison with the reference interval.

COMPARISON SETTINGS GROUP BOX

In addition, you can create a data set for the significance by selecting the **Create a Data Set for Significance** check box.

The significance is calculated for either ERS (**Show Significance for ERS** radio button) or ERD (**Show Significance for ERD** radio button).

To configure the reference interval, in the **Reference Interval Settings** group box you select either the **Based on Time** radio button for a time-based setting or the **Based on Data Points** radio button for a data point-based setting.

REFERENCE INTERVAL SETTINGS GROUP BOX

You can also specify that either the mean (**Reference Uses Mean** radio button) or the median (**Reference Uses Median** radio button) is to be used.

You make the settings for the averaging of the segmented data in the **Segment/Channel Selection** group box, as described in section 12.4.6, “Average”.

SEGMENT/CHANNEL SELECTION GROUP BOX

The number of available segments is displayed under **Available Segments**.

It is possible to obtain an average for all segments or a selected range of segments by selecting either the **Use Full Range** or **Specify Range of Segments** button. If you select the **Specify Range of Segments** radio button, you can specify the range of segments to be included in the **From** and **To** text boxes.

You can also specify whether only the segments with odd segment numbers (segment 1, 3, 5, etc.) or even segment numbers (2, 4, 6, etc.) are to be averaged by selecting the **Calculate with Odd - Even Segments** check box and then selecting the **Use Only Odd Segments** or **Use Only Even Segments** radio button.

Another option is individual channel mode, which you activate by selecting the **Enable Individual Channel Mode** check box. Individual channel mode allows you to run averaging on each channel separately. If only one channel in a segment has been marked as bad, the other channels are still used for averaging. As a result, the number of segments included in averaging may be different for each channel. If you do not select the check box, all segments that contain a “bad interval” marker are rejected in their entirety.

Before you can use individual channel mode, you have to take a number of steps by way of preparation. You will find more information on this in section 12.4.6, “Average”.

[KP95] J. Kalcher, G. Pfurtscheller, Discrimination between phase-locked and non-phase-locked event-related EEG activity. *Electroencephalography and Clinical Neurophysiology*, 94(1995), 381-384.

REFERENCES

12.4.4 Grand Average

Grand Average is a secondary transform. It is used to create one or more grand averages from different averages. SUMMARY

The result is stored in secondary history files in the current workspace.

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Result Evaluation > Grand Average**. PROCEDURE

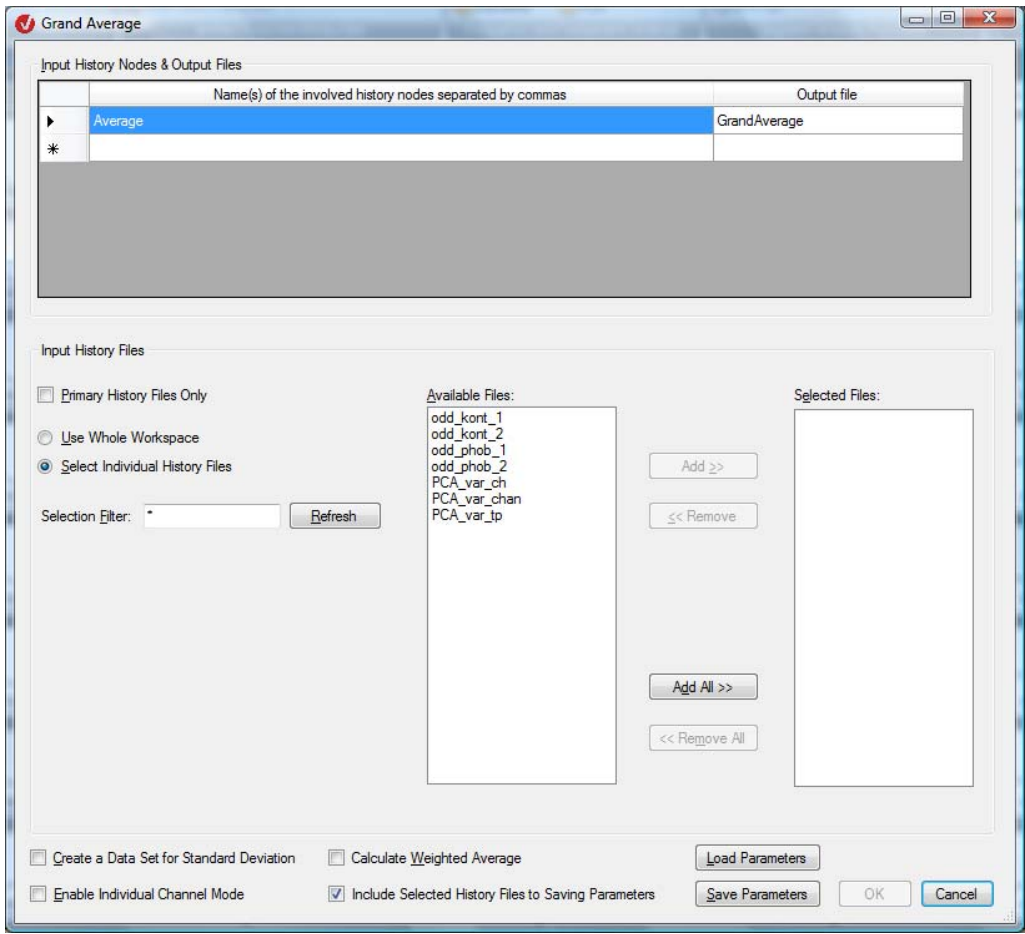


FIGURE 12—96 GRAND AVERAGE DIALOG BOX

You can specify the following in the table:

- In the **Name of the Involved History Nodes separated by commas** column, you specify the names of the data sets involved, separated by commas.
- In the **Output file** column, you specify the name of the output files.

In the **Input History Files** group box, you can make the following settings:

INPUT HISTORY FILE
GROUP BOX

- If you select the **Primary History Files Only** check box, you restrict the list under **Available Files** to primary history files.
- If you select the **Use Whole Workspace** radio button, all the available files in the workspace are included in the calculation of the grand average.
- If you select the **Select Individual History Files** radio button, you can select individual history files.
- In the **Selection Filter** text box, you specify the selection filter. This filters selectable files by means of name criteria. An asterisk (*) stands for one or more characters, and a period (.) stands for a single character. If the workspace contains the files "Test1H2", "Test2G" and "Hest5", for example, the string "Test*" filters out the files "Test1H" and "Test2G" (i.e. makes them available). The filter ".est*" accepts all three files. Once you have set the filter, you click the **Refresh** button to refresh the selection of available files.
- All the available files are listed in the **Available Files** text box.
- The **Selected Files** text box contains all the selected files.
- To select one or more files or remove them from the list of selected files, you select them and then click the **Add** or **Remove** button. The **Add All** and **Remove All** buttons do the same for all files.

In the lower part of the dialog box, you can make the following settings:

- If you select the **Create a Data Set for Standard Deviation** check box, an additional data set is created. This contains the standard deviation.
- To activate individual channel mode, you select the **Enable Individual Channel Mode** check box. This check box allows you to include data sets that have channels missing in averaging. As a result, the number of segments included in averaging can be different for each channel.
- If you select the **Calculate Weighted Average** check box, the average nodes included in the calculation of the grand average are weighted with the number of segments included in them.
- If you select the **Include Selected History Files to Saving Parameters** check box, the selected history files are stored in the file for the parameters used.
- You can use the **Load Parameters** button to load previously saved settings from a parameter file and then use or change them.
- The **Save Parameters** button allows you to save the settings you have made in parameter files so that they can be used again. If you do this, the dialog box that appears allows you to save the list of selected files as well as the other parameters.

On completion, the new files appear in the lower part of the History Explorer.

12.4.5 Segmentation

The Segmentation transform allows you to subdivide an EEG into segments.

SUMMARY

The sections of the EEG data set that do not meet the segmentation criterion are automatically suppressed. In other words, the resulting data set appears as a sequence of segments that meet the criterion.

Existing segment boundaries are respected during segmentation. In other words, no new segments are created within which another segment boundary is located.

The result of segmentation can be either a data set with multiple segments or a separate data set for each segment calculated.

In addition, you can also further segment an already segmented data set using additional criteria (subsegmentation). We advise you to use subsegmentation when you want to average different stimuli in a data set separately having carried out artifact correction beforehand. In this case, you select all the stimulus markers first, segment the data set and then carry out ocular artifact correction. You can subsegment the resulting corrected data set again separately for each stimulus marker.

No previous processing steps are required before the transform is used. To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Segmentation**.

PROCEDURE

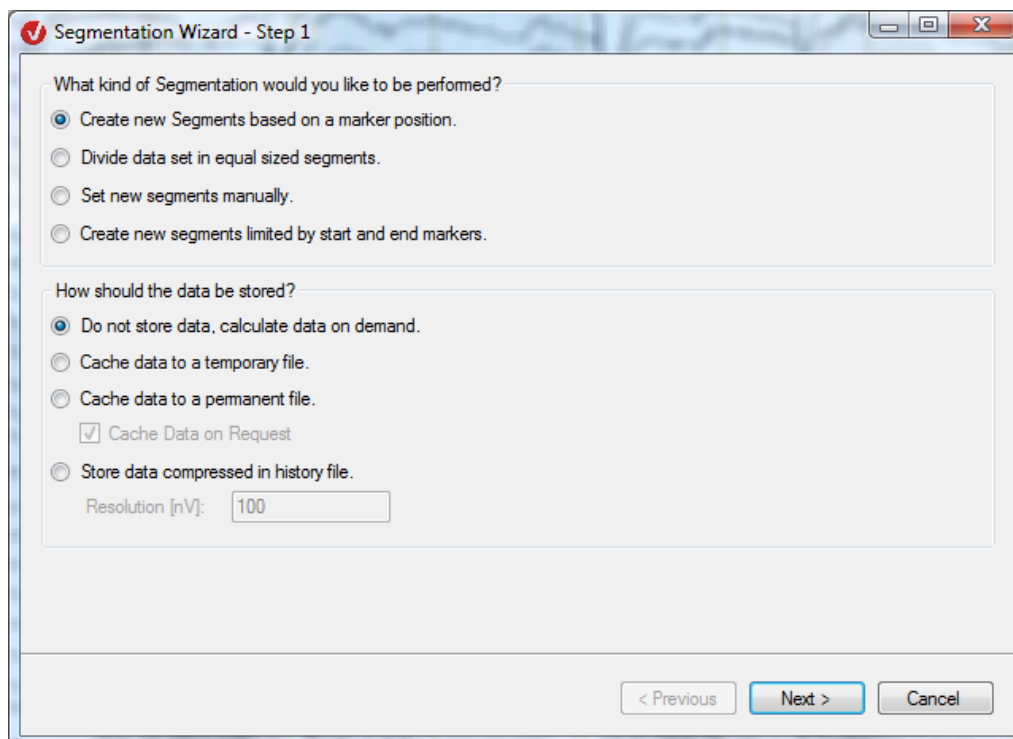


FIGURE 12—97 SEGMENTATION WIZARD, PAGE 1

You can make the following settings:

In the **What kind of Segmentation would you like to be performed?** group box, you specify the segmentation criterion or type. The following radio buttons are available:

“WHAT KIND OF
SEGMENTATION...”
GROUP BOX

- **Create new Segments based on a marker position:** Segmentation is carried out relative to a marker position. A start position and an end position must be specified for the segmentation. The start and end positions can also be before the marker position. You can choose any marker types.
- **Divide data set in equal sized segments:** The data set is subdivided into segments of the same length.
- **Set new segments manually:** You specify the segments manually.
- **Create new segments limited by start and end markers:** The beginning and end of the segment are defined by markers.

In the **How should the data be stored?** group box, you specify the storage options for the data. The following radio buttons are available:

„HOW SHOULD THE
DATA BE STORED?”
GROUP BOX

- **Do not store data, calculate data on demand:** The data is not stored. It is created on request.
- **Cache data to a temporary file:** The data is stored in a temporary file on the hard disk.
- **Store data compressed in history file:** The data is stored compressed in the history node.

In the **Resolution [nV]** text box, you can specify the resolution (precision) of the compression.

You will find detailed information on the storage options in the subsection entitled “Additional information: storage options” in this chapter.



Once you have made your selections, the **Next** button takes you to the second page of the wizard.

If you selected marker-based segmentation (**Create new Segments based on a marker position**), on the second page of the wizard you select from the list of available markers (**Available Markers** list box) one or more markers to be used for the purpose of segmentation (these then appear in the **Selected Markers** list box).

MARKER-BASED
SEGMENTATION

In the **Advanced Boolean Expression** text box, you can enter the selection criteria of the advanced Boolean expressions. You can specify marker names together with time windows in milliseconds and the operators “not”, “and” and “or”. You will find detailed information on the advanced Boolean expression function in the subsection entitled “Additional information: advanced Boolean expressions” in this chapter.

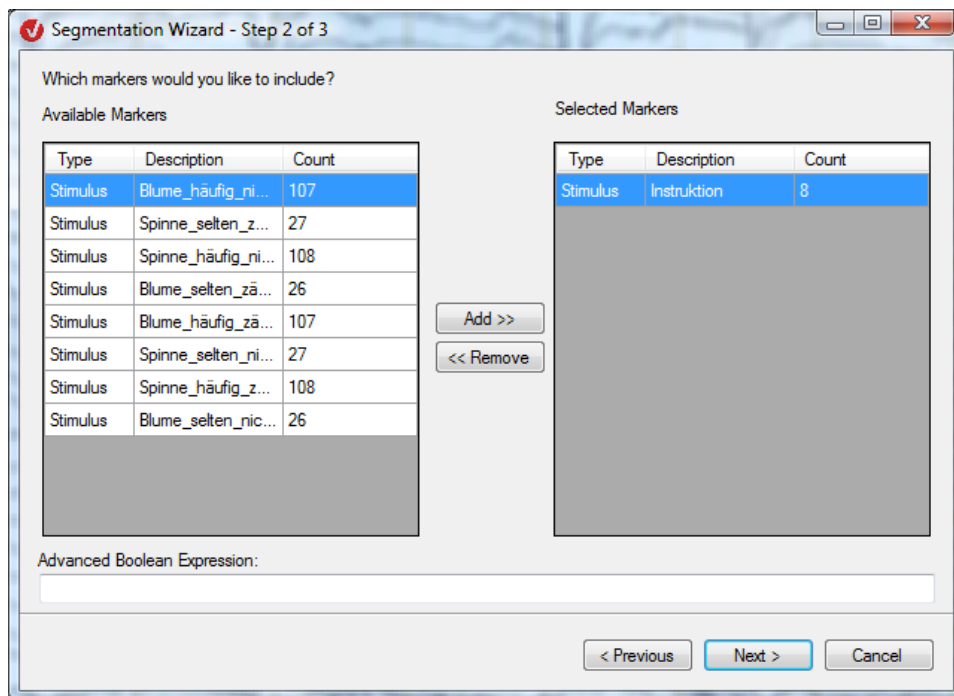


FIGURE 12—98 SECOND PAGE OF THE SEGMENTATION WIZARD, MARKER-BASED SEGMENTATION

Once you have made your selections, the **Next** button takes you to the third page of the wizard.

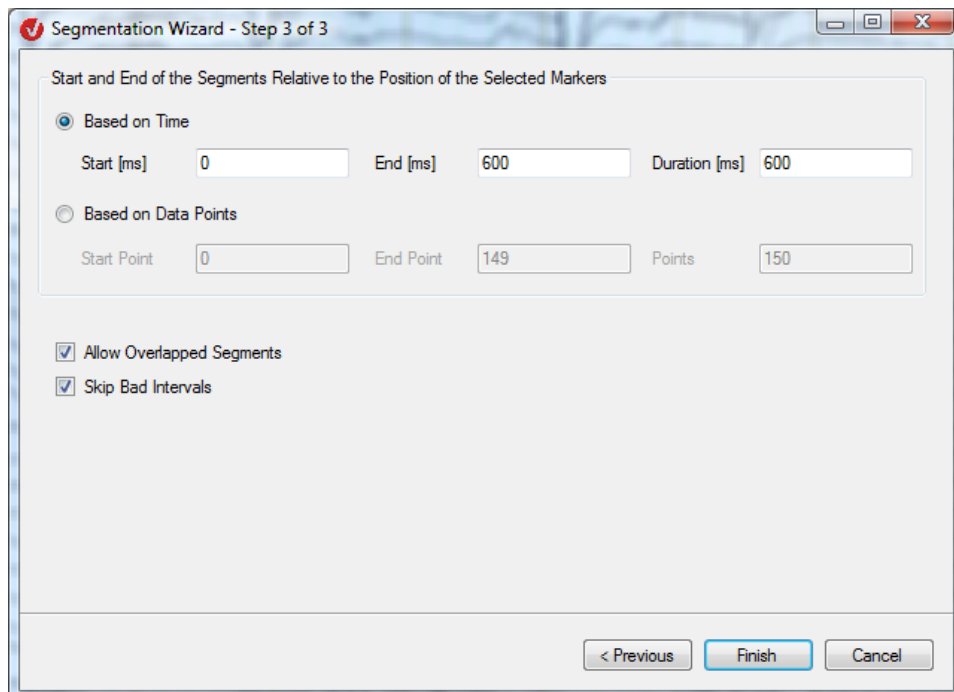


FIGURE 12—99 THIRD PAGE OF THE SEGMENTATION WIZARD, MARKER-BASED SEGMENTATION

On the third page of the wizard, you specify the relative positions of the interval based on time specifications (**Based on Time** radio button) or data points (**Based on Data Points** radio button). In the **Start [ms]** and **End [ms]** text boxes, you specify the beginning and end of the interval, and in the **Duration [ms]** text box you specify its length.

(If you make an entry in one of the six text boxes, the values in the other text boxes affected by it are adjusted accordingly.)

If you select the **Allow Overlapped Segments** check box, overlapping segments are included in segmentation. If you do not select this check box, only the first segment of two overlapping segments is included.

If you select the **Skip Bad Intervals** check box, segments that contain “bad interval” markers are not included. The “bad interval” markers are set when the Data Inspector transform is used. If you use the Average transform subsequently in individual channel mode (see section 12.4.6, “Average”), you should on no account select the **Skip Bad Intervals** check box.

The **Finish** button concludes your settings for marker-based segmentation.

If you selected time-based segmentation (**Divide data set in equal sized segments** radio button), you can make the following settings on the next page of the Segmentation Wizard:

TIME-BASED
SEGMENTATION

In the **Size of Segments** group box, you specify the size of the interval for the segment. You can specify the interval size in seconds. To do this, you select the **Based on Time** radio button and enter the desired value in seconds in the associated text box. You can also specify the size of the interval in points by selecting the **Based on Data Points** radio button and entering a value in the associated text box.

In the **Overlap Segments** group box, you can also specify how the segments are to overlap. As when specifying the segment’s interval size, you can specify the values in seconds (by selecting the **Based on Time** radio button and making an entry in the associated text box) or data points (by selecting the **Based on Data Points** radio button and making an entry in the associated text box).

If you select the **Skip Bad Intervals** check box, segments that contain “bad interval” markers are not included.

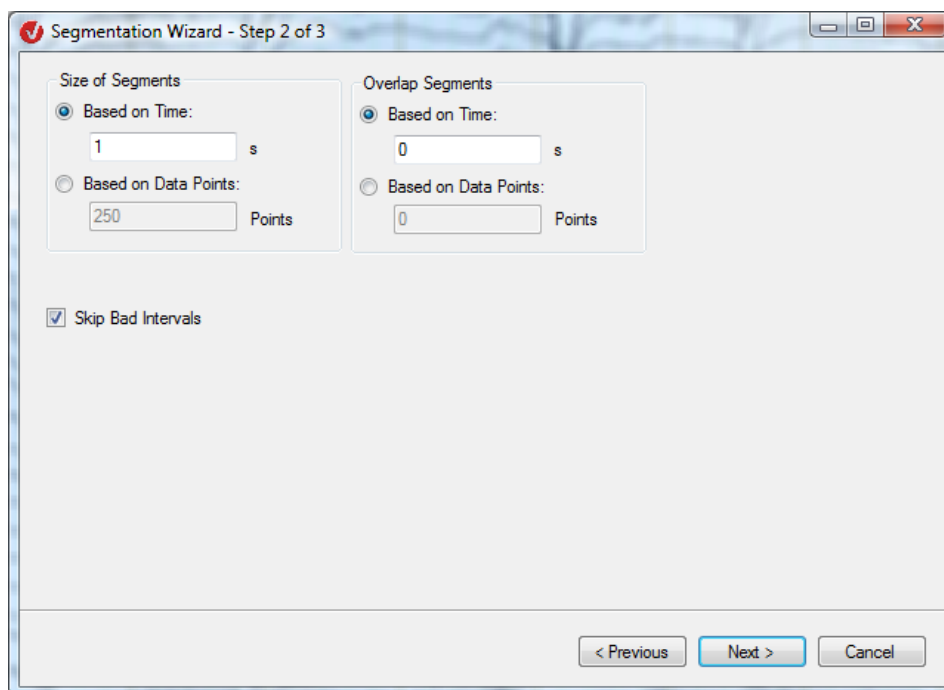


FIGURE 12—100 SECOND PAGE OF THE SEGMENTATION WIZARD, TIME-BASED SEGMENTATION

Once you have made your selections, the **Next** button takes you to the third page of the wizard.

On the third page, you are asked whether you want to create a separate data set for each new segment. This allows you to further process each segment separately.

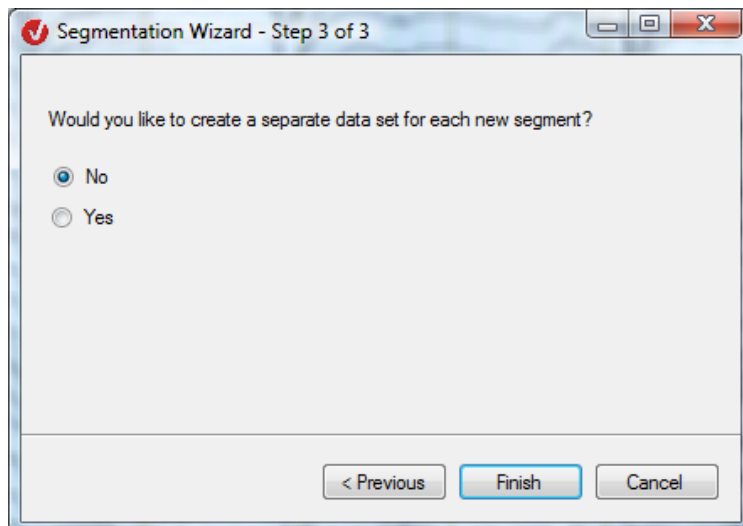


FIGURE 12—101 THIRD PAGE OF THE SEGMENTATION WIZARD, TIME-BASED SEGMENTATION

The **Finish** button concludes your settings for time-based segmentation.

If you specified that new segments are to be specified manually (by selecting the **Set new segments manually** radio button), you enter the new segments on the second page of the Segmentation Wizard.

SPECIFYING SEGMENTS
MANUALLY

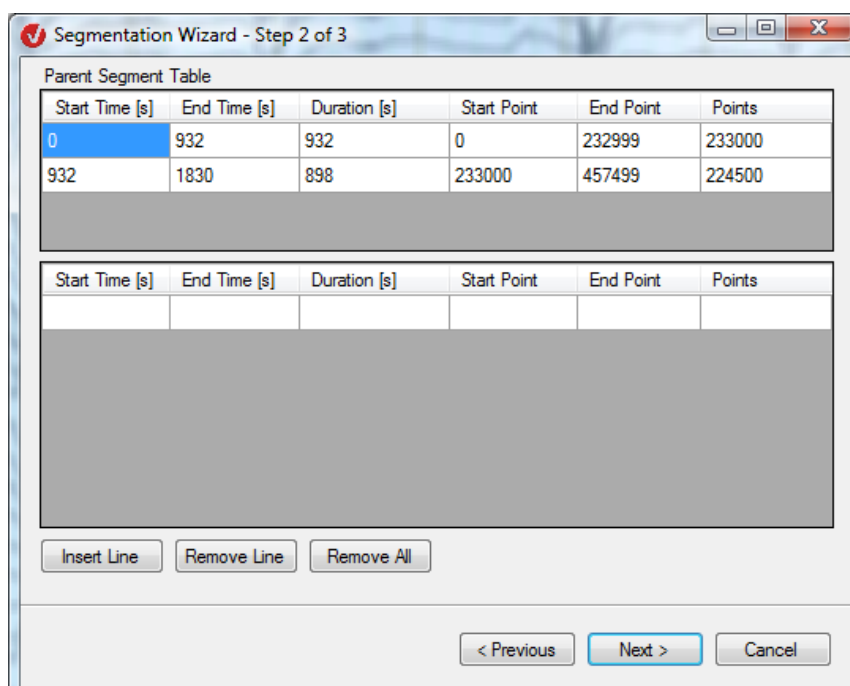


FIGURE 12—102 SECOND PAGE OF THE SEGMENTATION WIZARD, MANUAL SPECIFICATION OF SEGMENTS

The second page of the wizard contains two tables. The first table (**Parent Segment Table**) contains the segments that already exist in the parent node. You enter the new segments in the second table. You can specify the beginning, end and duration of the new segment based on time and data points. (If you make an entry in one of the six text boxes, the values in the other text boxes affected by it are adjusted accordingly.)

If a new segment goes beyond the boundary of an existing segment, an error message (**Segment intersects a parent segment**) appears at the edge of the dialog box. If this happens, make a new entry.

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

Once you have made your selections, the **Next** button takes you to the next page of the wizard.

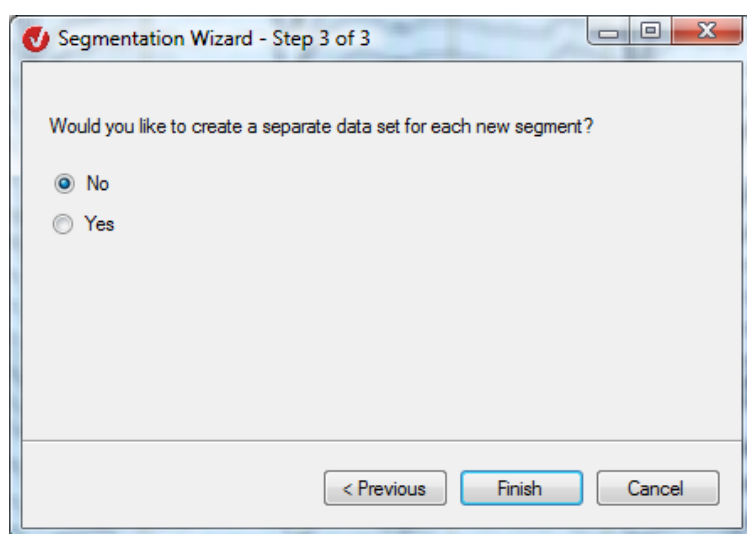


FIGURE 12—103 THIRD PAGE OF THE SEGMENTATION WIZARD, MANUAL SPECIFICATION OF SEGMENTS

The **Finish** button concludes your settings for the manual specification of segments.

If you specified segmentation based on start and end markers (by selecting the **Create new segments limited by start and end markers** radio button), you select the corresponding markers on the second page of the Segmentation Wizard.

SEGMENTATION BASED
ON START AND END
MARKERS

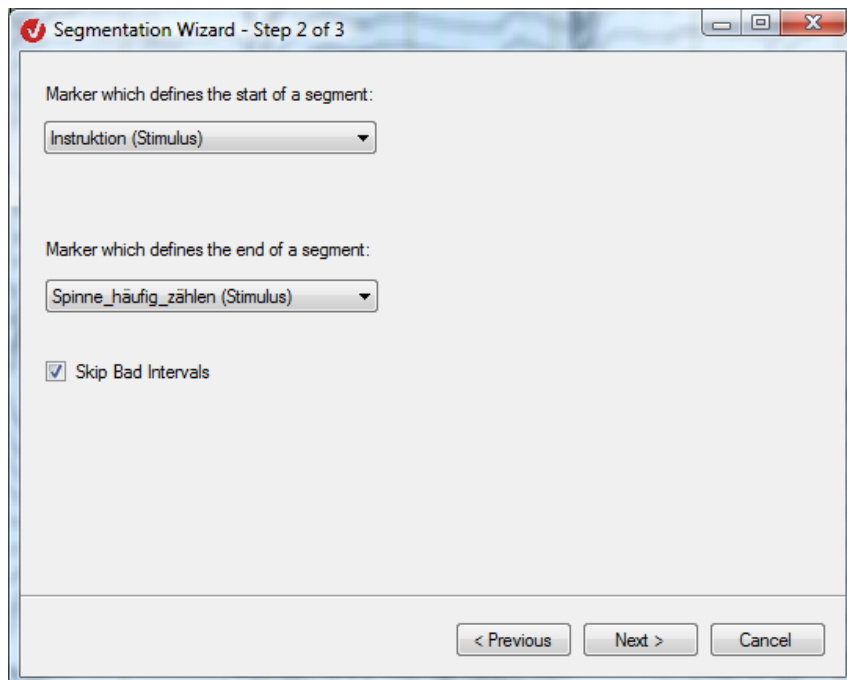


FIGURE 12—104 SECOND PAGE OF THE SEGMENTATION WIZARD, SEGMENTATION BASED ON START AND END MARKERS

You specify the start marker by choosing an item from the **Marker which defines the start of a segment** drop-down list and the end marker by choosing an item from the **Marker which defines the end of a segment** drop-down list.

If you select the **Skip Bad Intervals** check box, segments that contain “bad interval” markers are not included.

Once you have made your selections, the **Next** button takes you to the third page of the wizard.

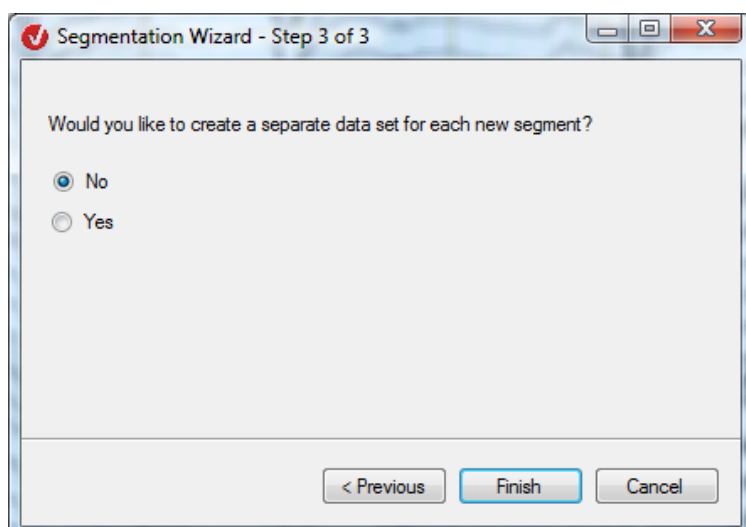


FIGURE 12—105 THIRD PAGE OF THE SEGMENTATION WIZARD, SEGMENTATION BASED ON START AND END MARKERS

On the third page, you are asked whether you want to create a separate data set for each new segment. This allows you to further process each segment separately.

The first start marker found is linked with the first end marker found to form a segment, the second start marker is linked with the second end marker and so on. Consequently, it is also possible to create overlapping segments. If an end marker is found without a preceding start marker, it is ignored. Start markers for which no end marker is found by the end of the data set are also ignored.

In the case of most transforms, it is not the results that are stored temporarily but information that describes the result of the operation. In the case of the Segmentation transform, this information consists of the position of the new segments in the data set.

ADDITIONAL
INFORMATION: STORAGE
OPTIONS

If you request data for display or further processing (transform or export), it is recalculated by the transform object. The advantage of this approach is that no intermediate files are generated for the various operations yet all intermediate results are nevertheless retained.

A disadvantage, however, is that the speed of certain steps – such as Ocular Correction, Baseline Correction and Average – is reduced as a result of the constant recalculation.

To counteract these negative effects, the results of the Segmentation transform can be stored temporarily in a cache file. The transform then accesses the cache file when data is requested.

Temporary and persistent cache files are available to you for storing the segmentation data. You can also store the data directly in the history file.

Persistent cache files are stored in the same folder as history files. They are saved permanently and not deleted until the associated transform node is deleted from the history tree by means of the **Purge Deleted Nodes** function. You can consider these cache files as being part of the history file. However, this method of storage is more efficient and allows even larger volumes of uncompressed data to be stored. Note that persistent cache files of a node continue to use storage space on the hard disk until the node is finally deleted from the cache for deleted nodes.

Temporary files only exist for as long as the history file is open. If the history file is opened again after being closed, the temporarily stored information is still available, but it is nevertheless recalculated on request. You should therefore carry out operations that follow segmentation without closing the history file.

If you subsequently want to carry out further operations following segmentation, you can recreate the temporary cache file. To do this, you open the history file and right-click a history node for segmentation. This opens a context menu from which you choose **Cache Data** to recreate the cache file.

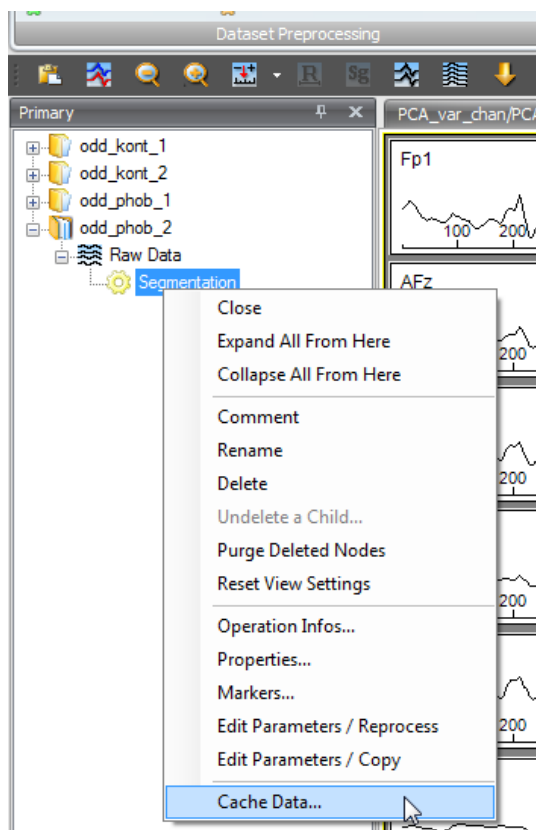


FIGURE 12—106 CACHE DATA MENU COMMAND

To access the folder in which the temporary files are stored, you choose **File > Configuration > Administration**. In the **Cache Path** text box, you can select the folder by using the **Browse** button.

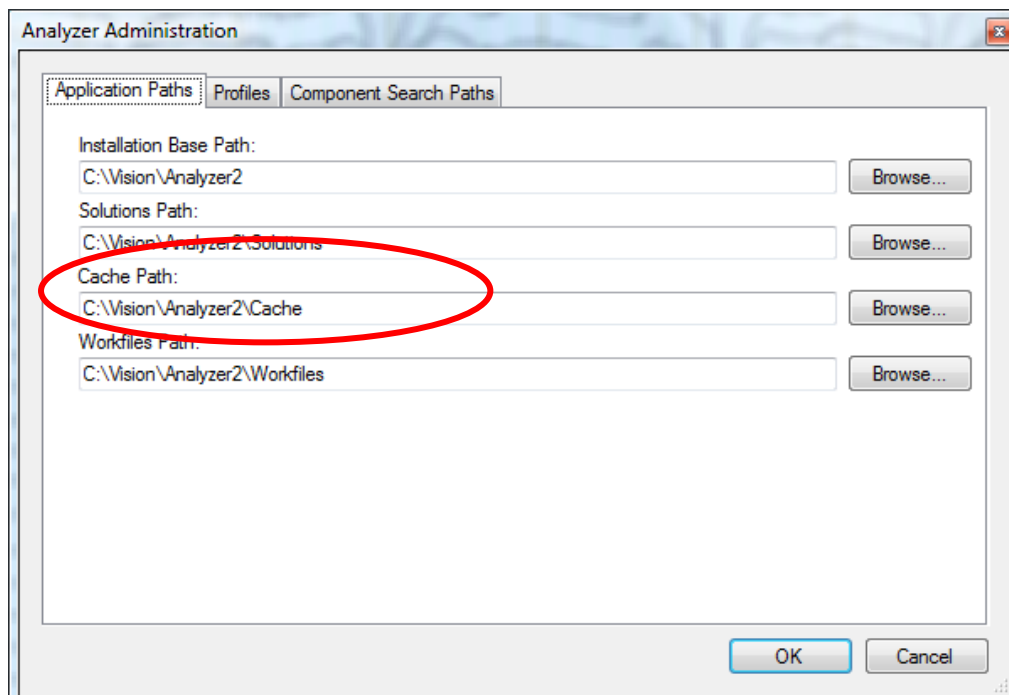


FIGURE 12—107 SELECTING THE CACHE FOLDER IN THE ANALYZER ADMINISTRATION DIALOG BOX

After averaging, the cache is no longer required because the Average transform stores the result in the history file.

As an alternative to persistent or temporary cache files, you can also store the data directly in the history node. This means the raw data is no longer needed for subsequent operations that access the segmented data. This is particularly advantageous when the raw data of a workspace is distributed across multiple CDs and, for example, a PCA is to be carried out.

The Segmentation transform compresses the data before it is stored. The Analyzer works internally with floating-point numbers only, but these are unsuitable for compression and have to be converted into integers first. To this end, you have to specify a resolution (precision). For EEG data this resolution should be about 100 nV (nanovolts, $1 \mu\text{V} = 1000 \text{ nV}$), which is 0.1 μV . A lower value means a higher resolution but less compression.

The data is generally stored segment by segment, regardless of the storage option selected. This can result in problems if you have created very long segments because the computer may not have enough RAM. Very long segments are therefore subdivided into smaller blocks when they are saved.

ABE is a kind of conditional segmentation that is only used for segmentation relative to a marker. It is used, for example, to select those segments in which a test subject has pressed a response button within a certain time after the triggering of a stimulus.

ADDITIONAL
INFORMATION:
ADVANCED BOOLEAN
EXPRESSIONS

Essentially, ABE allows segment selection to be made dependent on the existence or absence of one or more markers in one or more intervals relative to the reference marker. The markers can be of any type (segment markers, reference markers, DC correction etc.).

The following are examples of entries made in the **Advanced Boolean Expression** text box:

- You select a reference marker. You only want to include segments in which the test subject pressed the button R1 between 50 and 100 ms after the reference marker. The following expression should be entered in the text box:

R1(50,100)

- If you want to include all segments in which the test subject pressed the button R1 between 50 and 100 ms after the reference marker and also pressed the button R2 between 100 and 200 ms after the reference marker, the expression is:

R1(50,100) and R2(100,200)

- If you want to include segments in which the test subject pressed either R1 or R2 within the above intervals, the expression is:

R1(50,100) or R2(100,200)

- If you only want to include segments when either only R1 or only R2 was pressed within the above interval (exclusive OR), you can use the following expression:

R1(50,100) and not R2(100,200) or not R1(50, 100) and R2(100,200)

Consider which operators take precedence when you form the expressions. The “not” operator takes the highest precedence, followed by “and” and then “or”. You can change the precedence by using parentheses: Expressions in parentheses are calculated first.

- not (R1(50,100) or R2(100,200))

In this example, the expression “R1(50,100) or R2(100,200)” is calculated first, and the result is negated by the operator “not”. Consequently, all segments in which the test subject pressed either R1 within 50 to 100 ms or R2 within 100 to 200 ms are not included. Alternatively, you could use the following expression:

not R1(50,100) and not R2(100,200)

You can also enter negative values in the **Advanced Boolean Expression** text box. Negative values always relate to the time before the reference marker.

Any spaces are ignored, and no distinction is drawn between uppercase and lowercase. Consequently, “r 1(1, 2)” is identical to “R1(1,2)”. In the ABE – in contrast to the reference marker – all markers with the same sequence of characters are handled in the same way regardless of spaces. In other words, the marker value “r 1” is equivalent to “r1” and “R1”.

12.4.6 Average

The Average transform is used for averaging segmented data.

SUMMARY

This transform is typically used after:

PREREQUISITE FOR USE

- Filtering (optional)
- Segmentation
- Ocular Correction (optional)
- Artifact Rejection
- Local DC Detrend (optional)
- Baseline Correction

When using individual channel mode with the Average transform, note the subsection entitled “Additional information: individual channel mode” in this chapter.



Note that you make settings for marker types, exclude segments with incorrect subject responses and make other configuration settings in the Segmentation transform, not here.



To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Average**.

PROCEDURE

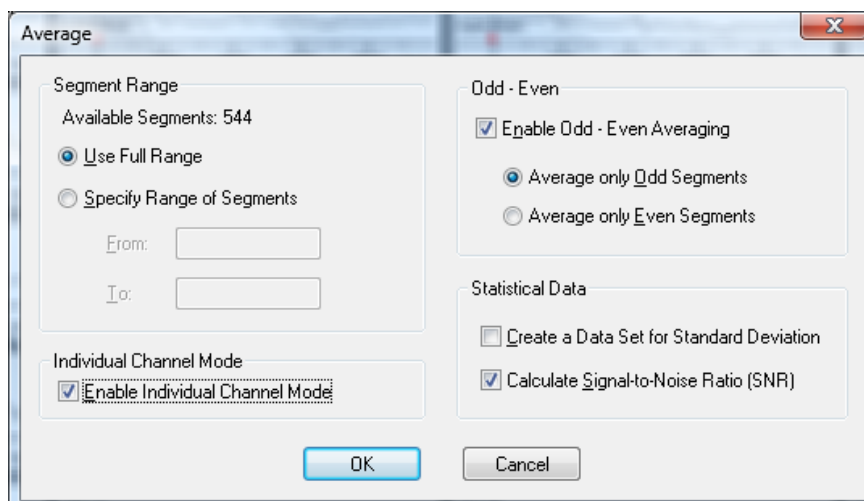


FIGURE 12—108 AVERAGE DIALOG BOX

You can make the following settings:

In the **Segment Range** group box, you specify the time range whose segments are to be included in averaging.

SEGMENT RANGE
GROUP BOX

- The number of available segments is displayed under **Available Segments**.
- If you select the **Use Full Range** radio button, all segments are included in averaging.
- If you select the **Specify Range of Segments** radio button, you can specify the range of segments to be included in the **From** and **To** text boxes.

If you select the **Enable Individual Channel Mode** check box, you activate individual channel mode, which allows bad intervals to be taken into account channel by channel. If you do not activate individual channel mode, all segments that contain a “bad interval” marker are rejected in their entirety.

INDIVIDUAL CHANNEL
MODE GROUP BOX

If you select the **Enable Odd-Even Averaging** check box, the **Average Only Odd Segments** and **Average Only Even Segments** radio buttons become available. These radio buttons allow you to specify whether only segments with odd numbers (segment 1, 3, 5, etc.) or only segments with even numbers (2, 4, 6, etc.) are to be averaged.

ODD-EVEN GROUP BOX

The segments in the specified time range (under **Segment Range**) are used as the basis for the count.

If you select the **Create a Data Set for Standard Deviation** check box, the standard deviation is output as a new data set.

STATISTICAL DATA
GROUP BOX

If you select the **Calculate Signal-to-Noise Ratio (SNR)** check box, the signal-to-noise ratio is calculated and stored in the operation information.

If you use individual channel mode, each channel is treated separately instead of all channels from every segment being included in averaging. If a channel in a segment has been marked as bad, all the other channels are still used for averaging. Consequently, the number of segments included in averaging may differ from channel to channel.

ADDITIONAL
INFORMATION:
INDIVIDUAL CHANNEL
MODE

Before you can use individual channel mode, you have to take a number of steps by way of preparation.

- If you use the Data Inspector transform, you have to activate individual channel mode there as well (see also section 12.2.5, “Data Inspector”).
- During segmentation you must not suppress the bad intervals (see section 12.4.5, “Segmentation”).
- If you use the Artifact Rejection transform instead of or in addition to the Data Inspector transform, you must also activate individual channel mode there in order to merely mark channels rather than reject entire segments (see section 12.2.4, “Artifact Rejection”).

The signal-to-noise ratio (SNR) is a measure of the quality of the EEG signal. Since there is no exact information available on either the signal or the noise in the EEG, your average total powers must be estimated statistically.

ADDITIONAL
INFORMATION: SIGNAL-
TO-NOISE RATIO

The average noise power of the EEG is calculated for each channel first. It is assumed that averaging eliminates the noise. In a second step, the average noise power is then calculated from the total of the squares of the differences between the EEG value and the average value, divided by the number of points minus 1.

In order to ascertain the average power of the signal in the EEG, you first calculate the total power of a channel of the EEG. The total power is obtained by calculating the mean of the squares for all data points of the channel before averaging.

It can be assumed that the signal and noise are uncorrelated. Consequently, the average power of the signal is equal to the difference between the average total power and the average noise power.

The SNR is then calculated from the quotient of the average signal power and the average noise power.

The result of the SNR calculation is stored in the resulting history node as a description. You obtain the result and other information by right-clicking the icon or displaying a context menu in the view and choosing the **Operation Infos** menu command. A window opens, showing information on the transform that has been performed. (You will find detailed information on the commands on the context menu in section 5.1, “The new user interface of the Analyzer”).

12.4.7 Baseline Correction

The Baseline Correction transform is used to correct the baseline of each segment.

SUMMARY

Correction is generally performed before averaging. An interval in a segment is defined in which the average voltage level corresponds to the new zero point of the segment values. In other words, the average (baseline) of the points in the defined interval is ascertained, and this is subtracted from all points in the segment. This operation is carried out for all the channels in the data set.

The Baseline Correction transform is typically used after:

PREREQUISITE FOR USE

- Segmentation
- Artifact Rejection
- Filtering (optional)
- Ocular Correction (optional)
- Local DC Detrend (optional)

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > Baseline Correction**.

PROCEDURE

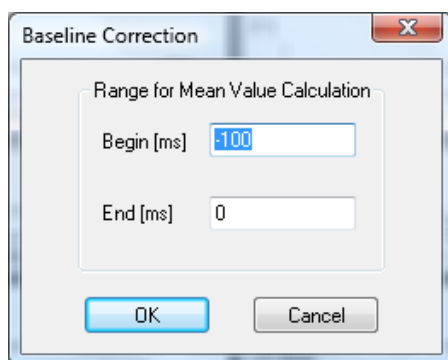


FIGURE 12—109 BASELINE CORRECTION DIALOG BOX

You can select any interval to be used to obtain the average voltage. It is generally positioned where activity is at its lowest level – ideally before the stimulus or other reference markers. To do this, you specify the values for the beginning (**Begin [ms]**) and end (**End [ms]**) of the interval in milliseconds.

Note that if you do not use the Baseline Correction transform, there may be a flattening off of the average signal.

ADDITIONAL
INFORMATION

12.4.8 DC Detrend

This DC Detrend transform calculates the DC trend from the EEG signal.

SUMMARY

Two different methods are used, depending on whether the transform is applied before or after segmentation.

If you apply the transform before segmentation, global trend correction is carried out, as described in [Hen93]. To begin with, the average voltage is calculated for each prestimulus interval of the specified marker type. In a second step, the average voltage is calculated for every DC reset in an interval directly before the DC reset. The difference between the average voltage before the DC reset and the average voltage of the first prestimulus interval after this DC reset is added as an offset to all voltage levels after this DC reset. In a third step, all average values calculated for the prestimulus intervals along the time axis and corrected by adding the offset are taken into account and the trend is ascertained by applying linear regression to this data. Only intervals that do not contain a DC reset are included in the calculation. Finally, the trend is subtracted from the original data, taking into account the DC offset.

To minimize the impact of DC trends on ocular artifact correction as far as possible, it is advisable to perform DC trend correction before ocular artifact correction.

RECOMMENDED USE

To display the dialog box for the transform, you choose **Transformations > Segment Analysis Functions > DC Detrend**.

PROCEDURE

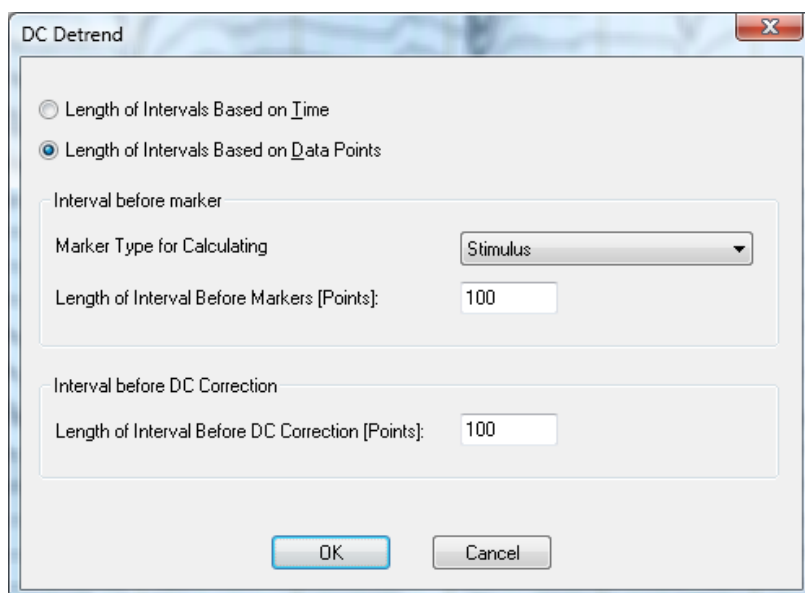


FIGURE 12—110 DC DETREND DIALOG BOX

You can make the following settings for the algorithm:

- The **Length of Intervals Based on Time** and **Length of Intervals Based on Data Points** radio buttons allow you to specify the interval length in milliseconds or data points, respectively.
- From the drop-down list box you choose the marker type for the calculation of the prestimulus intervals (**Marker Type for Calculating**). You then specify the length of these intervals in the **Length of Interval Before Markers [ms]** text box.
- In the **Length of Interval Before DC Correction [ms]** text box, you specify the length of the intervals before DC trend correction. These are used to calculate the average voltages and the offsets for the subsequent data.

If you apply the DC Detrend transform after segmentation, local trend correction is carried out. A linear function is subtracted from the data of each segment. The slope and limit values of this linear function are calculated for every segment from a certain interval at the beginning and end of the segment.

You can make the following settings:

- The **Intervals Based on Time** and **Intervals Based on Data Points** radio buttons allow you to specify whether the intervals are based on time or data points.
- In the **Interval at Segment Start** and **Interval at Segment End** text boxes, you specify the length of the interval – in milliseconds or data points – at the beginning and end of the segment.

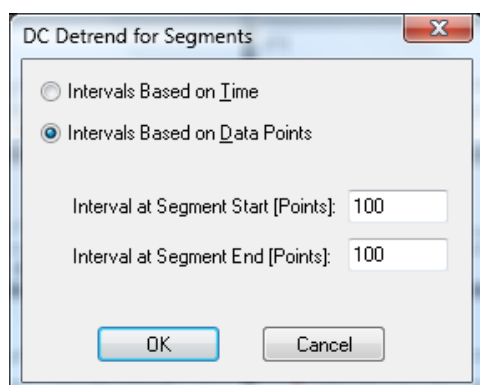


FIGURE 12—111 DC DETREND FOR SEGMENTS DIALOG BOX (FOR LOCAL DC TREND CORRECTION)

[Hen93] E. Hennighausen et al., A correction method for DC drift artifacts. REFERENCES
Electroencephalography and clinical Neurophysiology, 86 (1993), 199-204.

12.5 Transforms in the Comparison and Statistics group

12.5.1 t-Test

It is often not possible to estimate reliably on the basis of two EEG curves – the grand averages of two groups or two experimental conditions, for example – whether visible differences are also statistically significant.

SUMMARY

Conversely, with examinations of a more exploratory nature, it is often not possible to clearly ascertain from the available averages the intervals in which the conditions or groups have particularly marked differences. In all these cases, it can be very useful to calculate t-values for the data.

The t-Test transform permits the calculation of paired and unpaired t-tests as well as t-tests against zero.

It can be applied to segmented and unsegmented data as well as to averaged data and grand averages.

No preliminary work is necessary on the data (obtaining the differences or a priori averaging of the data, for example) in order to apply the t-test. Nor do the data set lengths of reference and comparison nodes have to match. In this case, the t-test is only carried out for the common time range.

The t-Test transform is typically used after:

PREREQUISITE FOR USE

- Segmentation

To display the dialog box for the transform, you choose **Transformations > Comparison and Statistics > Statistical Analysis > t-Test**.

PROCEDURE

The dialog box that appears contains radio buttons (**Paired t-Test** and **Unpaired t-Test**) that allow you to choose between a paired or unpaired t-test.

For the unpaired t-test, you can use the **Equal Variance** check box to specify whether equal variance is to be assumed between the two groups compared. Since this is a common assumption in EEG research, this check box is selected by default. However, if you know that this assumption does not apply, clear this check box.

Please note that an F-test for equal variance is not carried out in the t-Test transform. If you select this check box, the formula corrected for variance inequality is used.



If you select the **Enable Individual Channel Mode** check box, you activate individual channel mode, which allows bad intervals to be taken into account channel by channel. If you clear the check box, bad intervals are taken into account segment by segment.

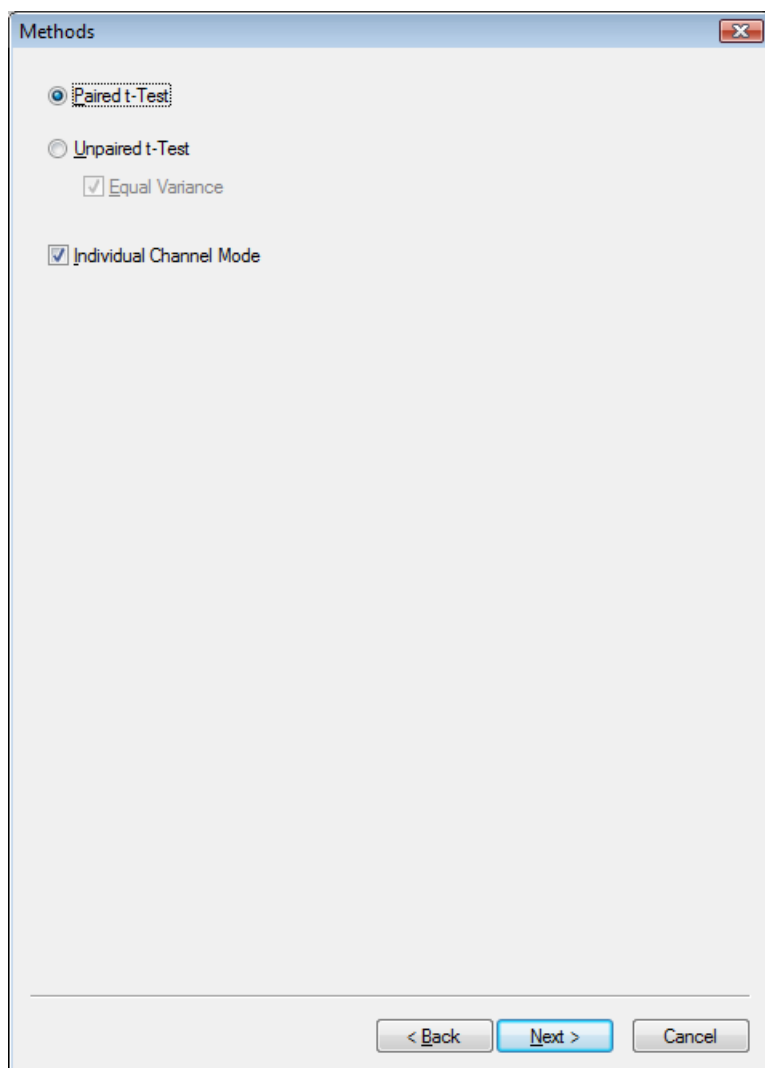


FIGURE 12—112 T-TEST DIALOG, FIRST PAGE

If you selected the paired t-Test in the first page of the dialog, the second page offers you the choice between a regular paired t-test (**Test Against Second Dataset**) and a t-test against zero (**Test Against Zero**), which is a special case of the paired t-test. This tests whether the values differ significantly from zero.

If you want to carry out your paired t-test against a reference node, you can select this from the list of existing history files.

In addition, by selecting the **Use Relative Path for Template or Drag and Drop** check box you can specify whether the comparison node is to be determined and stored relative to the reference node. In this way, for example, you can carry out the same t-test for each history file when running history templates, without having to specify the comparison data sets explicitly each time.

Please note, however, that this check box is only available for comparison nodes that are in the same history file as the reference node. When you select the check box, all the history files except your current one are removed from the list of available history files.



If you selected the unpaired t-test in the first page of the dialog, the next page offers you the same options as for the paired t-test. The only difference is that the option of a test against zero is not available to you.

Depending on whether you select a paired t-test, an unpaired t-test or a t-test against zero, all the required calculation steps are carried out (e.g. obtaining the differences across all segments in the paired t-test for segmented data, averaging of the differences and calculation of the t-values).

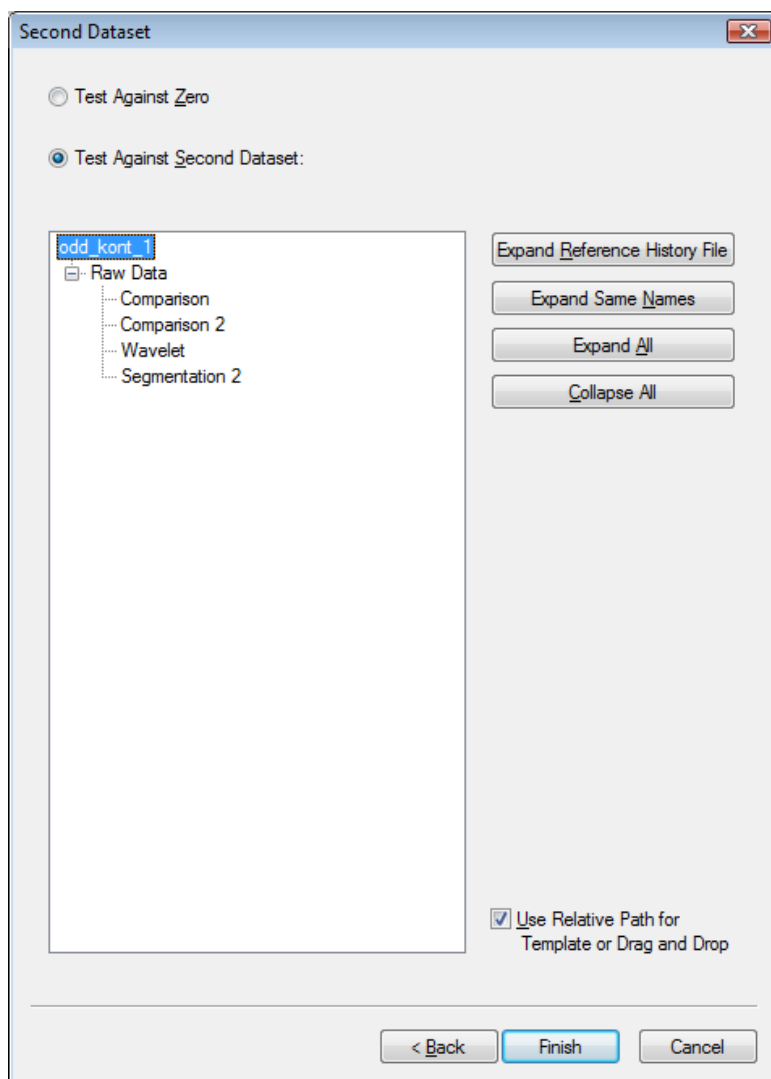


FIGURE 12—113 SELECTING THE T-TEST TYPE OF THE SECOND DATA SET

12.5.2 Cross Correlation

The Cross Correlation transform enables you to calculate the cross correlation between two channels in a segmented EEG. It is a statistical measure of the dependency of two channels. Time- and frequency-shifted dependencies are also calculated. If the transform is applied to complex data, the complex cross correlation is calculated.

SUMMARY

The averaged Cross Correlation transform is typically used after:

PREREQUISITE FOR USE

- Segmentation

To display the dialog box for the transform, you choose **Transformations > Comparison and Statistics > Cross Correlation**.

PROCEDURE

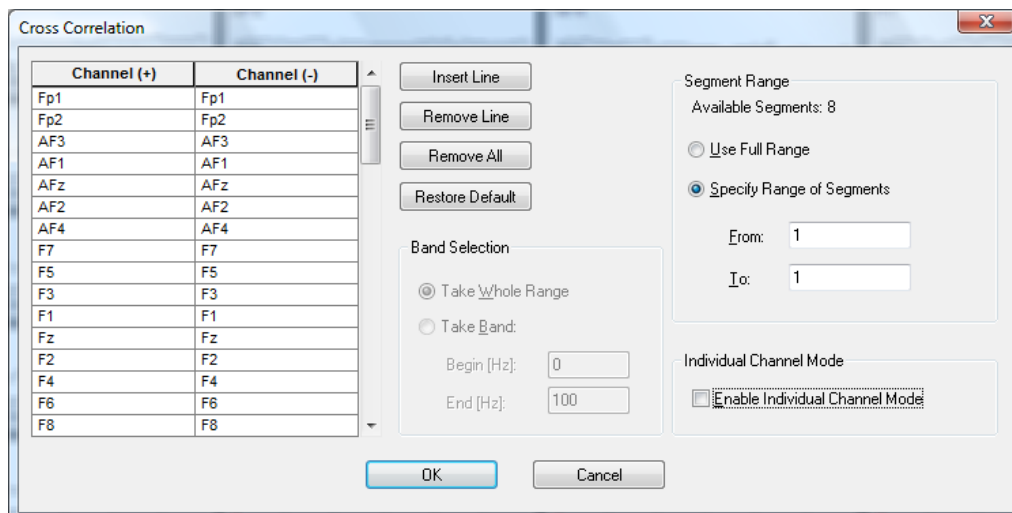


FIGURE 12—114 CROSS CORRELATION DIALOG BOX

The calculation is carried out as follows:

- First, the cross correlation between the specified pairs of channels is calculated segment by segment using the following formula:
- $$\text{CrCorr}(c_1, c_2)(j) = \sum_i (c_1(i) - \text{Avg}(c_1)) (c_2(i+j) - \text{Avg}(c_2)) / (\text{StdDev}(c_1) * \text{StdDev}(c_2)),$$
- $i = 1, \dots, \text{segment length}, j = 1 - \text{segment length}, \dots, \text{segment length}$
- Avg: average of all values in the segment
- StdDev: standard deviation of all the values in the segment
- The value 0 is added to the channels outside the segment for the purpose of the calculation.
- In a second step, an average is obtained across all segments for each of these pairs.

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together. The **Restore Default** button fills the table with all the data.

When you apply the transform to data in the frequency domain, you can enter in the **Band Selection** group box a frequency band to which the calculation is to be restricted.

If you are working with data in the frequency domain, enter in the table the channels between which the cross correlation is to be calculated.

If you select the **Take Whole Range** radio button, all the available data is included in the calculation.

You select a specific frequency band by selecting the **Take Band** radio button and entering the beginning and end of the band in the **Begin [Hz]** and **End [Hz]** text boxes. You also have the option of selecting the entire frequency range. To calculate the auto correlation of a channel, select the channel name in both the left- and right-hand list box of a row in the table. As a result, you get the channels in which the average of the cross correlations is shown against the time or frequency shift.

The value shown for **Available Segments** is the total number of available segments.

If you want to use all the segments, you select the **Use Full Range** radio button. If you want to specify the range of segments to be included in the calculation, you select the **Specify Range of Segments** radio button.

If you select the **Enable Individual Channel Mode** check box, you activate individual channel mode, which allows bad intervals to be taken into account channel by channel. If you clear the check box, bad intervals are taken into account segment by segment.

12.5.3 Data Comparison

The Data Comparison transform allows you to compare two data sets or two channels of a data set after averaging. Currently, the module can carry out the following comparisons: SUMMARY

- Difference waves
- Cross-correlation

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Comparison and Statistics > Data Comparison**.

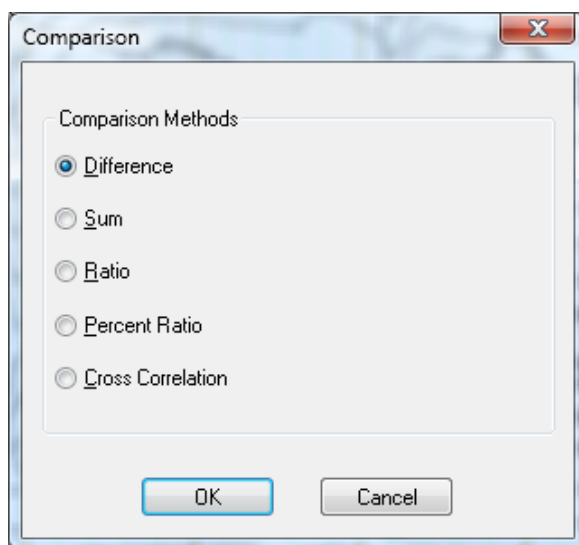


FIGURE 12—115 INITIAL COMPARISON DIALOG BOX

In the initial dialog box, you select the comparison method you want to use. The following methods are available:

- Calculation of difference waves (**Difference**)
- Calculation of the sum of two channels (**Sum**)
- Calculation of the ratio of the initial channel to the comparison channel (**Ratio**)
- Calculation of the ratio of the initial channel to the comparison channel as a percentage (**Percent Ratio**)
- Calculation of the cross-correlation (**Cross Correlation**).

In the calculation of ratios, the initial data value is divided by the other data value. If the other data value is zero, zero is used as the result.

In the next dialog box, the Comparison Wizard, you specify whether the comparison is to be carried out within the current data set (**Compare Channels**) or between two data sets (**Compare Datasets**).

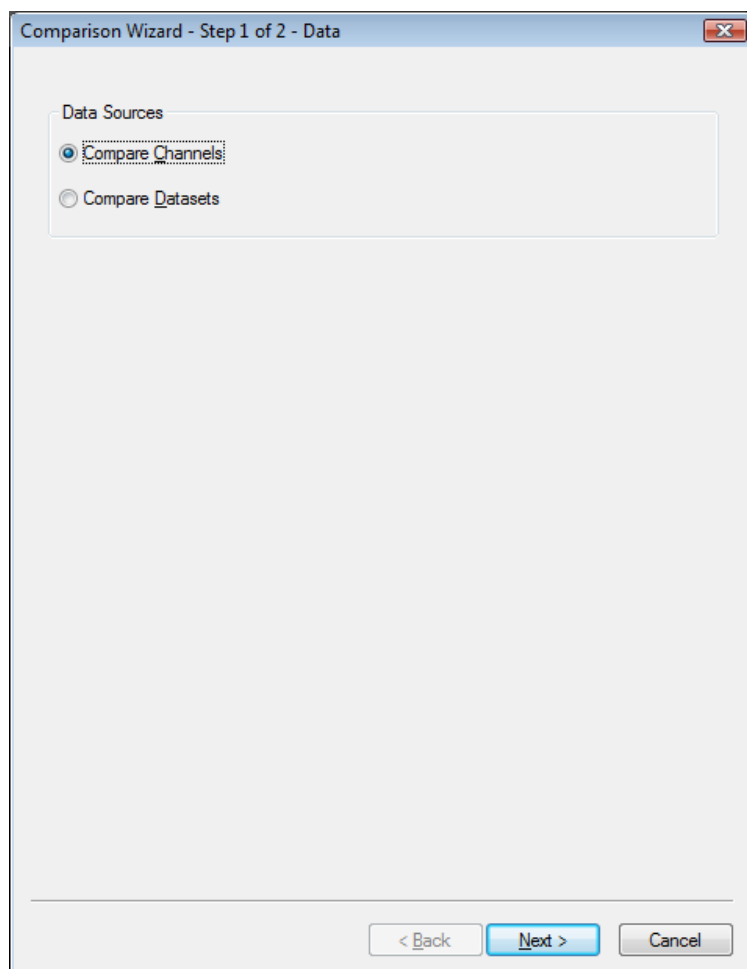


FIGURE 12—116 COMPARISON WIZARD, PAGE 1

If you opt for a comparison of channels within a data set, a channel selection dialog box is displayed. This allows you to select channel groups to be subtracted from each other.

You choose the channels from drop-down list boxes. The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table, remove individual rows or remove all rows.

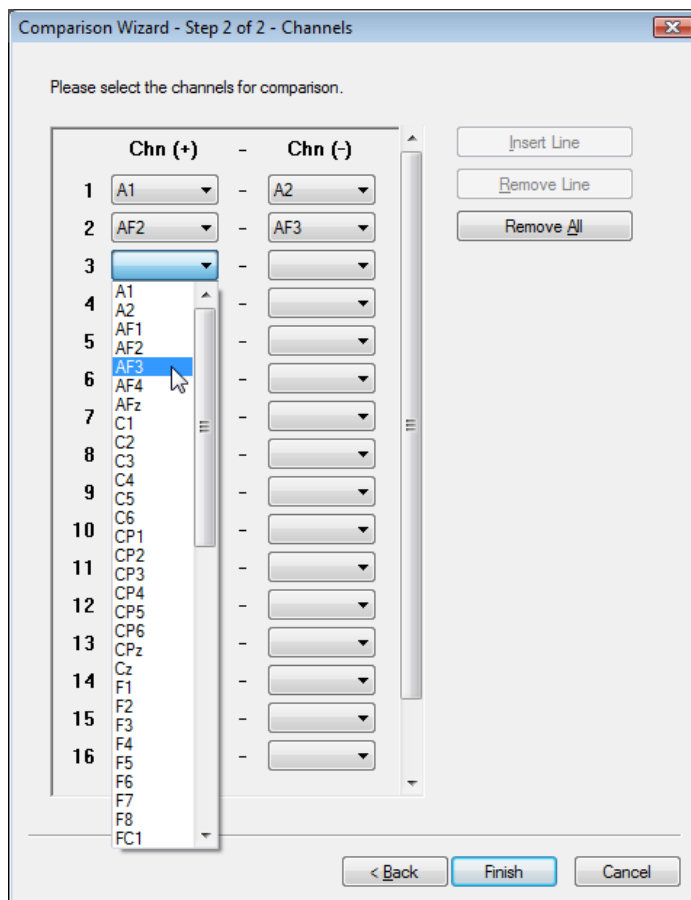


FIGURE 12—117 COMPARISON WIZARD, PAGE 2 WHEN THE COMPARE CHANNELS RADIO BUTTON IS SELECTED

If you opt for a comparison of two data sets, a data set selection dialog box is displayed. The dialog box contains a list of all the history files in the current workspace. You can open a data set by double-clicking its file name.

The following buttons make it easier for you to navigate in the table:

- **Expand History File:** Expands the current history file.
- **Expand Same Names:** Expands all history files that have a data set of the same name, up to this data set.
- **Expand All:** Expands all history files.
- **Collapse All:** Closes all history files.

If you select the **Keep Remaining Channels** check box, all channels that do not have a corresponding channel in the other data set are nevertheless retained.

The **Use Relative Path for Template or Drag and Drop** check box allows you to save the relative path of the data set for comparison. In other words, the history templates will always look for this data set in the same history file.

You select a data set by means of a double or single click. The **Finish** button concludes your entries.

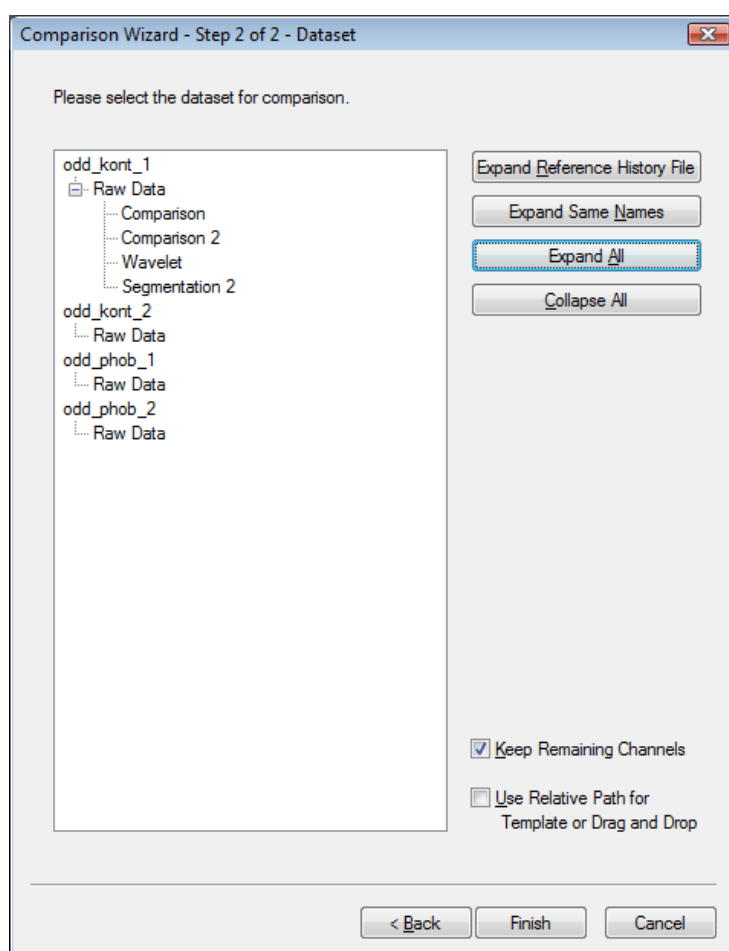


FIGURE 12—118 COMPARISON WIZARD, PAGE 2 WHEN THE COMPARE DATASETS RADIO BUTTON IS SELECTED

A view with overlays appears. The black line represents the result of the transform, the red line represents the initial node, and the blue line represents the other node for comparison.

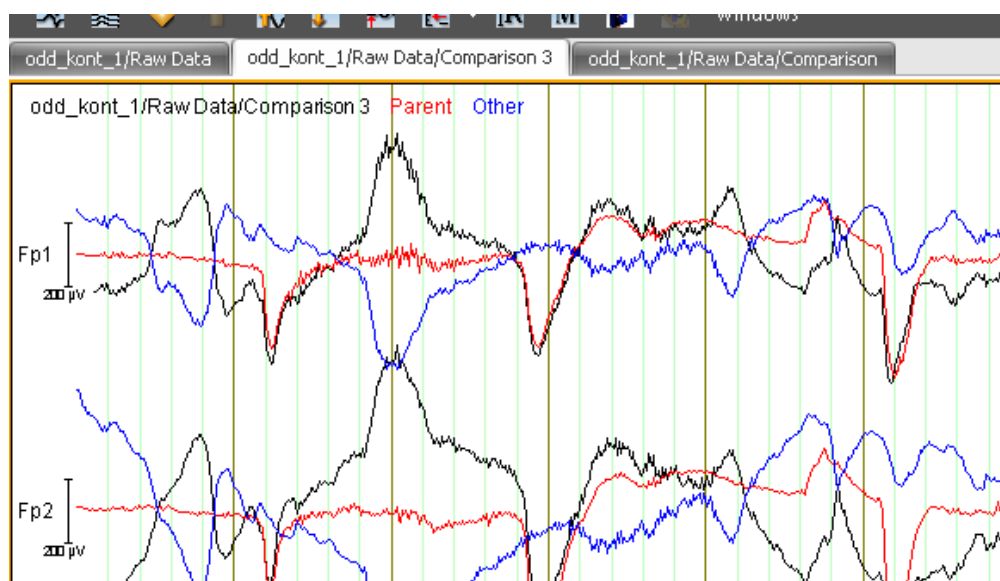


FIGURE 12—119 PART OF THE STANDARD VIEW (DATA SET OVERLAY)

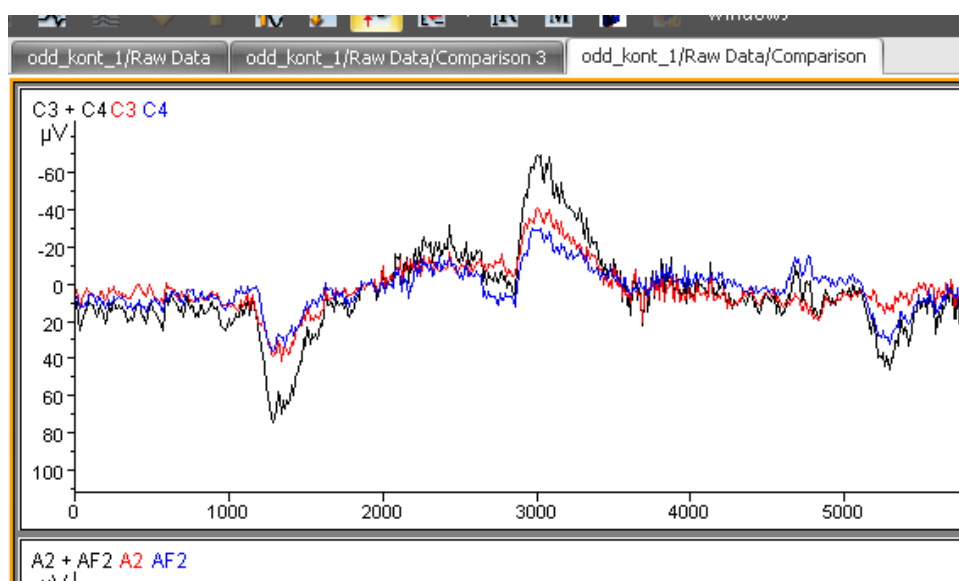


FIGURE 12—120 PART OF THE GRID VIEW (CHANNEL OVERLAY)

If you click the name of a node (when comparing data sets) or channel (when comparing channels) in the upper left corner of the view, the corresponding channel is deactivated or activated again.

The view context menu also contains the additional command **Display Static Overlays**. This allows you to switch between the overlays created by comparison and the normal overlays. You can only add other overlays to the node for comparison if this command does not have a check mark against it.

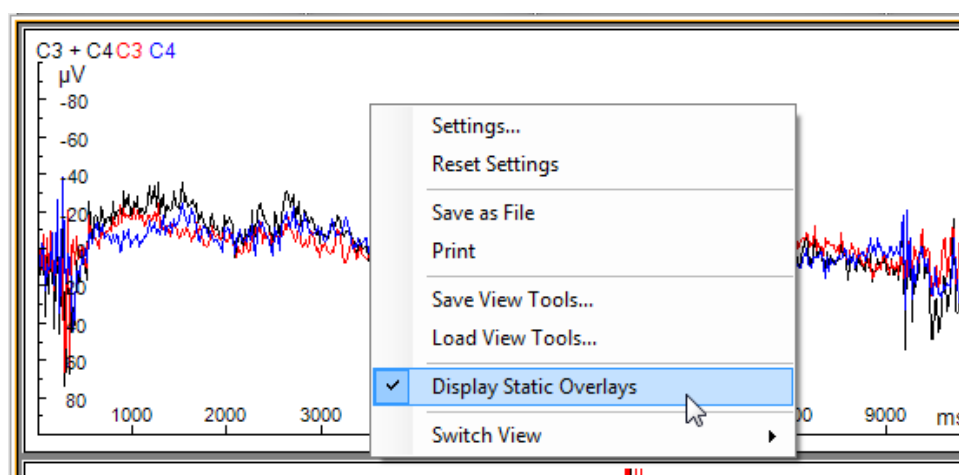


FIGURE 12—121 CONTEXT MENU CONTAINING THE DISPLAY STATIC OVERLAYS COMMAND

12.5.4 Covariance

The Covariance transform can be used as a preliminary step for various forms of coherence calculation. When the Formula Evaluator is used at the same time, it is possible to implement the majority of the methods described in the literature and other related methods.

SUMMARY

In contrast to the Coherence transform, the data output by the Covariance module is always of the same type as the processed input data. Consequently, it is possible, for example, to calculate and further process complex-valued coherence or to calculate the correlation of channels in the time domain.

The Covariance transform is typically used after:

PREREQUISITE FOR USE

- Segmentation

To display the dialog box for the transform, you choose **Transformations > Comparison and Statistics > Covariance**.

PROCEDURE

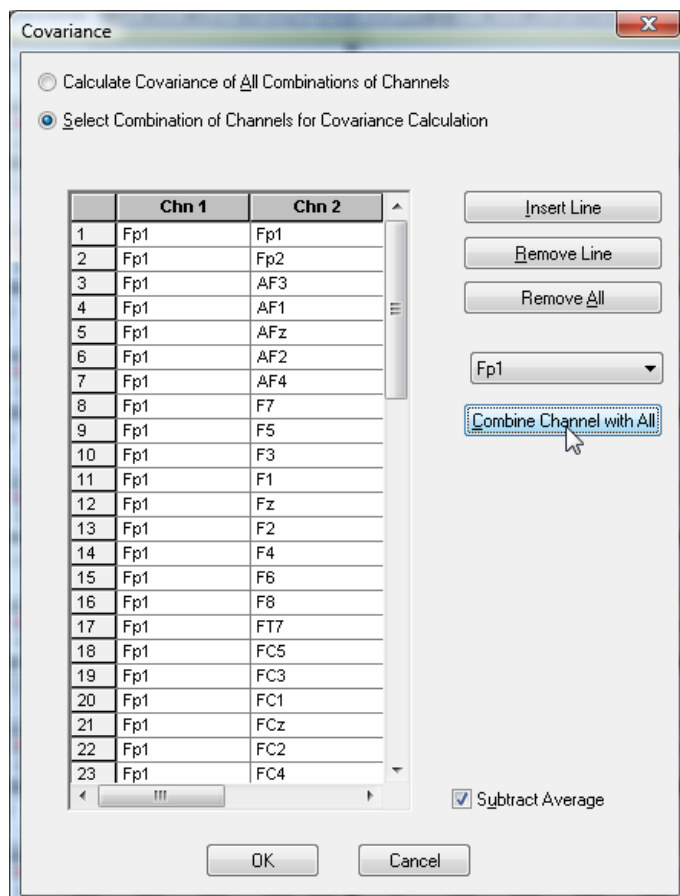


FIGURE 12—122 COVARIANCE DIALOG BOX

You specify whether all possible channel combinations (**Calculate Covariance of All Combinations of Channels** radio button) or only a selection of channel combinations (**Select Combination of Channels for Covariance Calculation** radio button) are included in the calculation.

If you decide on individual combinations, you can enter the channel combinations in the table. Alternatively, you can choose a channel from the drop-down list box on the right.

These two methods use the following formulas to calculate the covariance:

- $\text{Cov}(c_1, c_2)(x) = 1/N \sum (c_{1,i}(x) - \text{avg}(c_1(x))) (c_{2,i}(x) - \text{avg}(c_2(x)))^*$
- $\text{Cov}(c_1, c_2)(x) = 1/N \sum c_{1,i}(x) c_{2,i}(x)^*$

The **Subtract Average** check box allows you to specify whether method (1) or (2) is used. In both formulas, totaling is carried out using the segment number i. The average value obtained applies to the segments at a fixed time or at a frequency of x and with a fixed channel c.

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

If you click the **Combine Channel with All** button, all combinations of the selected channel are added to the table.

12.5.5 Coherence

The Coherence transform calculates the coherence between channels. Coherence is a measure of the dependency of the data between the individual channels over time. SUMMARY

The Coherence transform is typically executed after:

PREREQUISITE FOR USE

- The Fast Fourier transform

Note that calculation is only possible with complex frequency data.

To display the dialog box for the transform, you choose **Transformations > Comparison and Statistics > Coherence**. PROCEDURE

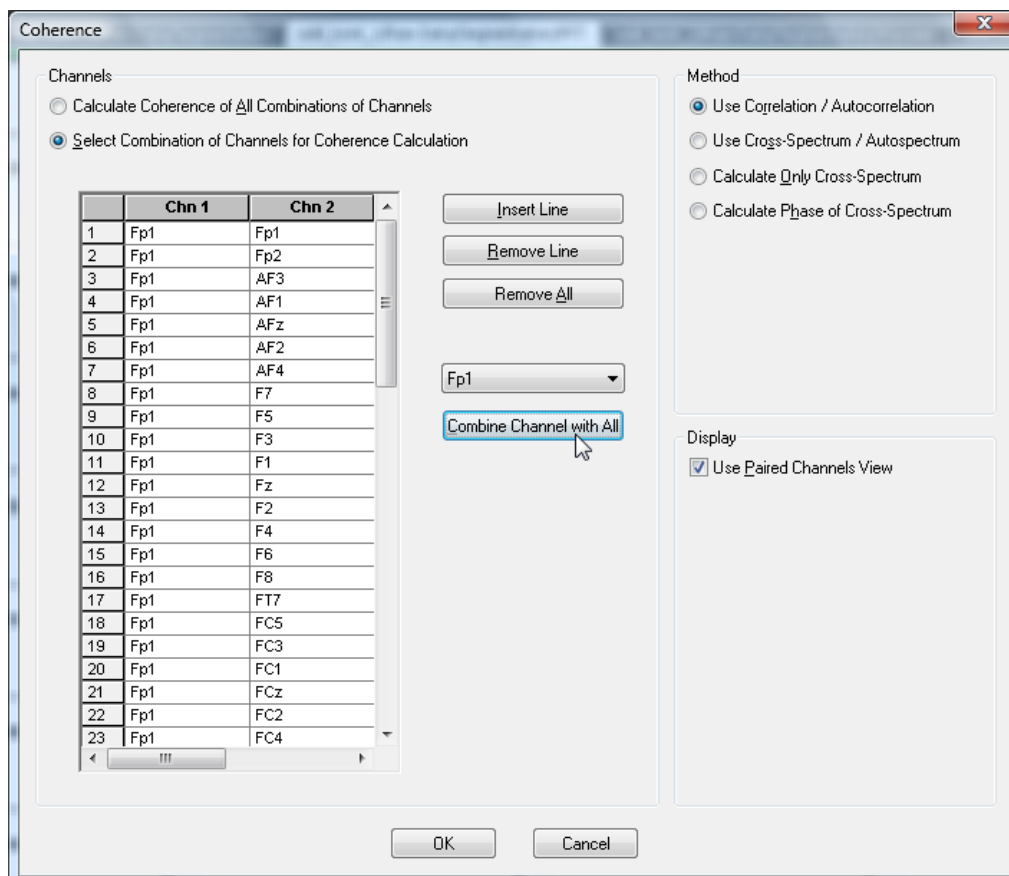


FIGURE 12—123 COHERENCE DIALOG BOX

The four radio buttons allow you to choose between four methods of calculating coherence:

METHOD GROUP BOX

- **Use Correlation / Autocorrelation:** quotient from correlation and autocorrelation
- **Use Cross-Spectrum / Autospectrum:** quotient from cross-spectrum and autospectrum
- **Calculate Only Cross-Spectrum:** calculation of the non-normalized cross-spectrum
- **Calculate Phase of Cross-Spectrum:** calculation of the phase of the cross-spectrum

The first method calculates the coherence using the following formula:

$$\text{Coh}(c_1, c_2)(f) = | \text{Cov}(c_1, c_2)(f) |^2 / (| \text{Cov}(c_1, c_1)(f) | | \text{Cov}(c_2, c_2)(f) |)$$

in conjunction with

$$\text{Cov}(c_1, c_2)(f) = \sum (c_{1,i}(f) - \text{avg}(c_1(f))) (c_{2,i}(f) - \text{avg}(c_2(f)))^*$$

In the second formula, totaling is carried out using the segment number i. The average is obtained with reference to the segments with a fixed frequency f and a fixed channel c.

The second method uses the cross-spectrum instead of the covariance. The formula is as follows:

$$\text{Coh}(c_1, c_2)(f) = | \text{CS}(c_1, c_2)(f) |^2 / (| \text{CS}(c_1, c_1)(f) | | \text{CS}(c_2, c_2)(f) |)$$

in conjunction with

$$\text{CS}(c_1, c_2)(f) = \sum c_{1,i}(f) c_{2,i}(f)^*$$

Here, too, totaling is carried out using the segment number i.

The third method merely calculates the cross-spectrum, as specified in the formula with CS.

The fourth method calculates the phase of the cross-spectrum. The phase is specified as a radian measure, and the curve is continued constantly at the transitions -Pi and +Pi in such a way that the range of values can theoretically extend across the entire range of real numbers but always specifies an angle (between the complex number vector and the real axis).

In methods 1 and 2, values between 0 and 1 are obtained for each frequency and each channel. In method 3, complex values are obtained, but only the amount is output.

You specify whether all possible channel combinations are to be included in the calculation (by selecting the **Calculate Coherence of All Combinations of Channels** radio button) or only a selection of combinations (by selecting the **Select Combination of Channels for Coherence Calculation** radio button).

CHANNELS TAB

The **Insert Line**, **Remove Line** and **Remove All** buttons allow you to add rows to the table and delete them again either individually or all together.

If you decide on individual combinations, you can enter the channel combinations in the table. Alternatively, you can choose a channel from the drop-down list box.

If you click the **Combine Channel with All** button, all combinations of the selected channel are added to the table.

If you select the **Use Paired Channels View** check box, the result is displayed in a two-part view. On the left, you see curves in the frequency domain that represent the coherence calculated for each frequency point and each channel combination. On the right, the coherence values between the channels are represented by lines. Their coloring reflects the coherence on a scale from 0 to 1. If the check box is cleared, the result is displayed in one of the frequency views.

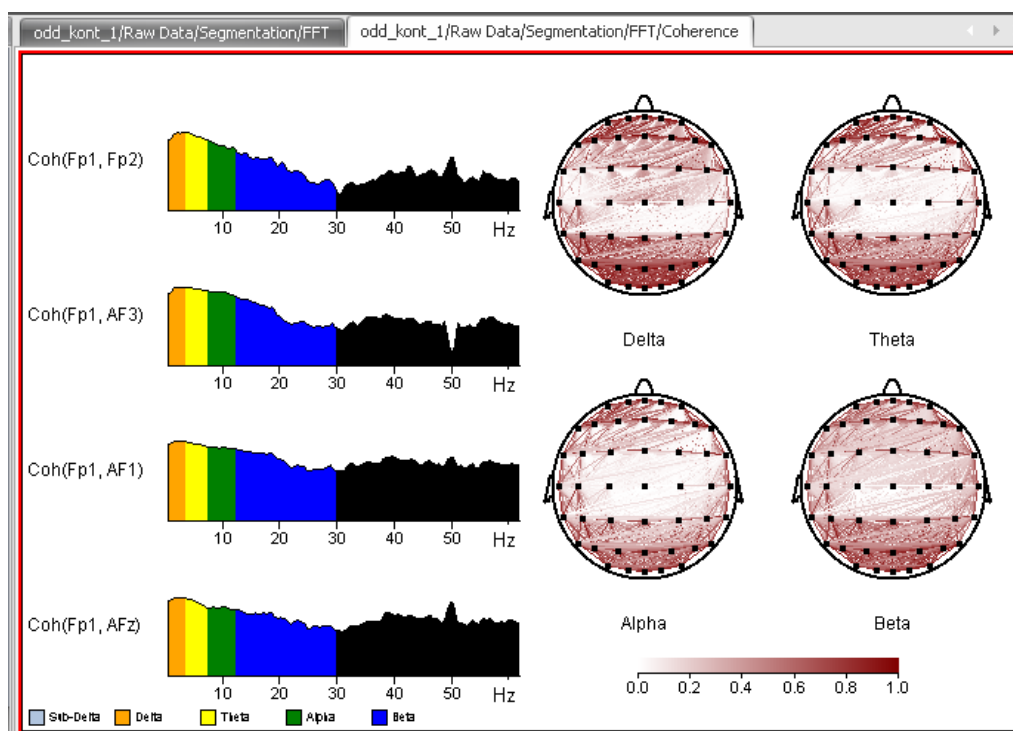


FIGURE 12—124 OUTPUT OF THE COHERENCE DATA

12.6 Transforms in the Special Signal Preprocessing group

12.6.1 LORETA

The LORETA transform allows you to view the LORETA data over the time range. Regions of interest (ROIs) are defined for this purpose. Each ROI is displayed in the Analyzer as a virtual channel.

SUMMARY

The virtual MR anatomical images are made available by the Montreal Neurological Institute of McGill University.



You call the required dialog box by choosing **Transformations > Special Signal Preprocessing > LORETA**.

PROCEDURE

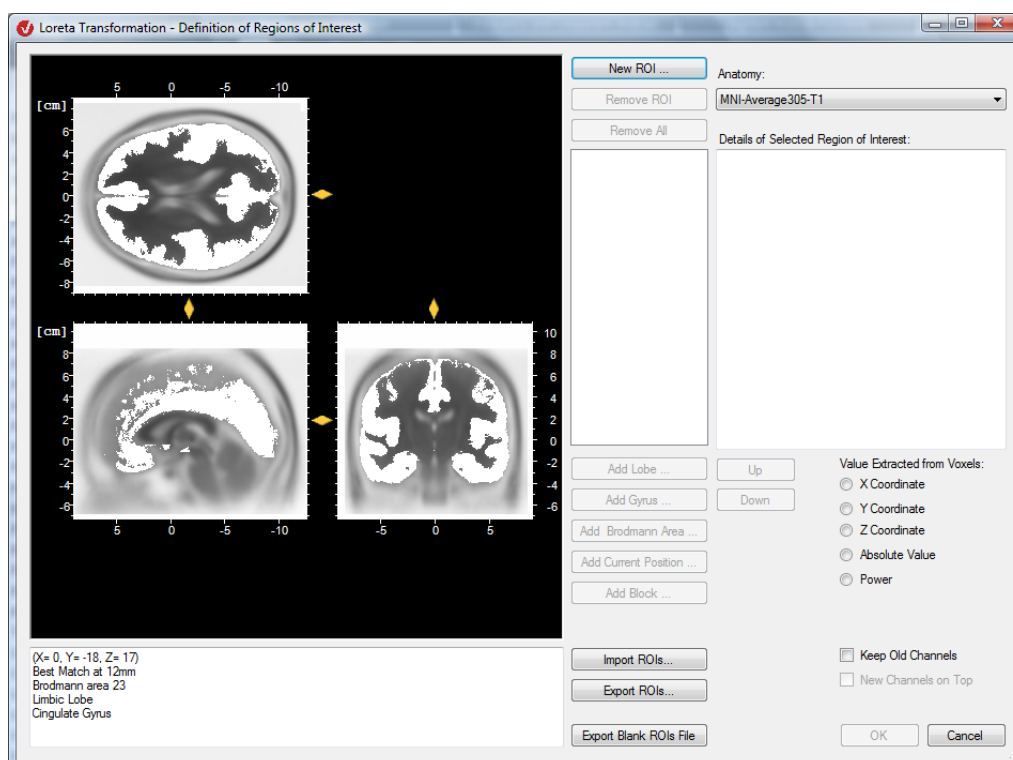


FIGURE 12—125 DIALOG BOX FOR THE LORETA TRANSFORM

Click **New ROI...** to create a new ROI. The **New Region** appears, in which you can enter the name of the new ROI. The name you enter here is also the name of the virtual channel. CREATING ROIS

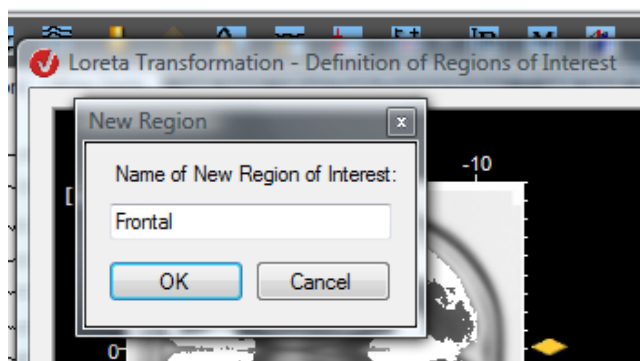


FIGURE 12—126 CREATING AN ROI

To add lobes to the ROI, click **Add Lobe....** You can use the **Left**, **Both** and **Right** radio buttons to specify whether the left lobe, right lobe or both lobes are to be added.

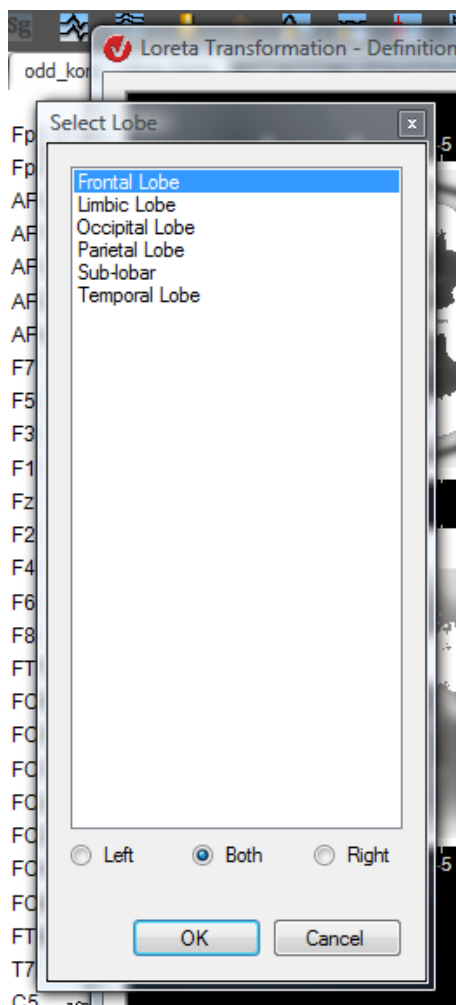


FIGURE 12—127 ADDING LOBES

You can use the **Add Gyri...** and **Add Brodmann Area...** buttons to add gyri and Brodmann areas to the ROI.

The **Add Current Position...** button allows you to add a specific position. You can choose whether to add the nearest voxel to the mouse pointer (by selecting the **Nearest Voxel** radio button) or to define a sphere with a specified radius around the current position (by selecting the **Sphere around Point** radio button).

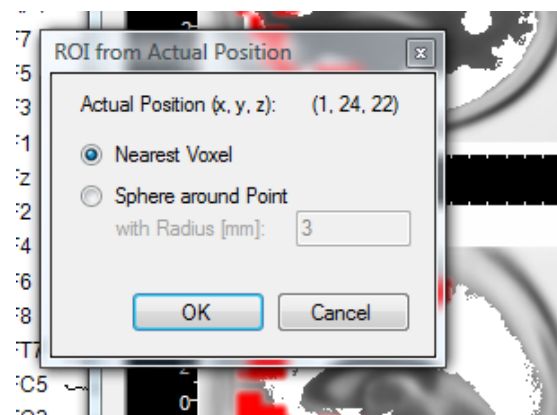


FIGURE 12—128 ADDING A SPECIFIC POSITION

The **Add Block...** button allows you to add a rectangular block, whose limits you can specify.

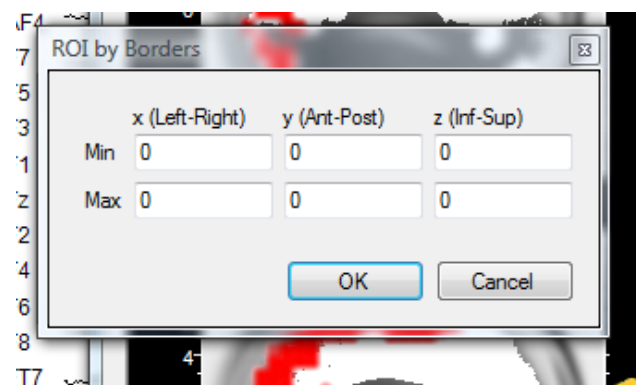


FIGURE 12—129 ADDING A BLOCK

The **Details of Selected Region of Interest** box lists everything specified.

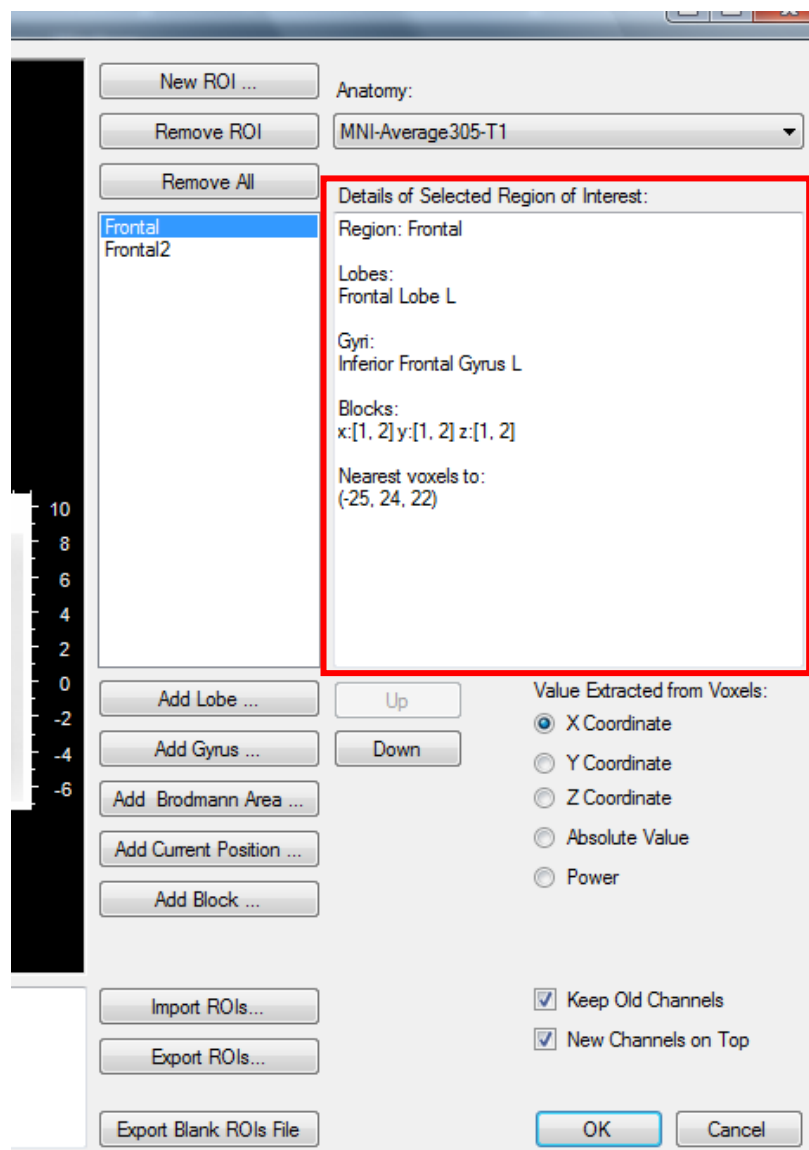


FIGURE 12—130 PART OF THE LORETA TRANSFORM DIALOG BOX, CONTAINING A LIST OF THE COMPONENTS OF THE ROI “FRONTAL”

From the **3D Anatomy** drop-down list, you can choose a virtual MR anatomical image.

ADDITIONAL SETTINGS

The **Remove ROI** and **Remove All** buttons allow you to remove ROIs individually or all at once.

In the **Value Extracted from Voxels** group, you can specify which value is to be calculated for the virtual channel from the corresponding ROI. You can choose the x-coordinate, y-coordinate, z-coordinate, absolute value of the coordinates or power (square of the value).

The **Keep Old Channels** check box allows you to specify whether the original channels are to be retained. The **New Channels on Top** text box allows you to specify whether the virtual channels are to be displayed before the original channels in the view.

The **Up** and **Down** buttons allow you to specify the order of the ROIs in the data set.

The **Import ROIs...** button imports ROIs that have already been defined. The **Export ROIs...** button allows you to export ROIs you have created as an .xml file so that they can be used subsequently.

The **Export Blank ROIs File** button exports voxel data, including the anatomical data, in a .csv file. You can open this file in Excel, for example, define the ROIs manually and re-import them as a .csv file.

The **OK** starts the calculation of the transform matrix and gives you the ROIs as new virtual channels. You can use the other modules of the Analyzer to work with these.

[PML94] R.D. Pascual-Marqui, C.M. Michel, D. Lehmann, Low resolution electromagnetic tomography: a new method for localizing electrical activity in the brain. International Journal of Psychophysiology, 18 (1994) 49-65.

REFERENCES

12.6.2 MR Correction (MRI scanner artifact correction)

In Version 1.0 of the Analyzer, both forms of MRI artifact correction were grouped together in the same transform (MRI Artifact Correction). In Version 2.0 of the software, there are separate transforms for scanner artifact correction and pulse artifact correction.



The scanner artifact correction transform allows the detection and correction of artifacts that occur during the recording of an EEG in an MRI scanner as a result of changes to the magnetic field in the scanner.

SUMMARY

The methods used in scanner artifact correction are based on techniques described in [Alloo].

PRELIMINARY REMARKS
ON METHODOLOGY AND
NOTES FOR USERS

The basic principle behind the correction of scanner artifacts is that the intervals interfered with by the MRI scanner are averaged. The averaged scanner artifact curve is then subtracted from the original curve in the affected intervals. This generally does not completely eliminate the scanner artifacts. Consequently, you should subject the data in the corrected ranges to a further correction by means of filters included in the transform.

It is possible to separate the detection of scanner episodes from scanner artifact correction and, as an initial step, to merely mark up the artifacts. The correction can therefore be based either on the detection method or on markers that already exist in the EEG.

You can use markers in order to define the intervals affected by scanner artifacts. Markers can be created by the scanner directly or by means of a macro. The quality of the averaged artifact curve to be subtracted from the individual sections in a subsequent step depends directly on the precision with which the markers are set over the duration of the signal. The transform implements methods by means of which a reference point (generally the starting point) is always marked for the scanned intervals.

There are two methods available for this: the simple gradient method and the gradient method with TDD (template drift detection).

In the simple gradient method, the sum of the gradients of the curves between two data points in the selected channels is calculated. If this sum exceeds the set threshold, a “scan start” marker is set.

In the gradient method with TDD, the current scanned interval is also compared with the first scanned interval, and “drifts” and “shifts” are calculated by means of an interpolation method for each scanned sampling interval in which an artifact occurs.

“Drift” are the differences in time between the averaged artifact curve and the scanner artifact of each interval. This drift is caused when the time of repetition (TR) of the scanner is not a multiple of the sampling rate. Consequently, the artifacts of the individual intervals drift by a fraction of a sampling interval even if the “scan start” markers are positioned perfectly.

ON DRIFTS AND SHIFTS

Drifts of the scanner rate in relation to the sampling rate no longer occur if the scanner and MR amplifier have been synchronized by means of the BrainVision SyncBox. This hardware option provides an ideal alternative to using TDC.



The information about drifts of a sampling interval is made available by the template drift compensation method when the artifacts are subsequently corrected. Moreover, the drift is adjusted appropriately at the beginning of the interval. This is of great benefit particularly in the case of continuous artifacts.

The TDD corrects certain marker positions by one or two points. These corrections are referred to as shifts. Their purpose is to compensate for the repeated effect of drifts.

If the scanner artifacts occur one after the other without being interrupted by artifact-free sections, it is very difficult to determine exactly where the next interval begins. Against this background, template drift detection can often significantly improve the positioning of the “scan start” markers.

In the simple gradient method, the accuracy with which the beginning of the artifact is detected does not necessarily increase when a larger number of channels are included. We therefore recommend that you use a single channel for this. Ensure that this channel actually contains all the existing scanner artifacts.

The accuracy of template drift detection, on the other hand, does increase when more channels are used. Results can therefore improve if you select a larger number of channels than you do for the simple gradient method.

The interval to be corrected can be moved relative to the starting point obtained (by means of markers or methods) in accordance with the selected interval range. If you enter negative values for the starting point when selecting the interval range, the beginning of the interval is positioned before the marked reference point.

It is possible to detect and correct artifacts in one and the same process, although you can also do it in two steps: PREREQUISITE FOR USE

- 1. Search the scanned intervals and set markers. You can then execute further transforms to analyze the time-related stability of the markers found (compare the marker position with the beginning of the scanner artifact). You should carry out checks like this, in particular, when you want to use external markers. The Analyzer’s “Marker Timing” solution is ideal for the analysis of the artifact markers. It shows the time between successive markers as a time-voltage curve.
- 2. Correct the scanned intervals.

You call the required dialog box by choosing **Transformations > Special Signal Processing > MR Correction**. PROCEDURE

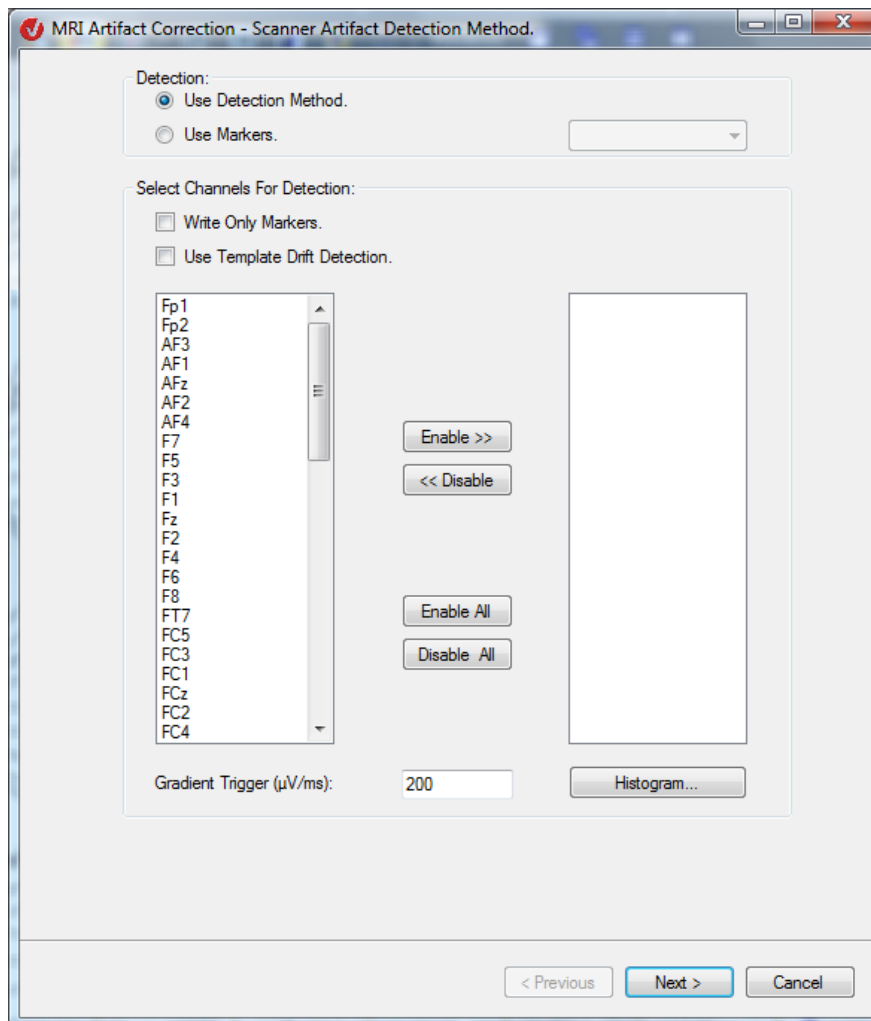


FIGURE 12—131 MRI ARTIFACT CORRECTION DIALOG, PAGE 1

You can separate the detection of scanner episodes from scanner artifact correction and, as an initial step, merely apply markers to the scanner artifacts. The correction can therefore be based either on the detection method or on markers that already exist in the EEG. The **Detection** group box allows you to specify whether you want to use the detection method (**Use Detection Method** radio button) or markers (**Use Markers** radio button) for artifact detection. You should select the **Use Markers** radio button if the scanned intervals are defined by existing markers. You select markers from the drop-down list box, which contains all the markers set in the EEG.

If you select the **Use Detection Method** radio button, you can use the **Write Only Markers** function. This function is used only to set markers; no artifact correction is performed. Artifact detection is thus carried out for either the current or a future correction. In this case, the markers found can be read if you apply the scanner artifact correction transform again and select the **Use Markers** radio button.

If you select the **Write Only Markers** check box and clear the **Use Template Drift Detection** check box, the artifacts are detected in that the marker positions are accepted as artifacts.

If you select both the **Write Only Markers** check box and the **Use Template Drift Detection** check box, the artifacts are detected by means of template drift detection (TDD).

If you carry out artifact detection with the **Use Template Drift Detection** check box selected, the quality of artifact correction is improved because template drift detection (TDD) corrects certain marker positions by calculating shifts in order to compensate for the effect of the drifts of the scanner.

Unlike in BrainVision Analyzer 1.0, it is possible to select the **Use Template Drift Detection** check box when the **Use Markers** radio button is selected. This is because it is not certain that the selected markers have drifts as user properties. This is the case when you use external markers.

The two large boxes in the lower part of the dialog box allow you to select the channels for which artifact detection is to be carried out.

In the **Gradient Trigger ($\mu\text{V}/\text{ms}$)** text box, you can specify the value of the gradient trigger. The **Histogram...** function helps you to determine a suitable gradient trigger. If you click this button, the **Gradient Histogram** dialog box appears.

The histogram displays the frequency distribution of the gradients and thus allows you to set a suitable gradient trigger. The gradient trigger is a limit value for automatically determining the scanner artifacts. The point in the EEG graph at which the gradient is greater than the gradient trigger is taken as the beginning of the artifact.

EXPLANATION

The **Display** button allows you to indicate the position of the value entered in the Trigger text box in the histogram. The **+/-** buttons allow you to resize the image.

The optimum gradient trigger value depends, among other things, on the channel selection.

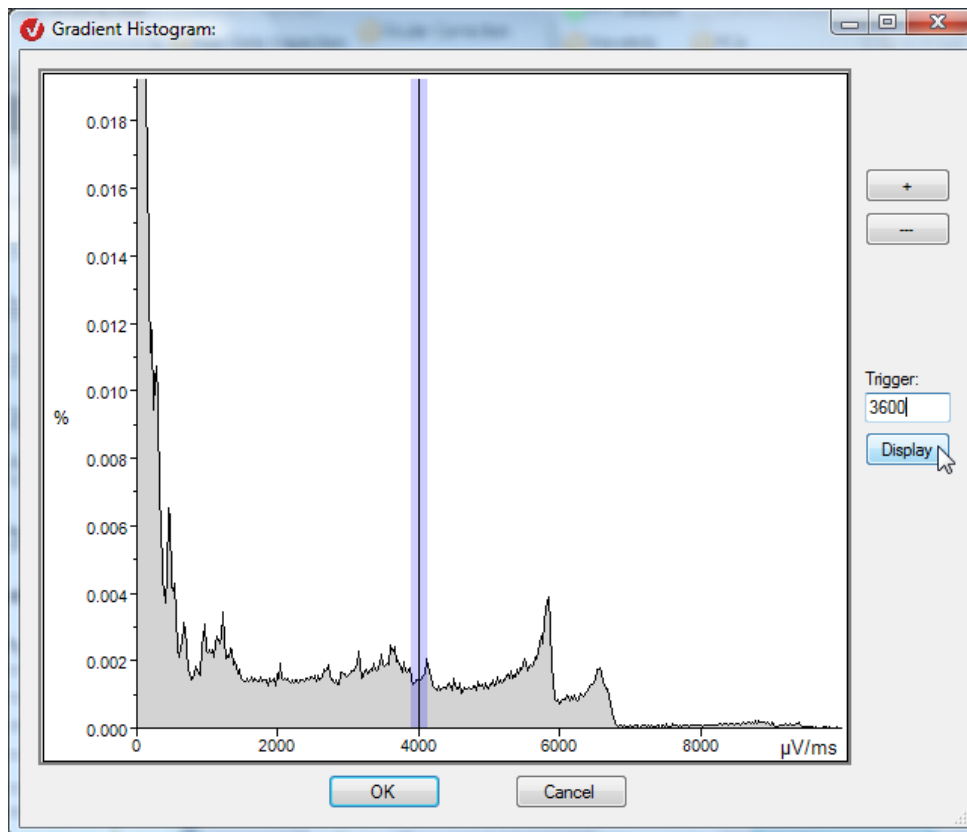


FIGURE 12—132 HISTOGRAM

The **Enable/Disable** and **Enable All/Disable All** buttons allow you to select the channels to which the gradient criterion is to be applied.

If you select **Artifact Type > Continuous** and **Select Channels for Detection > Write Only Markers**, the dialog contains no further pages. You conclude your settings by clicking the **Finish** button.

The **Next** button takes you to the second page of the dialog.

The screenshot shows a Windows-style dialog box titled "MRI Artifact Correction - Artifact Type and Interval Range." The dialog is divided into two main sections: "Interleaved Artifacts:" and "Continuous Artifacts:". In the "Interleaved Artifacts:" section, the "Based on Data Points:" radio button is selected. It has three input fields: "Start Point:" with the value 0, "End Point:" with the value 250, and "Points:" with the value 250. In the "Continuous Artifacts:" section, the "Based on Time:" radio button is selected. It has two input fields: "Offset [ms]:" with the value 0 and "TR [ms]:" with the value 1200. Below the "Continuous Artifacts:" section, there is another set of input fields for "Based on Data Points:" with "Start Point:" at 0 and "Points:" at 300. At the bottom of the dialog, there are three buttons: "< Previous", "Next >", and "Cancel". The "Next >" button is highlighted with a blue border.

FIGURE 12—133 MRI ARTIFACT CORRECTION DIALOG, PAGE 2

In the **Artifact Type** group box, you specify whether the scanner artifacts are interrupted (**Interleaved**) or continuous (**Continuous**).

- The **Interleaved** radio button allows you to detect scanned intervals when the intervals containing artifacts are followed by sections of the EEG that contain no scanner artifacts.
- The **Continuous** radio button allows you to detect scanned intervals containing artifacts when these intervals succeed each other without interruption. Specify the value of the scan period in the **TR [ms]** text box. The intervals are delimited by means of the time of repetition.

You can also make additional settings for the marker position or the point at which the artifact begins. You can specify the positions based on time or data points (using the **Based on Time** or **Based on Data Points** radio button).

If you make an entry in one of the six text boxes, the values in the text boxes affected by it are adjusted accordingly.

If you select the **Select Channels for Detection > Write Only Markers** check box, the wizard contains only pages 1 and 2.



FIGURE 12—134 MRI ARTIFACT CORRECTION DIALOG, PAGE 3

In the **Baseline Options** group box on the third page of the dialog, you can specify whether baseline correction is to be carried out before averaging and which period of the interval (relative to the marker, in other words to the reference point) is to be used for this. To do this, select the **Enable Baseline Correction for Average** check box. Baseline correction is carried out by averaging the data in the time range specified in the **Start** and **End** text boxes. This average is calculated channel by channel and subtracted from each data point in the interval.

**BASILINE OPTIONS
GROUP BOX**

We recommend that you always carry out baseline correction because it prevents jumps from occurring in the corrected EEG. Without baseline correction, the base level influences the calculation of the scanner artifact and is also subtracted at correction.

If you select the **Compute Baseline Over the Whole Artifact** check box, the baseline is calculated precisely across the whole artifact. The **Start** and **End** text boxes are no longer accessible.

For some EEGs, the method for obtaining the baseline delivers better results when the baseline is calculated within an interval that is partially outside the artifact. In this case, enter a relatively large negative value (e.g. -300) in the **Start** text box and a relatively small positive or negative value (e.g. between -25 and 25) in the **End** text box.

For other EEGs, the method delivers better results when you calculate the baseline within the artifact. In this case, enter a relatively small positive value in the **Start** text box and a relatively large positive value in the **End** text box. To calculate the baseline within the artifact, you can also use the default: **Compute Baseline Over the Whole Artifact**.

The **Average Options** group box contains the four methods of selecting the intervals for the calculation of the averaged artifact curve. They are template calculation using all the intervals, correlation, sliding average calculation and template drift correction (TDC).

**AVERAGE OPTIONS
GROUP BOX**

All four methods are based on subtracting templates (averages) from the artifacts. These templates are always calculated by averaging the artifacts. The EEG sections marked as “bad intervals” are not included in the template calculations. However, they are corrected as far as possible by means of template subtraction.

Depending on the method selected, not all the scanned intervals are used to calculate the templates, since data in some intervals cannot be used in the calculation and would falsify the averages obtained.

In the template calculation method with all intervals (the first radio button in the group box), clearly, all the scanned intervals are used. In the correlation method, only those intervals are included in the calculation that have at least a minimum correlation with the existing averaged artifact curve. In the sliding average calculation, a sliding average of the intervals is calculated. If you have used template drift detection to obtain the intervals, you can use the template drift compensation method to distribute the intervals to a number of averaged artifact curves, depending on the drift.

Note that the Detect Saturation function from Version 1.0 of the Analyzers is not included in the MR transform. This is because the Data Inspector transform provides more flexible methods for the same purpose.



1) If you select the **Use All Scanned Intervals for Average** radio button, all the scanned intervals are used in the template calculation, and there is no need to make any further settings. All artifact sections of the EEG that are identified by markers are included in averaging.

DESCRIPTION OF THE 4
METHODS: METHOD 1

2) If you select the **Select Scanned Intervals for Average by Following Criteria** radio button, the template calculation is based on the correlation method [Alloo]. In this method, the inclusion of individual artifacts in the template depends on whether they correspond to the averaged template.

METHOD 2

In the **Start at Interval Number** text box, you specify the interval at which averaging begins, and consequently you can eliminate from the averaging a specific number of episodes at the beginning of the measurement. This makes sense when your MR system inserts “dummy volumes” at the beginning of a measurement to stabilize the system. These “dummies” often have anything from a slightly different to a significantly different structure over time from the MR volume measurements. Consequently, including these “dummies” in the averaged artifact would make this template less representative.

In the **Include Always Following Number of Intervals from Start Interval** text box, you specify the number of intervals that must be included in the averaging in order to obtain a useful value for the subsequent correlation.

The value in the **Include Other Intervals Only If Correlation Exceeds** text box is used as follows:

If you select the **Common Use of All Channels for Bad Intervals and Correlation** check box, the correlation of each of the interval’s channels with the corresponding channel of the template is calculated. If this correlation is greater than the value in the **Include Other Intervals Only If Correlation Exceeds** text box, the interval’s channel is included in the template calculation. If the correlation is lower, the corresponding channel is not included.

If you clear the **Common Use of All Channels for Bad Intervals and Correlation** check box, the correlation of all the interval’s channels with the corresponding channels of the template is calculated as a first step. If a correlation is lower than the value in the **Include Other Intervals Only If Correlation Exceeds** text box, a switch is made to the next interval, and the channels from the affected interval are not included in the template calculation. If all the correlations are greater than this value, the entire interval is included in the template calculation.

We recommend that you do not select the **Common Use of All Channels for Bad Intervals and Correlation** check box if you are using the second method of the two described because correction is more precise when more intervals per channel are included in the template calculation.



In the following example, four intervals are ignored at the beginning, but the following five intervals are included in the template calculation. All other intervals must have a correlation of 0.8 with the template to be included in the template calculation:

☒ Select Scanned Intervals for Average by Following Criteria:

Start at Interval Number:	<input type="text" value="5"/>
Include Always Following Number of Intervals from Start Interval:	<input type="text" value="5"/>
Include Other Intervals Only If Correlation Exceeds:	<input type="text" value="0.8"/>

The **Upper Limit for Number of Intervals** check box and text box allow you to limit the number of intervals to be included in the template calculation in order to reduce the processing time.

The **Write Markers for Low Correlation** check box allows you to put a “low correlation” marker on intervals that do not meet the correlation criterion specified in the **Include Other Intervals Only If Correlation Exceeds** text box.

If you select the **Common Use of All Channels for Bad Intervals and Correlation** check box, a global marker is set for all channels. If, on the other hand, you clear this check box, a separate marker is set for each channel.

3) The **Use Sliding Average Calculation** option addresses the following problem with combined EEG and MRI measurement: As soon as the subject moves his or her head in the scanner even slightly, the resulting EEG artifacts are modified, in some cases considerably. This substantially reduces the quality of a template calculated across all intervals. A solution to this problem is to calculate the template by means of a sliding average of a selected number of intervals.

METHOD 3

A separate template is calculated for each interval to correct the interval.

Example: Let's assume you have entered the value 10 in the **Number of Intervals for Sliding Average** text box. The following 21 intervals are therefore included in the template calculation: the interval itself and the 10 preceding and 10 subsequent intervals.

Note that the sliding method in Version 1.0 of the Analyzer differs from the method in Version 2.0. In the former, only the 10 intervals preceding the current interval in our example would be used in the calculation of the template.

Another way to solve the problem (of the subject moving his or her head) is to position “head movement” markers manually. The Edit markers transform allows you to position these markers at those points in the EEG at which the subject clearly moved his or her head. The EEG sections delimited by markers are considered as separate EEGs by the scanner artifact correction transform. Consequently, separate template calculation and correction is carried out for each of these sections.

4) The template drift compensation method (TDC) uses several artifact templates to reduce problems caused by the drifting of the scanned intervals in relation to each other by fractions of a sampling interval (template drift). The method is based on using for averaging only those intervals that have similar template drift.

METHOD 4

We would like to point out again here that TDC does not have to be used if scanners and MR amplifiers are synchronized with each other by means of the BrainVision SyncBox.



Note that you can only use the TDC method if you selected the **Use Template Drift Detection** check box to measure the template drift when detecting the scanned intervals.

The drift in relation to the ideal position is assigned to each scanned interval as a fraction of a sampling interval between -0.5 and 0.5. A range of these drifts is assigned to each of the artifact templates managed by template drift compensation. For the purpose of averaging, each template takes into account only those intervals that fall within its range.

In the **Number of Templates To Use** text box, you specify the number of templates used. If you use a large number of templates, the correction should be more precise. However, fewer intervals are included in the calculation of each template in this case. Consequently, the significance of the template is reduced.

If you select the **Drift-differences and Shifts in Operation Infos** check box, all drift differences and shifts are added to the operation information. The drift differences are not nominal drift values; instead, they represent the difference between two successive drifts.

For a better selection of the number of templates used, you can also base yourself on the values of the drift differences or the distribution of the drifts.



The **Next** button takes you to the fourth page of the dialog:

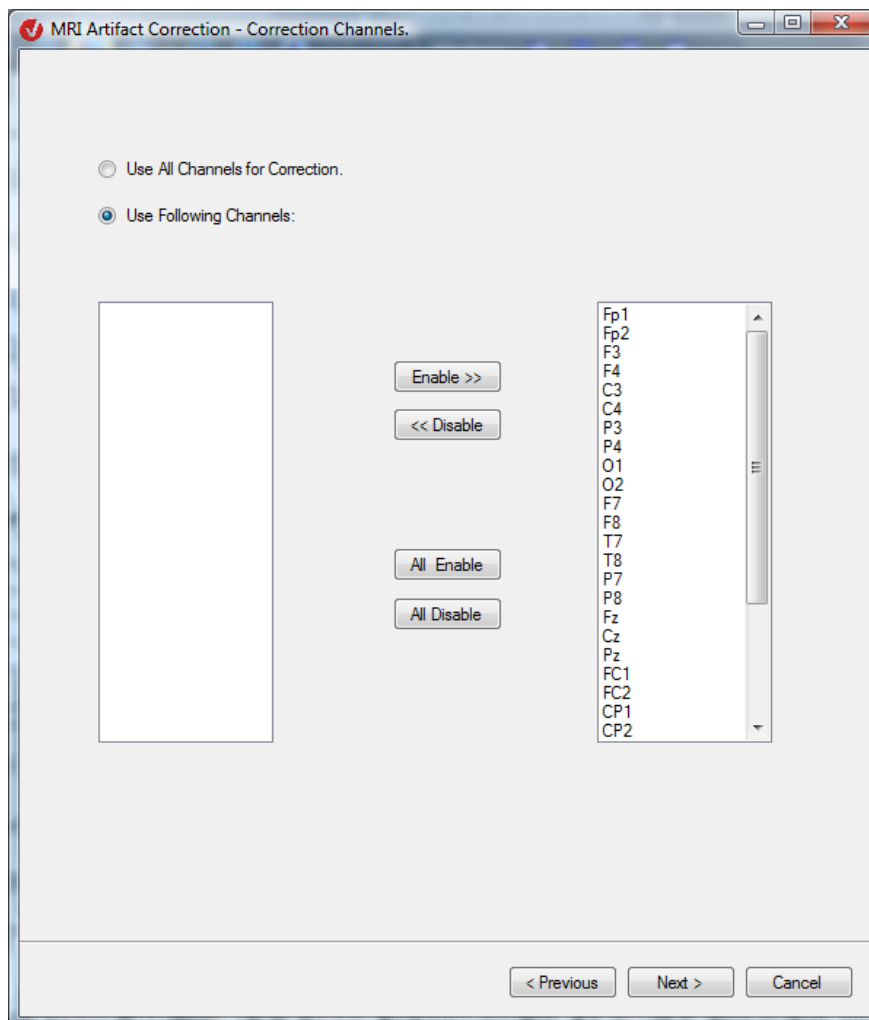


FIGURE 12—135 MRI ARTIFACT CORRECTION DIALOG, PAGE 4

The dialog box allows you to select the channels for which the correction is to be carried out. You can select all the channels (**Use All Channels for Correction**) or make a selection from those that are available (**Use Following Channels**). You can also use the **Enable >>/<< Disable** and **All Enable/All Disable** buttons to make your selection.

The **Next** button takes you to the fifth page of the dialog:

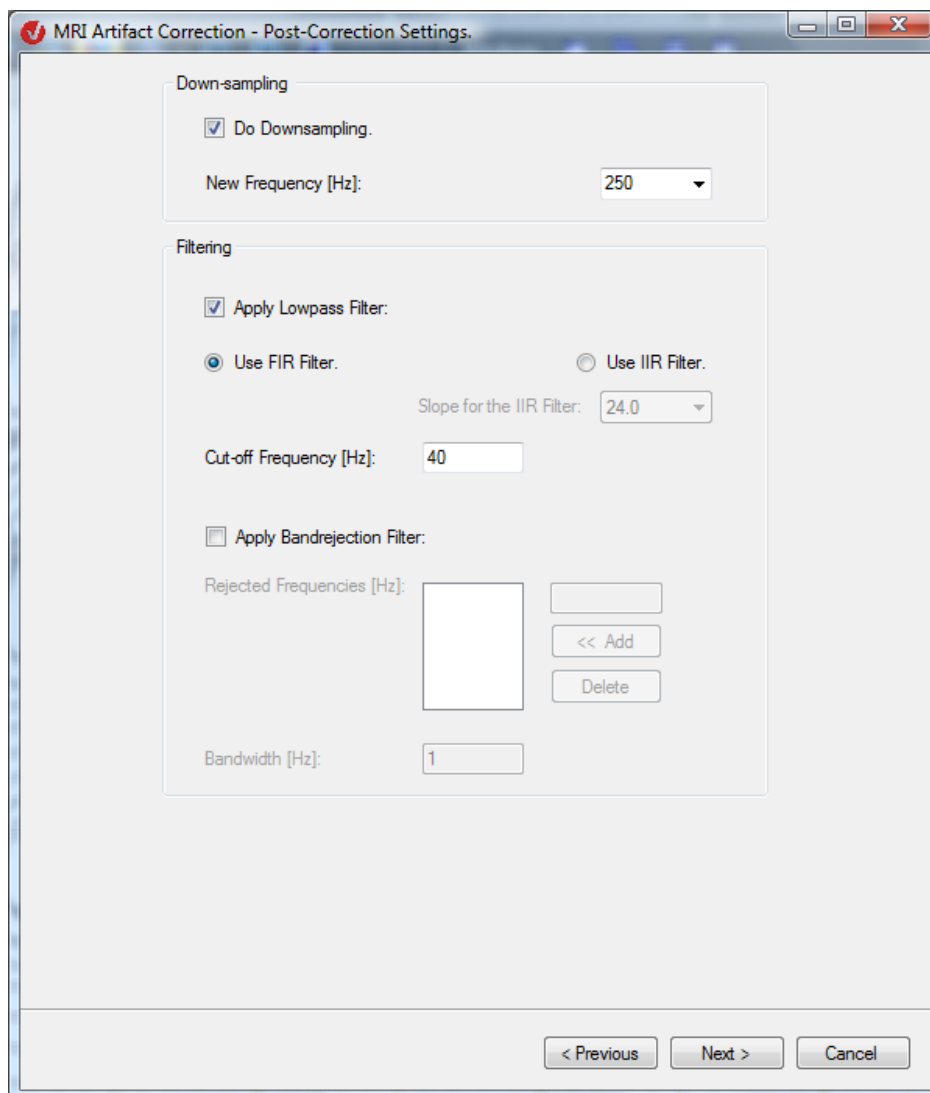


FIGURE 12—136 MRI ARTIFACT CORRECTION DIALOG, PAGE 5

The EEG is recorded in the scanner with a very high sampling frequency so that the scanner artifacts can be detected correctly and subsequently corrected. However, data with high frequencies takes a lot of time to process and requires a great deal of storage space. You should therefore carry out downsampling following artifact correction. To do this, select the **Do Downsampling** check box.

DOWN-SAMPLING
GROUP BOX

The **New Frequency** check box contains the value of the output frequency. This is the nominal value of the sampling rate of the output data. (Note that in Version 1.0 of the Analyzer the downsampling factor was specified at this point.) You can either enter a value or choose one from the drop-down list box.

If you decide to enter a value rather than choose one from the list, the frequency you specify may be adjusted to the nearest possible frequency when you move the cursor out of the **New Frequency** box. This is because downsampling can only be carried out with factors that are integers in order to avoid interpolation effects.

In the **Filtering** group box, you can make filter settings. Filtering is necessary if residual frequencies that do not have a physiological origin remain after the correction of the EEG.

FILTERING GROUP BOX

There are two filter types available: low-pass and band-rejection filters. The **Apply Lowpass Filter** function filters frequencies that are higher than the value entered in the **Cut-off Frequency [Hz]** text box.

You can also choose between the two filter types **FIR** (finite impulse response) and **IIR** (infinite impulse response). You specify the gradient of the IIR filter by choosing one of the two values from the **Slope for the IIR Filter** drop-down list box.

The FIR filter used here is the same as the filter used in Version 1.0 of the Analyzer and is very strong. Analyzer 2.0 therefore offers you the option of using an IIR filter. This IIR filter is a typical Butterworth filter, as used in the Filters transform.

The **Apply Bandrejection Filter** function (the band-rejection filter used here is an FIR filter) filters out the frequencies in the **Rejected Frequencies [Hz]** text box with the bandwidth specified in the **Bandwidth** text box.

You can use the **Apply Bandrejection Filter** function (the band-rejection filter used here is an FIR filter) to filter out specific frequency ranges. You can specify these ranges in the **Rejected Frequencies [Hz]** and **Bandwidth** text boxes. In the former you enter the averages, and in the latter the bandwidth of the frequency ranges. In order to enter values in the **Rejected Frequencies [Hz]** text box, enter them in the text box to its right and then click **Add**. To remove one or more values, select them and then click **Delete**.

The **Next** button takes you to the **Store Corrected Data in History Node** dialog box:

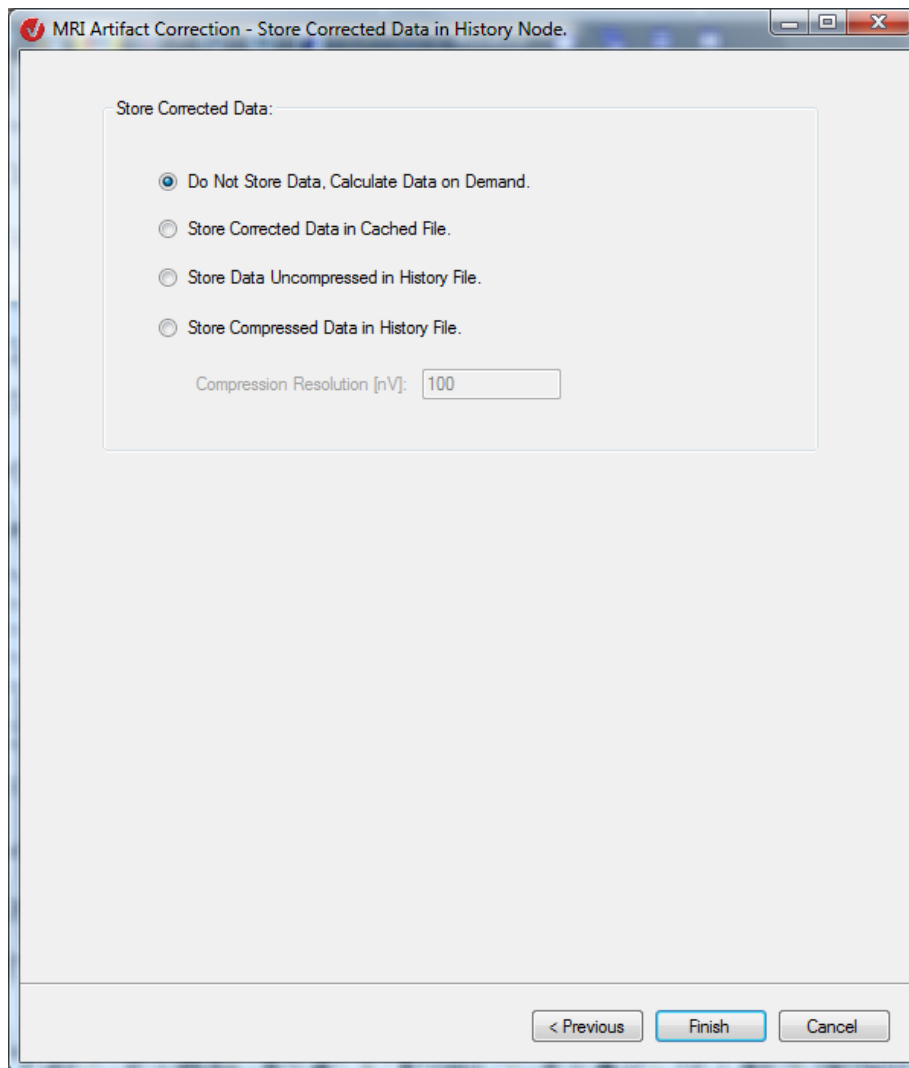


FIGURE 12—137 MRI ARTIFACT CORRECTION DIALOG, PAGE 6

This allows you to specify the storage options for the data calculated so that the subsequent operations can be performed more quickly:

- **Do Not Store Data, Calculate Data on Demand:** The data is not stored. Instead, it is calculated on demand.
- **Store Corrected Data in Cached File:** The data is stored in a cache file.

We recommend that you use this option to avoid increasing the size of the history files.

- **Store Data Uncompressed in History File:** The data is stored uncompressed in the history file that belongs to the data set.
- **Store Compressed Data in History File:** The data is stored compressed in the history file that belongs to the data set. Compression means the data takes up less storage space, but precision is reduced.

In the **Compression Resolution [μV]** text box, you specify the coefficient by which the data is to be compressed. The default value is 100.

Click the **Finish** button to start artifact correction.

[Alloo] P.J. Allen et al., A Method for Removing Imaging Artifact from Continuous EEG Recorded during Functional MRI. Neuroimage 12 (2000), 230-239. REFERENCES

12.6.3 CB Correction (pulse artifact correction)

In Version 1.0 of the Analyzer, both forms of MRI artifact correction were grouped together in the same transform (MRI Artifact Correction). In Version 2.0 of the software, there are separate transforms for scanner artifact correction and pulse artifact correction.



This transform allows the detection of pulse beats and the correction of pulse artifacts (cardioballistic artifacts) that occur during the recording of an EEG in an MRI scanner.

SUMMARY

Although it is theoretically possible to detect and correct pulses in one and the same process, it is not advisable – particularly not when the quality of the correction using the selected parameters for a given data set cannot be assessed. We therefore recommend that you break the process down into two separate steps:

RECOMMENDATIONS ON
THE USE OF THE
MODULE

- (1) Search for ECG episodes before correcting the pulse artifacts. Unless you perform the search for pulse artifacts in semiautomatic mode, we recommend that in this step you merely set markers and then analyze their structure over time. The Analyzer's "Marker Timing" solution is ideal for the analysis of the pulse markers. It shows the interval between successive markers as a time-voltage curve.
- (2) Correct the pulse artifacts.

The advantage of subdividing the process into different steps is that the interim results can be analyzed, permitting intermediate steps to be performed manually or automatically, for example adjustments to markers or an artifact search using the Raw Data Inspector.

To display the relevant dialog box, you choose **Transformations > Special Signal Processing > CB Correction**.

PROCEDURE

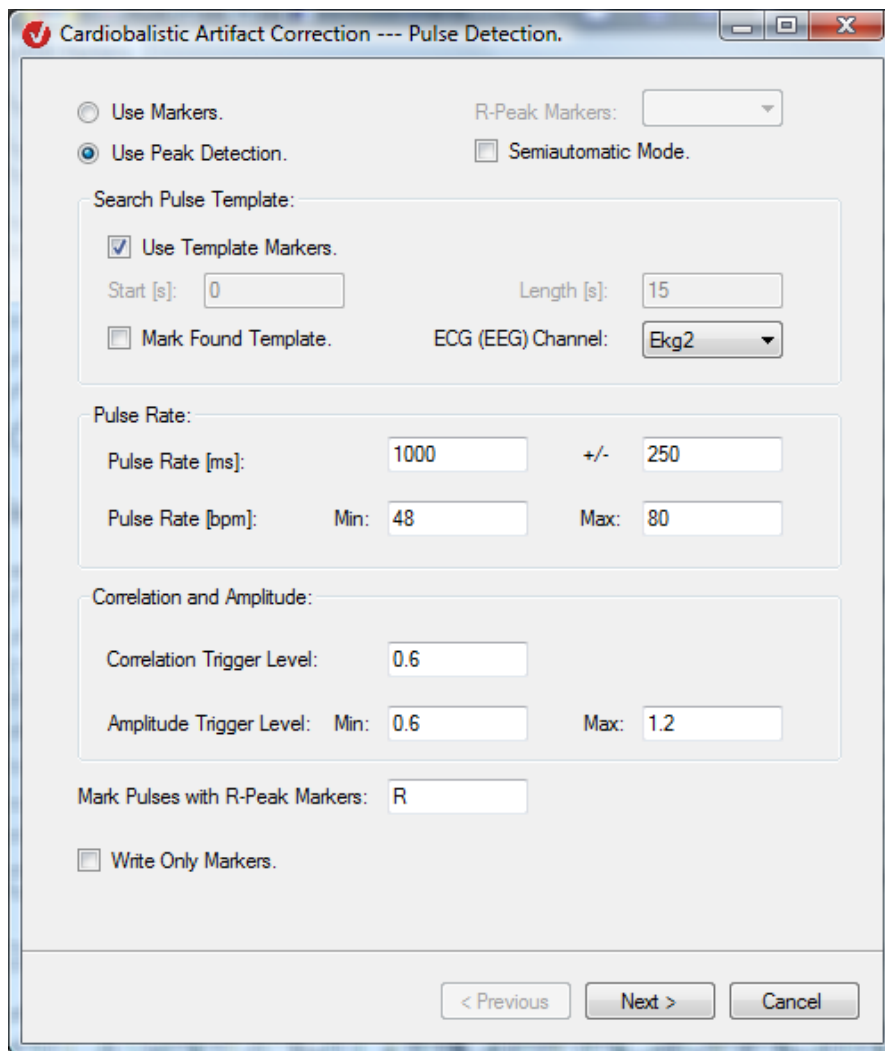


FIGURE 12—138 CARIOBALLISTIC ARTIFACT CORRECTION DIALOG, PAGE 1

At this point, you specify whether you want to use the peak detection method (**Use Peak Detection**) or markers (**Use Markers**) for artifact detection.

If you select the **Use Markers** radio button, the markers already set in the EEG are used to determine the pulse intervals, and artifact correction is performed for those pulses that are identified by a marker. You select the markers that are to function as R-peak markers in the EEG from the **R-Peak Markers** drop-down list, which contains the names of all the markers set in the EEG.

Note that these markers do not necessarily correspond to the point identified as the R-peak in heart physiology; they are a recurring attribute of the pulse, allowing the time at which the pulse beats occur to be identified.

If you select the **Use Peak Detection** radio button, the pulse peaks (R-peaks) are detected and marked; this is done either for the current correction or, if you have selected the **Write Only Markers** check box, for a future correction.

The **Semiautomatic Mode** check box allows you to enable/disable semiautomatic mode for subsequent editing of the results of pulse detection.

In the **Pulse Rate** group box, you make the pulse rate settings (the interval between two pulses). The pulse rate can be specified both in ms (as a time value) and in bpm (beats per minute). You specify the average pulse rate and associated tolerance range (**+/-**) in ms and the minimum and maximum tolerance values (**Min.** and **Max.**) in bpm.

When you change the value in one of the four text boxes and position the mouse pointer in another text box, the values in the text boxes affected by this are adjusted as appropriate.



In the pulse detection process, the values in the **Correlation and Amplitude** group box play the following role:

In the intervals in which the current correlation is greater than the value in the **Correlation Trigger Level** text box, maximum correlations are searched for. If the value of the amplitude at the maximum correlations lies strictly between the minimum and maximum amplitude triggers, this value is identified as the pulse peak. The **Correlation Trigger Level** value is always between 0 and 1.

The default values for the amplitude in the **Min.** and **Max.** text boxes are 0.6 and 1.2. If the default values do not lead to satisfactory results, adjust the values for **Min** and **Max** down/up.

In the **Mark Pulses with R-Peak-Marker** text box, you can enter the name of the R-peak marker.

If you have selected the **Write Only Markers** check box, there are no further parts to the dialog because no artifact correction is performed. All that happens is that pulses are marked. Click **Finish** to finish making your settings.

If the **Write Only Markers** check box is not selected, the **Next** button takes you to the second page of the dialog.

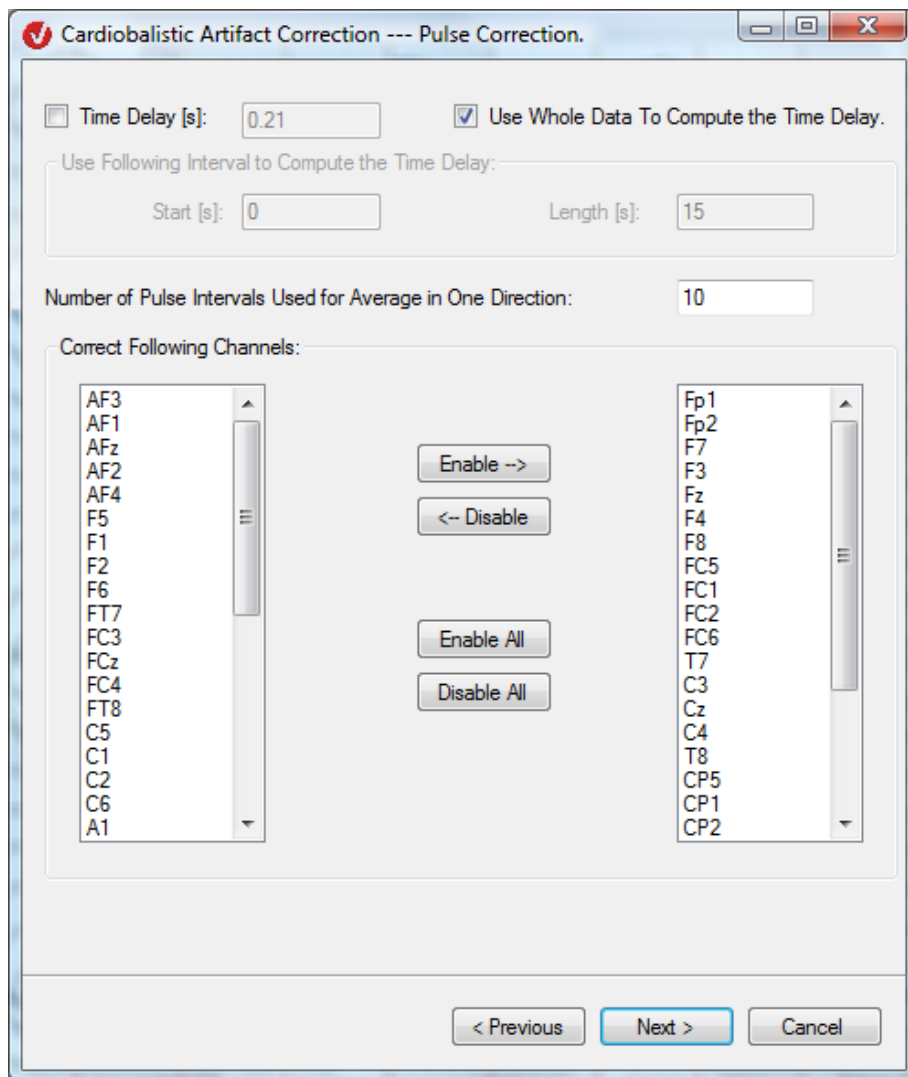


FIGURE 12—141 CARDBALLISTIC ARTIFACT CORRECTION DIALOG, PAGE 2

You can either specify a time delay (by selecting the **Time Delay [ms]** check box and entering the value) or have it calculated (**Time Delay Computation**). The time delay is the delay between the heartbeat and the occurrence of the artifacts caused by it in the EEG channels.

To enter a time delay, select the **Time Delay** check box and enter the desired value in the associated text box. If you do not select the check box, the time delay is calculated automatically.

If you decide to have the time delay calculated automatically, enter the beginning and length of the interval in which the calculation is to be carried out in the **Start [s]** and **Length [s]** text boxes.

If, on the other hand, you select the **Use Whole Data to Compute the Time Delay** check box, the entire data set is used to calculate the time delay, and the **Start [s]** and **Length [s]** text boxes are no longer accessible.

By means of the **Number of Pulse Intervals Used for Average in One Direction** option, the template is calculated using a sliding average of a selected number of intervals.

CORRECTION GROUP
BOX

A separate template is calculated for each interval to correct the interval. For example, let's assume you have entered the value 10 in the **Number of Pulse Intervals for Average in One Direction** text box. The following intervals are therefore included in the template calculation: the interval itself and the 10 preceding and subsequent intervals – a total of 21 intervals.

Note that the pulse correction process in Version 1.0 of the Analyzer differs from the process in Version 2.0. In the former, only the 10 intervals preceding the current interval in our example would be used in the calculation of the template.



You use the two list boxes below this to select channels.

The **Next** button takes you to the third page of the dialog:

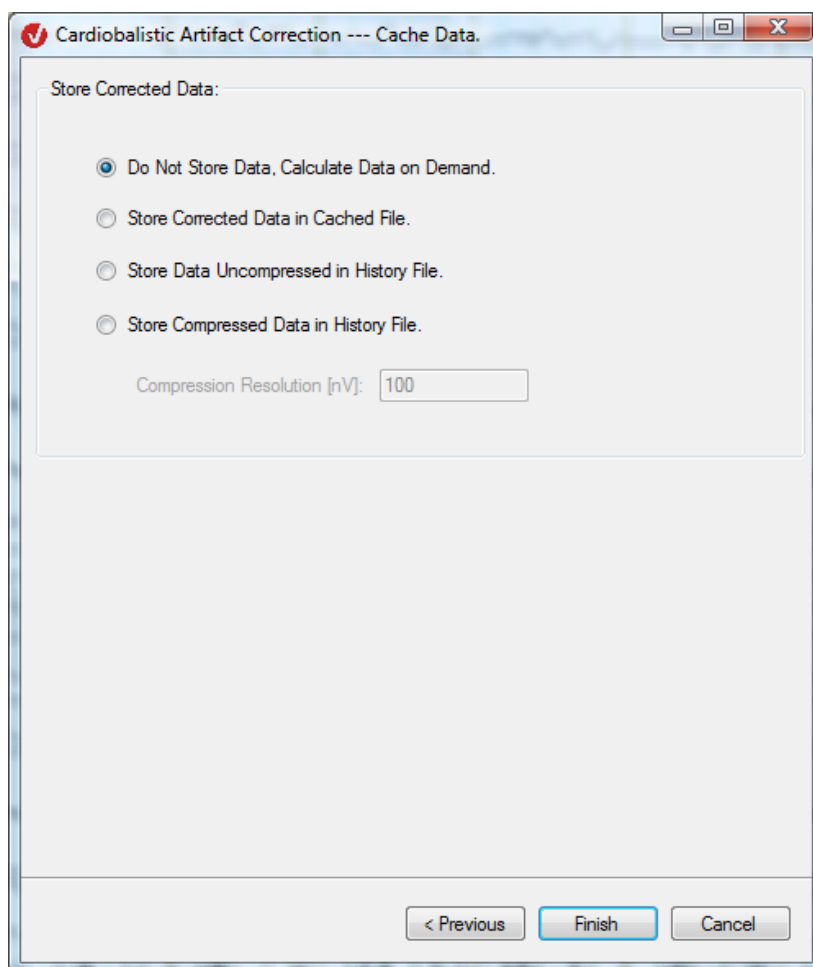


FIGURE 12—142 CARIOBALLISTIC ARTIFACT CORRECTION DIALOG, PAGE 3

This allows you to specify the storage options for the data calculated so that the subsequent operations can be performed more quickly:

- **Do Not Store Data, Calculate Data on Demand:** The data is not stored. Instead, it is calculated on demand.
- **Store Corrected Data in Cached File:** The data is stored in a cache file.

We recommend that you use this option to avoid increasing the size of the history files.

- **Store Data Uncompressed in History File:** The data is stored in a history file uncompressed.
- **Store Compressed Data in History File:** The data is compressed and stored in a history file. Compression means the data takes up less storage space, but precision is reduced.

In the **Compression Resolution [μ V]** text box, you specify the coefficient by which the data is to be compressed. The default value is 100.

If you selected the **Semiautomatic Mode** check box in the Pulse Detection Parameters dialog box, the artifact correction process is started when you click **Finish**.

On the other hand, if you did not select the **Semiautomatic Mode** check box, a data window opens in semiautomatic mode. This allows you to modify the results of pulse artifact correction subsequently. The temporary **Peak Detection** semiautomatic view dialog box appears on the right-hand side of the window.

To examine the pulse peaks in detail, click the channel label to display the channel specified in the **ECG (EEG) Channel** text box. The channel initially contains only red and green markers. Yellow markers are added subsequently.



FIGURE 12—143 MARKERS IN SEMIAUTOMATIC MODE

The colors have the following significance:

- The green markers indicate points that are clearly pulse peaks as far as the peak detection process is concerned.
- The red markers indicate points that are potentially pulse peaks but do not meet all the mathematical conditions for this.
- The yellow markers indicate red or green markers that have been confirmed or moved by the user.

Rules for the colors:

- If you click or move a green or red marker, it turns yellow.
- A yellow marker does not change its color if it is moved.
- If you click a yellow marker, it is deleted.
- If you click anywhere in the channel, a yellow marker is created.

The **Undo** and **Redo** buttons in the lower part of the temporary semiautomatic view dialog box allow you to reverse and restore the changes.

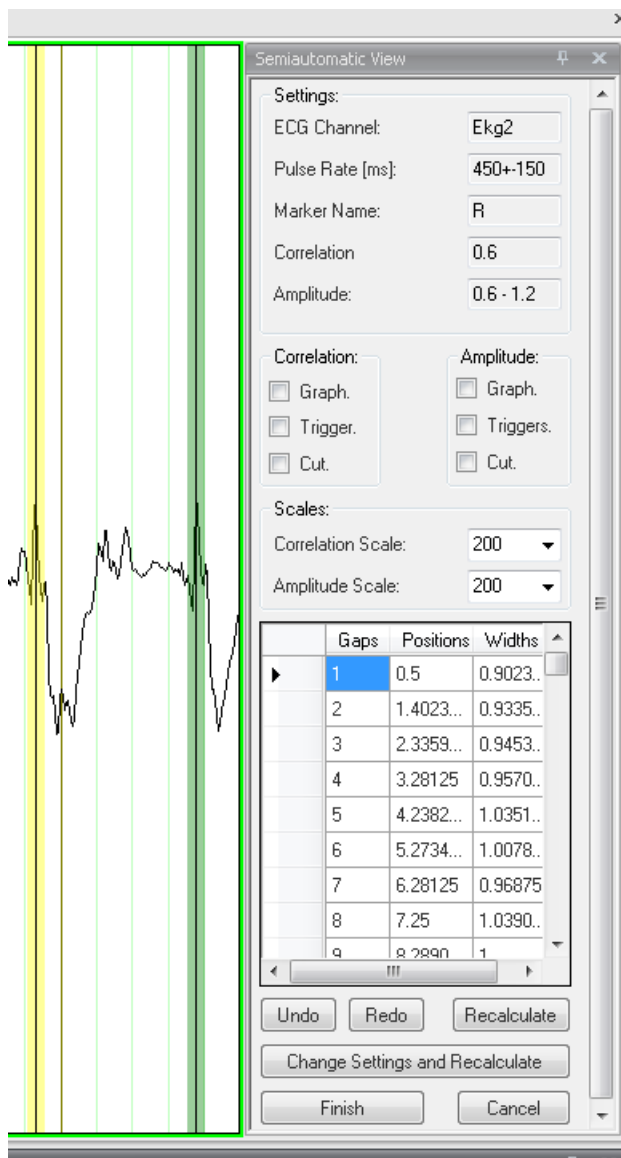


FIGURE 12—144 SEMIAUTOMATIC VIEW

When you terminate semiautomatic mode by clicking **Finish**, the green and yellow markers – but not the red ones – are treated as pulse peaks.

The **Settings** group box at the top of the **Peak Detection** semiautomatic view dialog box contains the most recently selected parameters for calculating:

- The name of the selected channel
- The interval between two pulses with a tolerance range
- The marker name
- The correlation trigger
- The amplitude trigger

The table shows the intervals in which not enough peaks were detected. These intervals are known as gaps. If you double-click a row in the table, the view switches to show the position of the gap. The table is continuously updated when the markers are deleted or confirmed.

If you select the **Correlation > Graph** check box, the correlation graph is displayed in the channel as an overlay. The **Correlation Scale** list box contains the factor used to display the correlation. By changing this value, you can change the size of the correlation graph in order to adjust it to the display of the EEG.

CORRELATION AND
AMPLITUDE GROUP
BOXES

If you select the **Correlation > Trigger** check box, the correlation trigger is displayed.

The **Correlation > Cut** function shows either:

- The correlation wherever it is greater than the correlation trigger (only within these intervals is a search carried out for the maximum correlations)
- or
- The constant trigger value wherever the correlation is lower than the correlation trigger

The green markers indicate local maximum correlations obtained within the intervals by means of the “correlation > correlation trigger” attribute.

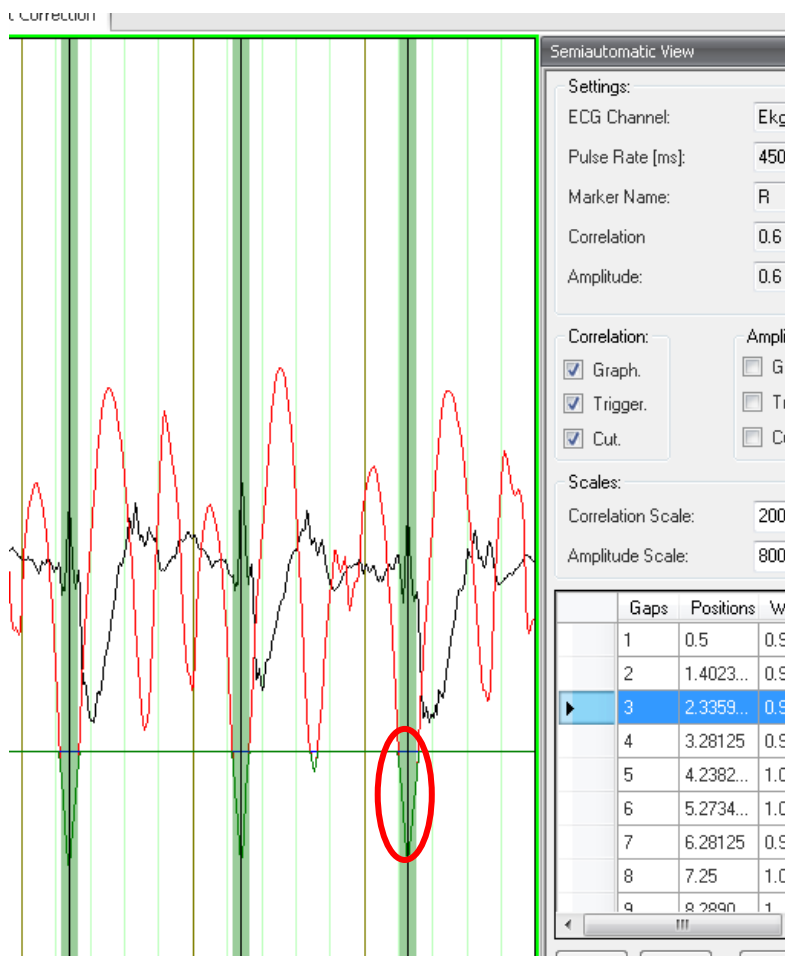


FIGURE 12—145 CORRELATION TRIGGER (GREEN LINE) AND LOCAL MINIMUM CORRELATION

If you select the **Amplitude > Graph** check box, the amplitude graph is displayed in the channel as an overlay. The Amplitude Scale list box contains the factor used to display the amplitude.

If you select the **Amplitude > Trigger** check box, both amplitude triggers are displayed.

The **Amplitude > Cut** function shows either:

- The constant value of the minimum trigger if the amplitude is lower than the minimum trigger value ($A < \min$)
or
- The amplitude graph if A is greater than the minimum and lower than the maximum ($\min < A < \max$)
or
- The constant value of the maximum trigger if A is greater than the maximum ($A > \max$)

Consequently, only the pulse peaks that meet the criteria “correlation > correlation trigger” and “min. amplitude trigger < amplitude < max. amplitude trigger” are output as reliable peaks.

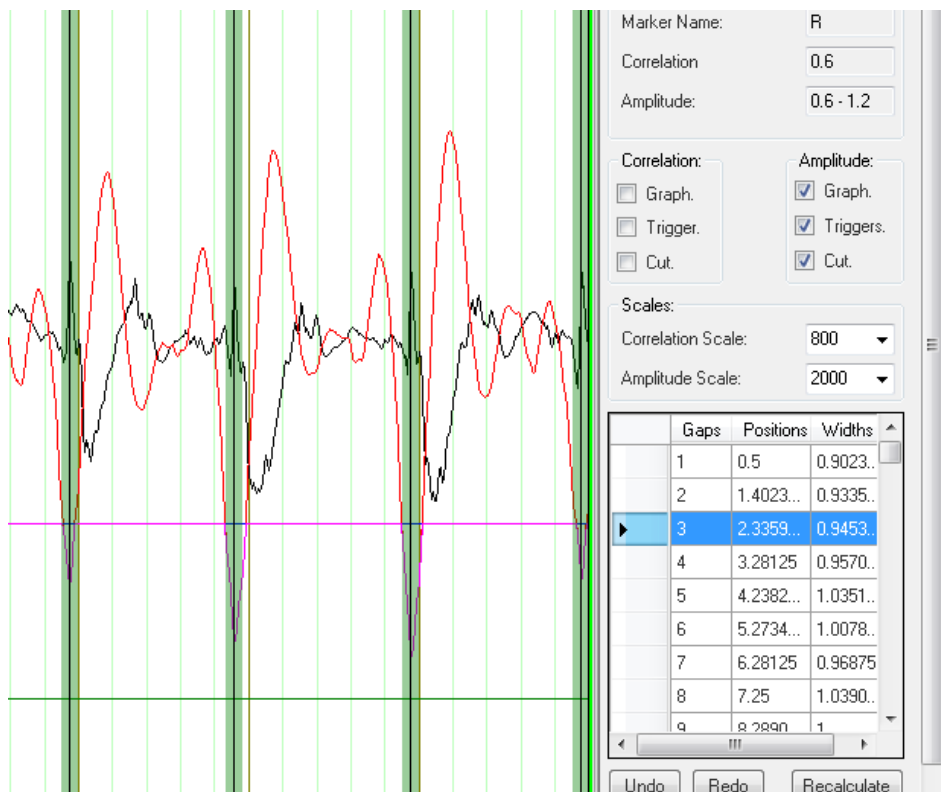


FIGURE 12—146 MINIMUM (PINK) AND MAXIMUM (GREEN) AMPLITUDE TRIGGERS

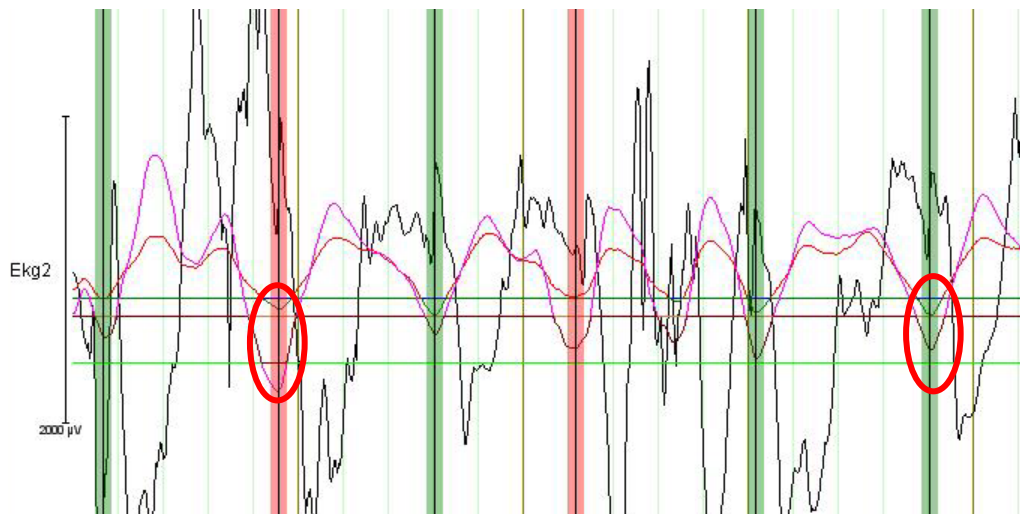


FIGURE 12—147

In Figure 12—147, you can see in the highlighted area on the left that the local maximum correlation is greater than the correlation trigger. However, the amplitude is outside the permissible amplitude range. A red marker is therefore used here (unreliable peak). In the highlighted area on the right, the criteria “correlation > correlation trigger” and “min. amplitude trigger < amplitude < max. amplitude trigger” are met, so the corresponding peak is output as a reliable peak (green marker).

The pulse template is identified in the channel by a light blue marker. This marker also contains an internal peak marker (a vertical black line with a circle). Both the position and size of the marker and the position of the internal marker can be changed.

If you press the right mouse button and then choose **Move Template Here**, you can move the template to the required position in the EEG:

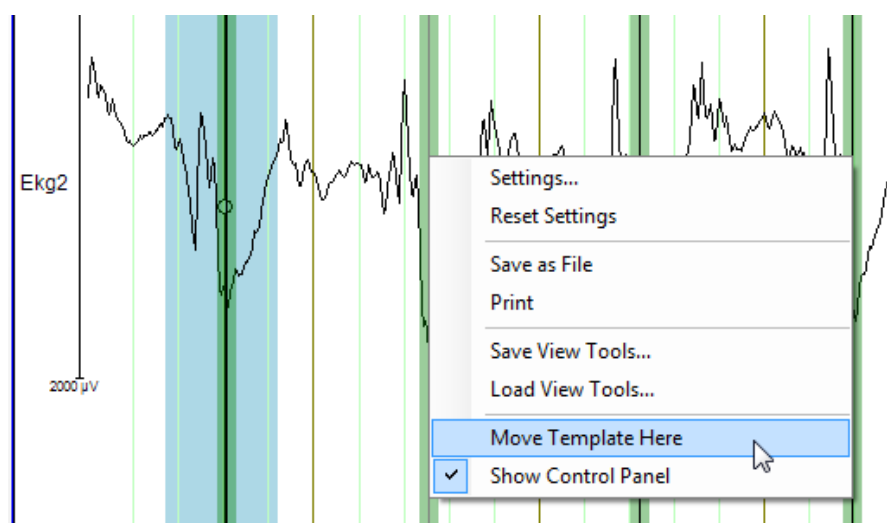


FIGURE 12—148 PULSE TEMPLATE, “MOVE TEMPLATE HERE” FUNCTION

Click the **Recalculate** button to recalculate the markers when the template has been moved.

The **Change Settings and Recalculate** button displays the **Change Settings** dialog box. This dialog box contains the same elements for peak detection as the main **Pulse Detection** dialog box. It also contains the **Use Marked Template** and **Find Another Template** radio buttons.

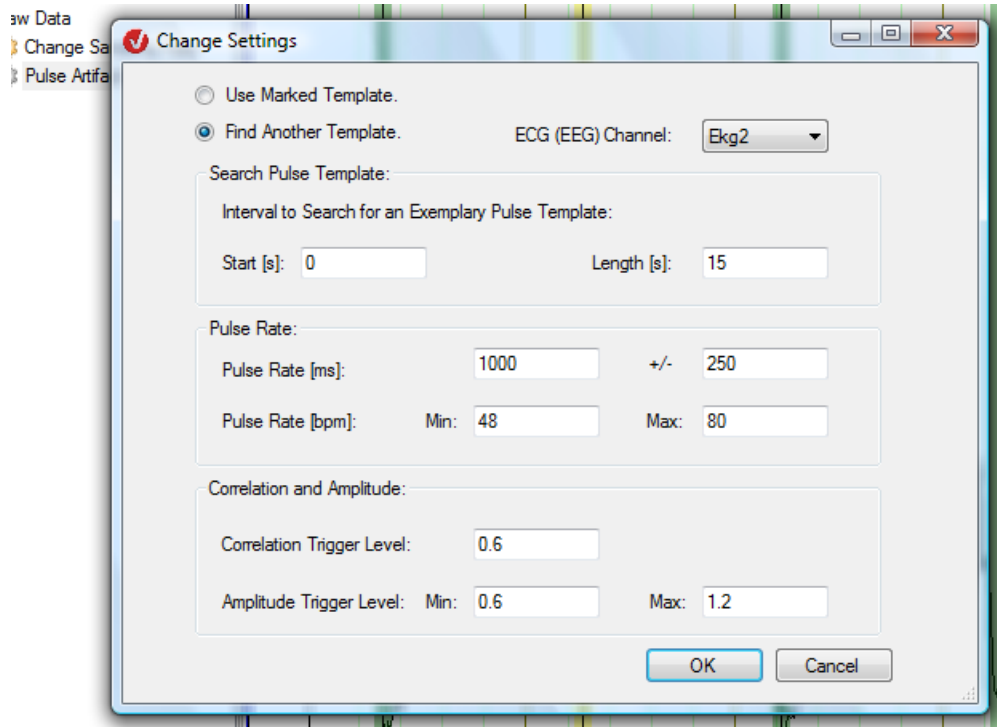


FIGURE 12—149 DIALOG FOR CHANGING THE SETTINGS SUBSEQUENTLY

If you select the **Use Marked Template** radio button, the existing template is used. If you select **Find Another Template**, a new template is obtained.

Click the **OK** button to conclude and apply your settings.

Click the **Finish** button in the temporary semiautomatic view to start artifact correction.

As with MRI scanner artifact correction, the correction of pulse artifacts is based on a template averaging process. Because the pulse beats are extremely variable, only the sliding method can be used successfully. The first step is to reliably detect the ECG episodes in order to determine precisely the time at which the artifacts associated with a heartbeat begin. It is not absolutely essential to determine the R-peak position here; it is enough to obtain a clearly defined, recurring attribute of the ECG recording.

METHOD

It is possible to separate the detection of pulse episodes from pulse artifact correction and, as an initial step, to highlight the pulse attributes. The correction can therefore be based either on the detection method or on markers that already exist in the EEG.

The correlation method compares the ECG curve over time with a template curve in terms of their shape and amplitude and searches for peaks in those sections in which the correlation exceeds a specific threshold.

Because of the great variety of EEG/ECG recordings and situations, it is difficult to apply the parameters used in one case to another case. Semiautomatic mode was introduced to allow suitable parameters to be found and to provide an insight into the detection process.

In order to calculate averages for the pulse artifacts in the EEG channels, the trigger times obtained are transferred from the ECG channel to the EEG channels, taking into account a selectable time delay. The correction is performed over an interval that includes the trigger point. The length of the interval corresponds to the average spacing between R-peaks. To obtain the average pulse curve, corresponding intervals of the preceding and following sections of the EEG are used. Linear trends are calculated before averaging. Sections identified as bad intervals are excluded from the calculation. The correction involves subtracting the calculated average pulse curve from the EEG. This is performed separately for each ECG episode and each channel.

[All98] P.J. Allen et al., Identification of EEG Events in the MR Scanner: The Problem of Pulse Artifact and a Method for Its Subtraction. *Neuroimage* 8 (1998), 229-239. REFERENCES

12.7 Transforms in the Others group

12.7.1 Data Cache

The Data Cache transform allows the data of the parent node to be saved so that it can be accessed more quickly than if it had to be recalculated. SUMMARY

The Data Cache transform always queries the data of the parent node at fixed intervals. Segmented nodes are saved segment by segment. Non-segmented nodes are saved at user-definable intervals.

Whether or not the Data Cache transform can be used effectively depends on the preceding transformations. Some transforms, such as the Average transform or the Fast Fourier transform, always save their data in the history node. Others, such as the MR Correction transform, have parameter options that allow data to be stored temporarily.

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Others > Data Cache**.

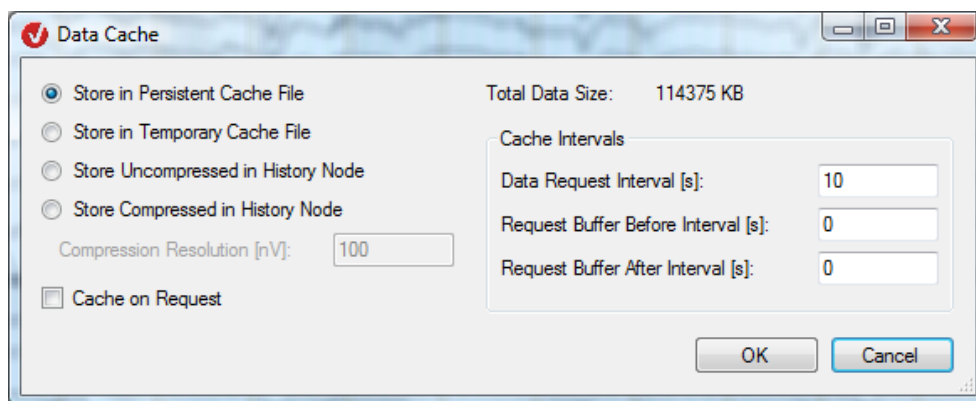


FIGURE 12—150 DATA CACHE DIALOG BOX

The four radio buttons in the dialog box allow you to choose between four different methods of data storage:

- **Store in Persistent Cache File:** The data is stored in a permanent file on the hard disk.
- **Store in Temporary Cache File:** The data is stored in a temporary file on the hard disk.
- **Store Uncompressed in History Node:** The data is stored in the history node uncompressed.
- **Store Compressed in History Node:** The data is compressed and stored in the history node.

In the **Compression Resolution [nV]** text box, you can specify the resolution (precision) of the compression. The resolution for EEG data should be about 100 nV (nanovolts, $1 \mu\text{V} = 1000 \text{ nV}$), i.e. 0.1 μV . A lower value means a higher resolution but less compression.

Note that persistent cache files continue to use storage space on the hard disk until the associated transform node is removed from the cache for deleted nodes by means of the **Purge Deleted Nodes** function.



Note also that when very large quantities of data are stored uncompressed in the history node, this can result in increased access times.



The **Cache Data on Request** check box is only relevant to the first two storage methods. If the check box is selected, the cache is only calculated the first time you request the data. If the check box is cleared, the data is only calculated when you conclude your entries with **OK**.

Regardless of the **Cache Data on Request** check box, the data of the parent node is always requested in segments or the intervals used.

Total Data Size indicates the total volume of the uncompressed data.

The text boxes in the **Cache Intervals** group box are only relevant in the case of non-segmented data:

- **Data Request Interval [s]:** The data is always written to the cache at intervals of n seconds.
- **Request Buffer Before Interval [s]:** The data is also requested from the parent node n seconds before the actual cache interval.
- **Request Buffer After Interval [s]:** The data is also requested from the parent node n seconds after the actual cache interval.

Consequently, the cache consists of several intervals of the length specified in the text boxes in the **Cache Intervals** group box. For each of these intervals, a quantity of data is requested from the parent node that corresponds to the sum of all three values. The request before and after the cache interval is relevant when settling times have to be taken into account, as with IIR filters, for example.

The four data storage methods always respect the above when data is not segmented. Consequently, the cache is always filled with the same data, regardless of the order in which it is structured.

12.7.2 Edit Markers

The Edit Markers transform allows you to set and edit markers.

SUMMARY

No previous processing steps are required before the transform is used.

PROCEDURE

To display the dialog box for the transform, you choose **Transformations > Others > Edit Markers**.

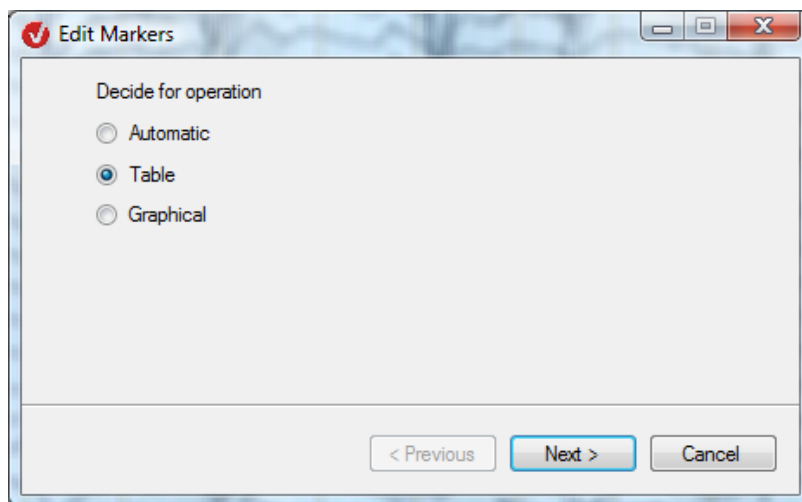


FIGURE 12—151 INITIAL EDIT MARKERS DIALOG BOX

To begin with, you specify the type of marker editing. You can choose from the following modes:

- **Automatic:** This mode is for editing existing, complete marker groups.
- **Table:** In this mode, you can set and edit individual markers. The markers are positioned with pinpoint precision.
- **Graphical:** This mode allows you to set and edit individual markers freely in the EEG.

If you select the **Automatic** radio button, the **Next** button displays the following dialog box:

AUTOMATIC MODE

Marker Type	Marker Description	New Marker Type	New Marker Description	Channel	Time Shift [ms]	Action on Markers
New Segment		New Segment		no change	0	modify

FIGURE 12—152 USER MARKERS DIALOG BOX AFTER YOU SELECT THE AUTOMATIC RADIO BUTTON

Each row in the table represents an editing rule. For each row, all the markers of the data set are selected with a suitable type and description and edited as specified. The rows are processed in the order in which they appear in the table.

The controls in the upper part of the dialog box make it easy to create new rows for the table. Existing rows can be edited directly in the table.

From the **Choose Marker Type** drop-down list, you choose the type of the marker to be changed. The list contains the marker types that exist in the data set. When changes are made, the **New Marker Type** text box is updated. From the **Choose Marker Description** drop-down list, you choose a description for the marker.

If you select the **Delete these Markers?** check box, all markers of the chosen type and with the chosen description are deleted.

The **New Marker Type** and **New Marker Description** text boxes allow you to change the marker type and description. The **Choose Channel** drop-down list allows you to choose the new channel for the markers. If the marker channel is not to be changed, you can select **No Change**.

In the **Time Shift in ms** text box, you specify the value for the time shift of the marker. The relevant marker is moved by this value to the left (negative value) or right (positive value) on the axis.

The **Clear** button deletes all entries and resets the **Choose Channel** function to **All**. The **Add** button adds the new editing rule to the table.

The **Move Row Up** and **Move Row Down** buttons allow you to change the position of the selected row in the table and thus the order of the various processing steps.

The **User Properties** button displays the following dialog box, which contains the user-specific marker properties. These properties apply to a single marker group in each case:

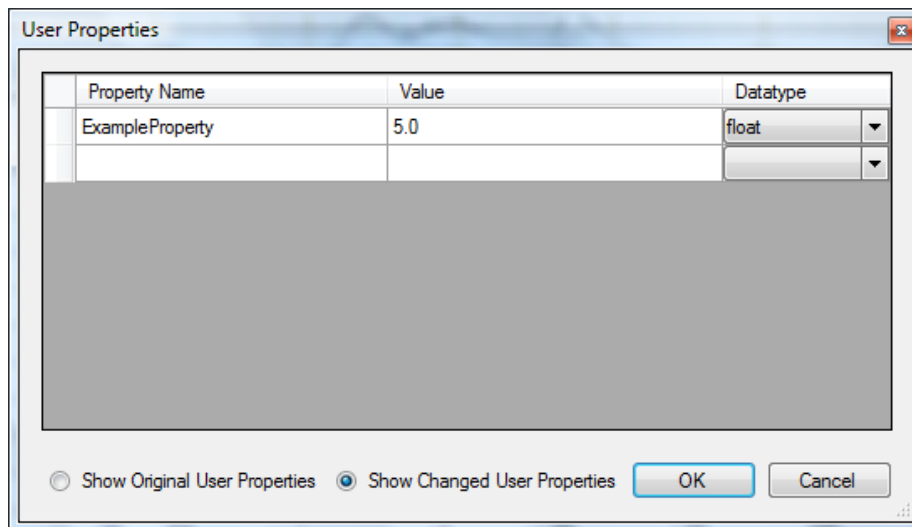


FIGURE 12—153 USER PROPERTIES DIALOG BOX, EDIT MARKERS TRANSFORM

In the **Property Name** cell, enter the name of the property. You can make any entry here. The **Value** cell contains the associated value. This value is assigned a programming data type that you choose from the drop-down list in the **Datatype** column.

The **Show Original User Properties** and **Show Changed User Properties** radio buttons allow you to specify whether the original user properties or the user properties you have edited are to be displayed.

You can delete existing user properties by selecting the row in the grid in the view of the changed user properties and pressing the **<Delete>** key to delete it. The row turns red, and the data type **NULL** appears in the **Datatype** column. Alternatively, you can specify the data type by choosing **NULL** from the drop-down list. To undo this deletion, you can set one of the other data types for the row at any time.

If you select the **Table** radio button, the Next button displays the following dialog box:

MANUAL MODE

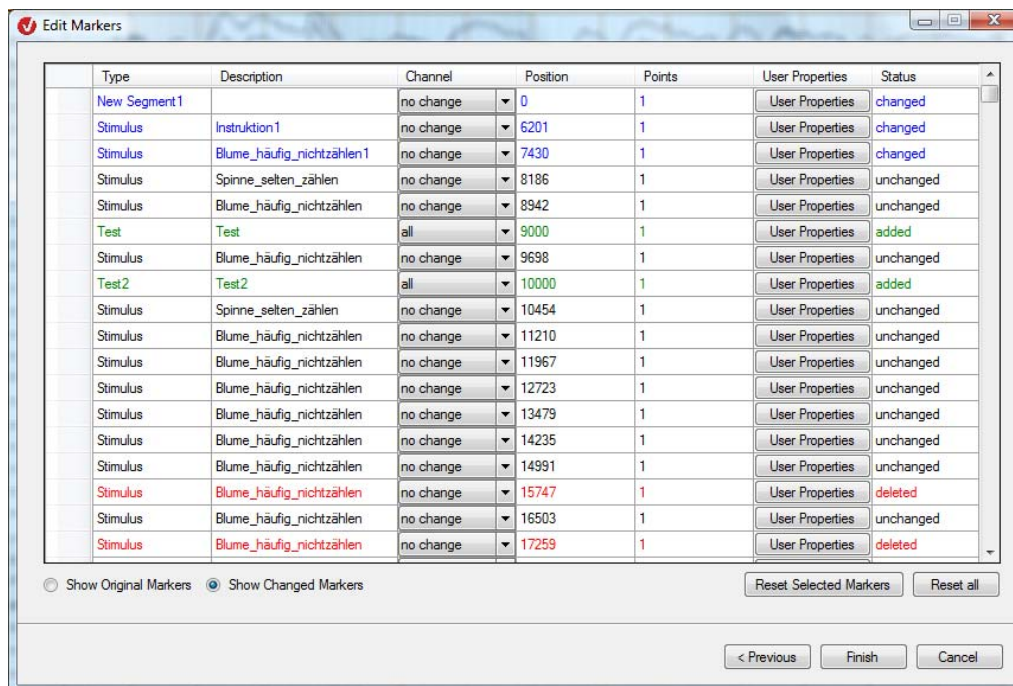


FIGURE 12—154 EDIT MARKERS DIALOG BOX AFTER YOU SELECT THE TABLE RADIO BUTTON

The table contains the type (**Type** column), the description (**Description** column), the associated channel(s) (**Channel** column), the marker position in ms (**Position** column), the line width of the marker (**Points** column), the user-specific properties (**User Properties** column) and the marker status (**Status**) for the markers set in the EEG.

A marker can have the following statuses: **unchanged**, **changed**, **deleted** and **added**. The **Status** column is updated automatically. The statuses have the following color codes:

- Unchanged markers: black
- Changed markers: blue
- Added markers: green
- Deleted markers: red

You change the entries in the **Type**, **Description**, **Position** and **Points** cells by double-clicking the cell. You select a channel from the drop-down list in the **Channel** column. You delete a column from the table by pressing the **<Delete>** key.

If you select the **Show Original Markers** radio button, the status of the markers in the original data set is displayed. If you select the **Show Changed Markers** radio button, the changed markers are displayed in the color coding corresponding to the changes made.

If you click the **Reset Selected Markers** button, the selected markers are reset to their original status. The **Reset All** button resets all markers to their original status.

The **User Properties** button displays a dialog box containing the user-specific marker properties. These properties apply to a single marker. This dialog box is the same as the **User Properties** dialog box in automatic mode.

If you select the **Graphical** radio button, the **Next** button displays a data window in interactive mode. The window contains a temporary Semiautomatic View dialog box that helps you with marker editing.

GRAPHICAL MODE

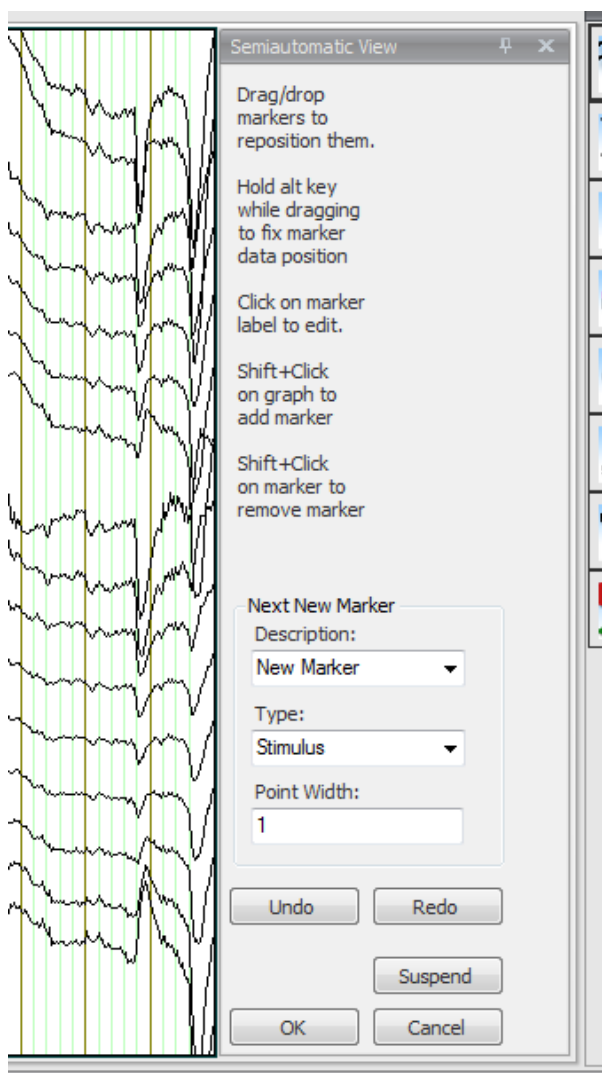


FIGURE 12—155 PART OF AN EEG WITH THE TEMPORARY SEMIAUTOMATIC VIEW DIALOG BOX AFTER SELECTING THE GRAPHICAL RADIO BUTTON

A marker must be active before you can edit it. If it is, the marker label is framed by a gray box. In the case of a marker with multiple points, the box appears as soon as you position the mouse pointer on the marker. In the case of a marker with only one point, the box appears when you position the mouse pointer on the marker label.

Shift+Click on Graph to add marker function:

You set a marker by holding down the **Shift** key and clicking in the graph. You can set the properties of the new marker using the controls under **Next New Marker**. This is useful when you want to create a number of markers of the same type. By means of a single mouse click you create a marker of the width specified in the **Point Width** text box. If you want to set a marker with a different number of points, hold the mouse button down and drag the mouse pointer to the left or right over the graph.

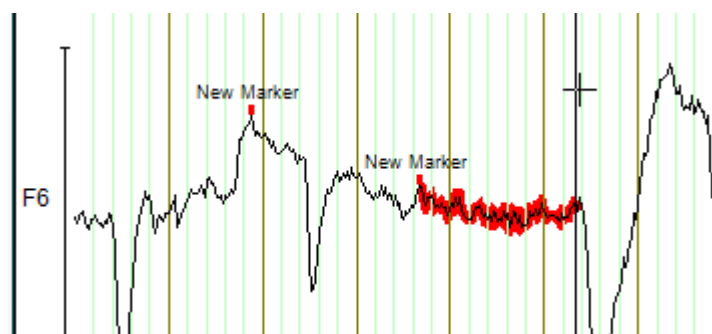


FIGURE 12—156 MARKERS WITH MORE THAN ONE POINT

Drag/drop markers to reposition them and Hold alt key while dragging to fix marker data position functions:

You change the position of a marker by clicking the marker, holding down the mouse button and dragging the marker to the desired position. The graph on which you are positioning the active marker changes color from black to orange.

You can place a marker on a graph, in a channel or in the margin along the bottom of the screen for all channels in the area of the marker. If you hold down the **Alt** key when dragging, the marker is placed on the new channel but remains on the same data point.

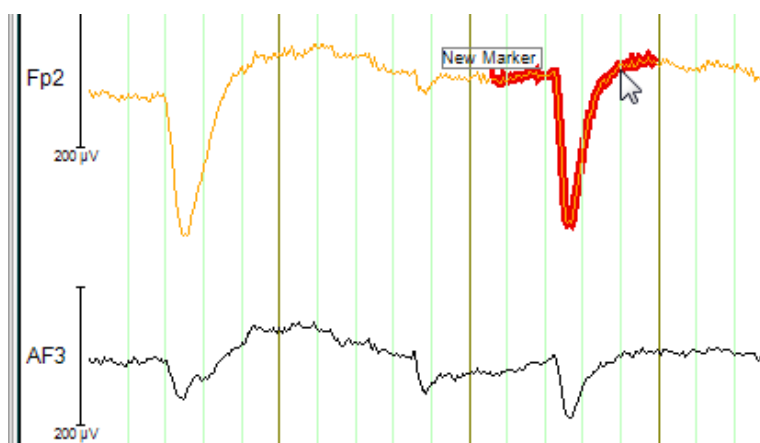


FIGURE 12—157 CHANGING THE POSITION OF A MARKER

Markers with multiple points have a positioning handle at each end with which you can change the size of the marker. The positioning handle becomes visible when you move the mouse pointer near the end of the marker.

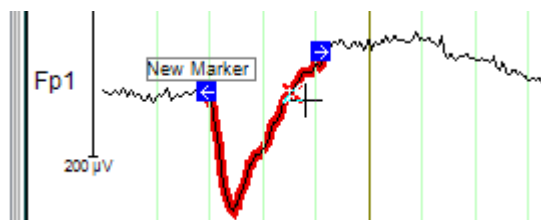


FIGURE 12—158 MARKER WITH POSITIONING HANDLES

Markers that apply to all channels and range highlighting can be resized in a similar way.



FIGURE 12—159 POSITIONING HANDLES OF A MARKER FOR ALL CHANNELS AND RANGE HIGHLIGHTING

Click on Marker Label to Edit function:

To edit a marker, click the marker or its label. A dialog box appears, in which you can change the marker's description (in the **Description** text box), type (in the **Type** drop-down list box) and width (in the **Point Width** text box).

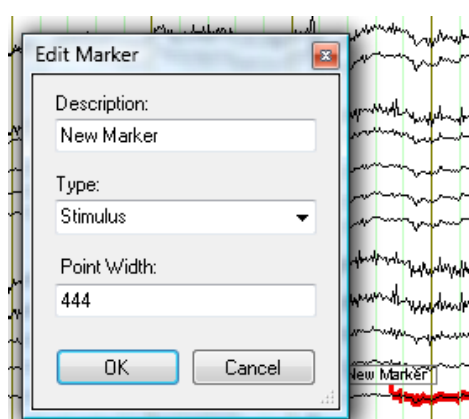


FIGURE 12—160 DIALOG BOX FOR EDITING MARKERS IN GRAPHICAL MODE

Shift+Click on Marker to Remove Marker function:

To delete a marker, press the **Shift** key and click the marker or its label.

The controls in the **Next New Marker** group box set the properties of the next marker created with **⌘Shift** plus a mouse click. From the **Description** and **Type** drop-down list boxes, you can either choose a description or type from those already in the data set or enter a new text. In the **Point Width** text box, you specify the length of the marker in data points.

The **Undo** and **Redo** buttons in the lower part of the temporary semiautomatic view dialog box allow you to reverse and restore the changes.

If you want to interrupt your editing of the markers and resume later, you click the **Suspend** button. The Edit Markers transform is highlighted in red in the list of history nodes, and all the processing steps carried out continue to apply until you open the node again with a double-click. No transforms or anything else can be applied to the interrupted node.

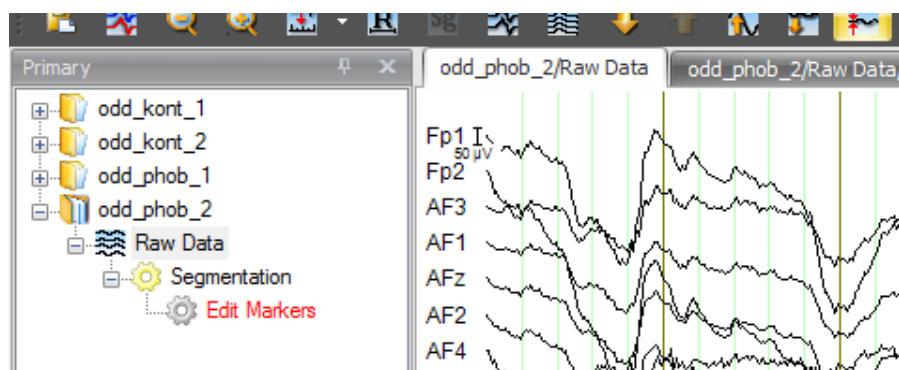


FIGURE 12—161 INTERRUPTED MARKER EDITING

If you click the **Cancel** button, interactive mode is terminated and the operations performed are not saved.

12.7.3 MATLAB®

The software package MATLAB® from MathWorks has become established in the scientific world for a variety of reasons. Its numerous libraries for signal processing and visualization, some of which are available free, have made MATLAB® a valuable tool in the field of brain research as well. Of all the libraries that are available in this field of application, the EEGLab package has made a particular name for itself.

SUMMARY

MATLAB® and the Analyzer have different strengths in terms of functionality and user guidance, so they complement each other ideally. The MATLAB® transform allows data to be exported from the Analyzer to MATLAB®, processed there and then imported back into the Analyzer. In this way, MATLAB® processing methods are integrated in the Analyzer, in a similar way to macros, and can also be used in history templates.

In order to use the transform, you must have a valid license for MATLAB® Version 7.4 or higher installed on your computer. This is not shipped with BrainVision Analyzer; you have to purchase the license directly from MathWorks. Simply installing a MATLAB® runtime environment does not allow you to run the MATLAB® transform.

PREREQUISITE FOR USE

The transforms of the Analyzer can essentially be subdivided into two categories:

PRELIMINARY REMARKS

There are transforms that calculate and store their data when the history node is created, and there are transforms that first create a history node and do not calculate the data and make it available until requested to do so by views or subsequent transforms. The transforms of the first category include the Average transform and the Fast Fourier transform (FFT). The data calculated by these transforms differs so fundamentally in its structure from the original data that it makes sense to calculate it fully and store it each time the transform is called.

The transforms belonging to the second category include filtering transforms and the RMS transform. A section of these transforms can be calculated using sections of the original data set. The original data sets that use these transforms are generally of the same order of magnitude as raw data. Calculating and storing all of this data would be very heavy on resources, which is why calculation on request makes more sense.

The MATLAB® transform supports both procedures. This means you can select the most suitable option, depending on the original data and the scope of the required calculation in MATLAB®.

To display the dialog box for the transform, you choose **Transformations > Others > Matlab**.

PROCEDURE

Depending on whether you want to calculate the data when the node is created or on request (see the preliminary remarks), select the **Calculate Data on Creation of Node** or **Calculate Data on Request** radio button. The appearance of the dialog box differs depending on which radio button you select:

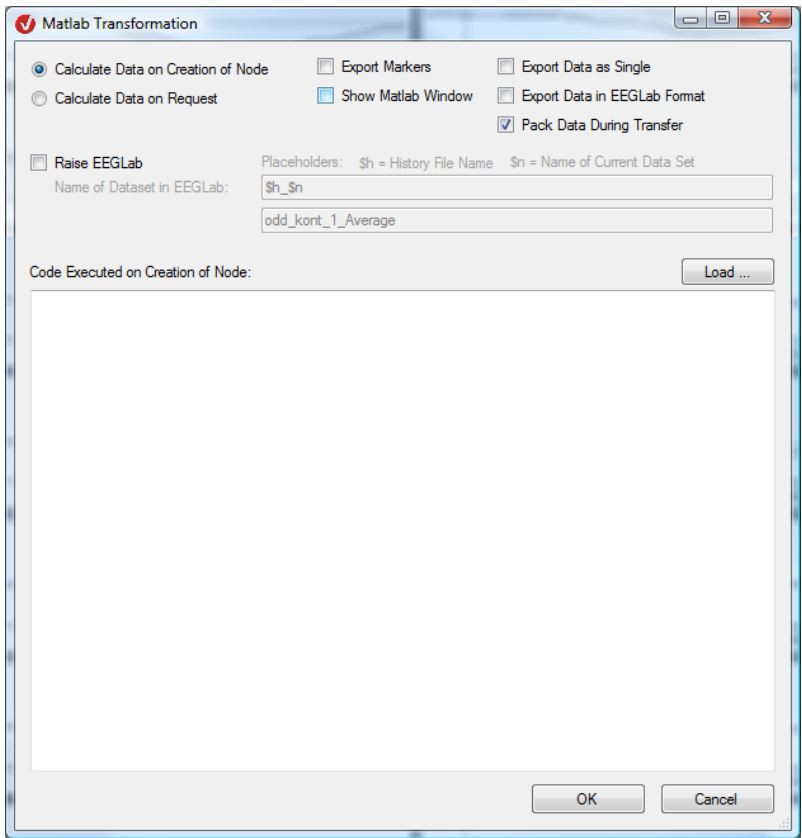


FIGURE 12—162 MATLAB® DIALOG BOX WITH THE CALCULATE DATA ON CREATION OF NODE RADIO BUTTON SELECTED

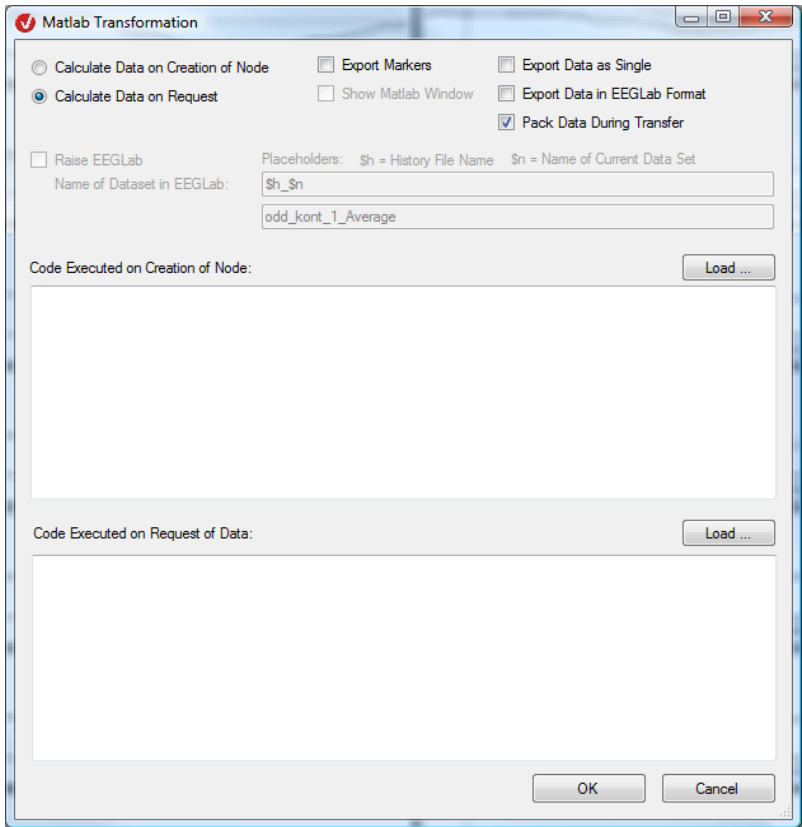


FIGURE 12—163 MATLAB® DIALOG BOX WITH THE CALCULATE DATA ON REQUEST RADIO BUTTON SELECTED

If you select the **Calculate Data on Creation of Node** radio button, a large text box appears in which you can enter the MATLAB® code to be processed. Enter all the code required to process the EEG data, change properties and create new markers in the **Code Executed on Creation of Node** text box.

If you select the **Calculate Data on Request** radio button, two text boxes appear for MATLAB® code. In the first of these text boxes, you enter all the MATLAB® commands that you want to be executed when the node is created. These will generally involve changes to the EEG properties or the creation of new markers. Note that if you select this radio button, for performance reasons no EEG data is made available to you at this stage. The EEG data is not transferred to MATLAB® until requested by subsequent transforms or views. In the lower text box, you enter the code for the processing of this data.

You will find examples of the use of these two radio buttons at the end of the chapter.



Data can be exported to MATLAB® in two different formats: a simple matrix format or the EEGLab format.

To select the EEGLab format, select the **Export Data in EEGLab Format** check box. The EEGLab format is adequately documented so it is not necessary to provide a description of it here.

The matrix format of the data, which you get when you do not select the check box, has the following structure:

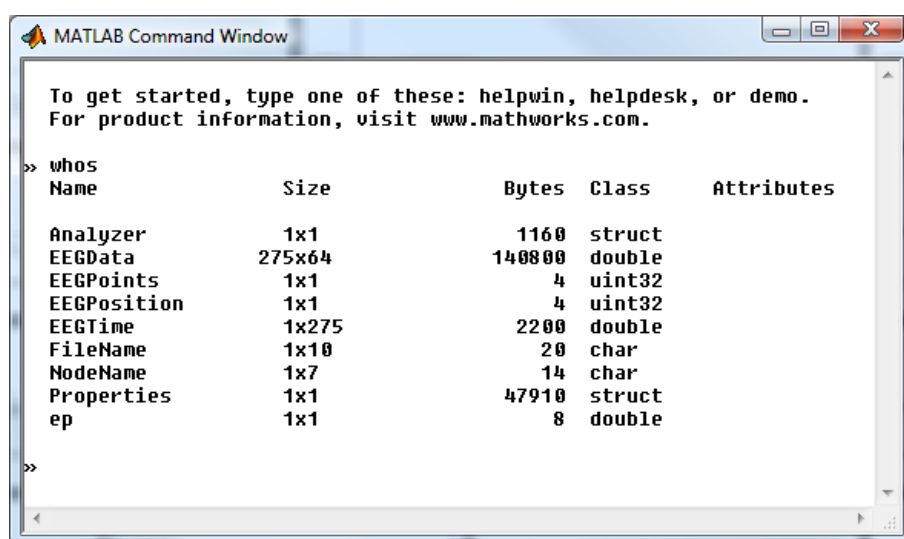
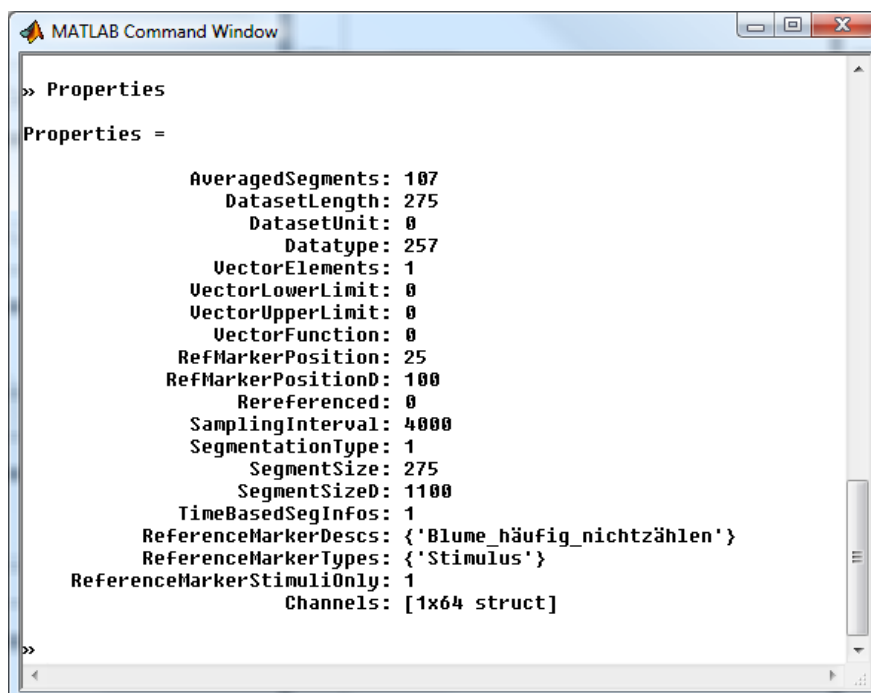


FIGURE 12—164 DATA IN SIMPLE MATRIX FORMAT

The exported EEG data is stored in a MATLAB® matrix with the name EEGData. The data points correspond to the rows of the matrix, and the channels correspond to the columns. In the case of segmented data, the matrix has an additional dimension that corresponds to the individual segments. This format is ideal for further processing by the signal processing and data visualization commands (filter, plot, etc.) contained in MATLAB®. The EEG properties are contained in the MATLAB® Properties variable.



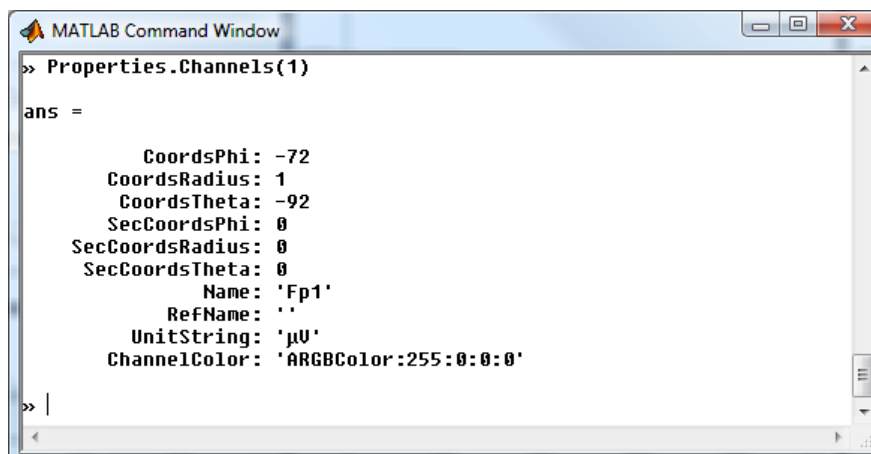
```

>> Properties
Properties =
    AveragedSegments: 107
    DatasetLength: 275
    DatasetUnit: 0
    Datatype: 257
    VectorElements: 1
    VectorLowerLimit: 0
    VectorUpperLimit: 0
    VectorFunction: 0
    RefMarkerPosition: 25
    RefMarkerPositionD: 100
    Rereferenced: 0
    SamplingInterval: 4000
    SegmentationType: 1
    SegmentSize: 275
    SegmentSizeD: 1100
    TimeBasedSegInfos: 1
    ReferenceMarkerDescs: {'Blume_häufig_nichtzählen'}
    ReferenceMarkerTypes: {'Stimulus'}
    ReferenceMarkerStimuliOnly: 1
    Channels: [1x64 struct]
>>

```

FIGURE 12—165 PROPERTIES VARIABLE

This is a variable of the type struct, in which the individual properties can be accessed by means of their names. This also applies to any user properties in the data set. The individual properties are stored in MATLAB® according to their type. The channel properties, for example, can be accessed via the field of structs called Channels.



```

>> Properties.Channels(1)
ans =
    CoordsPhi: -72
    CoordsRadius: 1
    CoordsTheta: -92
    SecCoordsPhi: 0
    SecCoordsRadius: 0
    SecCoordsTheta: 0
    Name: 'Fp1'
    RefName: ''
    UnitString: 'µV'
    ChannelColor: 'ARGBColor:255:0:0:0'
>> |

```

FIGURE 12—166 CHANNEL PROPERTIES

It is similar with the markers. By default, these are not exported to MATLAB® because this could involve the export of large volumes of data. To export markers to MATLAB®, you have to select the **Export Markers** check box explicitly in the dialog box. A variable called Markers then becomes available to you in MATLAB®. This is a field of structs. As with the properties, these structs provide access to the individual marker properties.

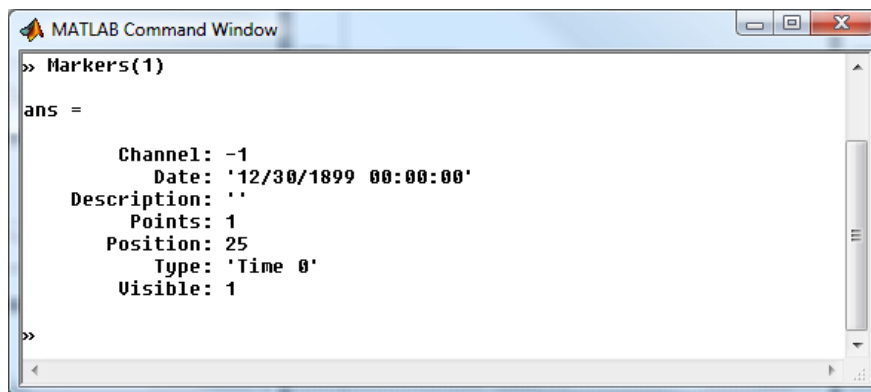


FIGURE 12—167 MARKERS VARIABLE

The EEGPosition and EEGPoints variables specify the position and length of the EEG data in the overall data set. They are relevant primarily when the EEG data is processed on request. Otherwise, the position is 1 and the length is the length of the original data set.

The FileName variable specifies the name of the history file, and the NodeName variable specifies the name of the history node. The Analyzer variable contains information about the Analyzer. You can also use these variables in template mode to program flexible behavior in MATLAB® scripts.

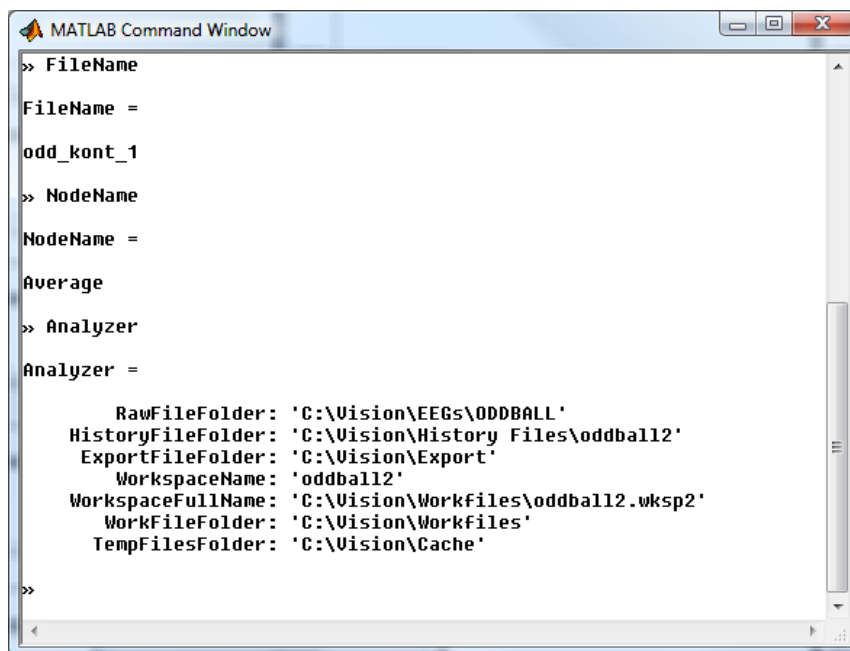


FIGURE 12—168 VARIABLES WITH INFORMATION ON THE NODE AND THE ANALYZER ENVIRONMENT

The EEGTime variable, which is exported together with segmented data, contains a time vector of the EEG data set. This can be used, for example, in the plot function for drawing the time axis.

The data is imported into the Analyzer again from the variables described above. In other words, changes in Properties and EEGData are imported back into the Analyzer as changes. The current status of the transform does not allow changes to be made in the markers. However, you can create new markers by creating a variable in MATLAB® called NewMarkers that has a similar structure to the Markers variable.

In addition to the options described above, you can also make the following settings in the dialog box:

Export Data as Single: To save storage space when there are large volumes of data, the EEG data is stored as floating-point numbers with single precision.

Pack Data During Transfer: When large volumes of data are transferred to MATLAB®, storage bottlenecks can occur there because MATLAB® loads matrices in contiguous portions of main memory. If you select this check box, a pack command is called in MATLAB® at regular intervals during the transfer of data in order to enlarge the contiguous portion of main memory. If you do not transfer large volumes of data, we recommend that, in order to obtain better performance, you do not select this check box.

Show Matlab Window: This setting opens a MATLAB® command window following data export. Processing is suspended in the Analyzer, and the following message window appears.

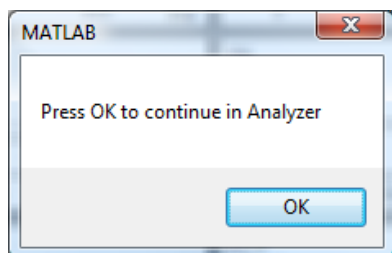


FIGURE 12—169 MESSAGE WINDOW

You can then execute commands interactively in MATLAB® and examine and edit data. Note that these commands entered interactively are not returned to the Analyzer. They are thus not suitable for History Template mode. However, interactive mode is ideal for familiarizing yourself with the data in MATLAB® and compiling commands that you can enter in the MATLAB® command field when the MATLAB® transform is called subsequently.

When you click **OK** in the message window, the Analyzer resumes processing, imports the data from MATLAB® and writes it to the history node created.

The procedure is similar for **Raise EEGLab**. In this case, the interactive user interface of EEGLab appears in addition to the MATLAB® command window. The package must be installed on your computer, and the paths must be registered with MATLAB®. If you select the **Raise EEGLab** check box, you can specify the name of the data set in EEGLab. You can use the placeholders \$h and \$n for this, as elsewhere in the Analyzer.

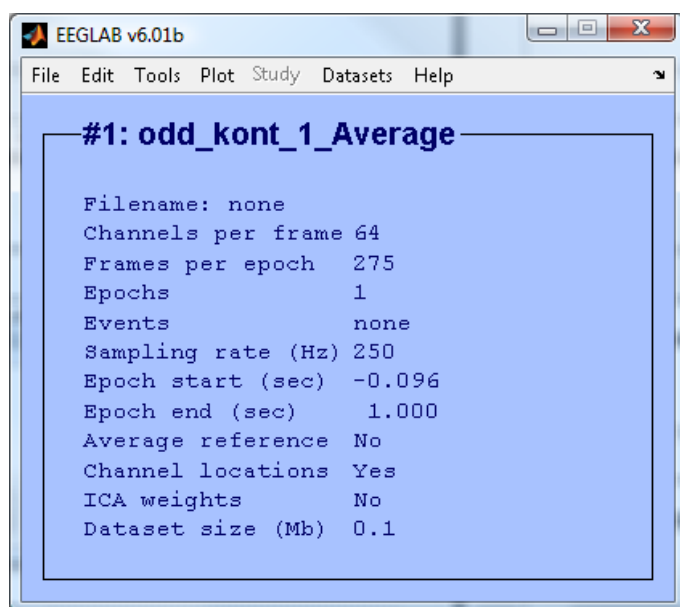


FIGURE 12—170 INTERACTIVE EEGLAB USER INTERFACE

Note that it only makes sense to select the **Show Matlab Window** and **Raise EEGLab** check boxes for working interactively with MATLAB®/EEGLab if the data is calculated and stored when the history node is created.

In the operation information of the Analyzer, you will find, in addition to the parameters that are set, including the MATLAB® code, the contents of a variable called Description, which you can define and to which you can assign values in MATLAB®. In this way, it is possible to transfer information from the calculation in MATLAB® to the operation information of the Analyzer.

The functionality of the MATLAB® transform is illustrated below using two examples.

EXAMPLES

Example 1: Simple plot with MATLAB®

In this example, the plot function of MATLAB® is used to display the EEG data. The exported matrix already has the appropriate format for this.

For this example, select a node with a short data set (an Average data set, for example). The example does, of course, work with longer data sets, but that requires more resources.

Select **Calculate Data on Creation of Node** and **Show Matlab Window**. In the code text box, enter the following command:

```
plot(EEGTime, EEGData);
```

Then run the transform by clicking the **OK** button.

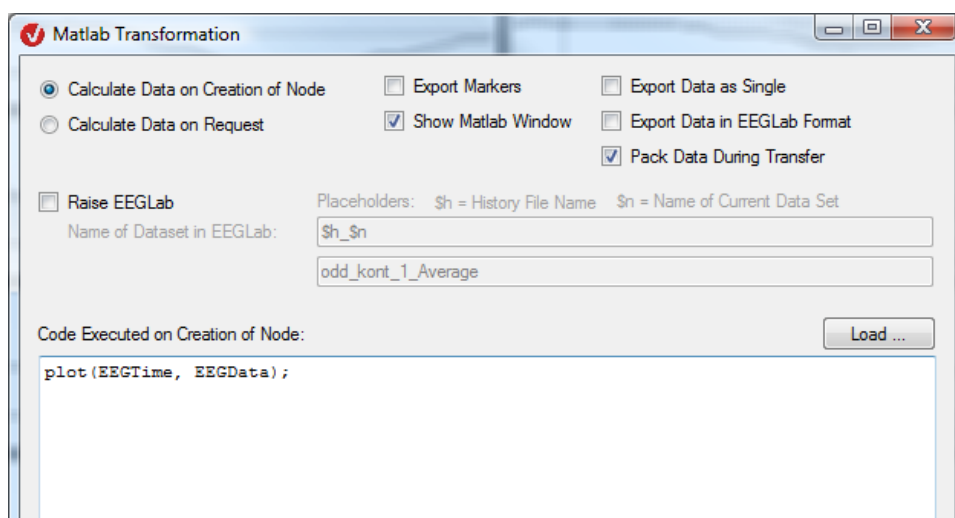


FIGURE 12—171 EXAMPLE: SIMPLE PLOT 1

MATLAB® is called, and an additional window opens. This contains a MATLAB® plot of the EEG data.

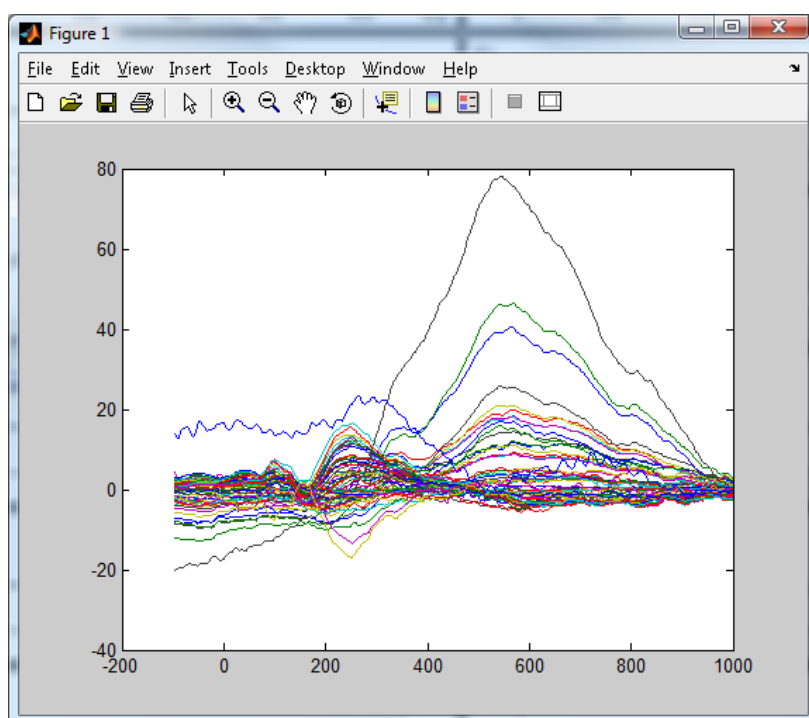


FIGURE 12—172 MATLAB® PLOT OF THE EEG DATA

When you click **OK** in the message window, MATLAB® is closed again and a new node is created that contains the data of the original node because, apart from the plotting of the data in MATLAB®, no further operations have been executed.

If you want to navigate through the MATLAB® plots using the Analyzer navigation function, specify that the graph is to be created on request. For this example you can use a larger data set (a raw data set, for example).

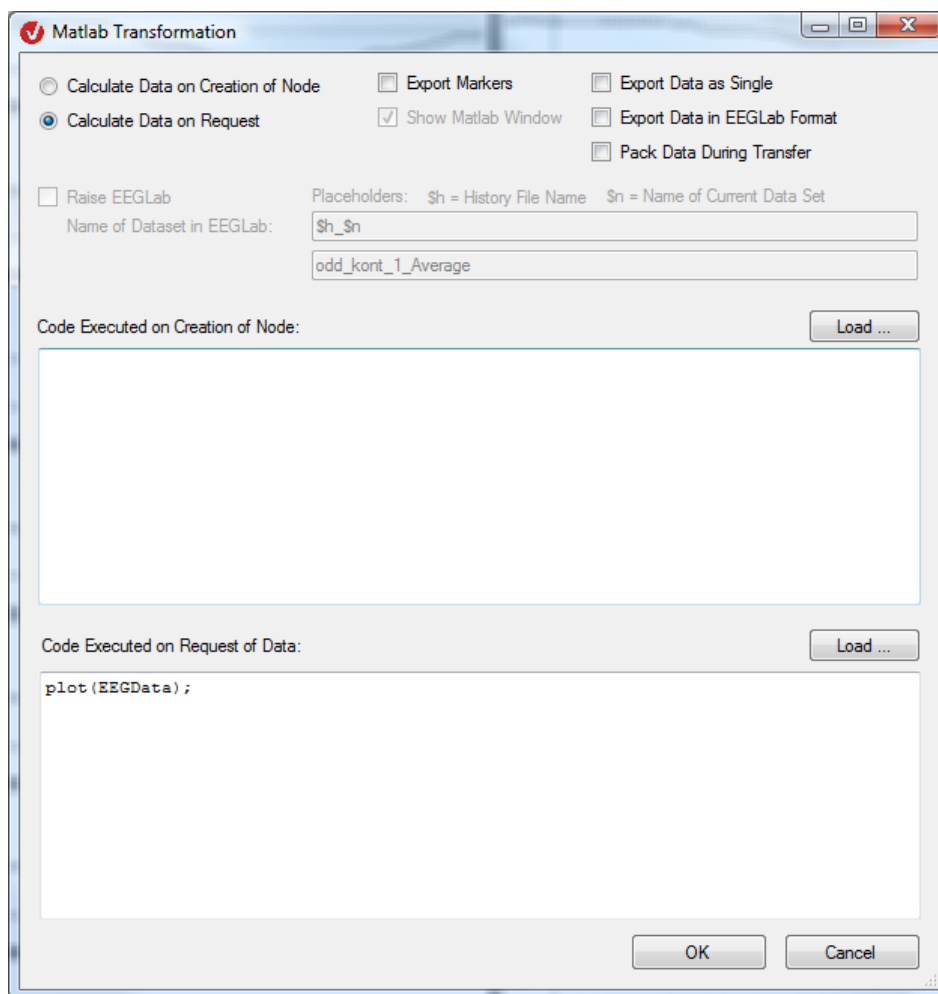


FIGURE 12—173 EXAMPLE: SIMPLE PLOT 2

A new node appears in the Analyzer that displays the same data as the original data set. In this case, no data is stored additionally in the history node. In addition, a MATLAB® plot window appears whose display changes when you navigate in the Analyzer.

Example 2: FIR filter with MATLAB®

MATLAB® offers comprehensive signal processing methods. For example, you can use two commands to create an average FIR filter. Because this kind of filter tends to be used on raw data, the **Calculate Data on Request** radio button is provided:

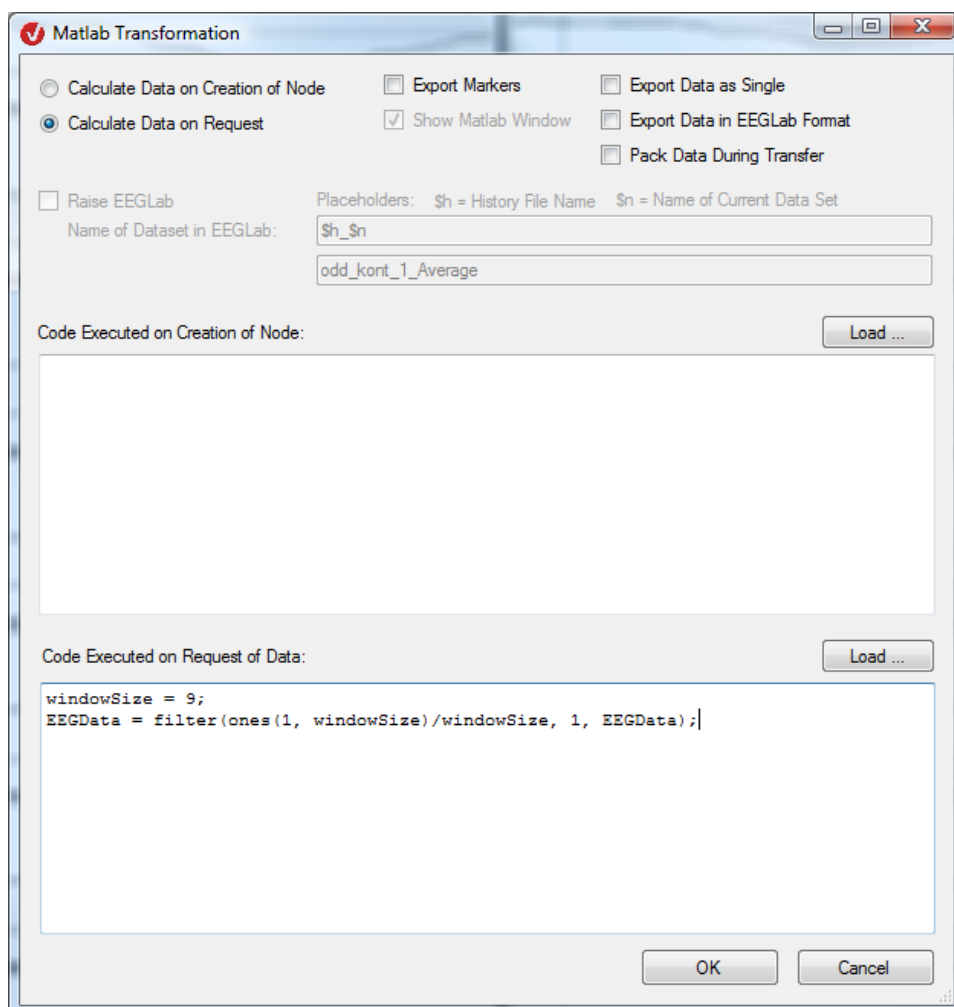


FIGURE 12—174 EXAMPLE OF THE CREATION OF AN FIR FILTER

In this case, an FIR filter with a length of 9 is created with constant filter coefficients of $1/9$. If necessary, you can use the MATLAB® functions to define more complex FIR filters.

When you execute the MATLAB® transform with the above parameters, you get a new history node that makes the filtered data available on request with the help of MATLAB®. Compare the data with the raw data in the Analyzer using the overlay function, and try navigating through the data set. Try the transform out in a history template as well.

12.7.4 Topographic Interpolation

The Topographic Interpolation transform allows virtual EEG channel values to be obtained on the basis of real existing values. The background to topographic interpolation is the spatial distribution of the electrodes on the surface of the head. The purpose is to establish the comparability of the EEG data with external data.

SUMMARY

The Topographic Interpolation transform is used in two cases:

It is used when the channels of two different EEGs are to be compared, but the EEGs differ in their channel configuration. Additional, virtual channels are created for the EEG that correspond to those of the data set to be compared.

The transform is also used when an error-ridden or defective channel has to be replaced (for example, because of excessive noise or a failed electrode during recording of the EEG). In this case, the Edit Channel function is used first to remove the affected channel from the data set. In a second step, the corresponding value is calculated by means of topographic interpolation. The virtual channel that has been calculated is then added to the EEG data set.

Note that the EEG data set must have at least four channels with coordinates.

PREREQUISITE FOR USE

To display the dialog box for the transform, you choose **Transformations > Others > Topographic Interpolation**.

PROCEDURE

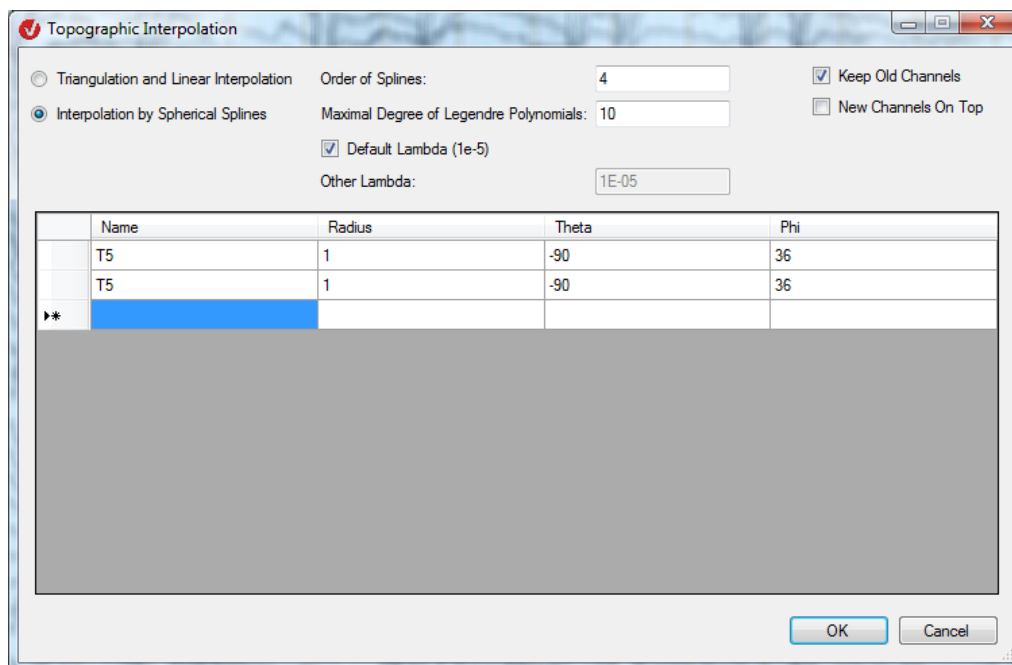


FIGURE 12—175 TOPOGRAPHIC INTERPOLATION DIALOG BOX

In the **Topographic Interpolation** dialog box, you specify whether the data is to be calculated by triangulation and linear interpolation (**Triangulation and Linear Interpolation** radio button) or interpolation with splines (**Interpolation by Spherical Splines** radio button).

If you decide on interpolation with splines, you enter the spline order in the **Order of Splines** text box and the maximum degree of the Legendre polynomial in the **Max. Degree of Legendre Polynomials** text box.

If you select the **Default Lambda** check box, the default value of 10^{-5} (1e-5) is automatically accepted. If you clear the check box, you can enter a different value.

We recommend that you enter a value of 10 in the **Max. Degree of Legendre Polynomials** text box and a value of 10^{-5} (1e-5) in the **Lambda** text box.



If you clear the **Keep Old Channels** check box, the output data set contains only the interpolated channels. If you select it, the data set contains both the old and new channels.

The **New Channels On Top** check box allows you to specify whether new channels are added at the beginning or end of the list of channels. This setting is only relevant if you have selected the **Keep Old Channels** check box.

In the table, you enter the name (in the **Name** column), Radius (in the **Radius** column) and coordinates (in the **Theta** and **Phi** columns) of the channel created by interpolation.

Please note the following special rule: If you enter a channel name of a channel that already exists in the EEG, this channel is no longer included in the output data set. (However, this is only relevant if you have selected the **Keep Old Channels** check box.) The original channel is always used in interpolation, regardless of the special rule.

Note that it is not possible to enter one and the same channel name in the table. You receive an error message if you do this.



Two different interpolation methods are used: triangulation and linear interpolation and interpolation by spherical splines. In triangulation and linear interpolation (**Triangulation and Linear Interpolation** radio button), the surface of the head is triangulated (divided up into triangles), and the values are calculated for each triangle by means of linear interpolation.

ADDITIONAL
INFORMATION

Interpolation by spherical splines (**Interpolation by Spherical Splines** radio button) consists of a set of basic spline functions. The form of the basic functions is influenced by the **Order of Spline** parameter. The spherical splines are calculated by means of an approximation method. The degree of accuracy of the result of the calculation depends on the Maximum Degree of Legendre Polynomials and Lambda parameters. We recommend that you enter a value of 10 in the **Max. Degree of Legendre Polynomials** text box and a value of 10^{-5} (1e-5) in the **Lambda** text box. Experience has shown that these values lead to satisfactory results. Because they are used so frequently, the results are also comparable. If you select the **Default Lambda** check box, the default value of 10^{-5} (1e-5) is automatically applied. If you clear the check box, you can enter a different value. We recommend that you only do this if you know that the value you enter will meet your requirements.

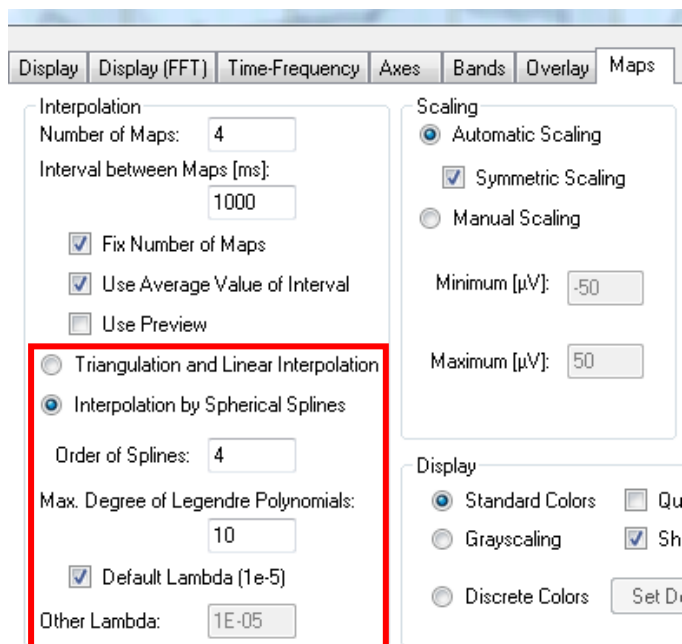


FIGURE 12—176 SELECTING THE INTERPOLATION METHOD ON THE MAPS TAB OF THE DEFAULT VIEW SETTINGS DIALOG BOX

[Pergo] F. Perrin et al., Spherical splines for scalp potential and current density mapping. *Electroencephalography and clinical Neurophysiology*, 72 (1990), 184-187, together with the correction in *Electroencephalography and clinical Neurophysiology*, 76 (1990), 565.

REFERENCES

13 Add-ins

13.1 Marker Navigation

The Marker Navigation add-in allows you to navigate to selected markers.

To display the add-in, you choose **Add Ins > Tools > Marker Navigation**. A dockable window opens in the upper part of the view.

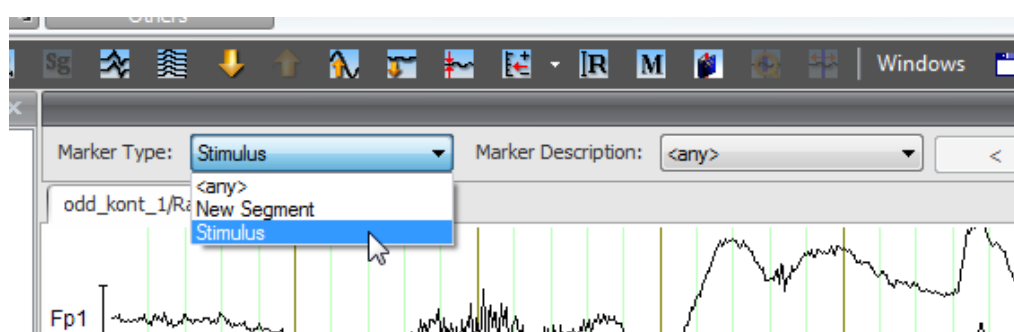




FIGURE 13—1 MARKER NAVIGATION INTERFACE ELEMENT

The **Marker Type** and **Marker Description** drop-down list boxes contain all the marker types and marker descriptions in the associated data set. You can use the drop-down list boxes to navigate to specific markers. To navigate to any type or any description, choose **<any>** from the corresponding drop-down list box.

The buttons  and  allow you to navigate to the next or previous marker that meets the criteria chosen from the **Marker Type** and **Marker Description** drop-down list boxes. If the data set does not contain a combination of marker type and description, the buttons are inaccessible.

If you navigate to a marker in this way, the marker appears in the middle of the part of the EEG that is displayed. The marker appears in green in the marker window.

Note that the Marker Navigation add-in does not change the channel display. In other words, markers may not be visible in the channels.



If you have multiple data sets open, navigation is carried out separately for each data set, and that includes the selection of the marker type and description.

13.2 Analyzer Video

The Analyzer Video add-in is for playing video data and EEG data synchronously.

The prerequisite for the operation of the plug-in is that Codec must be installed. You will find Codec and notes on its installation on the BrainVision CD.

Open an EEG data set containing a video sequence, and call the add-in by choosing **Add Ins > Plug In > Analyzer Video**. A dockable video window opens in the upper part of the view.

The video view is possible for both raw data and derived history nodes (transforms).



FIGURE 13—2 COMBINED EEG/VIDEO PLAYBACK

The date and time of the video recording are displayed at the top of the window.

The video window contains the buttons **Play**, **Pause** and **Stop**. The **Sync. EEG** button allows you to synchronize the EEG manually with the current video position.

The transparent bright blue highlighting indicates the position in the EEG. If you activate the marker by clicking the data displayed, the context menu allowing you to select transforms does not appear. To display this menu, you then have to right-click the data.

If you select the **Video is Master** check box, the navigation in the EEG follows the navigation in the video. In other words, if you change the position of the slider for the video, the slider for the EEG jumps to the corresponding position in the EEG view.

If you select the **EEG is Master** check box, the navigation in the video follows the navigation in the EEG. In other words, if you change the position of the slider for the EEG, the slider for the video jumps to the corresponding position in the video.

If both check boxes are selected, navigation in the EEG and video is fully synchronized.

13.3 Generic Data Header

The Generic Data Header add-in allows you to generate header files for the Generic Data Reader (GDR).

To call the add-in, you choose **Add Ins > Others > Generic Data Header**.

The Select Data File dialog box appears, in which you can select a file containing EEG data. The **Generic Data Header** dialog box then appears.

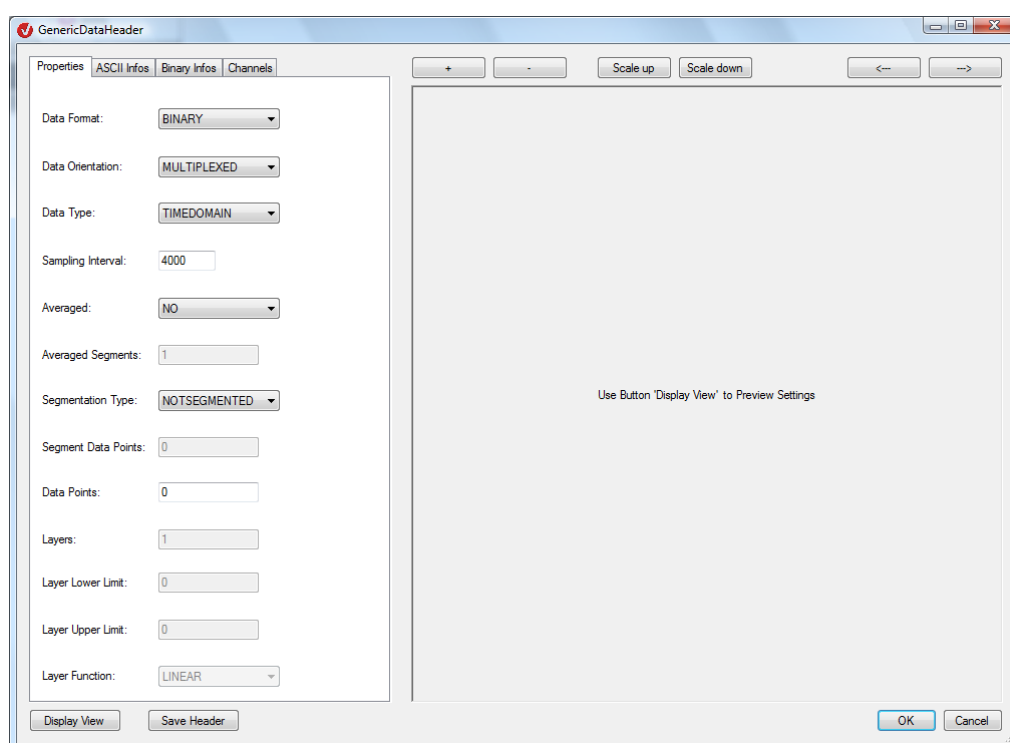


FIGURE 13—3 GENERIC DATA HEADER DIALOG BOX

The dialog box allows you to make entries for the .vhdr file to be created. On the various tabs (**Properties**, **ASCII Infos**, **Binary Infos** and **Channels**), you can make appropriate entries for your EEG. You will find detailed information on the settings in section 16.1.2, “Generic Data Reader”.

On the **Channels** tab, you can specify the number of channels in the EEG in the **Number of Channels** text box. Click **Refresh** to add new rows to the table or delete rows from the table.

You can also rename the channels in the table, among other things. However, we recommend that you find out how many channels there are before you start renaming them.

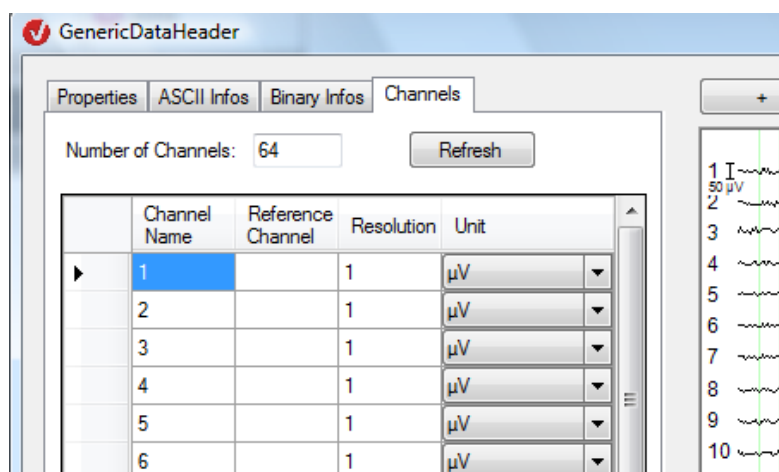


FIGURE 13—4 RENAMING CHANNELS

The **Save Header** button saves your entries and creates the .vhdr file. Once the header file has been created, you can display the data on the right-hand side of the dialog box by clicking **Display View**. The label on the button then changes to **Update View**. If you make changes to the settings, you can update the view by clicking **Update View**.

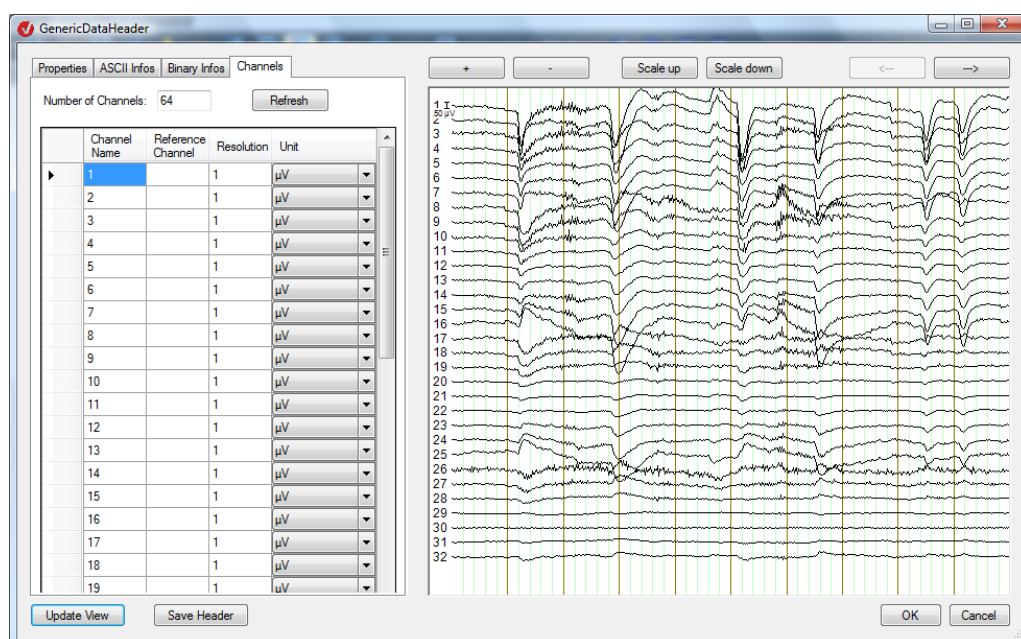


FIGURE 13—5 DISPLAY OF THE EEG

The buttons **+** / **-**, **Scale up/Scale down** and **<--** / **-->** allow you to navigate in the EEG displayed.

13.4 LORETA

The functions of the LORETA add-in are the same as the functions of LORETA as a transient view. You will find a detailed description in section 14.3.



The difference between LORETA as a transient view and as an add-in is as follows: As a transient view, LORETA is tied to a selected data set. As an add-in, on the other hand, the display of the data relates to the current view, and it is possible to switch between the different views.

To execute LORETA as an add-in, you choose **Add Ins > Others > Loreta**.

14 Transient transforms

The transient transforms are exclusively for the temporary display and inspection of the EEG data. They are transient because their result is not stored anywhere.

You call the transient transforms by using the mouse to select a point or section of the EEG.

A context menu appears when you release the mouse button, offering you a selection of transforms (3D Head View, CSD Map, FFT, Loreta, Map, Zoom).

If you select one of these transforms, the current data window is divided into two. The result of the transform is displayed on the right. It applies to the currently selected point or section. If you change the position of the marker, the transient view is updated.

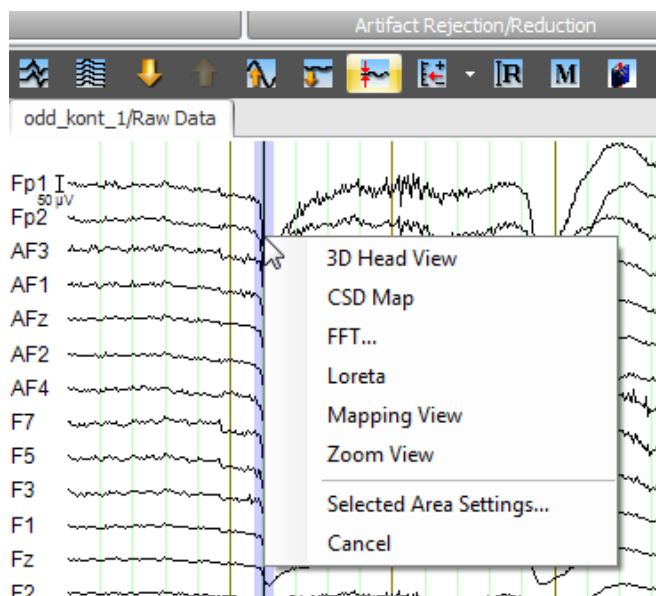


FIGURE 14—1 FIRST MENU FOR CALLING THE TRANSIENT TRANSFORMS

Alternatively, you can select a section of the EEG, right-click in the EEG to display the context menu and choose an item from the **Transient Views** submenu.

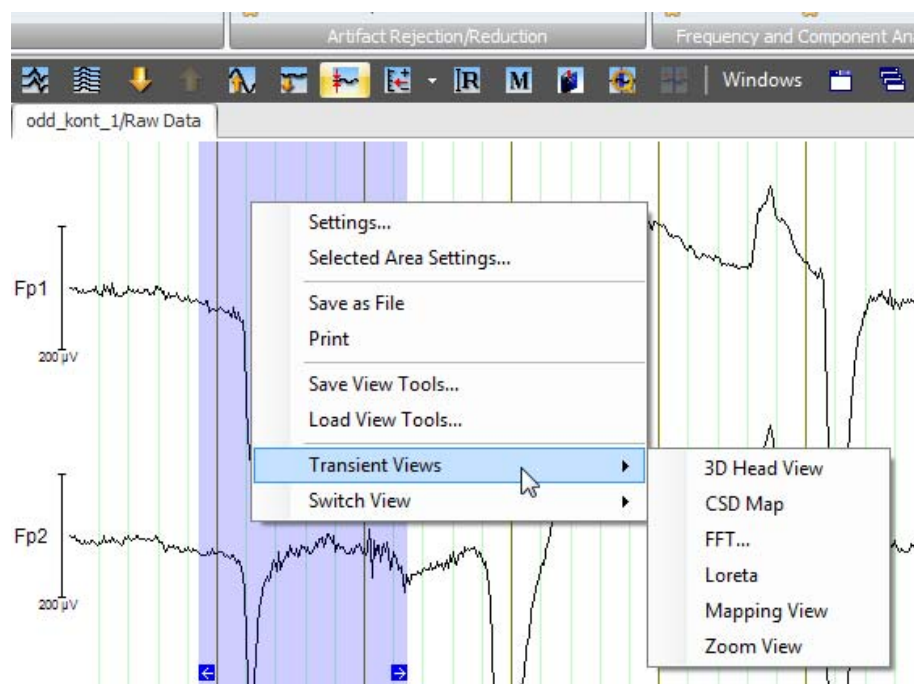



FIGURE 14—2 SECOND MENU FOR CALLING THE TRANSIENT TRANSFORMS

When you select one of these transforms, the current data window is divided into two. The result of the transform is displayed on the right. It applies to the highlighted section of the EEG. If you change the position of the highlighted section by positioning the mouse over it, holding down the mouse button and moving the mouse pointer horizontally, the result of the transient view is updated.

The dockable window on the right has a separate toolbar at the top, which allows you to change the settings of the transient view.

You can change the size of the subwindow for the display of the transient transforms by using the mouse to move the separating bar between the subwindows.

You close the right-hand subwindow by clicking the cross  in its title bar.

14.1 3D Map

The 3D Map option creates a 3D topographic map that displays the voltage distribution on the head in the time or frequency domain.

In order to generate the map, the program requires information about the position of the electrodes. If you used electrode names on the 10/10 or 10/20 principle when recording the EEG, the program should have this information. However, if you used other channel names, you can use the Edit Channels transform to enter the correct coordinates. You will find detailed information on this in section 12.1.6, “Edit Channels”.

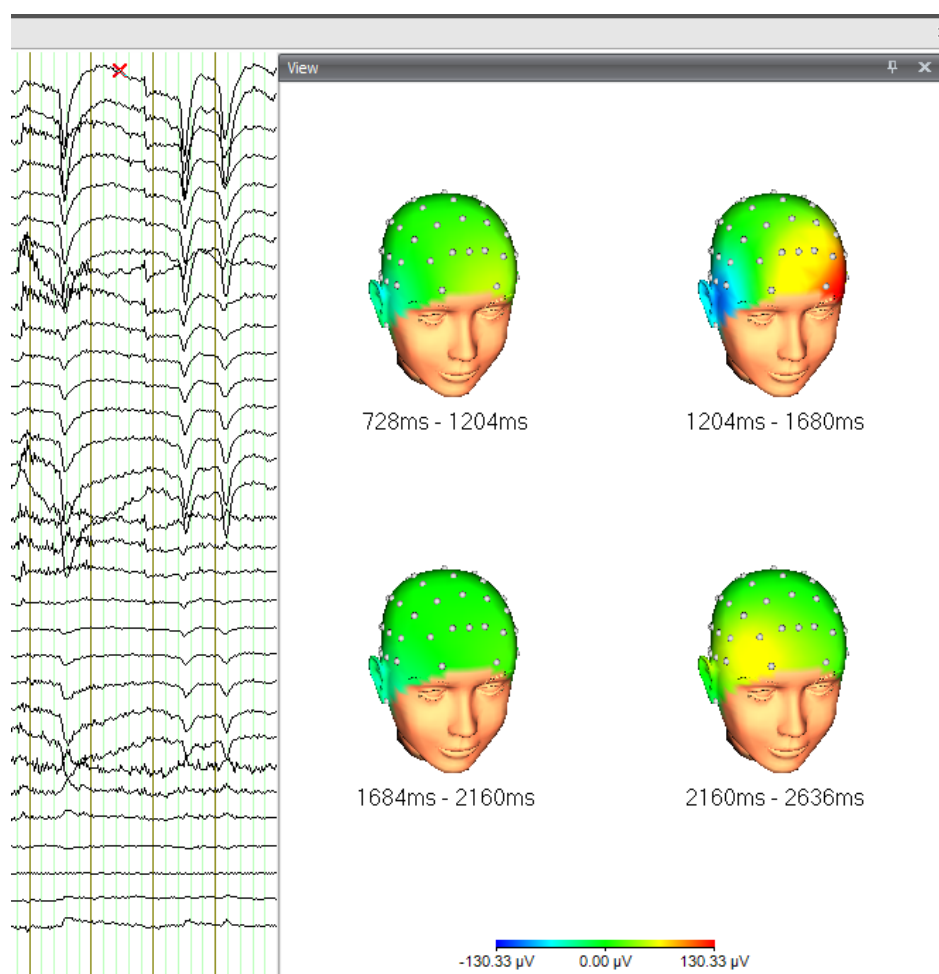


FIGURE 14—3 3D MAP

You will find more information on the 3D map in section 9.2.4.

14.2 Current Source Density (CSD)

You will find detailed information on the CSD Interpolation transform in section 12.4.6.

If you use the CSD transform in its transient form, the current source density is represented in a map. An order of 4 and a polynomial degree of 10 are used implicitly for the calculation.

To display the result of the transient CSD transform to best effect, we recommend that you use interpolation by means of spherical splines for the map. You do this by selecting the **Interpolation by Spherical Splines** radio button on the **Maps** tab of the **Default View Settings** dialog box (see also section 7.3.2, “Category-related view settings”).

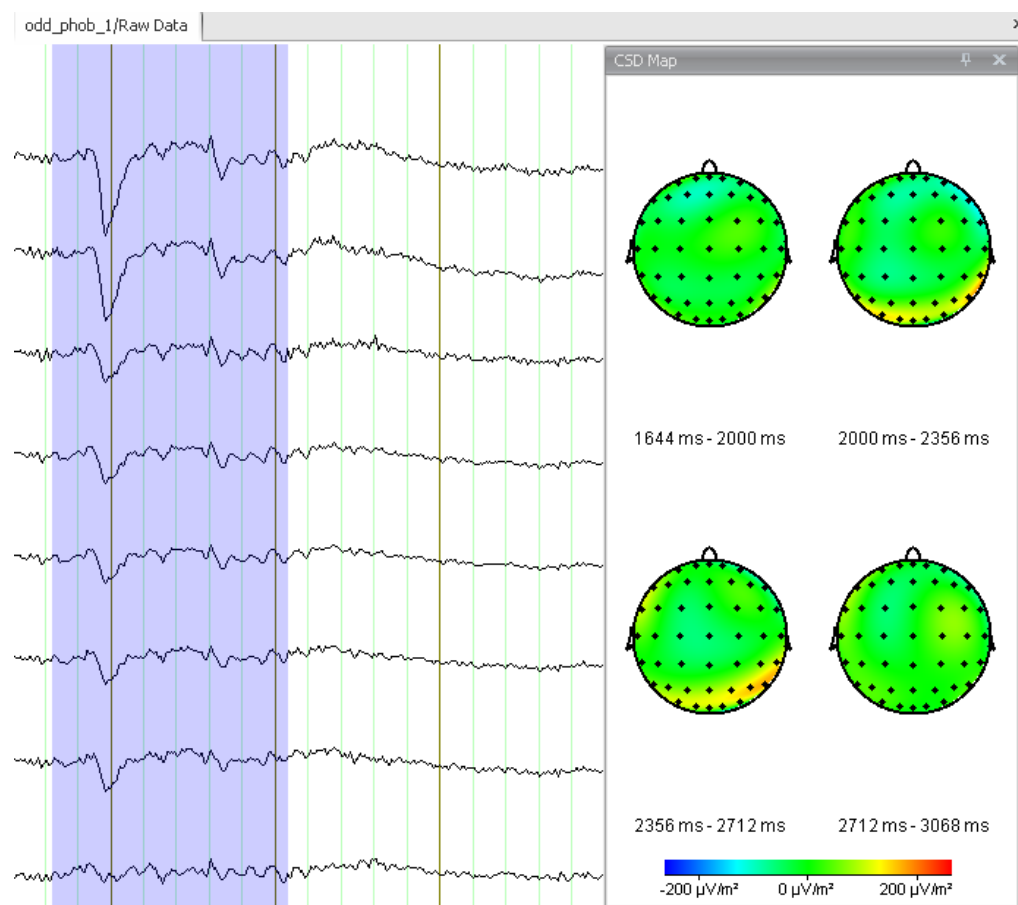


FIGURE 14—4 CSD MAP

14.3 LORETA

The LORETA transient view is for source localization by means of the **Low Resolution Brain Electromagnetic Tomography** method of R. D. Pascual-Marqui. SUMMARY

The virtual MR anatomical images are made available by the Montreal Neurological Institute of McGill University.



You can use LORETA on a data point, a selected range of the EEG or the currently displayed section of the EEG. PROCEDURE

You begin by selecting a point or range in the EEG. A context menu appears. Choose the **Loreta** command from the menu.

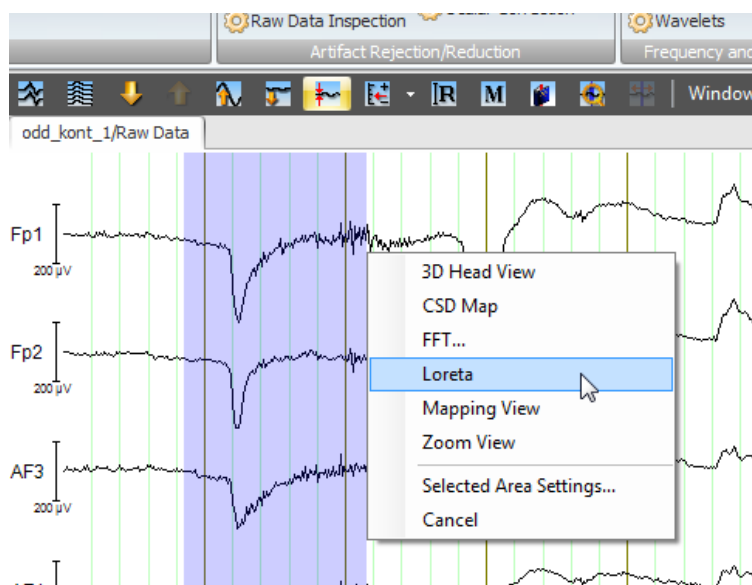


FIGURE 14—5 CONTEXT MENU FOR CALLING LORETA

A dockable window opens. The window contains three cross-sections through a virtual head.

The window works in the same way as a map: You can use the mouse to move the point or range highlighting. The display of the cross-sections changes to reflect this.

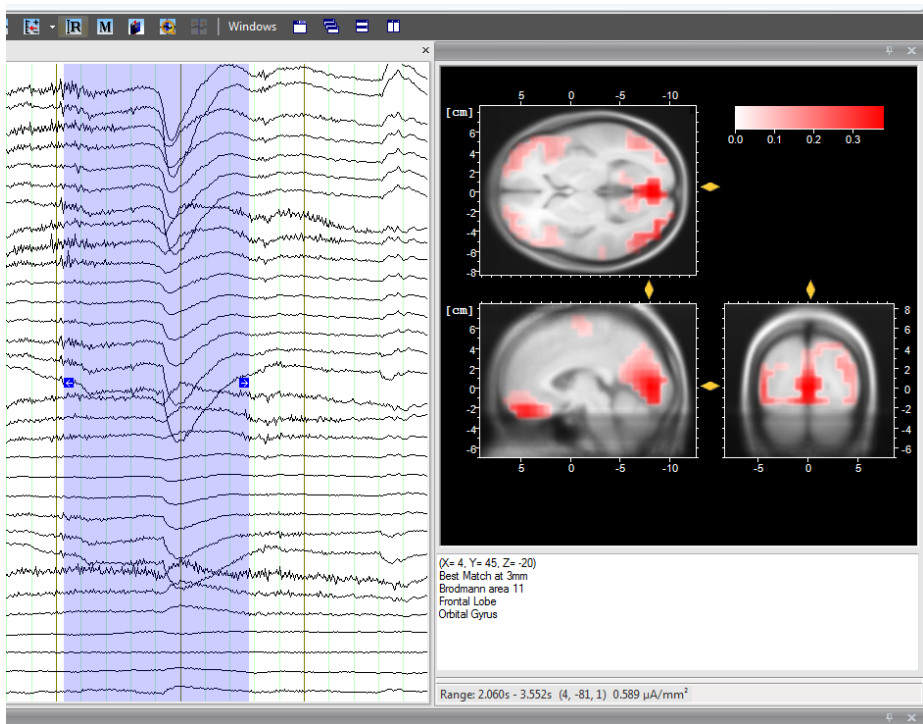


FIGURE 14—6 DOCKED LORETA WINDOW

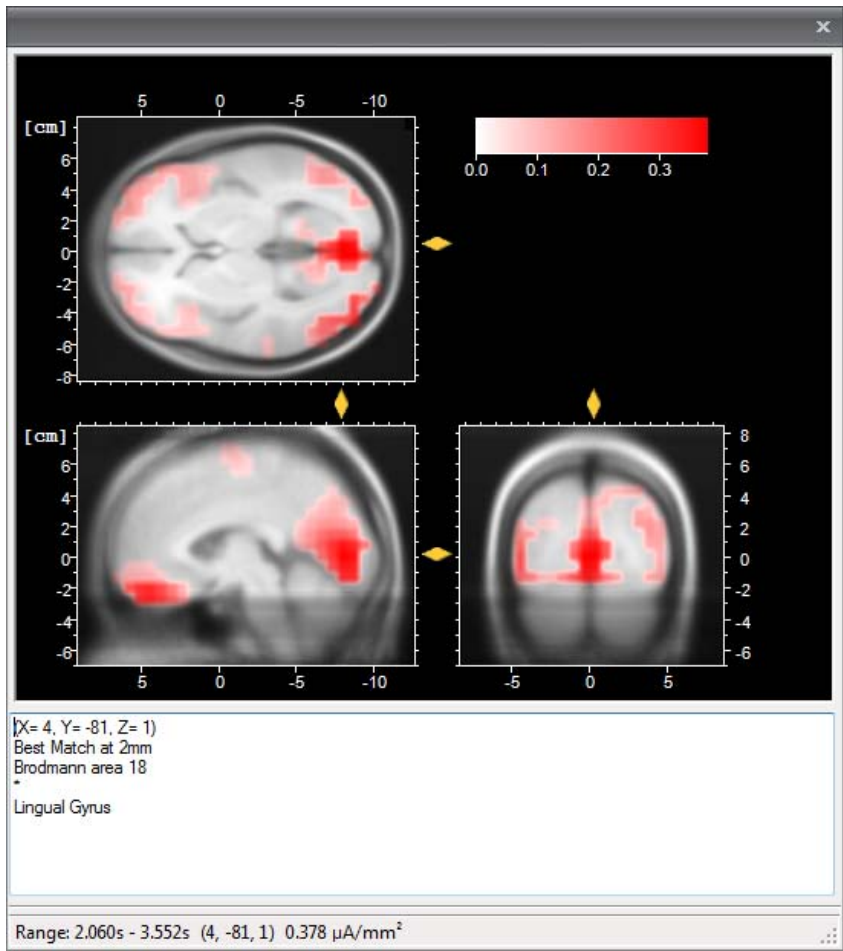


FIGURE 14—7 LORETA WINDOW, DETAILED VIEW

(1) You can navigate in the cross-sections or layers of the tomography either by using the mouse to move the four yellow sliders on the borders of the cross-sections in the desired direction or by clicking a point in the cross-section and using the mouse wheel to scroll up and down. When you click in a cross-section, the position of the sliders is updated.

NAVIGATION

(2) If you move the highlighting in the EEG in the view window and then release the mouse button, the display in the LORETA window is updated.

In the status bar of the LORETA window, **Range** indicates the range or point selected in the view (range or single-point highlighting), the cross-section coordinates of the sliders (in parentheses) and the current flow density.

LORETA WINDOW

The information box above the status bar, which relates to the position of the mouse in the LORETA window, provides the following information (in this order):

- The parentheses contain the cross-section coordinates of the current position of the mouse pointer (crosshair). When you move the mouse pointer around the cross-section, the coordinates displayed change accordingly.
- The value for **Best match at** specifies the distance from the current mouse position of the next voxel containing stored physiological data. This is the data from the LORETA program.
- The next three lines indicate the associated anatomical data of the brain areas in the vicinity of the mouse pointer.

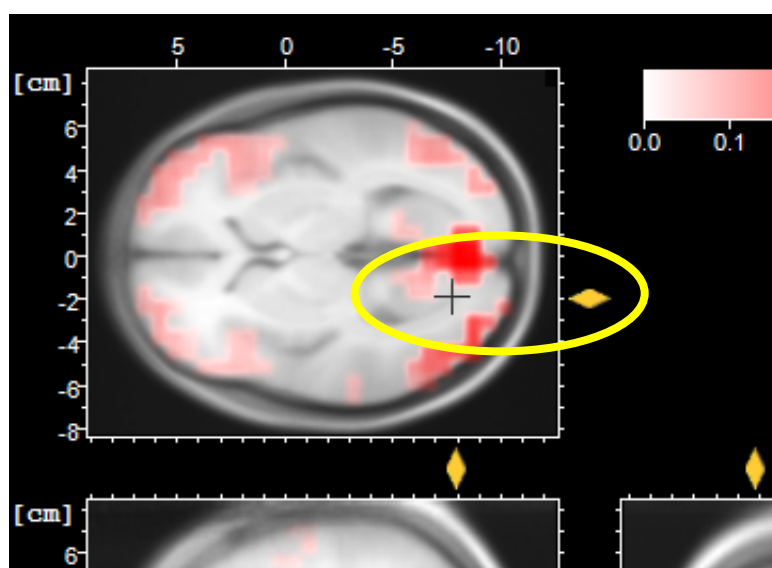


FIGURE 14—8 DISPLAY OF THE MOUSE POINTER IN THE CROSS-SECTION

If the mouse pointer is positioned outside the three cross-sections, the information box displays the values of the current intersection of the three cross-sections.



You display the context menu of the LORETA window by right-clicking in the window. The context menu contains the following commands:

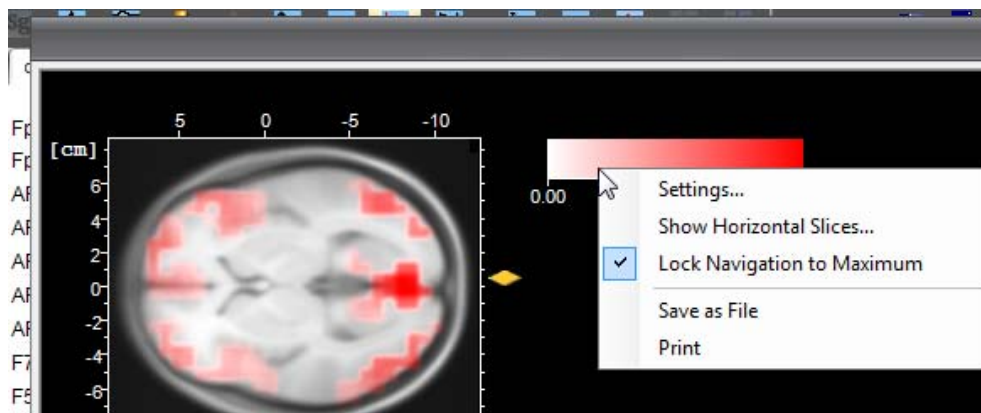


FIGURE 14—9 CONTEXT MENU OF THE LORETA WINDOW

Save as File saves the LORETA view as a file. The graphics formats EMF, BMP, PNG and JPEG are available to you.

Print opens the dialog box for printing the LORETA view.

Lock Navigation to Maximum: If you choose this command, the display focuses on the position with the strongest brain activity.

Settings... opens the associated dialog box for changing the settings:

- From the **3D Anatomy** drop-down list, you can choose a virtual MR anatomical image.
- You can also switch between automatic and manual scaling.

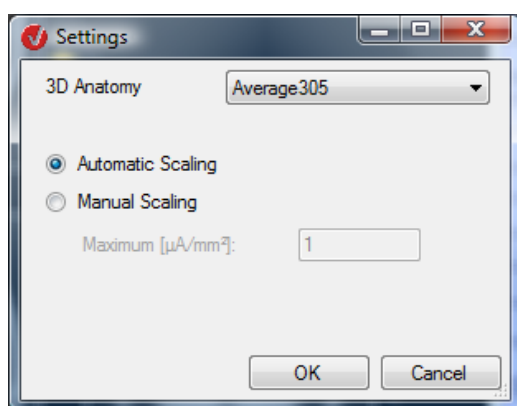


FIGURE 14—10 SETTINGS DIALOG BOX

Show Horizontal Slices... opens a new window (**Horizontal Slices**) containing horizontal cross-sections (z-axis) at fixed intervals. If you right-click in the window, the associated context menu appears. This contains two commands:

- **Settings...** displays the **Borders and Step** dialog box, in which you can specify the minimum and maximum z-coordinates and the size of the steps (in the **Step** text box).
- **Export as Bitmap...** allows you to export the file as a bitmap.

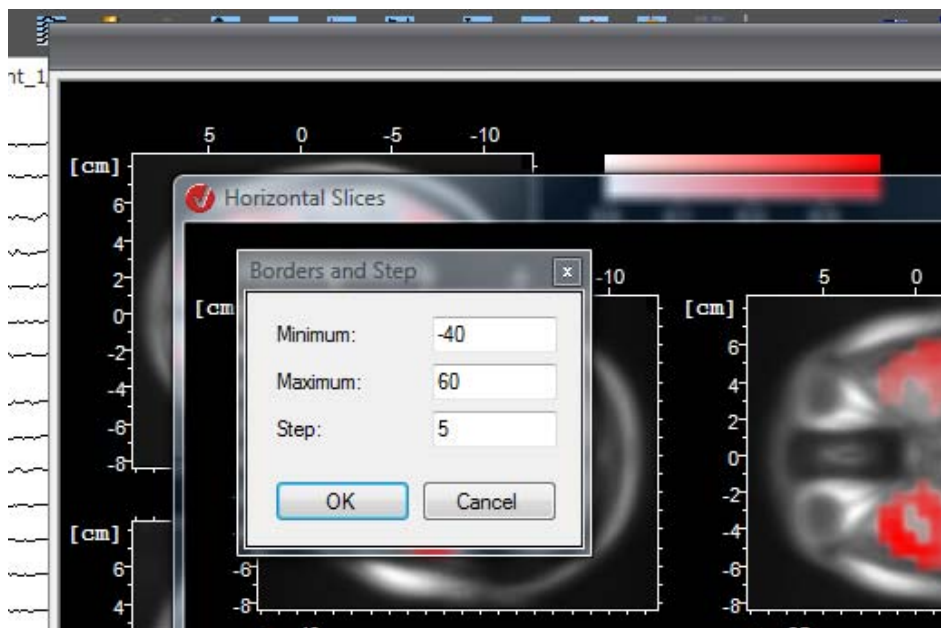


FIGURE 14—11 DIALOG BOX FOR DISPLAYING THE HORIZONTAL CROSS-SECTIONS, INCLUDING SETTINGS DIALOG BOX

14.4 Fast Fourier transform (FFT)

The FFT displays the frequency spectrum of the current section. It always uses the standard view and the currently selected montage.

The transient view also has a separate toolbar.

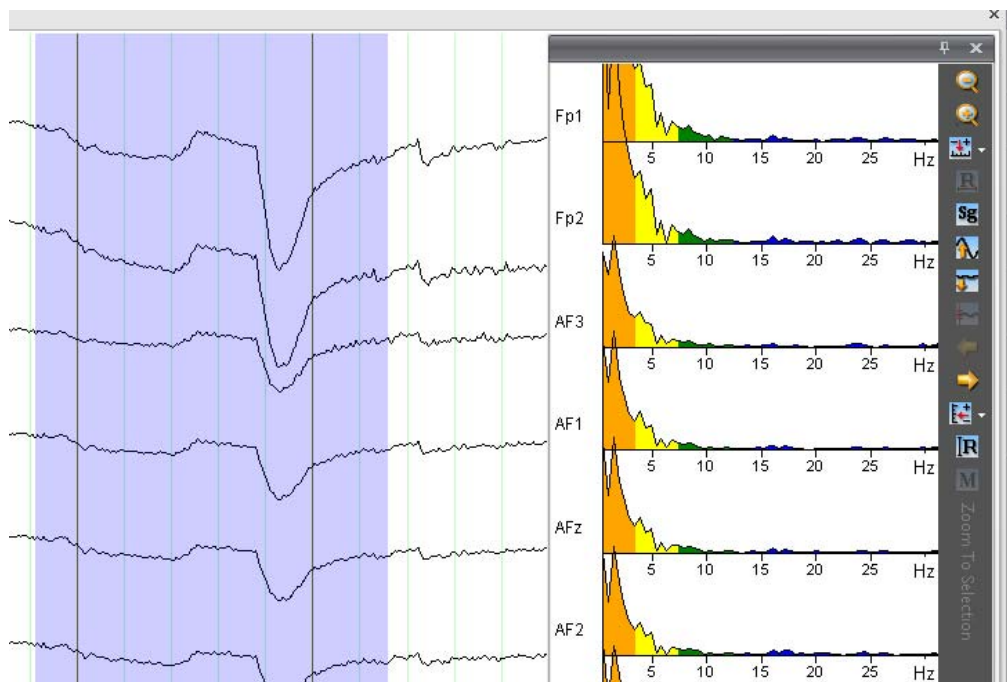


FIGURE 14—12 FFT AS A TRANSIENT TRANSFORM

14.5 Map

The Map option creates a 2D topographic map that displays the voltage distribution on the head in the time or frequency domain.

As with the 3D Map transient transform, valid head coordinates are required to display the 2D map. If you used electrode names on the 10/10 or 10/20 principle when recording the EEG, the program should have this information. However, if you used other channel names, you can use the Edit Channels transform to enter the correct coordinates. You will find detailed information on this in section 12.1.6, “Edit Channels”.

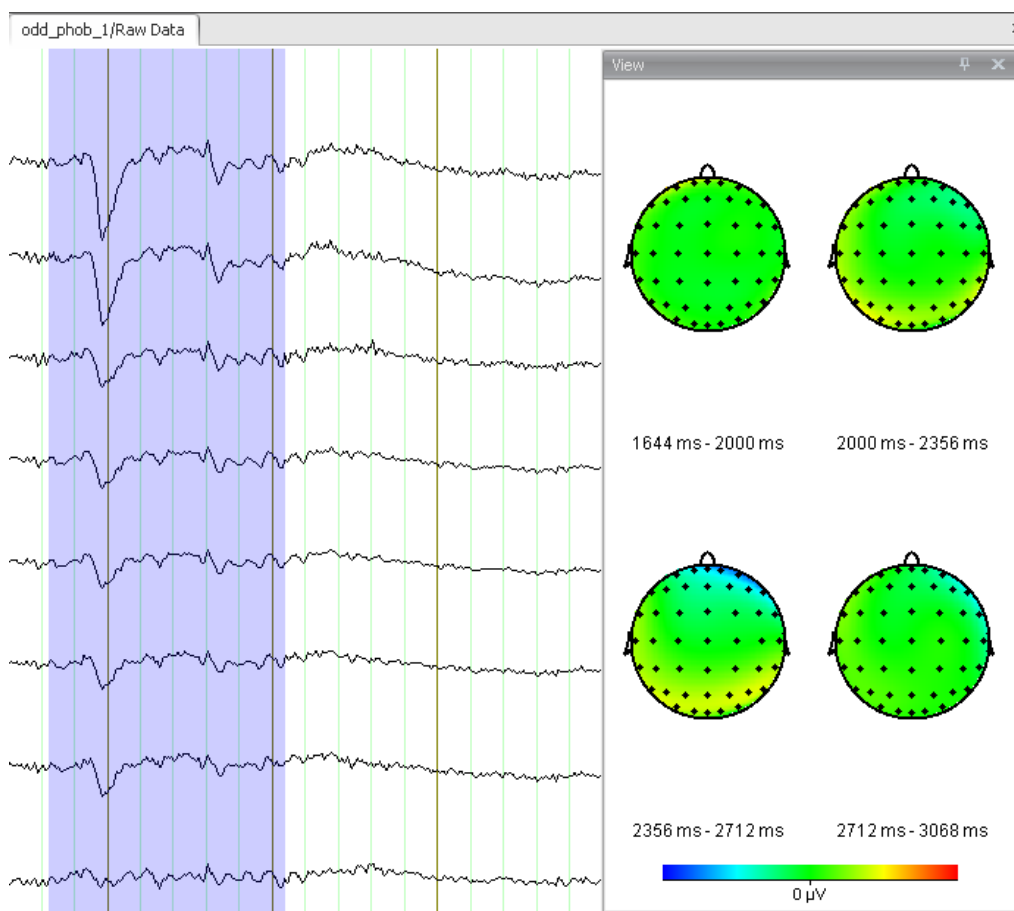


FIGURE 14—13 2D MAP

14.6 Zoom

The Zoom option enlarges (zooms) the display of the current EEG section. It always uses the standard view and the currently selected montage.

The transient view has a separate toolbar.

Note that the zoom function is only available for the time domain.

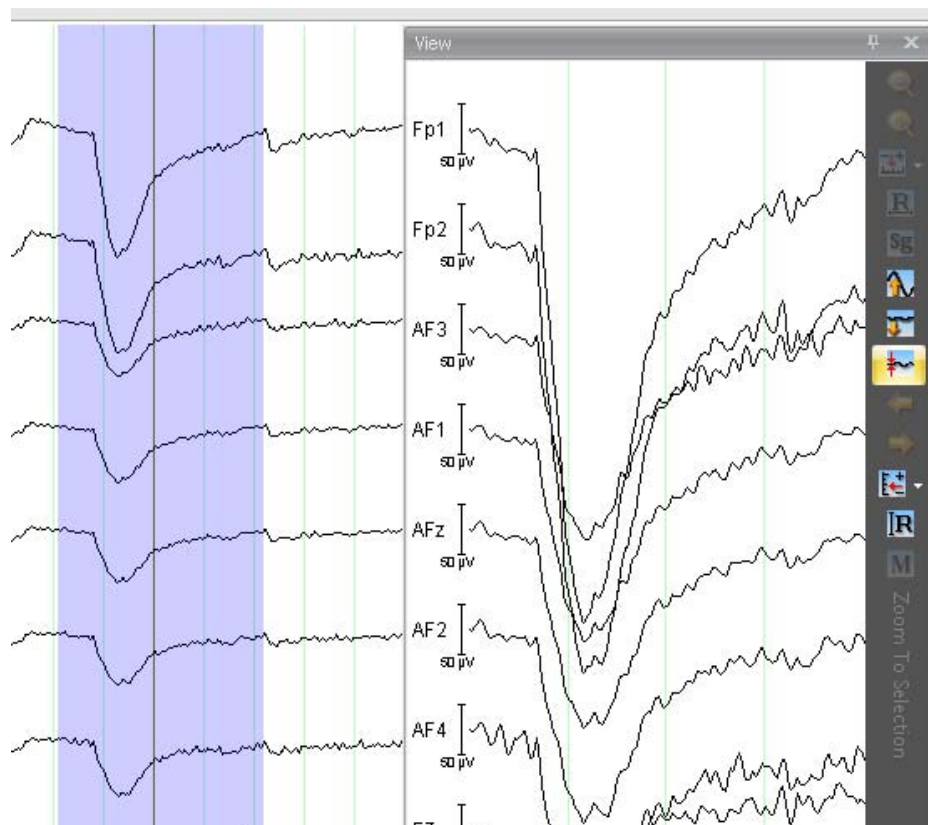


FIGURE 14—14 ZOOM

15 Export components

The export components can be used to export data sets, markers, area dimensions and so on to files so that they can be further processed using other programs. You will find the export components on the **Export** tab.

As with transforms, there are two groups of export components: simple exports (in the **NodeExport** group) and multiple exports (in the **Multiple Export** group). Simple export components always have a single input data set. ASCII exports provide an example. Multiple export components always have multiple input data sets. They include the Peak Information Export component, which creates a table of peak values on the basis of a selection of history files or history nodes.

In contrast to multiple export components, simple export components can operate with templates. They can also only be executed when a data set is displayed – in the same way as primary transforms – and always relate to the active data set window.

The simple export components provide placeholders for the name of the history file (\$h) and the name of the current data set (\$n). The advantage of using placeholders is that export components can also be used in history templates without existing exported files being overwritten constantly. This can be illustrated by an example in which there are two history files: “EEG1” and “EEG2”. The “Average” data set is exported for both, and the name “\$h_\$n” is entered. The resulting file names are “EEG1_Average” and “EEG2_Average”.

If you have selected a block in the current data set, you can use the simple export components to export this block exclusively.

You specify the folder for the export files by choosing **File > Workspace > New** or by choosing **Edit** and then entering it in the **Export Files** text box in the **Edit Workspace** dialog box.

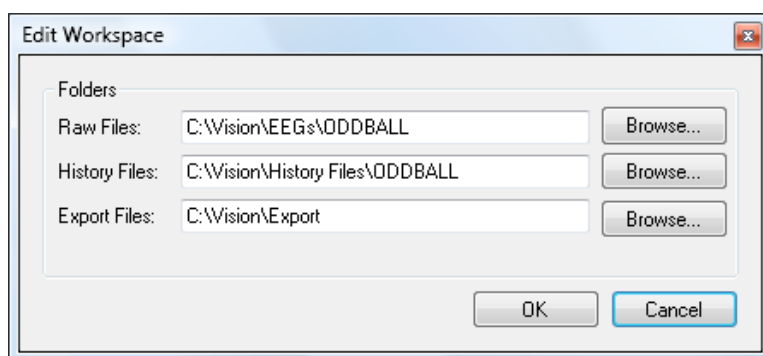


FIGURE 15—1 SPECIFYING THE EXPORT FOLDER

The next two sections of this chapter describe all the simple and multiple export components that are currently available with the Analyzer. The structure of this chapter is based on that of the Ribbon: All the export components contained on the **Export** tab are described one after the other (going from left to right).

When you have completed your entries, a dialog box containing the name and storage location of the export file appears. The dialog box below is an example for the Besa export component: NOTE

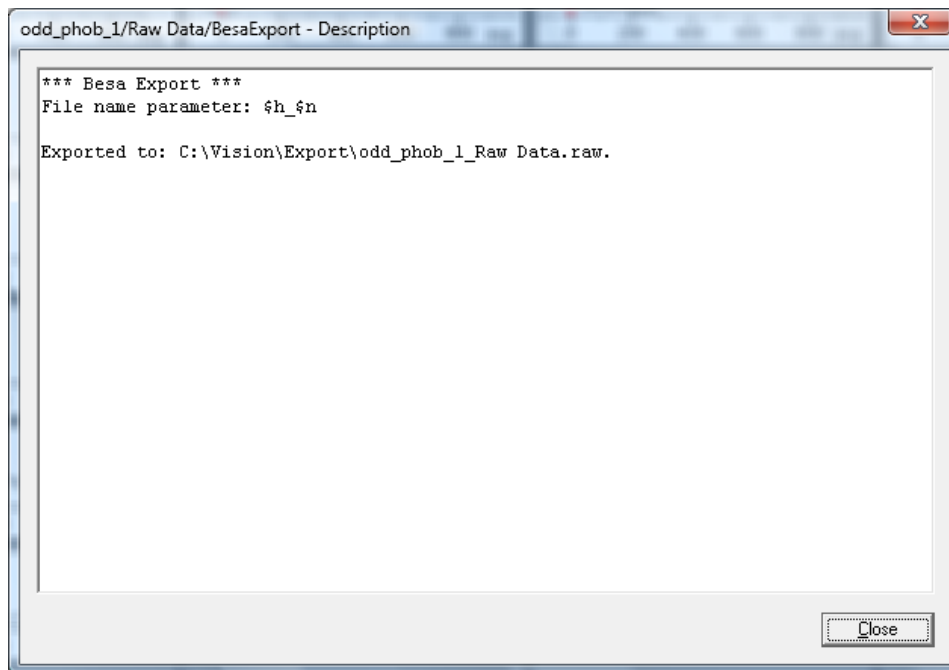


FIGURE 15—2 BESA EXPORT, INFORMATION ON THE EXPORT FILE

15.1 Simple export components

15.1.1 Besa Export

The Besa Export component exports the data set or section of the data set in BESA ASCII format. The exported file has the file name extension “.raw”. SUMMARY

To display the dialog box for the Besa Export component, you choose **Export > NodeExport > Besa....** PROCEDURE

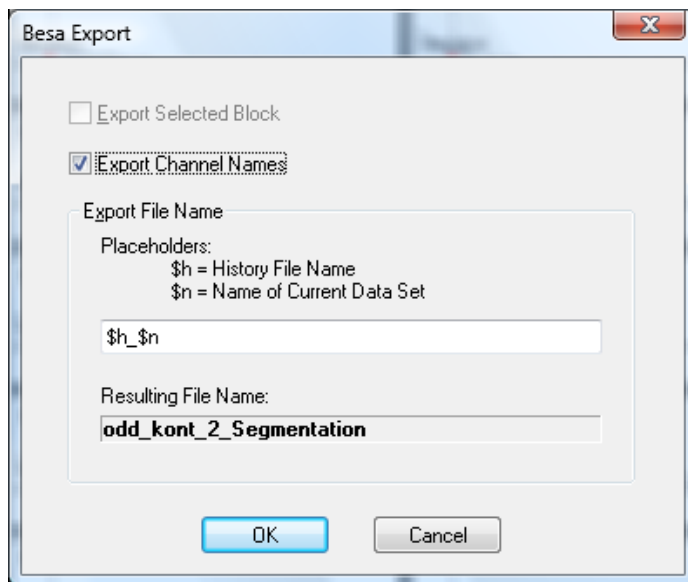


FIGURE 15—3 BESA EXPORT DIALOG BOX

You can make the following settings:

- If you select the **Export Selected Block** check box, only the selected block is exported. This check box is only accessible if you have selected a block.
- If you select the **Export Channel Names** check box, you can also export the channel names.
- The **Export File Name** text box allows you to enter the name of the export file, for which you can also use placeholders. The name you create in this way appears in the Resulting File Name text box.

15.1.2 EDF Export

The EDF Export component allows you to export EEG data in EDF or EDF+ format.

SUMMARY

To display the related dialog box, you choose **Export > NodeExport > EDF....**

PROCEDURE

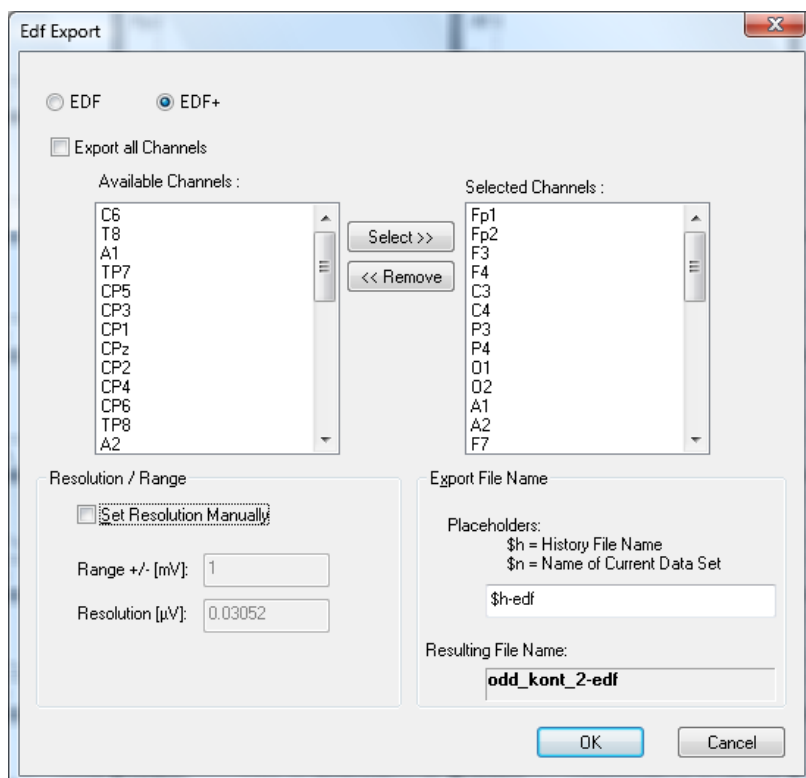


FIGURE 15—4 EDF EXPORT DIALOG BOX

You can make the following settings:

- The **EDF** and **EDF+** radio buttons allow you to specify whether the data is exported in EDF or EDF+ format.
- If you select the **Export all Channels** check box, all channels are exported.
- The **Select >>** and **<< Remove** buttons allow you to specify which of the available channels (in the **Available Channels** list box) are to be exported (i.e. included in the **Selected Channels** list box).
- If you select the **Set Resolution Manually** check box, you gain access to the **Range +/- [mV]** text box, in which you can specify the range of values for the data to be exported. In the **Resolution [µV]** text box, the corresponding resolution of the values is automatically adjusted.
- The **Export File Name** text box allows you to enter the name of the export file, for which you can also use placeholders. The name you create in this way appears in the **Resulting File Name** text box.

15.1.3 Markers Export

The Marker Export component saves selected markers in an ASCII file.

SUMMARY

To display the dialog box for the Markers Export component, you choose **Export > NodeExport > Markers....**

PROCEDURE

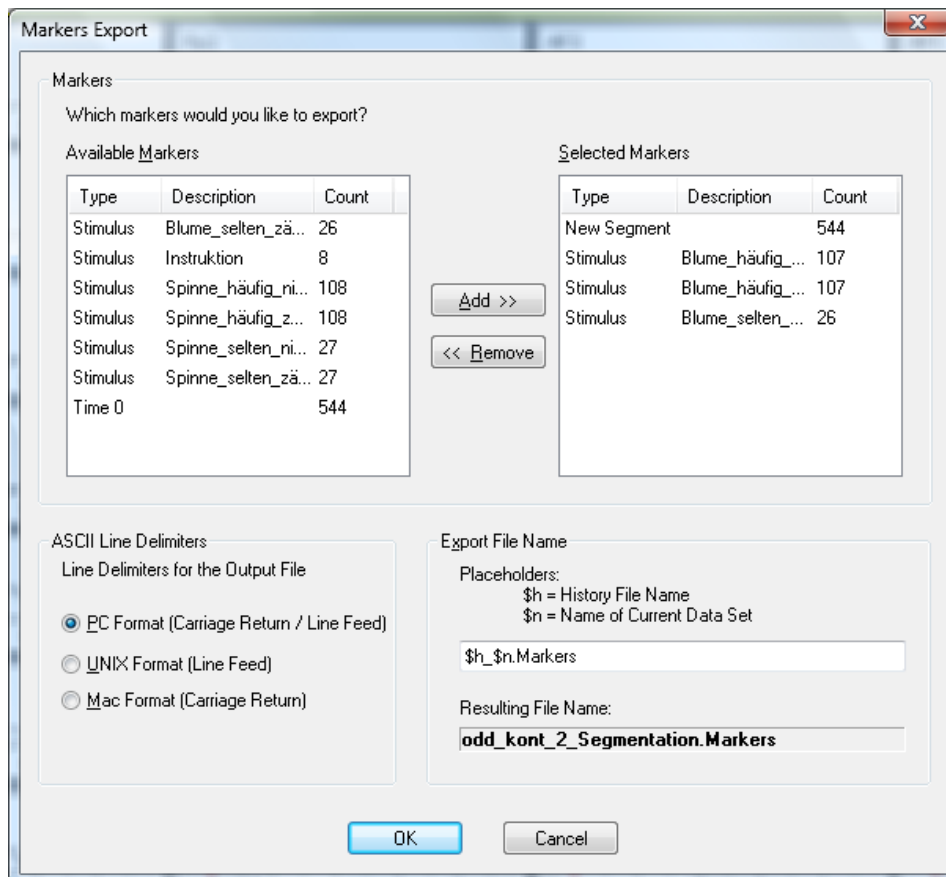


FIGURE 15—5 MARKERS EXPORT DIALOG BOX

You can make the following settings:

- The **Add >>** and **<< Remove** buttons allow you to specify which of the available markers (in the **Available Markers** list box) are to be exported (i.e. included in the **Selected Markers** list box).
- In the **ASCII Line Delimiters** group box, you can specify the format of line delimiters for all exported ASCII files in order to further process the data under different operating systems. The three commonly used formats for the majority of PC operating systems (**PC Format** radio button), Unix (**Unix Format** radio button) and Apple Mac (**Mac Format** radio button) are available for you to select.
- The **Export File Name** text box allows you to enter the name of the export file, for which you can also use placeholders. The name you create in this way appears in the **Resulting File Name** text box.

15.1.4 Generic Data Export

The Generic Data Export component allows you to export data – including complex data – in the time and frequency domains in ASCII or binary format. SUMMARY

To display the dialog box for the Generic Data Export component, you choose **Export > NodeExport > Generic Data Export....** PROCEDURE

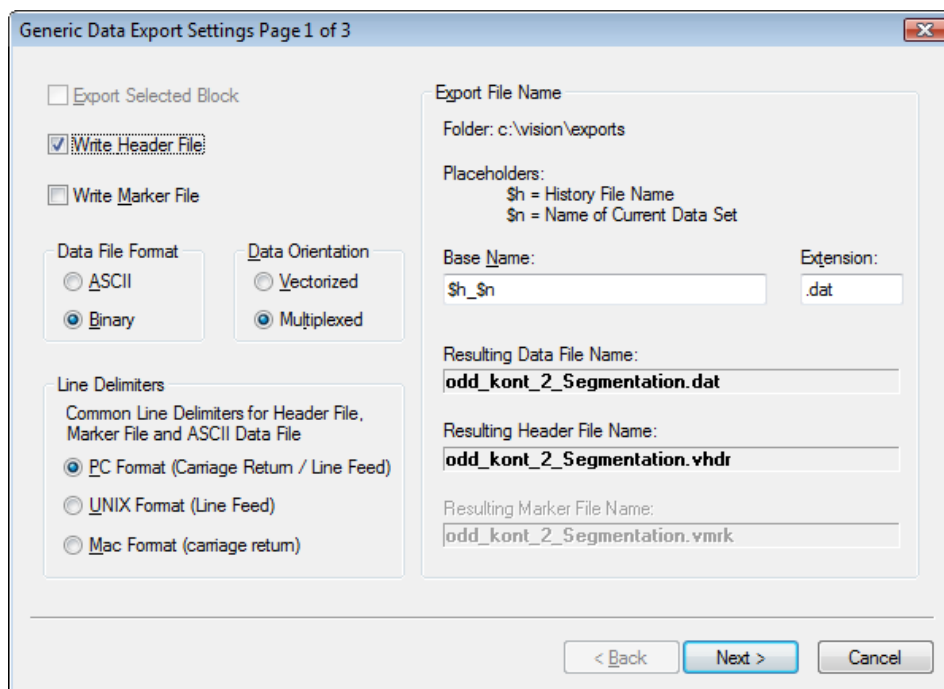


FIGURE 15—6 GENERIC DATA EXPORT DIALOG, FIRST PAGE

On the first page of the dialog, you can make the following settings:

- If you select the **Export Selected Block** check box, only the selected block is exported. This check box is only accessible if you have selected a block.
- If you select the **Write Header File** check box, a header file is created. You can also generate an ASCII header file containing information on channels, the sampling rate, data set type, etc. This header file is in the INI file format commonly used under Windows®.
- If you select the **Write Marker File** check box, a marker file is created. The marker file, which is also in INI format, lists all the existing markers together with their positions, types, descriptions, etc.
- In the **Data File Format** group box, you specify the format of the files to be exported. You can specify whether the data is to be exported in ASCII format (by selecting the **ASCII** radio button) or binary format (by selecting the **Binary** radio button). In the case of the ASCII export, the values are written directly in μV or μV^2 .

- In the **Data Orientation** group box, you specify the data orientation by selecting either the **Vectorized** or **Multiplexed** radio button.

This applies to the channels. Vectorized in this context means that all the data points of the first channel are written to the export file first, followed by those of the second channel, and so on. In an ASCII export, each channel to be exported is written to a separate line. Multiplexed means that the data of the first sampling time point is written first, followed by the data of the second sampling time point, and so on. In an ASCII export, the data of each sampling time point is written to a separate line. If you export complex data, the real part is written first, followed by the imaginary part.

- In the **ASCII Line Delimiters** group box, you can specify the format of line delimiters for all exported ASCII files in order to further process the data under different operating systems. The three commonly used formats for the majority of PC operating systems (**PC Format** radio button), Unix (**Unix Format** radio button) and Apple Mac (**Mac Format** radio button) are available for you to select.
- The **Export File Name** text box is for entering the name of the export file, for which you can also use placeholders. In the **Base Name** text box, you specify the base name of the file, and in the **Extension** text box its file name extension. The names you select for the export file, header file and marker file appear in the **Resulting Data File Name**, **Resulting Header File Name** and **Resulting Marker File Name** text boxes.

To proceed to the next page of the dialog, you click the **Next >** button.

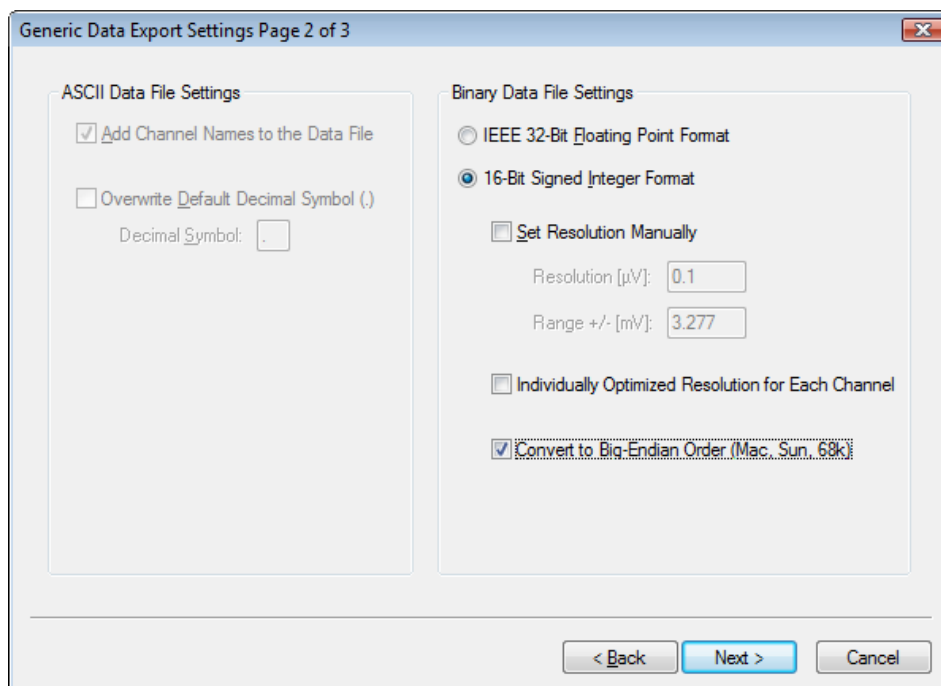


FIGURE 15—7 GENERIC DATA EXPORT DIALOG, SECOND PAGE

The second page of the dialog allows you to set ASCII or binary parameters. Depending on whether you have selected an ASCII or binary export, either the **ASCII Data File Settings** group box (on the left) or the **Binary Data File Settings** group box (on the right) is accessible.

In the **ASCII Data File Settings** group box, you can make the following settings:

ASCII GROUP BOX

- If you select the **Add Channel Names to the Data File** check box, the channel names are added to the file. In the case of multiplexed data, the channel names appear in the first line. Otherwise, they appear in the first column.
- If you select the **Overwrite Default Decimal Symbol (,)** check box, you overwrite your computer's default decimal symbol (point or comma) with the characters entered in the **Decimal Symbol** text box. Your computer's decimal symbol depends on its country settings.

In the **Binary Data File Settings** group box, you can make the following settings:

BINARY GROUP BOX

You select either the **IEEE 32-Bit Floating Point Format** or **16-Bit Signed Integer Format** radio button. If you select the former, as in the case of the ASCII export the values are written directly in μV or μV^2 .

The settings below the radio buttons are only applicable if you select the **16-Bit Signed Integer Format** radio button:

- If you select the **Set Resolution Manually** check box, you set the resolution at which the data is written manually. In the **Resolution [μV]** text box, you enter the resolution of the values, and in the **Range +/- [ms]** text box the range of the data to be exported. If you make an entry in one of these two text boxes, the value in the other text box is adjusted accordingly.

This resolution, – again in μV or μV^2 – specifies the minimum difference between two values to be stored. Since the 16-bit format is restricted to a maximum of 216 values, too high a resolution can result in data peaks being truncated. The range in mV that is achieved at the specified resolution is shown in the dialog. You can also enter this range instead of the resolution.

Alternatively, you can have the program calculate and set the optimum resolution. In this case, however, you should always export a header file as well, since this is the only place you will find the resolution that has been used.

- If you select the **Individual Optimized Resolution for Each Channel** check box, you can optimize the resolution for each channel in cases where you have the resolution calculated automatically. If you do not select the check box, a common resolution is selected for all channels.
- If you select the **Convert to Big-Endian Order** check box, the exported data is converted to big-endian order. If you want to work with exported integer data on a system such as a Mac or a SUN workstation, the least and most significant bytes of each value have to be stored the other way round in big-endian order.

To proceed to the final page of the dialog, you click the **Next** button.

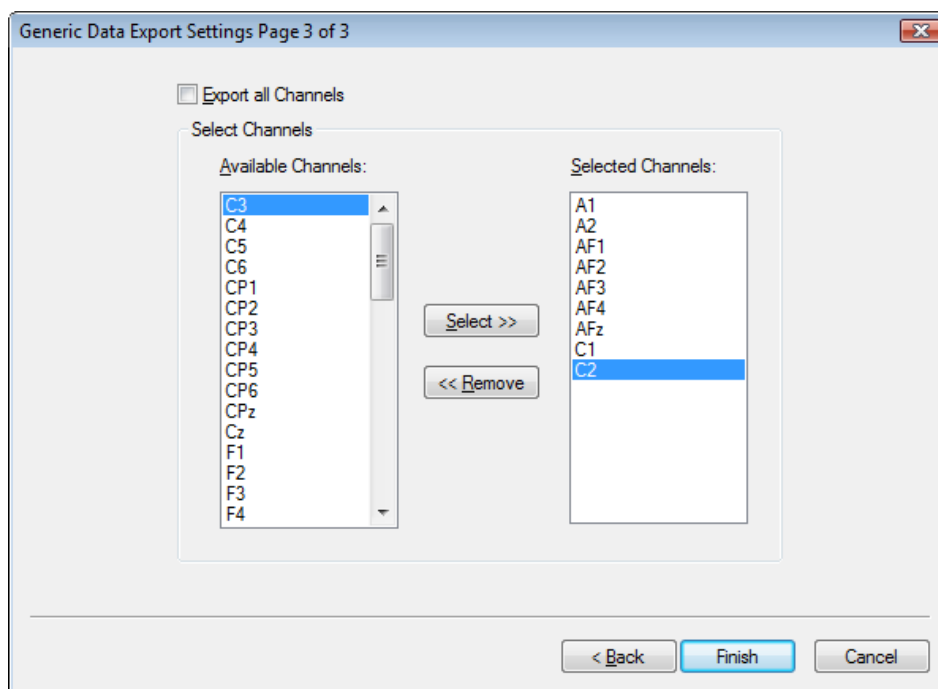


FIGURE 15—8 GENERIC DATA EXPORT DIALOG, THIRD PAGE

On the last page of the dialog, you specify that all channels are to be exported by selecting the **Export all Channels** check box.

If you do not select the check box, you can use the **Select >>** and **<< Remove** buttons to select which of the available channels (in the **Available Channels** list box) are to be included in the export (i.e. in the **Selected Channels** list box).

You click the **Finish** button to conclude your entries.

15.2 Complex export components

15.2.1 Area Information Export

You can use the Area Information Export component to export the area dimensions ($\mu\text{V} \cdot \text{ms}$ or $\mu\text{V} \cdot \text{Hz}$) of an interval, the average activity (μV) or the total activity in an interval to an ASCII table.

SUMMARY

To display the dialog box for the Area Information Export component, you choose **Export > Multiple Export > Area Information Export....**

PROCEDURE

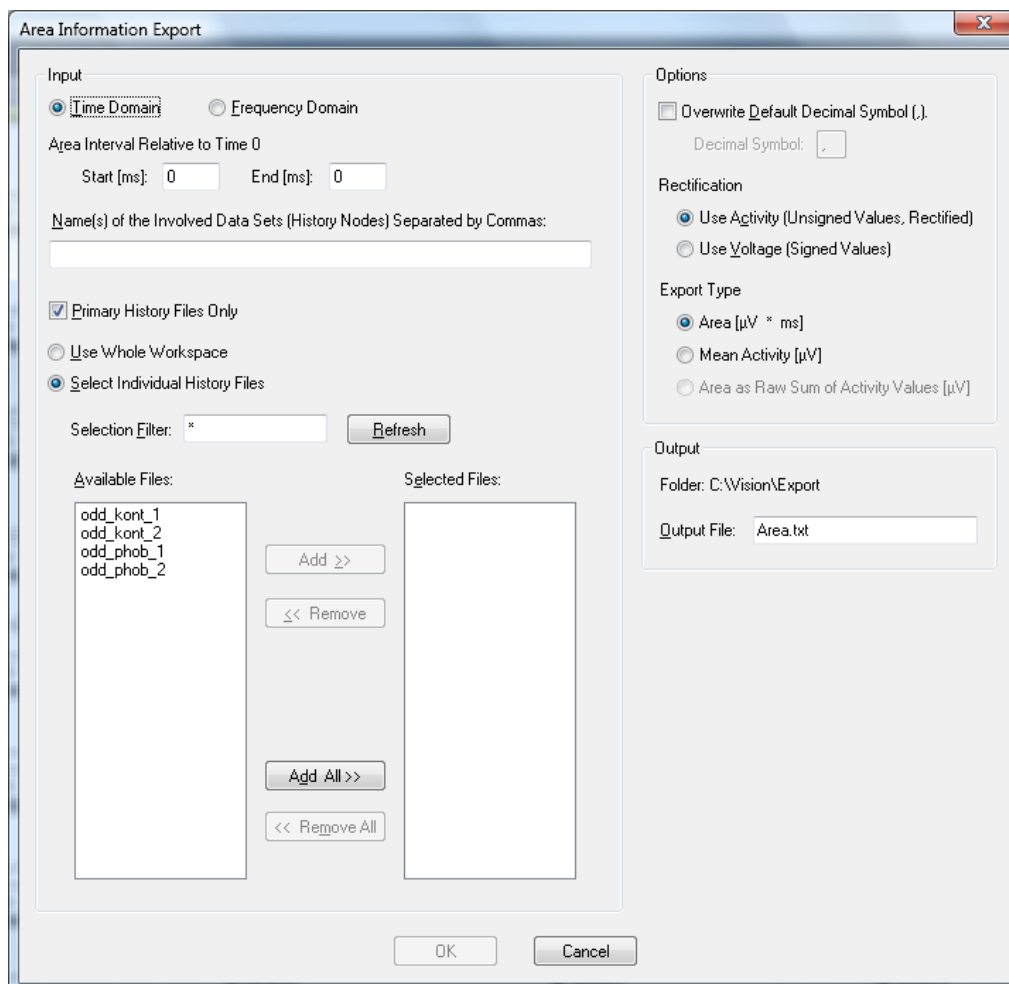


FIGURE 15—9 AREA INFORMATION EXPORT DIALOG BOX

In the **Input** group box, you can make the following settings:

INPUT GROUP BOX

- You specify whether the data to be exported is in the time domain (by selecting the **Time Domain** radio button) or the frequency domain (by selecting the **Frequency Domain** radio button).
- In the **Area Interval Relative to Time o Start [ms]** and **End [ms]** text boxes, you specify the interval to be exported.
- In the **Name(s) of the Involved Data Sets (History Nodes)** text box, you specify the names of the data sets (history nodes) involved, separated by commas.
- If you select the **Primary History Files Only** check box, you limit the **Use Whole Workspace** and **Select Individual History Files** radio buttons to primary history files.
- In the **Selection Filter** text box, you specify the selection filter. This filters selectable files on the basis of name criteria. An asterisk (*) stands for one or more characters, and a period (.) stands for a single character. If the workspace contains the files "Test1H2", "Test2G" and "Hest5", for example, the string "Test*" filters out the files "Test1H" and "Test2G" (i.e. makes them available). The filter ".est*" accepts all three files. Once you have set the filter, you click the **Refresh** button to refresh the selection of available files.
- All the available files are listed in the **Available Files** text box.
- The **Selected Files** text box contains all the selected files.
- To select one or more files or remove them from the list of selected files, you select them and then click the **Add** or **Remove** button. The **Add All** and **Remove All** buttons do the same for all files.

In the **Options** group box, you can make the following settings:

OPTIONS GROUP BOX

- If you select the **Overwrite Default Decimal Symbol (,)** check box, you overwrite your computer's default decimal symbol (point or comma) with the characters entered in the **Decimal Symbol** text box. Your computer's decimal symbol depends on its country settings.
- In the **Rectification** group box, you can specify whether the data is to be included in the calculation without preceding signs by selecting the **Use Activity (Unsigned Values, Rectified)** radio button or with preceding signs by selecting the **Use Voltage (Signed Values)** radio button. In the former case, the signal is rectified and the area or activity is then calculated.

This option is only available for data in the time domain. In the case of complex data, all calculations are automatically based on the absolute values.

- In the **Export Type** group box, you specify the type of calculation to be carried out for the data to be exported.

If you select the **Area** option, the area is exported. If you select the **Mean Activity** radio button, the average activity is exported. The **Area as Raw Sum of Activity Values** radio button is only available for frequency data. If you select it, the sum of the spectral line values of the defined range are exported without reference to the spectral line width.

The **Output** group box contains the storage location of the export file. In the **Output File** text box, you can specify the name and file name extension of the export file. OUTPUT GROUP BOX

15.2.2 Peak Information Export

The Peak Information Export component exports data on the position and voltage of peak markers that have been set in selected history files or nodes to an ASCII table. SUMMARY

The markers to be exported are usually set when the Peak Detection transform is used. PREREQUISITE FOR USE

To display the dialog box for the Peak Information Export component, you choose **Export > Multiple Export > Peak Information Export....** PROCEDURE

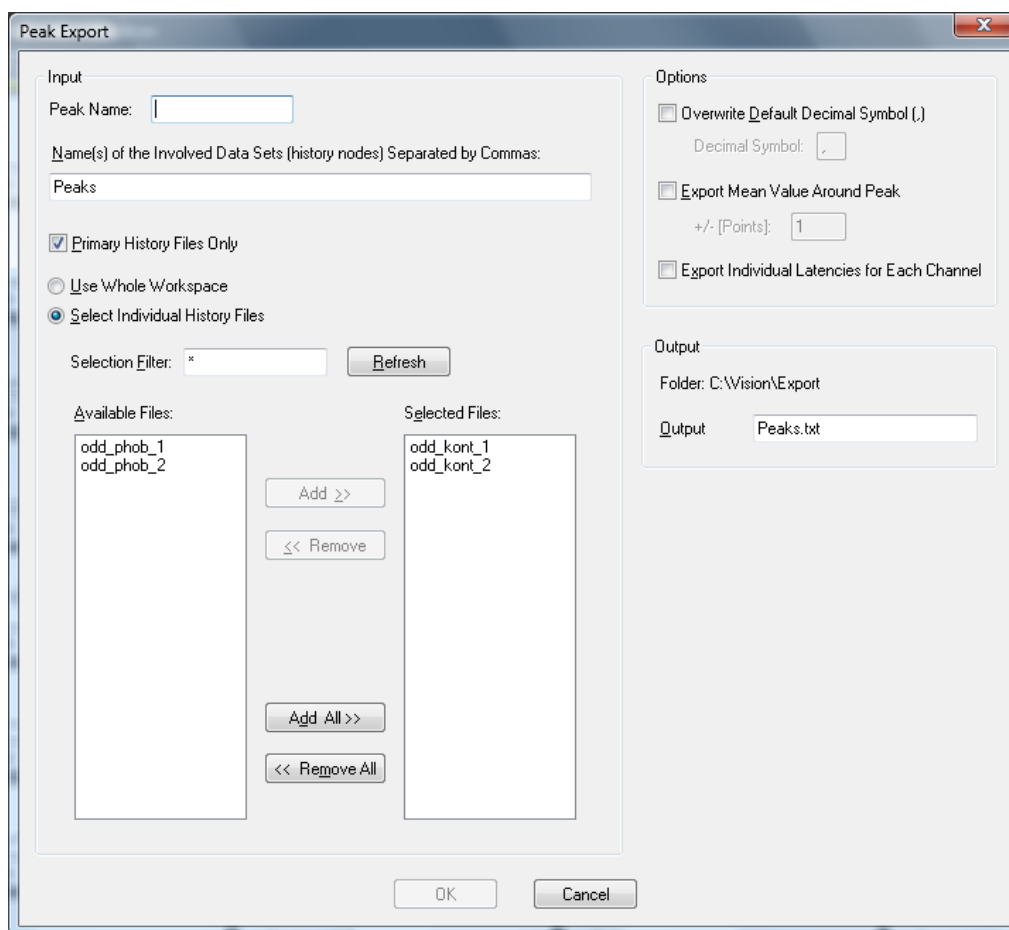


FIGURE 15—10 PEAK INFORMATION EXPORT DIALOG BOX

In the **Input** group box, you can make the following settings:

INPUT GROUP BOX

- In the **Peak Name** text box, you enter the name you gave the peak during peak detection.
- In the **Name(s) of the Involved Data Sets (History Nodes)** text box, you specify the names of the data sets (history nodes) involved, separated by commas.

- If you select the **Primary History Files Only** check box, you limit the **Use Whole Workspace** and **Select Individual History Files** radio buttons to primary history files.
- In the **Selection Filter** text box, you specify the selection filter. This filters selectable files on the basis of name criteria. An asterisk (*) stands for one or more characters, and a period (.) stands for a single character. If the workspace contains the files “Test1H2”, “Test2G” and “Hest5”, for example, the string “Test*” filters out the files “Test1H” and “Test2G” (i.e. makes them available). The filter “.est*” accepts all three files. Once you have set the filter, you click the **Refresh** button to refresh the selection of available files.
- All the available files are listed in the **Available Files** text box.
- The **Selected Files** text box contains all the selected files.
- To select one or more files or remove them from the list of selected files, you select them and then click the **Add** or **Remove** button. The **Add All** and **Remove All** buttons do the same for all files.

In the **Options** group box, you can make the following settings:

OPTIONS GROUP BOX

- If you select the **Overwrite Default Decimal Symbol (,)** check box, you overwrite your computer’s default decimal symbol (point or comma) with the characters entered in the **Decimal Symbol** text box. Your computer’s decimal symbol depends on its country settings.
- If you select the **Export Mean Value Around Peak** check box, the average value for the data around the peak is exported. In the **+/- [Points]** text box, you specify the width of this interval in points.

You can also obtain an average value around the peak and export it. To do this, you enter a value in the **+/- [Points]** text box indicating how many points before and after the point are to be included in averaging. A value of 2 means that 5 points are included in averaging (2 before, 2 after, and the peak position itself).

- If you select the **Export Individual Latencies for Each Channel** check box, individual latencies are exported for each channel.

If you used individual latencies for each channel in peak detection, you can also export these. If not, the latency of the first marker found in a data set is exported.

The **Output** group box contains the storage location of the export file. In the **Output File** text box, you can specify the name and file name extension of the export file.

OUTPUT GROUP BOX

15.3 Additional export components: LORETA

The LORETA export component allows you to export Analyzer data to a format that can be read by LORETA. The data is exported in two files: an .xyz file, which contains the coordinates of the electrodes, and a .dat file, which contains the actual EEG data.

SUMMARY

You display the required dialog box by choosing **Export > Others > Loreta Export**.

PROCEDURE

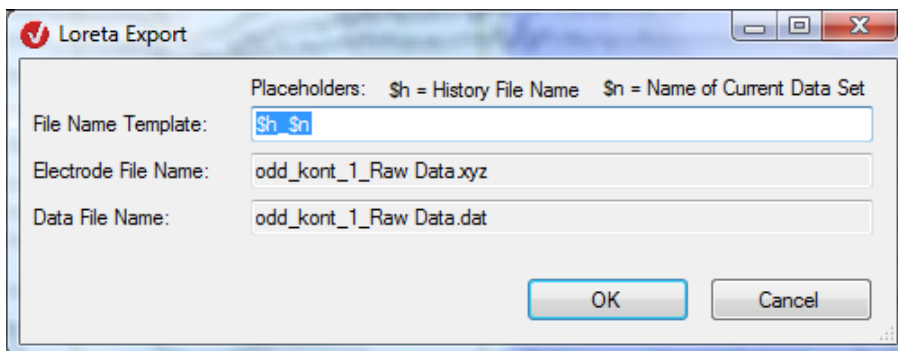


FIGURE 15—11 LORETA EXPORT DIALOG BOX

In the **File Name Template** text box, you specify the name of the export file. The placeholders \$h (for the name of the history file) and \$n (for the name of the current data set) are available to you.

16 Importing data, positions and markers

16.1 Importing data

In addition to the standard readers for many commercially used file formats, the Analyzer also allows user-defined formats to be imported.

For simple ASCII formats you may be able to use the Besa format. For more complex formats you should use the Generic Data Reader, which gives you an abundance of configuration options for describing your raw data.

16.1.1 Besa format

ASCII files can be imported in Besa format. This format has the following structure:

First line: general information

NPTS=<number of data points> TSB=<point in time 0 in ms> DI=<sampling interval in ms> SB=<scaling of data points in 1/ μ V> SC=<display scaling (is ignored)> NCHAN=<number of channels>

Example:

```
NPTS=1024 TSB=100 DI=3.90625 SB=1 SC=1 NCHAN=32
```

This is a data set with 1024 data points and a prestimulus interval of 100 ms. The digitization interval is 3.90625 ms, which corresponds to a sampling rate of 256 Hz. The scaling value for data points is 1, which means the values are specified directly in microvolts. The display scaling (SC) is ignored. The data set has 32 channels.

Second line: channel names

The channel names are listed in the second line, separated by spaces. Example:

```
Fp1 Fp2 F3 F4 etc.
```

Third and subsequent lines: data

The data values are entered as of the third line in the form of floating point numbers. The decimal symbol used is always a decimal point. Each line contains the data of one channel. The individual data values are separated by spaces.

If you store the data in a raw data folder, the Analyzer reads it in like a normal raw EEG.

You can create a sample file by exporting part of an EEG as a Besa file, as described in chapter 15, “Export components”.

16.1.2 Generic Data Reader

The Generic Data Reader (GDR) is used to read in EEG files of various formats for which there is no specific reader (e.g. proprietary laboratory formats). The reader uses a header file that describes a single EEG. This file is an ASCII file with the extension “.vhdr”. It normally gets the same base name as the raw data EEG described in it. The header file is stored in the raw data folder of the workspace.

The format of the header file is based on the Windows® INI format. It consists of various named sections containing keywords/values. Here is an extract from a header file:

```
Brain Vision Data Exchange Header File Version 1.0
; Data created from history path:
; P300b/Raw Data/Filters/Segmentation/BaselineCorrection/Average

[Common Infos]
DataFile=P300b_Average.dat
MarkerFile=P300b_Average.vmrk
DataFormat=ASCII
; Data orientation:  VECTORIZED=ch1,pt1,  ch1,pt2...,  MULTIPLEXED=ch1,pt1,
ch2,pt1 ...
DataOrientation=VECTORIZED
DataType=TIMEDOMAIN
NumberOfChannels=32
```

The first line identifies the header file and is mandatory.

A semicolon at the beginning of a line identifies a comment. Comments are ignored by the reader. Blank lines are also ignored. A section is identified by a line with a heading enclosed in square brackets. The header extract above, for example, contains the Common Infos section. A header file can contain an unlimited number of sections.

The lines that follow contain some of the keywords in this section together with the values assigned to them. A keyword can only occur once in a section. Its meaning depends on the section in which it occurs. There must not be a space before or after the equals sign. Most predefined keywords have a predefined value. This is used by the reader if a keyword is not found.

If you want to create a header file, it is best to export an EEG using the Generic Data Export component. This creates a header that is compatible with the GDR. Set the parameters in such a way that the format of the exported file is as close as possible to that of the one to be imported. You can then adapt the header to meet your specific requirements.

The various predefined sections are listed below with their keywords, meaning and default values.

Common Infos		
This section contains general information on the EEG file.		
Keyword	Meaning	Default value
DataFile	Name of the EEG file. If the name does not contain a path, it is assumed that the EEG file is in the same folder as the header file. The placeholder <i>\$b</i> can be used in the file name. It is replaced by the base name of the header file when the file is read in. Example: If the name of the header file is <i>Test.vhdr</i> , the entry DataFile=\$b-EEG.dat is interpreted as DataFile=Test-EEG.dat .	None, a value must be specified.
MarkerFile	Optional marker file. The marker file contains a list of markers assigned to the EEG. If no path is specified explicitly, the marker file is searched for in the folder containing the header file. The format of the marker file is explained below. The placeholder <i>\$b</i> can be used in the file name.	-
DataFormat	Data format. Possible values: ASCII, BINARY	ASCII
DataOrientation	Data orientation. Possible values: VECTORIZED The file begins with all the data points of the first channel, followed by all the data points of the second channel, and so on. MULTIPLEXED All the channels come one after the other for every data point. In other words, the data structure is multiplexed.	MULTIPLEXED

COMMON INFOS

COMMON INFOS
(CONTINUED)

Keyword	Meaning	Default value
DataType	Data type. Possible values: TIMEDOMAIN The data is in the time domain. FREQUENCYDOMAIN The data is in the frequency domain. FREQUENCYDOMAIN_COMPLEX The data takes the form of complex frequency values. Each real value is followed by an imaginary value. TIMEFREQUENCYDOMAIN The data exists in several layers, as in the case of the continuous wavelet transform, for example. Each channel is represented by a vector of data at a point in time. TIMEFREQUENCYDOMAIN_COMPLEX This type corresponds to TIMEFREQUENCYDOMAIN, except that here each value takes the form of a complex number.	TIMEDOMAIN
NumberOfChannels	Number of channels in the EEG file.	None, a value must be specified.
SamplingInterval	Sampling interval. The interval is specified in μ s in the time domain and in hertz in the frequency domain.	None, a value must be specified.
Averaged	This indicates whether the data set to be read in has been averaged. It is particularly relevant to the enabling and disabling of transforms on the Transformations menu. Possible values: YES – Yes, the data set represents data that has been averaged. NO – No, the data set represents data that has not been averaged.	NO
AveragedSegments	Number of segments included in averaging. This value is only evaluated when “Averaged=YES” is set.	0
SegmentDataPoints	If the data is segmented evenly, the number of data points per segment can be specified at this point.	0

Keyword	Meaning	Default value
SegmentationType	Segmentation type. Like Averaged, this variable is relevant to the enabling and disabling of transforms on the Analyzer's Transformations menu. Possible values: NOTSEGMENTED The data set has not been segmented. MARKERBASED The data set has been segmented on the basis of one or more marker positions. All segments have the same length. FIXTIME Segmentation was based on fixed times. All segments have the same length.	NOTSEGMENTED
DataPoints	Number of data points in the EEG file. If no predefined value has been specified, the data is read in up to the end of the file. In the case of binary data, the TrailerSize parameter in the [Binary Infos] section can be set as an alternative.	0
Layers	Number of layers in a multilayer EEG of the type <i>TIMEFREQUENCYDOMAIN(_COMPLEX)</i>	1
LayerLowerLimit	Lower limit in multilayer data. In the case of the type <i>TIMEFREQUENCYDOMAIN(_COMPLEX)</i> , the unit is hertz.	0
LayerUpperLimit	Upper limit in multilayer data	0
LayerFunction	Function that describes the intervals between the layers of multilayer data. Possible values: LINEAR Linear function LOGARITHMIC Logarithmic function	LINEAR

COMMON INFOS
(CONTINUED)

ASCII Infos This section is only relevant if ASCII is set for DataFormat in the Common Infos section.		
Keyword	Meaning	Default value
DecimalSymbol	Decimal symbol used in the EEG file. This symbol can be either a point or a comma. In the header file, the decimal symbol is always a point.	Point (.)
SkipLines	Number of header lines to be skipped	0
SkipColumns	Number of columns to be skipped at the beginning of a line	0

ASCII INFOS

Channel Infos Channel information. This section lists the individual channels and their properties.		
Keyword	Meaning	Default value
Ch<x>. x stands for the channel number. In other words, the keyword for the first channel is Ch1, for the second channel Ch2, etc.	Individual properties for the channel are specified separated by commas: <channel name>,<reference channel name>,<resolution in "unit">,<unit> Example: Ch1=Fp1,,1 The first channel has the channel name Fp1. The common reference channel is taken as the reference channel because no entry has been made. The resolution is 1 µV. The resolution is the value by which the value of the data point is multiplied to convert it to µV.	<channel number>,,1,µV. For channel 1, for example: Ch1=1,,1

CHANNEL INFOS

Binary Infos This section is only relevant if BINARY is set for DataFormat in the Common Infos section.		
Keyword	Meaning	Default value
BinaryFormat	Binary format. Possible values: IEEE_FLOAT_32 IEEE floating-point format, single precision, 4 bytes per value INT_16 16-bit signed integer UINT_16 16-bit unsigned integer	INT_16
ChannelOffset	Channel offset at which the data starts. The offset is only relevant to vectorized data. ChannelOffset and DataOffset can be used simultaneously.	0
DataOffset	Size of the offset in the file at which the actual data starts	0
SegmentHeaderSize	If the data is segmented evenly, the size of the segment header can be entered here in bytes.	0
TrailerSize	Size of the trailer of the EEG file in bytes. This parameter can be specified as an alternative to DataPoints in Common Infos in order to stop reading in the data before the end of the EEG file is reached.	0
UseBigEndianOrder	This only applies to integer formats. It specifies whether big endian order is used, i.e. whether the most significant byte is stored first (Macintosh, Sun). Possible values: YES Yes, big endian order is used. NO No, little endian order is used (corresponds to the Intel specification).	NO

BINARY INFOS

Coordinates Coordinates are listed here.		
Keyword	Meaning	Default value
Ch<x> “x” stands for the channel number. In other words, the keyword for the first channel is Ch1, for the second channel Ch2, etc.	Coordinates of an individual channel in the form: <radius>,<theta>,<phi> Example: Ch1=1,-92,-72 The coordinate system of the Analyzer is described in Appendix B.	If the value is not listed here, the Analyzer uses the electrode name of the channel, searches for the coordinates in the 10/10 system and uses them. If the channel name is unknown, the coordinates are set internally to 0,0,0.

COORDINATES

GDR-compatible marker file

The marker file has a similar structure to the header file with sections and keywords. It should have the file name extension “.vmrk” and the same base name as the associated EEG file.

The first line identifies the marker file, as follows:

```
Brain Vision Data Exchange Marker File Version 1.0
```

The various predefined sections are listed below together with their keywords, meaning and default values.

Common Infos This section contains general information on the marker file.		
Keyword	Meaning	Default value
DataFile	Name of the EEG file. If the name does not contain a path, it is assumed that the EEG file is in the same folder as the marker file. This information is not evaluated by the GDR.	-

MARKER: COMMON
INFOS

Marker Infos Marker information. The individual markers and their properties are listed in this section.		
Keyword	Meaning	Default value
Mk<x>. “x” stands for the marker number. In other words, the keyword for the first marker is Mk1, for the second marker Mk2, etc.	<p>Individual properties for the marker are specified separated by commas: <type>,<description>,<position>, <points>,<channel number>,<date> Example: Mk1=Time 0,,26,1,0 The first marker in this example has the type “Time 0”, no description, its position is at data point 26, its length is 1 data point, and the channel number is 0, which means that this marker applies to all channels. The date is optional. It is only evaluated if the marker type is New Segment. The date has the following format: 4 digits = year 2 digits = month 2 digits = day 2 digits = hour (24-hour system) 2 digits = minute 2 digits = second 6 digits = microsecond The result is a time resolution of a microsecond. Example: 19990311140312000000 means 11 March 1999, 14:03:12.003012</p>	-

MARKER INFOS

16.2 Importing markers and channel positions

To read in additional data along with the raw data (output files from your stimulator, for example), you can create a Basic macro that creates a new history node. This node inherits the data from the raw EEG. You can, however, delete markers and generate them anew. You can also change the names and positions of channels. You can use the Basic macro to open and read out ASCII files.

You will find examples of macros for reading in channel positions and markers in the BrainVision Analyzer Macro Cookbook.

17 Printout

File > Print > Print allows you to print the currently displayed section of the EEG. The usual Windows® dialog box for selecting the printer appears.

File > Print > Print Preview gives you a print preview. However, the actual output on the printer may differ from what you see in the preview. This depends on the quality of the printer driver you are using and is something over which we unfortunately have no influence.

If you print from the Ribbon, the active main view and its transient views are printed. If you want to print only the main view or only a transient view, you choose the **Print** command from the context menu of the relevant view.



To set headers, footers and margins, you choose the **File > Configuration > Preferences** menu command and then select the **Graphics Export/Output** tab.

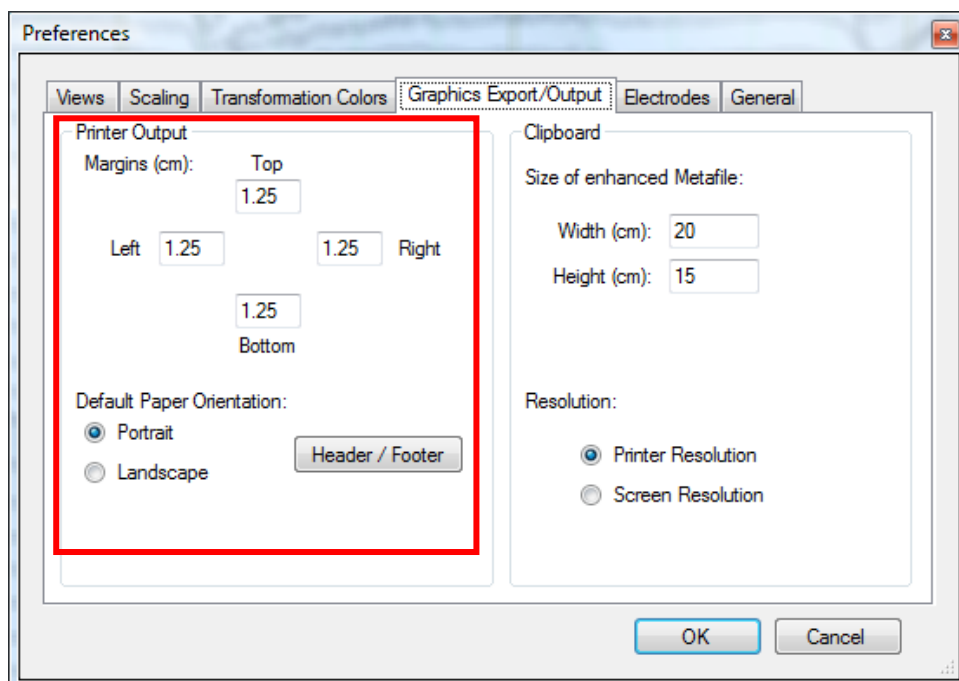


FIGURE 17—1 PRINTER SETTINGS

On this tab, you can specify whether the default orientation is portrait or landscape (by selecting the **Portrait** or **Landscape** radio button). Under **Margins (cm)**, you can specify the left (**Left** text box), right (**Right**), top (**Top**) and bottom (**Bottom**) margins of the printout in centimeters.

When printed, the view has the same proportions as the print area. It is easiest to check the positioning of view tools etc. in the printout if you adjust the size of the view window beforehand so that it has approximately the same proportions as the print area.

TIP

The **Header / Footer** button displays a dialog box in which you can configure headers and footers.

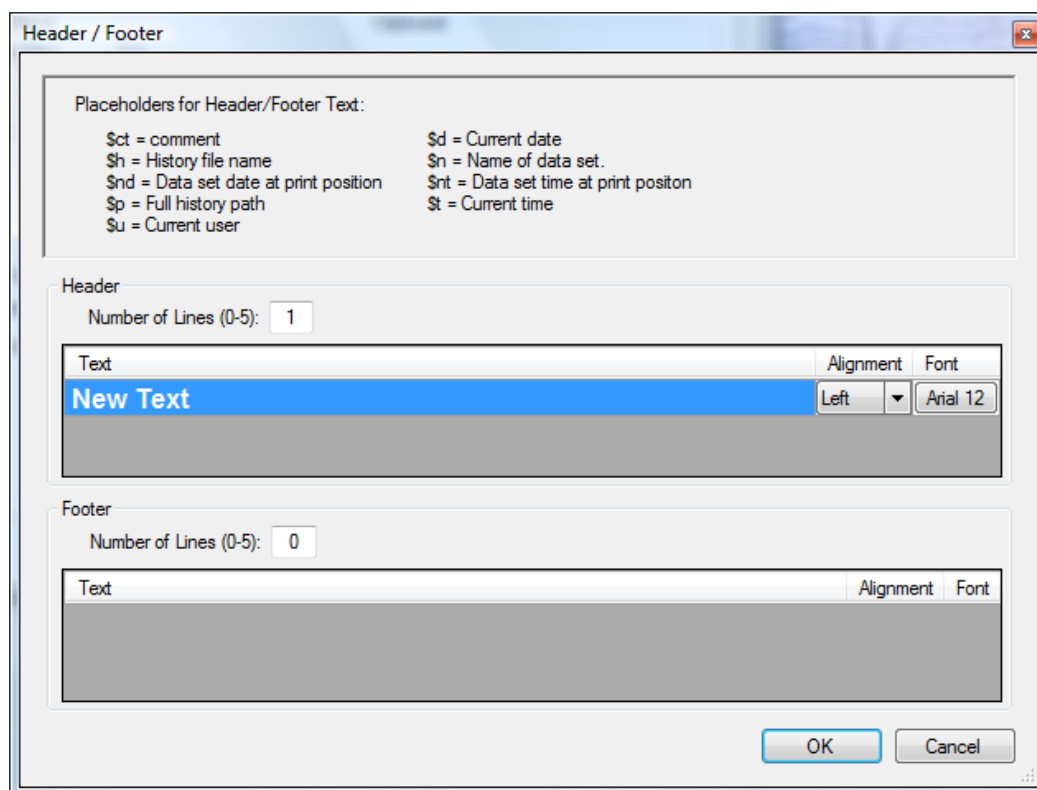


FIGURE 17—2 DIALOG BOX FOR DEFINING HEADERS AND FOOTERS

In this dialog box, you can define up to five headers and footers that are to appear in the printout. The dialog box contains two sections: **Header** and **Footer**. You specify the following:

- **Number of Lines:** Number of headers and footers

For each header and footer:

- **Text:** Here, you enter the text that you want to appear in the header/footer. You can also use placeholders, which are replaced with current values during printing or for the print preview. An example of a placeholder is \$n. If this placeholder is used anywhere in the text, the program replaces it during printing with the name of the data set to be printed. You will find a list of all the available placeholders below.
- **Alignment:** Here, you can specify whether the text is to be left-aligned (**Left**), centered (**Center**) or right-aligned (**Right**).
- **Font:** This button displays the Windows® font dialog box, where you can choose the font to be used for the text.

Placeholder	Meaning
\$ct	Comment: The comment you can enter for each data set is placed here. To enter a comment for a data set, move the mouse pointer to the data set in the History Explorer and right-click it. A context menu appears. Choose the “Comment” command and enter the comment.
\$d	Current date
\$h	Name of the history file
\$n	Name of the current data set
\$nd	Date of the data set at the beginning of the section being printed. Note that not all EEG formats contain date information.
\$nt	Time of the data set at the beginning of the section being printed. Note that not all EEG formats contain time information. In this case, it is assumed that recording begins at 0:00 hours. This means you see the time offset of the section being printed.
\$p	Full history path containing all the intermediate steps from the raw EEG to the current data set.
\$t	Current time
\$u	Computer user who is currently logged in

FIGURE 17—3 PLACEHOLDERS AND THEIR MEANING


If the printing facilities offered by the Analyzer do not meet your requirements, you can export graphics to programs such as MS Word, MS PowerPoint and Corel Draw for further processing, as described in chapter 18, “Graphical Export”.

18 Graphical export

You can export the currently displayed EEG to the clipboard as a vector graphic and process it further in other programs such as Word, PowerPoint or Corel Draw.

You can also export the currently displayed EEG to an image file. The graphics formats EMF, BMP, PNG and JPEG are available to you.

The functions described here allow you to export the active main view and its transient views. If you want to export only the main view or only a transient view, you choose the **Save as File** command from the context menu of the relevant view.

To export the EEG to the clipboard, you click the **Copy**  button on the toolbar.

EXPORTING TO THE
CLIPBOARD

Open the destination application (Microsoft Word, for example), and then choose **Edit > Paste**. The graphic appears in the current window of the destination application.

Alternatively, you can use the standard Windows® keys for this operation: **⌘-C** to copy the graphic from the Analyzer and **⌘-V** to paste it into most destination applications.

The Enhanced Metafile (EMF) format is used for the export. Most Windows® graphics programs support this format. You can change the graphic's default size of 16 x 12 cm by choosing **File > Configuration > Preferences** and then selecting the **Graphics Export/Output** tab. In the **Width (cm)** and **Height (cm)** text boxes, you then specify the width and height of the graphic.

In the **Resolution** group box, you can specify whether you want to use the screen resolution (by selecting the **Screen Resolution** radio button) or the generally higher printer resolution (by selecting the **Printer Resolution** radio button). Note that some programs have problems processing EMF data in printer resolution.

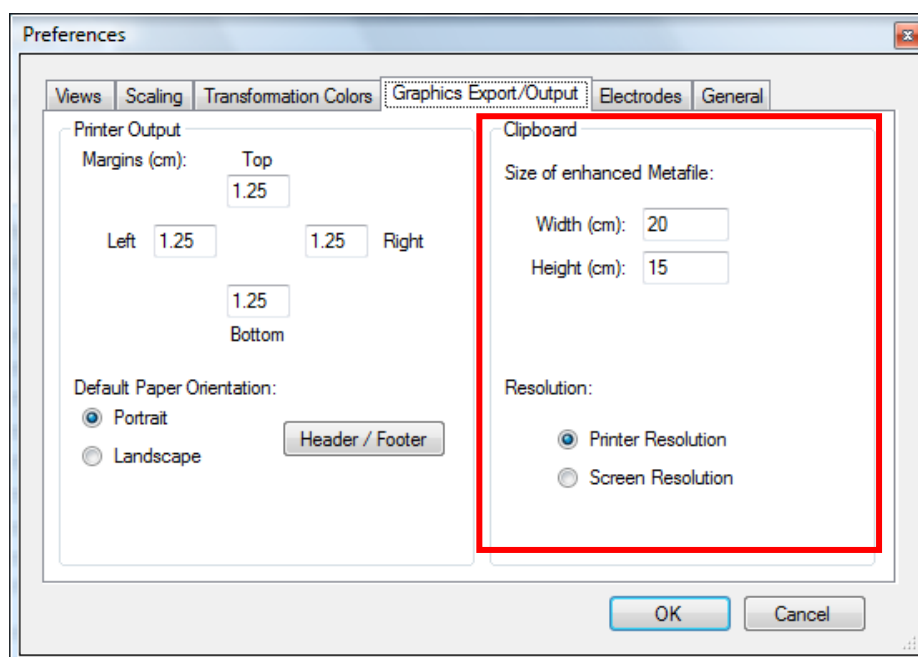


FIGURE 18—1 PREFERENCES DIALOG BOX FOR EXPORTING VIA THE CLIPBOARD

File > Print > Print to Graphics exports the current view to a file. A file selection dialog box appears. You choose the format of the file to be exported from the **Save as type** drop-down list in the lower part of the dialog box.

EXPORTING TO A FILE

As when exporting to the clipboard, you specify the size and resolution of the graphics file by choosing **File > Configuration > Preferences** and then selecting the **Graphics Export/Output** tab.

19 Appending multiple raw data sets

You can append multiple raw EEGs in order to process them as a single data set. This may be necessary if you interrupt data acquisition and want to resume it subsequently with a new output file.

The raw EEGs are not actually appended. Instead, they are merely assigned to a single history file (i.e. they are linked “virtually”).

The prerequisite for appending one raw EEG to another is that the main properties of the two data sets – channel name, sampling rate, etc. – must be identical.



To append a raw EEG, you first select the initial file in the History Explorer. To do this, you right-click the corresponding book icon and then choose **Append File...** from the context menu that appears.

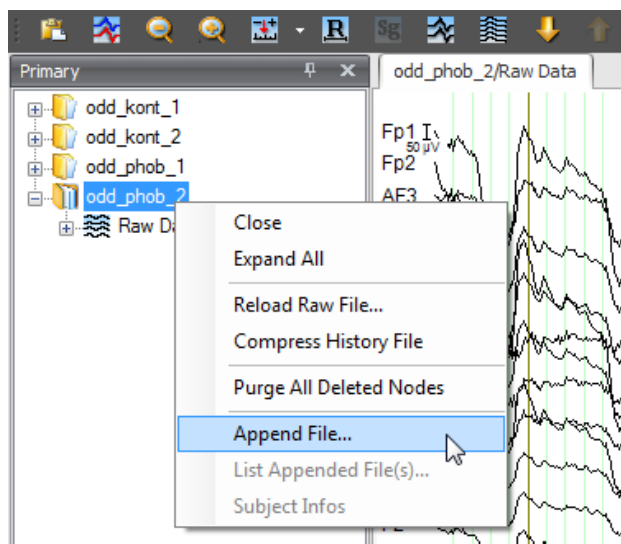


FIGURE 19—1 CONTEXT MENU OF A BOOK ICON

A warning is issued to the effect that any transforms you have run with this history file will be lost.

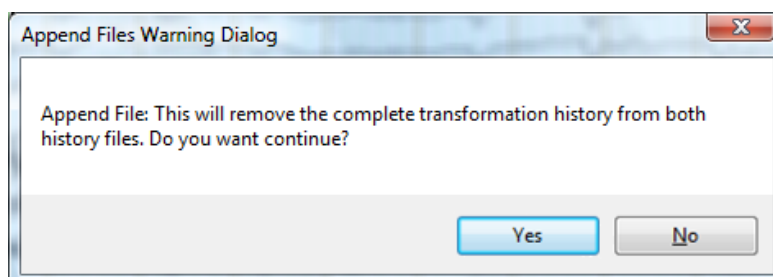


FIGURE 19—2 WARNING

Click the **Yes** button. A dialog box appears, in which you can select the raw data EEG to be appended.

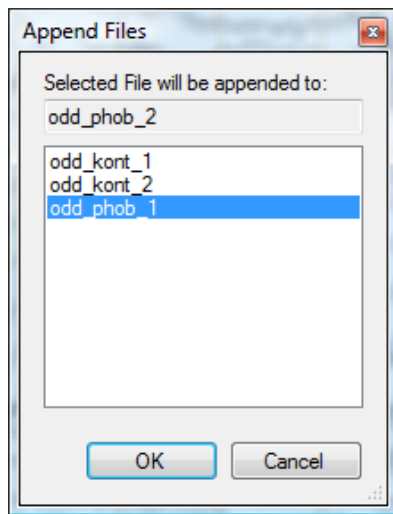


FIGURE 19—3 APPEND FILES DIALOG BOX FOR SELECTING A RAW DATA EEG

Click the **OK** button. The first history file is modified and the second one removed. The icon changes from a book into a stack of books.

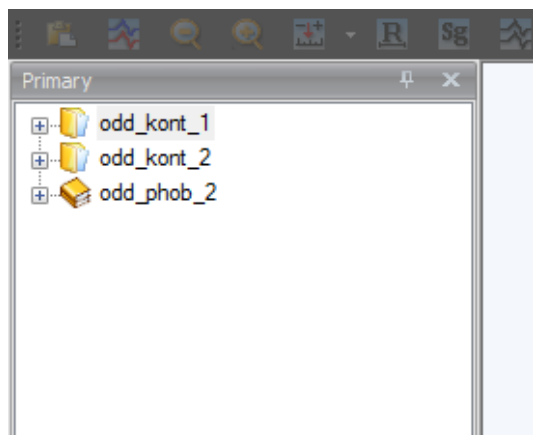


FIGURE 19—4 ICON FOR APPENDED RAW EEGS

You can also append other raw EEGs to this history file.

To find out which raw EEGs have been appended to the history file, you can right-click the corresponding book icon to display the context menu again. This now also contains the **List Appended File(s)** command. When you choose this, a dialog box appears. This contains information on the initial data set and the appended data sets.

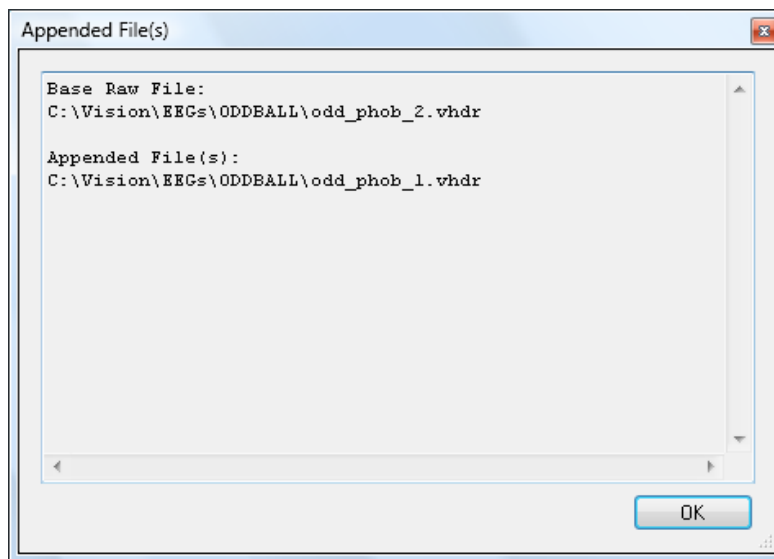


FIGURE 19—5 DIALOG BOX CONTAINING APPENDED DATA SETS

To cancel the appending of the data sets, you have to terminate the program and delete the associated history file (xxx.ehst) and history information file (xxx.hfinf) in the history file folder. The next time you start the Analyzer up, these files are automatically generated anew, and the EEGs are thus separated.

20 Solutions

The Analyzer offers many different options for data analysis and manipulation and program control.

INTRODUCTION

Data is analyzed and manipulated primarily by means of transforms, which contain all the basic steps for calculating evoked potentials, as well as many other standard methods used in neurophysiological research.

It is also possible to create user-defined macros for manipulating, importing and exporting data and controlling the Analyzer. The advantage of using macros is that individual solutions can be implemented with relatively little effort.

In order to create macros, however, you need a certain amount of programming knowledge. It is also essential to document macros in order to be able to follow what has been done. If the documentation is not stored together with the macros, there is a risk that the required documents will be lost or that they will apply to the wrong version of the macro. Finally, macros can be easily changed because they are easy to read, although this can also have undesirable side effects.

Solutions are used to counteract the disadvantages of macros. These are lightweight programs for dealing with a wide variety of problems and tasks. A solution is an individual file containing the executable code and the associated documentation.

The solutions are made available to you by Brain Products GmbH. You can install or delete solutions subsequently without any problems.

In contrast to macros, the source text of solutions cannot be modified. Consequently, the solution is always used unchanged.

You will find a collection of solutions in the **\Solutions** subfolder on the BrainVision CD. To install the solutions, you use the **InstallSolutions.exe** installation file, which is also located in the **\Solutions** subfolder. There are solutions, for example, for ECG and EMG processing, marker importing and ASCII exporting. You will find more solutions on the Brain Products website.

To access the base folder of the solutions, you choose **File > Configuration > Administration**. In the **Solutions Path** text box, you specify a folder, or you can use the **Browse** button to select one.

CREATING A FOLDER

If you are working in a network with several colleagues, we recommend using a shared base folder for the solutions.



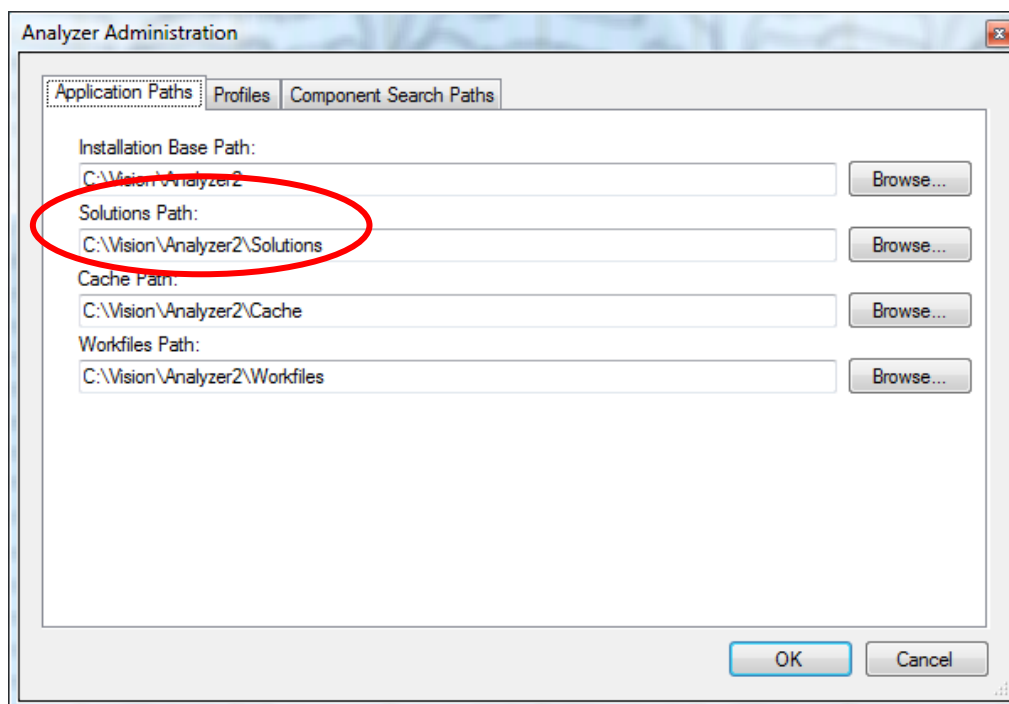


FIGURE 20—1 SELECTING THE BASE FOLDER FOR THE SOLUTIONS IN THE ANALYZER ADMINISTRATION DIALOG BOX

If you use the standard installation program, the solutions are automatically installed in thematically arranged subfolders. You can also install the solutions manually with separate categorization if you set up user-defined subfolders.

INSTALLATION

You can use Windows® Explorer to delete individual solutions and subfolders.

It is also possible to copy user-defined Analyzer macros to the solutions folder or a subfolder. These will then also appear on the **Solutions** tab.

The solutions appear on the **Solutions** tab on the Ribbon. The structure of the tab corresponds to the structure of the base folder and its subfolders. Consequently, each subfolder of the base folder is represented as a group. The solutions contained in the subfolders appear as buttons in the groups.

DISPLAY ON THE RIBBON

Solutions files have the file name extension ".vaso" (which is an abbreviation of **V**ision **A**nalyzer **S**olutions).

In our example the base folder is **C: \Vision\Analyzer2\Solutions**. It contains the subfolders **EKG** and **EMG**.

The solution for the **EKG** subfolder is called **EKG Markers.vaso**. This folder also contains an image for the button (**EKG Markers.png**).

The solution for the **EMG** subfolder is called **EMG Onset Search.vaso**. This folder also contains an image for the button (**EMG Onset Search.png**).

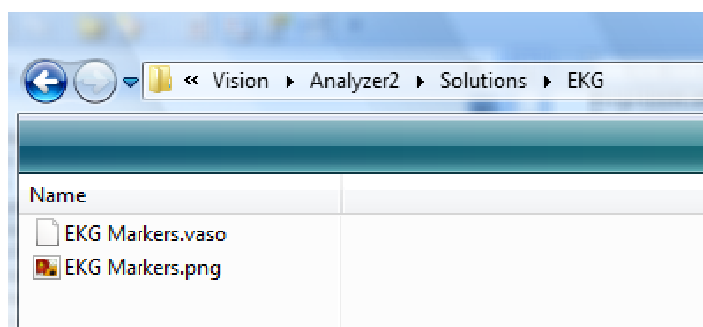


FIGURE 20—2 CONTENTS OF THE EKG MARKERS SUBFOLDER

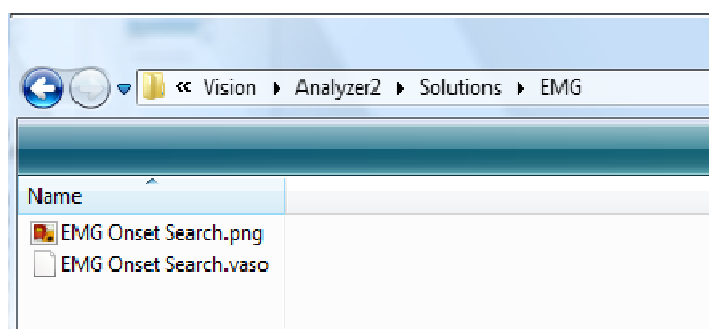


FIGURE 20—3 CONTENTS OF THE EMG ONSET SUBFOLDER

The **Solutions** tab for our example thus has the following structure:

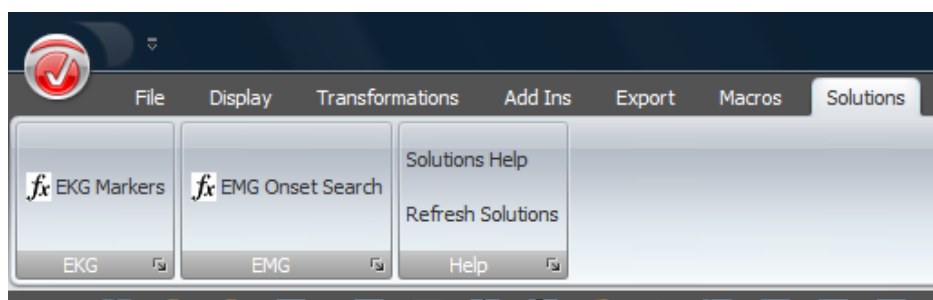


FIGURE 20—4 SOLUTIONS TAB

Proceed as follows to assign an icon to the button for a solution: In the subfolder of the solution base folder, add the image for the solution button as a bitmap or PNG image. It has the same name as the associated VASO file.

The **Refresh Solutions** button updates the Ribbon when you have made changes to the Solutions folder.

To display the documentation for the solutions, you choose **Solutions > Help**. The **Solutions Help Explorer** appears. The Solutions Help Explorer contains all the solutions and macros contained in the solutions folder.

If you click an item in the Explorer, a brief description appears in the **Description** text box. A double-click displays the associated documentation in full in a separate window. Alternatively, you can right-click the item and choose **Show Documentation** from the context menu.

If you double-click a macro, its source code is displayed.

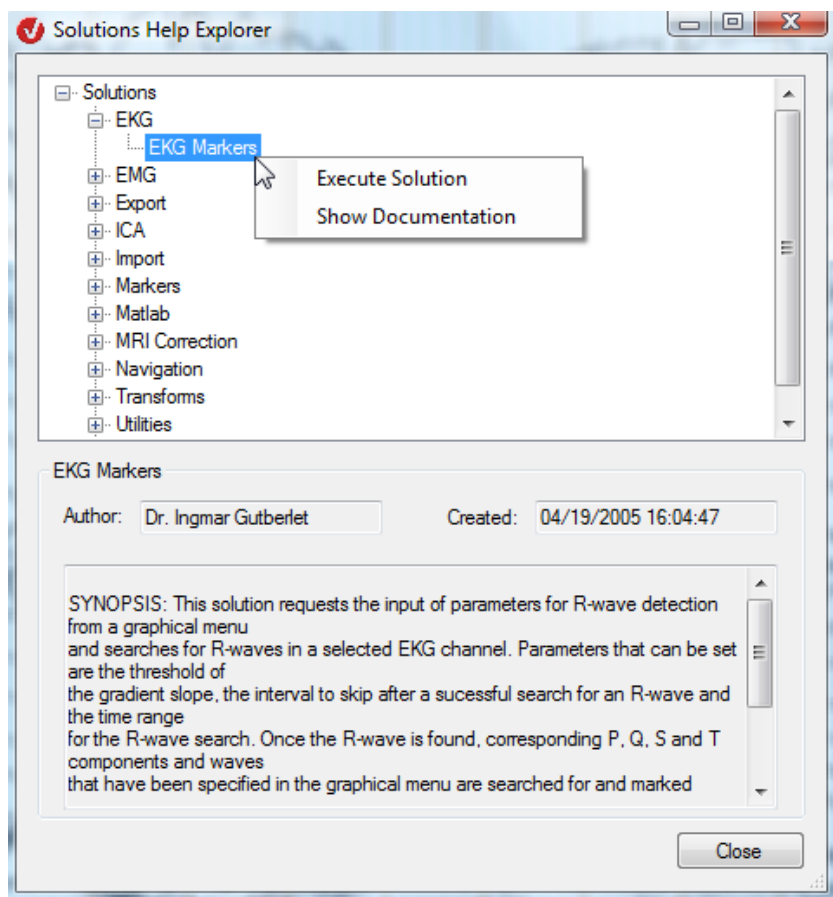


FIGURE 20—5 SOLUTIONS HELP EXPLORER

To apply a solution, you open a history file and click the solution on the **Solutions** tab. **APPLYING A SOLUTION** Alternatively, you can open the Solutions Help Explorer, right-click the solution in the Explorer and then choose **Execute Solution** from the context menu that appears.

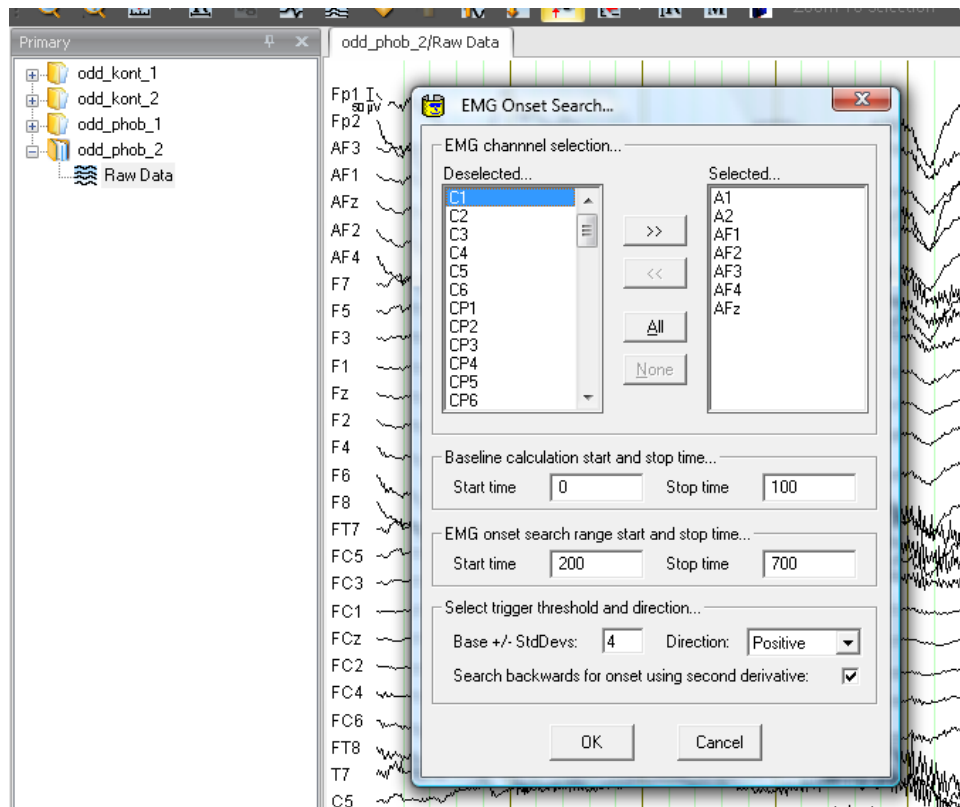


FIGURE 20—6 APPLYING THE EMG ONSET SOLUTION

Please contact Brain Products GmbH directly if you are interested in other solutions.



21 Analyzer help

You will find a list of the installed components and information on the software in the **Help** group on the **Help** tab.

You can also choose **Help > Documentation** to get the Analyzer's manuals.

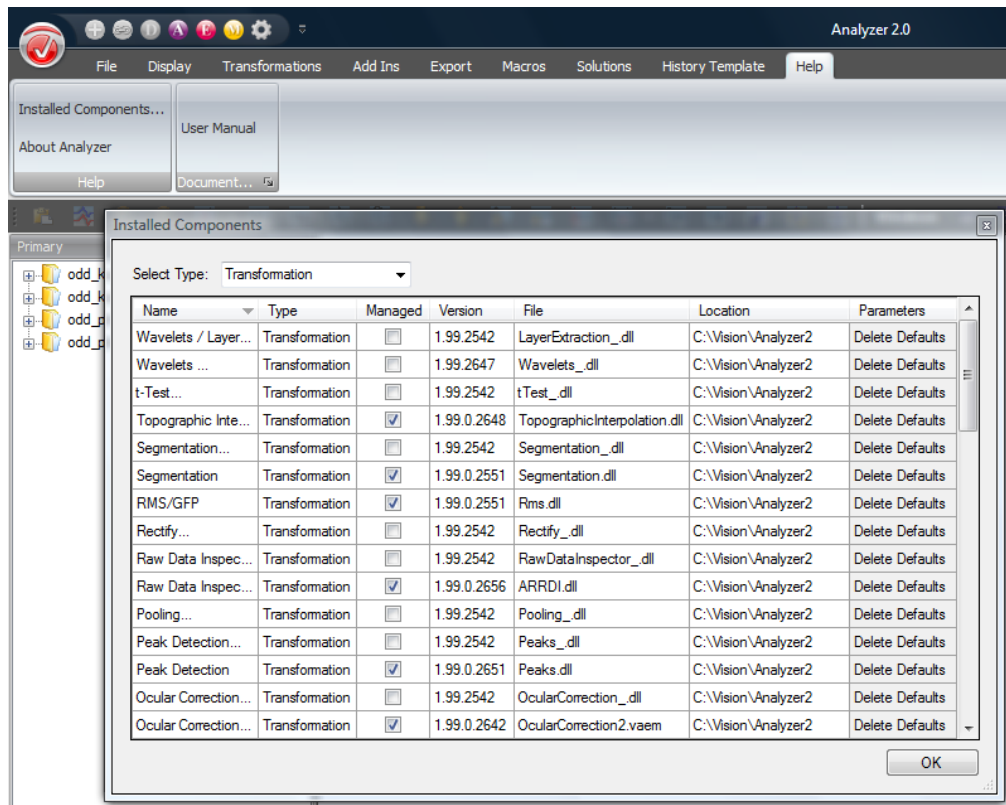


ABB. 21—1 LIST OF INSTALLED COMPONENTS ON THE HELP TAB

In the **Installed Components** dialog box, you can reset the default values of the parameters of the component by clicking **Delete Defaults** in the **Parameters** column. This is only possible for those component types that use parameters.

Appendix A: Raw data on removable media

Removable media are drives whose media are interchangeable – CD-ROM, ZIP and MO drives, for example.

If you use the same drive as a raw data source for different workspaces, a raw EEG may appear in several workspaces. This is because the Analyzer usually analyzes all raw EEGs in the raw data folder when the workspace is changed or the program is started up and creates history files where necessary.

The following rule applies to all removable media in order to simplify handling:

- (1) If there is at least one history file in the current workspace for which there is no equivalent in the form of a raw data set on the removable medium, and
- (2) if there are EEGs on the removable medium that have not already been read into the current workspace,

you are asked whether you want to add the raw data to the current workspace.

Note that the program can only detect removable media on the current PC, not on the network.



Appendix B: Electrode coordinate system

The electrode coordinate system used in the Analyzer is explained below. This coordinate system is used wherever electrode positions are needed, such as for mapping and for positioning electrodes in the head view.

You can change the electrode positions using the Edit Channels transform.

The axis system is defined in such a way that the z-axis runs through the vertex. The x-axis points to the right, and the y-axis to the front.

Spherical coordinates are used to specify the position of a point on the head. A set of coordinates consists of the three variables r , θ , and ϕ (radius, theta and phi).

The radius (r) specifies how far the point is away from the center of the coordinate system. It is specified in millimeters. The only exceptions are $r = 0$ and $r = 1$. $r = 0$ signifies an invalid position, for instance when the position of an electrode is not known, and $r = 1$ means that a standard diameter has been chosen for the radius. This can be used when the surface of the head is approximated by the surface of a sphere.

ϕ specifies the angle between the x-axis and the projection of the line connecting the point and the coordinate origin on the xy plane. $\phi > 0$ applies to the front right and rear left quarter of the sphere. $\phi < 0$ is for the front left and rear right.

θ is the angle between the z-axis and the line connecting the point and coordinate origin. In the left hemisphere, θ is < 0 . In the right hemisphere, $\theta > 0$.

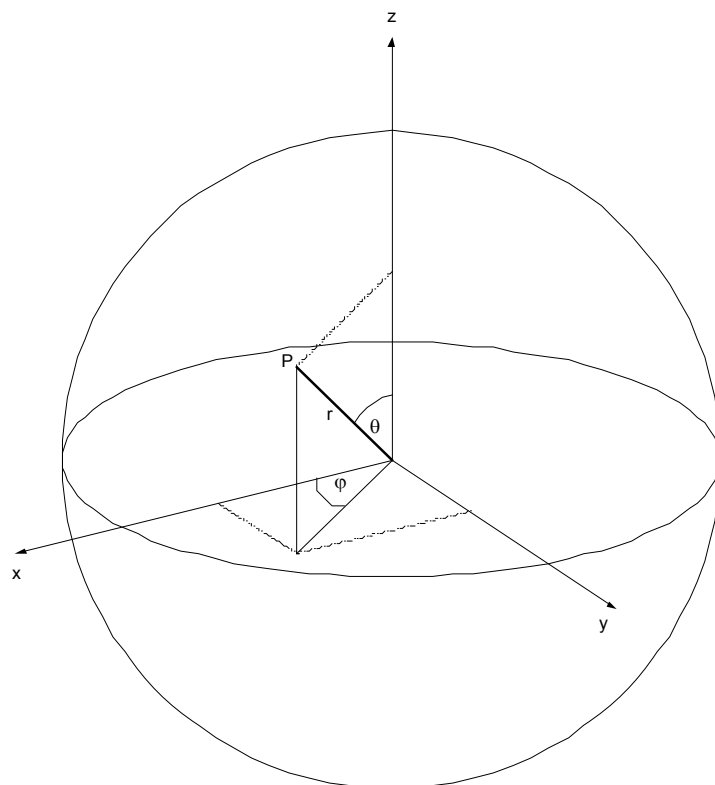


FIGURE B—1 COORDINATE SYSTEM

Appendix C: Markers (time markers)

All the markers used by the Analyzer are time markers. Time markers mark a point in time or a period of time in the EEG.

A marker can be an item of stimulus information that is used to ascertain evoked potential, but it can also mark a new segment or indicate that a DC correction was carried out at a certain time. Markers are an aid to orientation for segmentation and other transforms.

All markers in the Analyzer have the following five properties:

- **Type:** The type specifies the marker class, such as “Stimulus” or “New Segment”. There are different predefined types for specific tasks (see figure C—1). The color of the marker in the view depends on the type. Since the types are just ordinary texts, you can create new types by means of a macro, for example, or by setting markers manually.
- **Description:** This is the description given to a marker. It can also be regarded as a subclass. When you select markers (during segmentation, for example), in most cases you can make a selection by type and description. The description is also saved as text, and there are therefore no restrictions on its contents. The Analyzer or its reader components construct some texts (for EEG formats, for example) that store stimuli as numeric values. If an EEG contains a stimulus with the value 1, the reader component converts this value to the text “S 1”. The description is generally shown when the markers are displayed.
- **Position:** The position defines the data point at which the marker occurs in the EEG.
- **Points:** These are the data points over which a marker extends. In most cases, markers have a length of one point. There is only one type of predefined marker that extends across more than one point: the Bad Interval marker. This marker is set when you use the Data Inspector or Artifact Rejection transforms.
- **Channel Number:** A marker can be assigned to one or all channels (channel number o).

The New Segment marker also has the Date Time property, which means that the date and time of its occurrence is stored in every marker of this type, provided this information can be extracted from the raw EEG.

Type	Function	Color in view
Bad Interval	This indicates a bad interval owing to artifacts.	Pink or gray
Comment	This is used for a comment.	Black
DC Correction	A DC correction occurs with EEGs recorded using a DC acquisition system. There is usually a jump in the voltage levels of the data at this time.	Yellow
New Segment	This is used to mark discontinuities in the EEG. These include interruptions in the recording but also segmentation.	Green
Peak	This marker is set by peak detection routines.	Black
Response	This is the response of the subject.	Blue
This indicates a stimulus.	This indicates a stimulus.	Red
Threshold	This is set by the Level Trigger transform. Because of its proximity to the stimulus marker, it is the same color in the view.	Red
Time o	Time zero marker. This marker only comes into play after averaging. It marks the boundary between the prestimulus and poststimulus.	Long, black, dashed line
Voltage	This marker causes most views to show the voltage and time on the relevant channel.	Black

FIGURE C—1 TABLE OF PREDEFINED MARKER TYPES

Appendix D: Keyboard shortcuts

The following table shows the functions of keys and key combinations in the Analyzer.

Whether and which shortcuts are active depends on which control element the focus is on. If these control elements support keyboard input (e.g. the right arrow key for the primary history data in the History Explorer), this keyboard input is ignored in the view.



If the focus is on a view, the following shortcuts are active:

	Right arrow	Moves the selection/highlighting (if present) to the right	
	Left arrow	Moves the selection/highlighting (if present) to the left	
	Page Up	Displays the previous channel group	
	Page Down	Displays the next channel group	
Ctrl +	Right arrow	Next interval	
Ctrl +	Left arrow	Previous interval	
Ctrl +	Up arrow	Increases the scaling	
Ctrl +	Down arrow	Decreases the scaling	
Ctrl +	+	Zooms in	Numeric keypad
Ctrl +	-	Zooms out	Numeric keypad
Ctrl +	+	Zooms in	Keyboard
Ctrl +	-	Zooms out	Keyboard
Ctrl + Shift	Right arrow	Next interval in the transient view	
Ctrl + Shift	Left arrow	Previous interval in the transient view	
Ctrl + Shift	Up arrow	Increases the scaling in the transient view	
Ctrl + Shift	Down arrow	Decreases the scaling in the transient view	
Ctrl + Shift	+	Zooms into the transient view	Numeric keypad
Ctrl + Shift	-	Zooms out of the transient view	Numeric keypad
Ctrl + Shift	+	Zooms into the transient view	Keyboard
Ctrl + Shift	-	Zooms out of the transient view	Keyboard
Ctrl +	C	Copies the view to the clipboard	
Ctrl +	S	Saves the active history template	
Ctrl +	Tab	Switches to the next view tab	
Ctrl + Shift	Tab	Switches to the previous view tab	
	Del	In the History Explorer, in the history template: deletes a data set or secondary history file	
	F2	In the History Explorer, in the history template: renames a data set or a secondary history file	

Appendix E: Installing a network license (USB)

The BrainVision Analyzer Professional Edition network license (referred to in the following as Analyzer) is protected software.

In order to be able to use this license, you need to install the HASP HL Net key (referred to in the following as the USB dongle) and the network license server. This can be done on any computer in the network.

BrainVision Analyzer Version 1.05.0003 or higher and Windows® XP Service Pack 2 or Windows® Vista. REQUIREMENTS

Make sure your computer is connected to the network before proceeding with installation.

INSTALLATION STEPS

- 1. Install the HASP HL device driver.

The installation program for the HASP HL device driver is in the **DongleNetwork** folder on the BrainVision CD. In this folder, double-click the **HASPUserSetup.exe** installation file and follow the instructions of the installation program. You get to the folder by choosing **Browse the CD** in the CD's welcome screen.

- 2. Connect the USB dongle.

When the LED on the USB dongle lights up, you know that the installation has been successful.

- 3. Install the HASP License Manager.

The HASP License Manager is in the **DongleNetwork** folder on the BrainVision CD. In this folder, double-click the **lmsetup.exe** file and follow the instructions of the installation program. Select **Service** as the installation type and automatic port enabling for the firewall.

- 4. Enable the port for the firewall.

If you are using a firewall other than the one supplied by the Windows® operating system, enable port 475 for TCP and UDP.

The BrainVision Analyzer network licenses are now available to you.

Note that the licenses are only available to you if the computer has been started, the dongle is inserted and a network connection is active.



In addition, make sure that no other Vision Analyzer network license (either a USB dongle or LPT dongle) is active on the network.



You can install the drivers and programs on several computers. Consequently, you can attach the USB dongle to another computer in the event of a server failure.

Appendix F: Command-line parameters

The Analyzer supports a number of command-line parameters. To enter these, select the MS-DOS prompt. A prompt appears. Change to the Vision folder by entering the command **cd <folder>**.

Example:

```
C:\>cd c:\Vision
```

You can call the Analyzer with additional parameters.

Example:

```
C:\Vision>Analyzer -new -pPrinter
```

Alternatively, create a copy of the Analyzer shortcut placed on the desktop during installation. Then right-click the icon of the copy and choose **Properties** from the context menu that appears. A dialog box appears. On the **Shortcut** tab, append the parameters in the **Target** text box to the existing text.

Example:

```
C:\Vision\Analyzer.exe
```

Change to:

```
C:\Vision\Analyzer.exe -new -pPrinter
```

In this way, you can create several shortcuts on the desktop for different parameters.

Now we come to the parameters.

“-m<Macro>” calls the specified macro at program startup.

Example:

```
C:\Vision\Analyzer.exe "-mCompress All"
```

This calls the macro Compress All after program startup. Quotation marks are only needed if the macro name contains a blank. Note that the macro name must come immediately after the -m with no intervening blank.

The -new parameter forces a new program instance of the Analyzer. When the Analyzer is called more than once, the existing program instance is used. This parameter suppresses this behavior.

Example:

```
C:\Vision\Analyzer.exe -new
```

The -p<Profile-File> parameter uses the described user profile file during the session.

Example:

```
C:\Vision\Analyzer.exe -pPrinter
```

You could, for example, save all the settings for optimum printing in the profile file named Printer.

It is possible to combine different parameter types. Note that -p is always executed before -m.

Appendix G: Shortcuts to raw data

In Windows® it is possible to create what are known as shortcuts. You can create a shortcut, for example, by using the mouse to drag a file from one folder to another in Windows® Explorer while holding down the **⌘Ctrl** and **⌘Shift** keys. This creates a small file that points to the actual file.

The Analyzer can work with shortcuts to raw EEG files. These are treated in exactly the same way as if the original file was in the folder. This enables you to set up a workspace containing raw EEGs from various folders by creating shortcuts to the various raw EEGs in the raw data folder of this workspace. A raw EEG file can therefore also be analyzed in different workspaces without having to be copied to these workspaces.

Appendix H: BrainVision Electrode Files

These XML files contain a list of electrode coordinates.

Any number of <Electrode> tags can be enclosed between <Electrodes> tags. The <Electrode> tags each contain the name and spherical coordinates (as described in Appendix B) of a single electrode.

Please specify the spherical coordinates as floating-point numbers with a decimal point (.) as the decimal separator. The following example shows how the file is structured:

```
<Electrodes defaults="true">
  <Electrode>
    <Name>Fplx</Name>
    <Radius>1</Radius>
    <Theta>-90.5</Theta>
    <Phi>-72</Phi>
  </Electrode>
  <Electrode>
    <Name>Fp2x</Name>
    <Radius>1</Radius>
    <Theta>90.5</Theta>
    <Phi>72</Phi>
  </Electrode>
</Electrodes>
```

The “defaults” attribute of the <Electrodes> tag can be used to control whether the electrodes list is to be interpreted as a complete list (when the value “false” is set) or if the list is to be added to an underlying list of standard Analyzer coordinates (when the value “true” is set). If no value is set, “false” is assumed.