Software Manual

encevis 1.5

Contents

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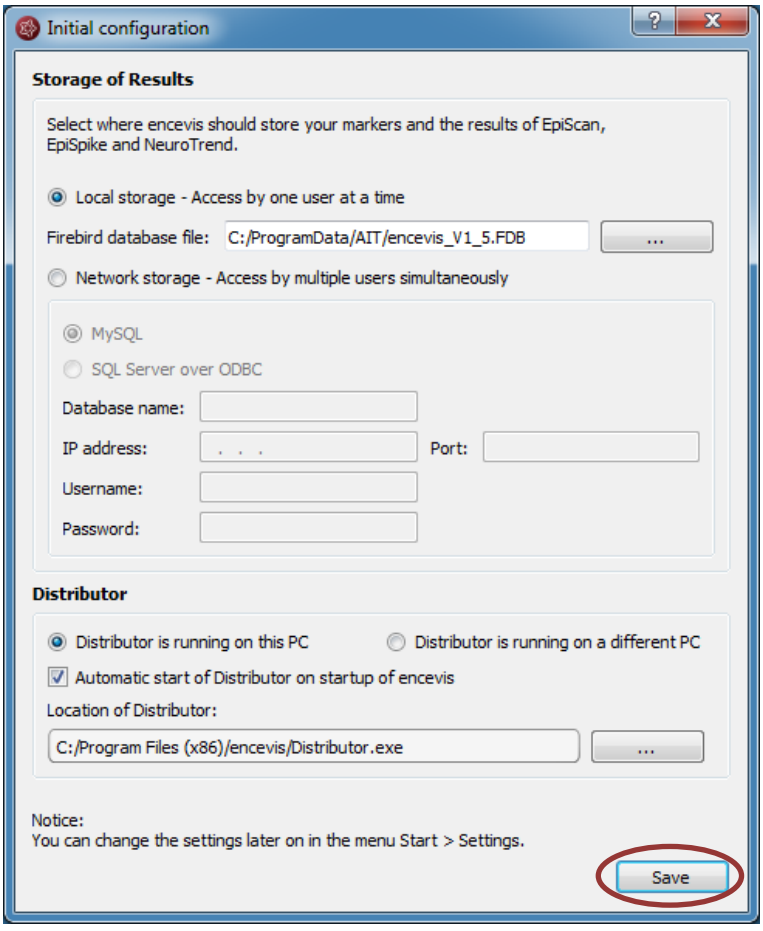
Quick Start Guide

Installation

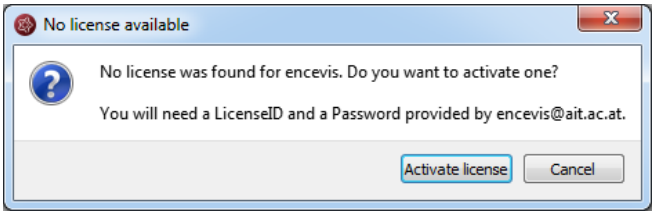
Once you have downloaded **encevis**, continue with the following steps:

1. Start the **encevisInstaller**, this will guide you through the installation process.
2. Start **encevis**.
3. The initial configuration window will pop up.
4. Press “**Save**”, to keep the default settings.

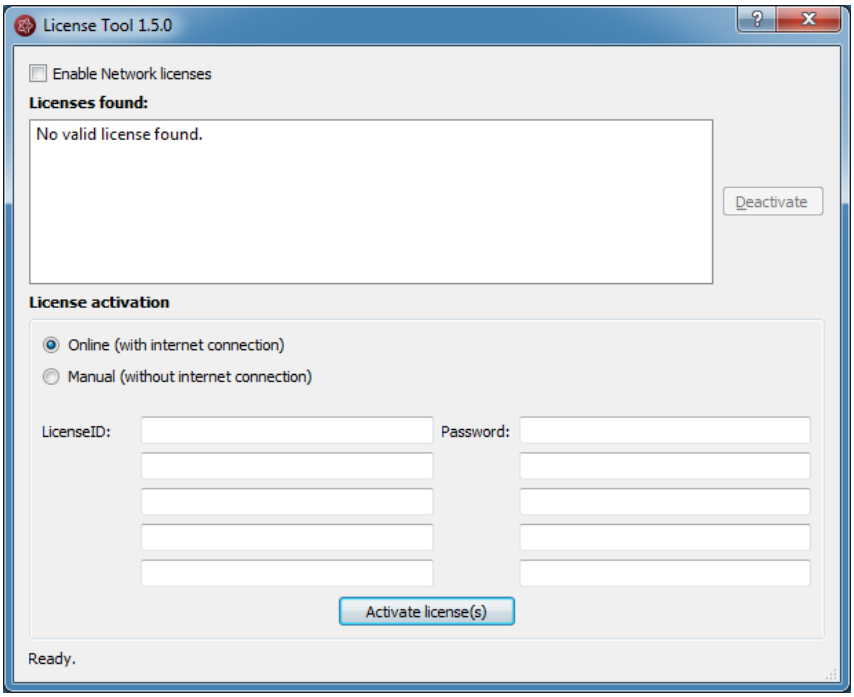


License activation

1. Start **encevis**.
2. Press the button “**Open EEG**”, the following window will pop up:

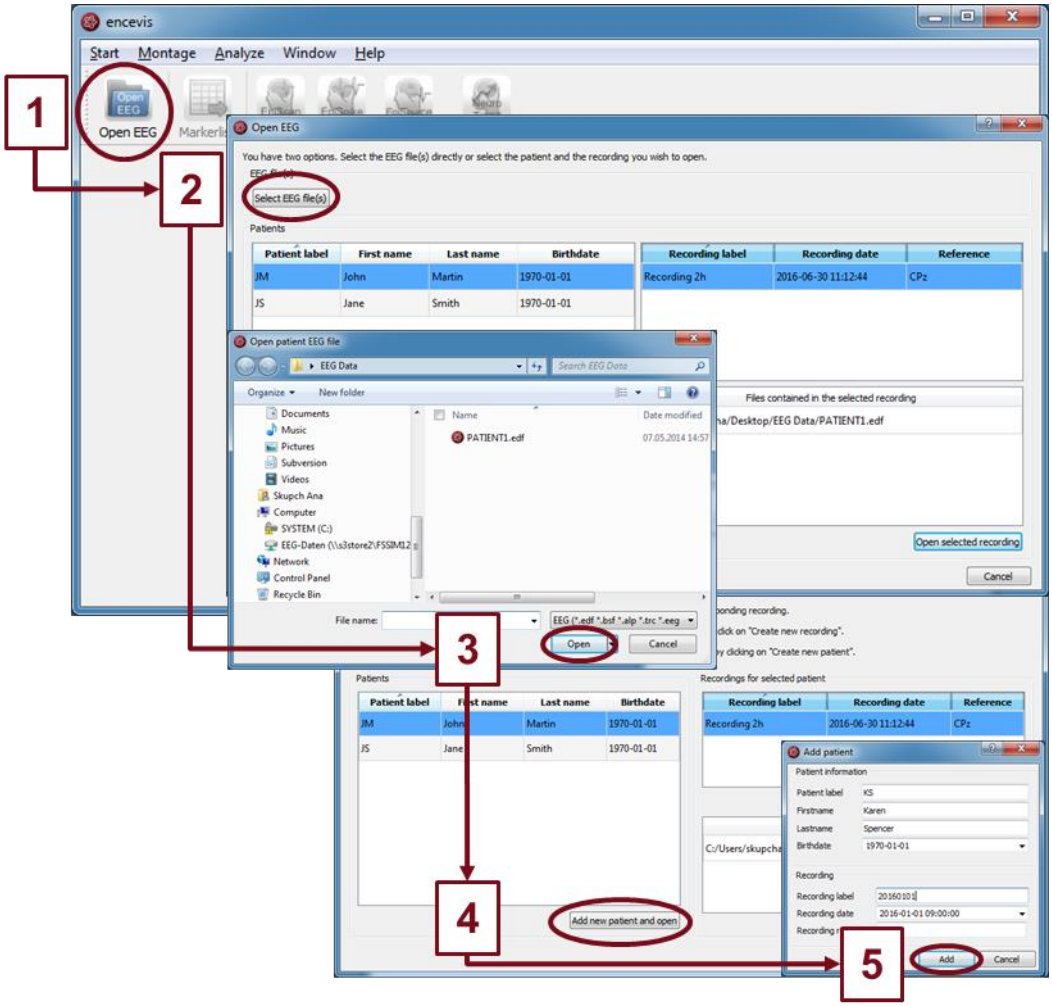


3. Press “**Activate license”**, the License Tool will pop up.



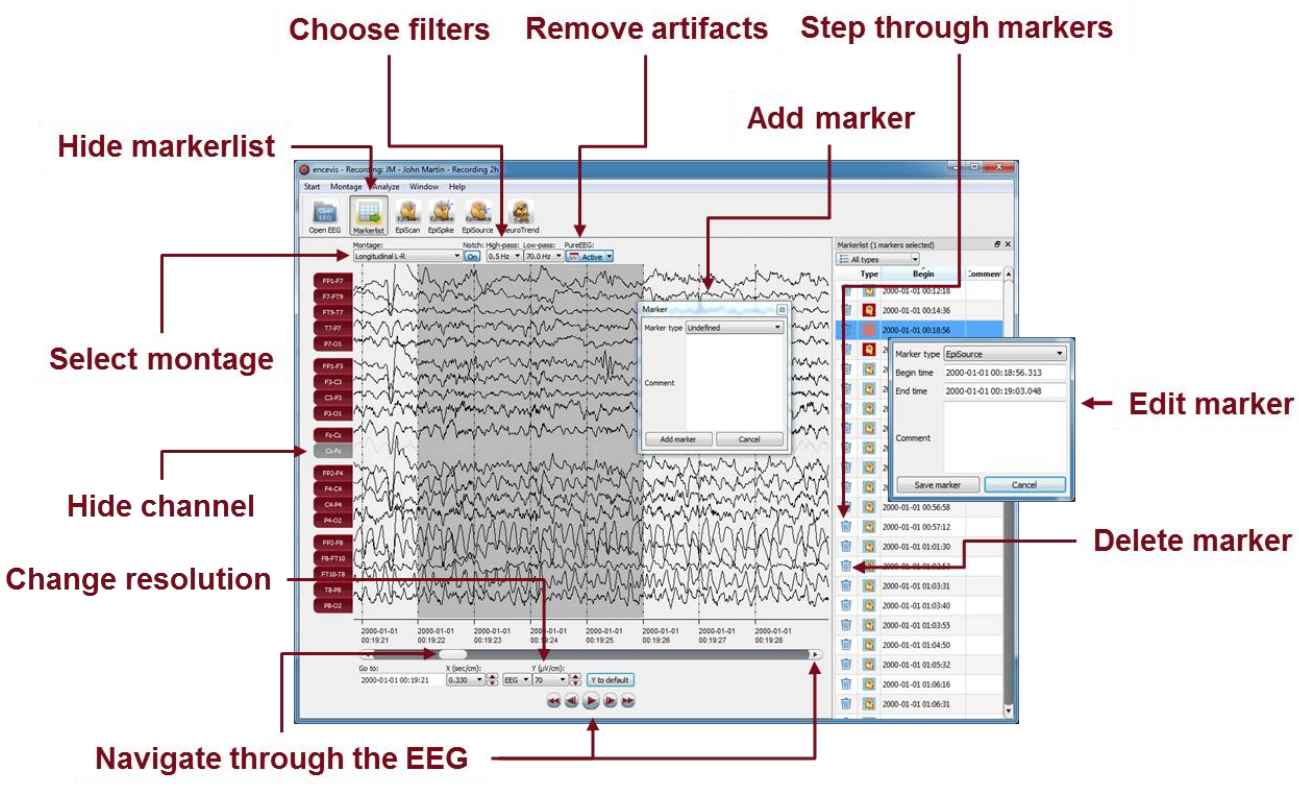
4. If you are connected to the internet, select „**Online**“ as activation mode. Otherwise, select “**Manual**” and contact your distributor in order to get the keys for the manual activation.
5. Enter the LicenseID and Password.
6. Press ”**Activate license(s)**“.

Open EEG file(s) in 5 steps



1. Press “**Open EEG**” or select the menu point **Start > Open EEG.**
2. Press “**Select EEG file(s)**”
3. Select the EEG file(s) that you would like to open.
4. If the file(s) are already registered in the EEG file management they will be opened immediately, otherwise a window will pop up. There, Press "**Add new patient and open**", a new window will pop up.
5. Fill in the fields of the "Patient information". Fill in the recording label and the recording date and the reference used for the EEG recording. Press "**Add**".

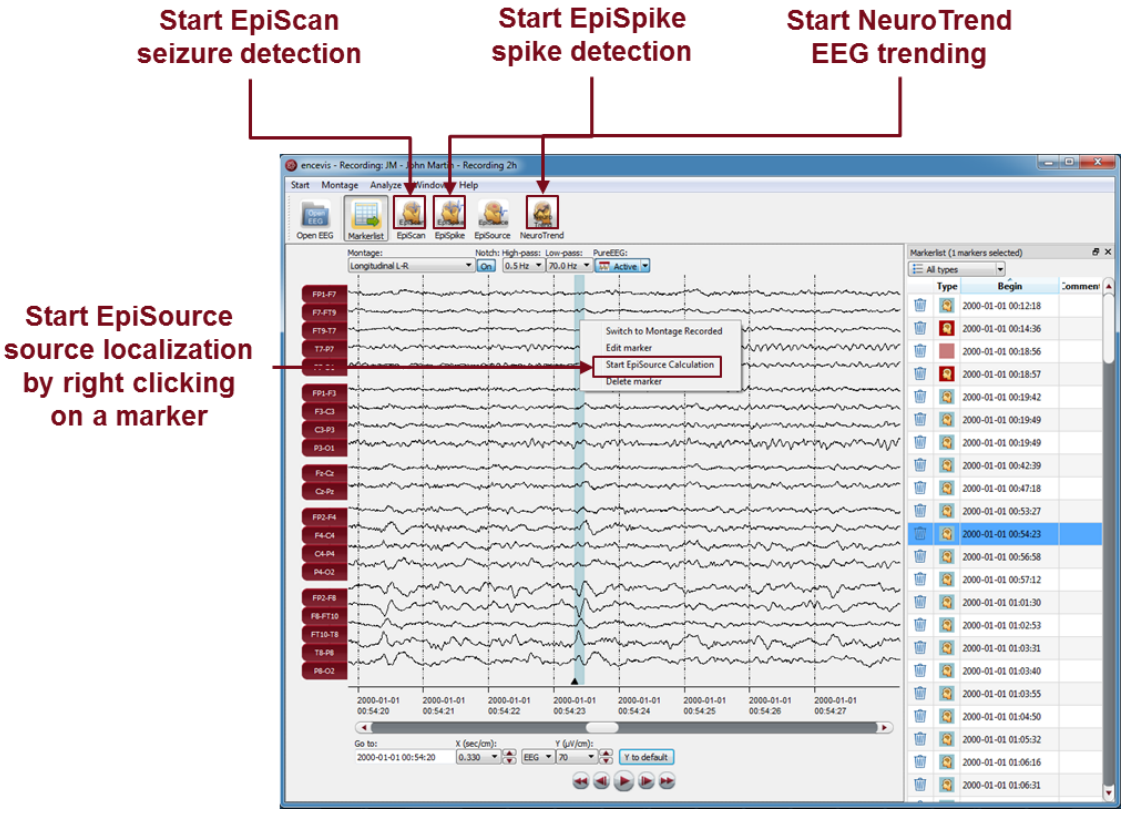
Review EEG



You have now the possibility to use all functionalities of encevis:

- Navigate easily through the EEG.
- Remove artefacts with PureEEG.
- Change the settings of the channels by selecting a montage and hide channels.
- Change the resolution in time and in voltage.
- Select notch, high-pass and low-pass filters.
- Watch the EEG in two windows at the same time.
- Create, review and change markers for special EEG events.
- Markers are saved with the data in the marker list and can be reviewed anytime.
- Start automatic EEG analysis.

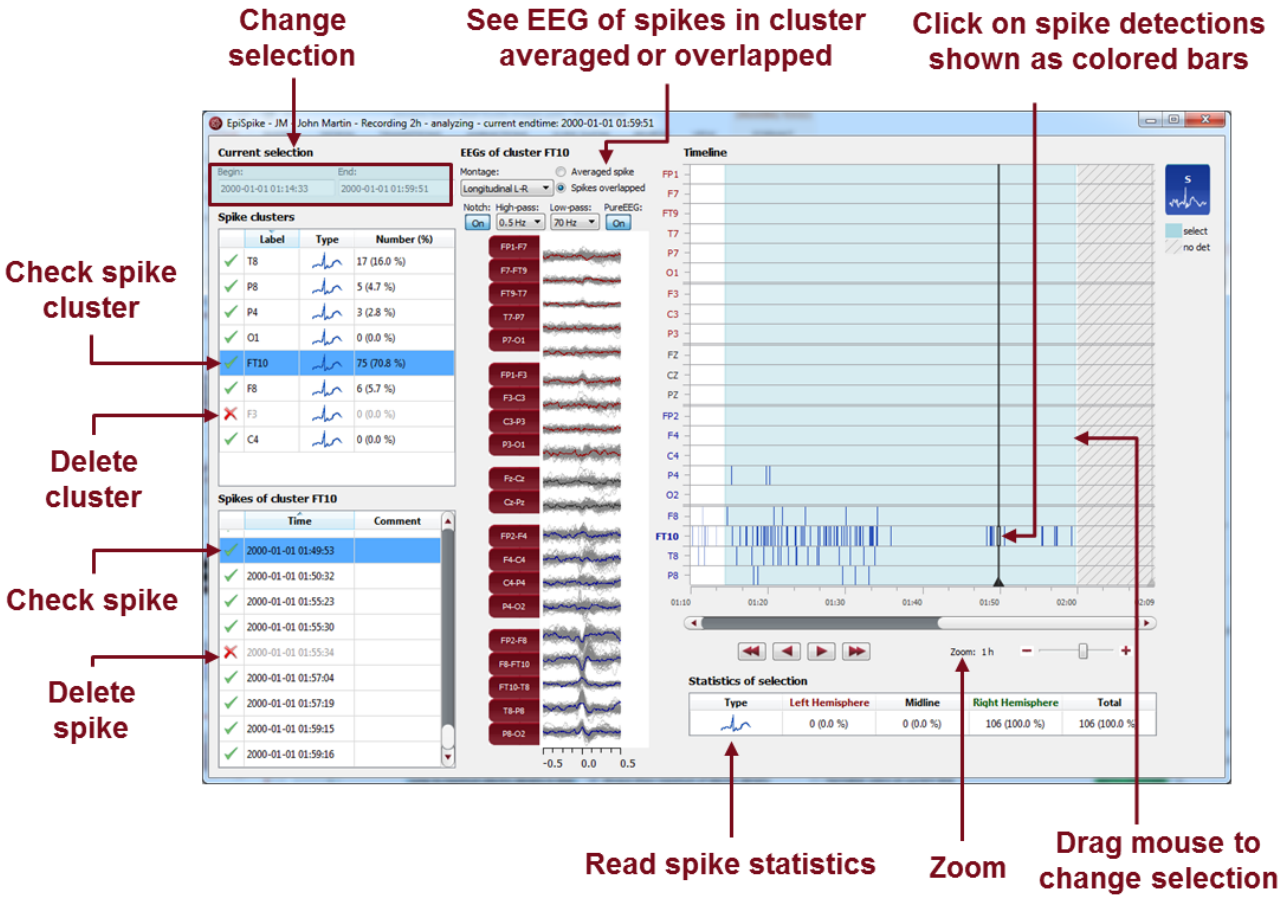
Start automatic EEG analysis



encevis offers you a series of automatic EEG analysis tools:

- EpiScan: the automatic seizure detection generates markers that you can easily review with the marker list.
- EpiSpike: the automatic spike detection detects spikes, clusters them by localization and visualizes the results for easy review.
- EpiSource: you can easily start the source localization on markers inserted manually or automatically. EpiSource has its own easy to use display.
- NeuroTrend: the advanced EEG trending calculates automatic detection of patterns, qEEG, aEEG, the heart rate based on ECG and visualizes the results on a single screen.

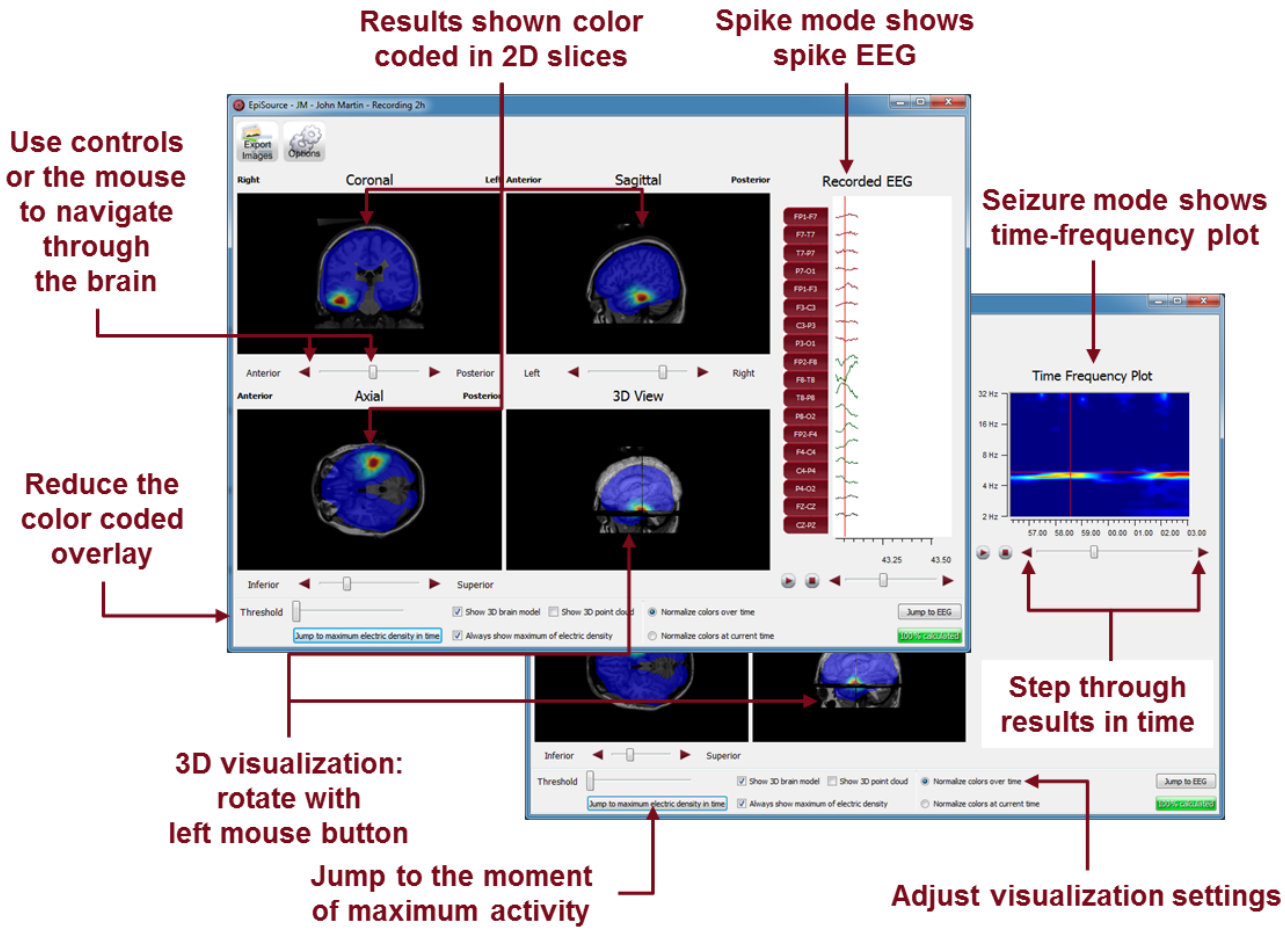
EpiSpike



Start EpiSpike and use all its functionalities:

- Start the detection on the complete time range or specify a time segment you are particularly interested in.
- Find the spike detections on a timeline as blue bars clustered and arranged by their localization.
- Zoom in and zoom out of the timeline using the mouse wheel.
- Click on a detection to see its EEG and find it in the spike list.
- Choose if you want to see the average spike EEG of the cluster or all spikes overlapped.
- Go through the lists of spike clusters and their spikes and remove detections you do not want.
- Change time of selection for review and statistics.
- Synchronize with the EEG in the EEG viewer.

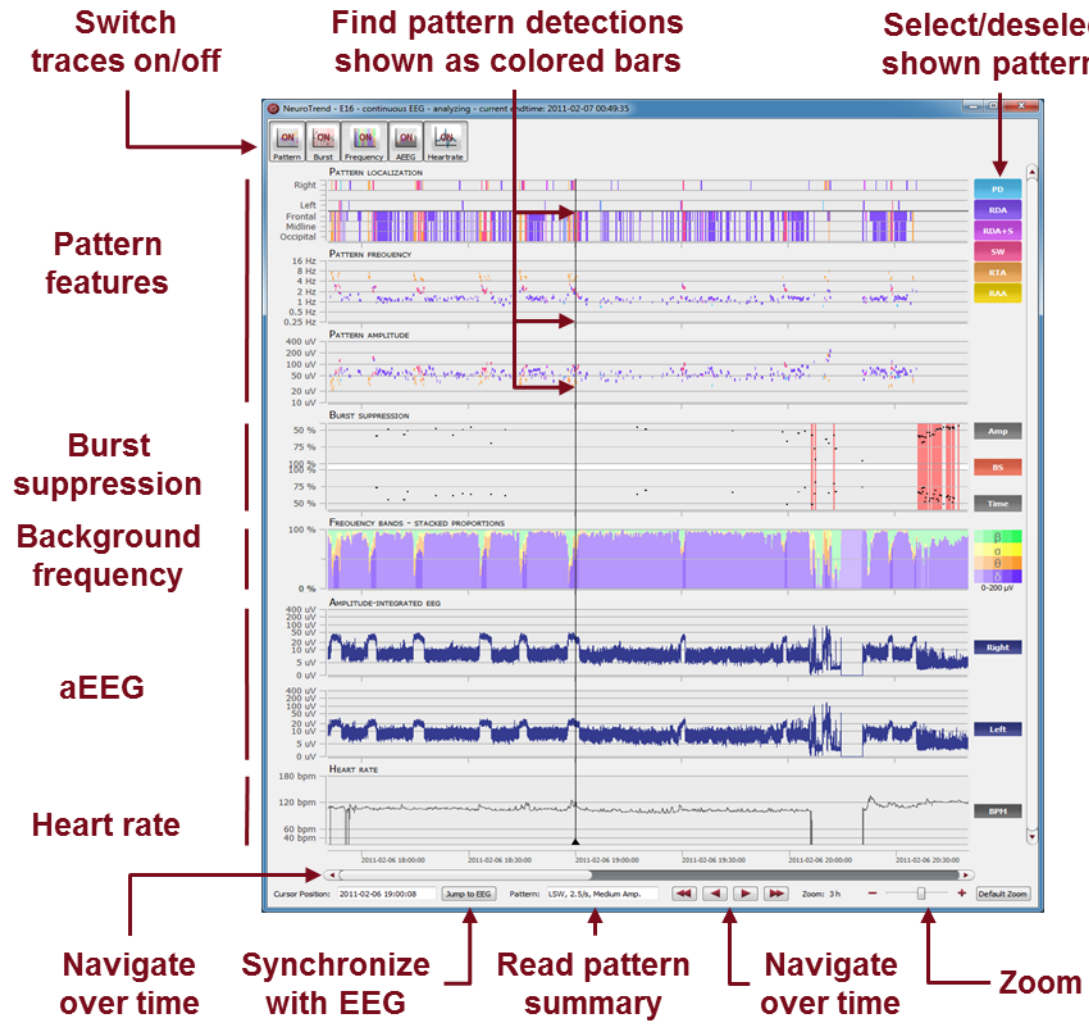
EpiSource



Start EpiSource and use all its functionalities:

- Choose between seizure mode (seizure markers: 1s-5min) and spike mode (spike markers: 20-500ms).
- See the results of the source localization as color-coded overlay to the structural MRI. High activity is red. Low activity is blue.
- Review the results in the three 2D slices (Coronal, Sagittal and Axial).
- Navigate through the slices using the controls or the mouse.
- Review the results in the 3D visualization.
- Zoom in and zoom out using the mouse on the screen.
- Step through the results in time or just jump to the time point of maximum activity.
- Adjust several visualization settings.
- Export the results as images.

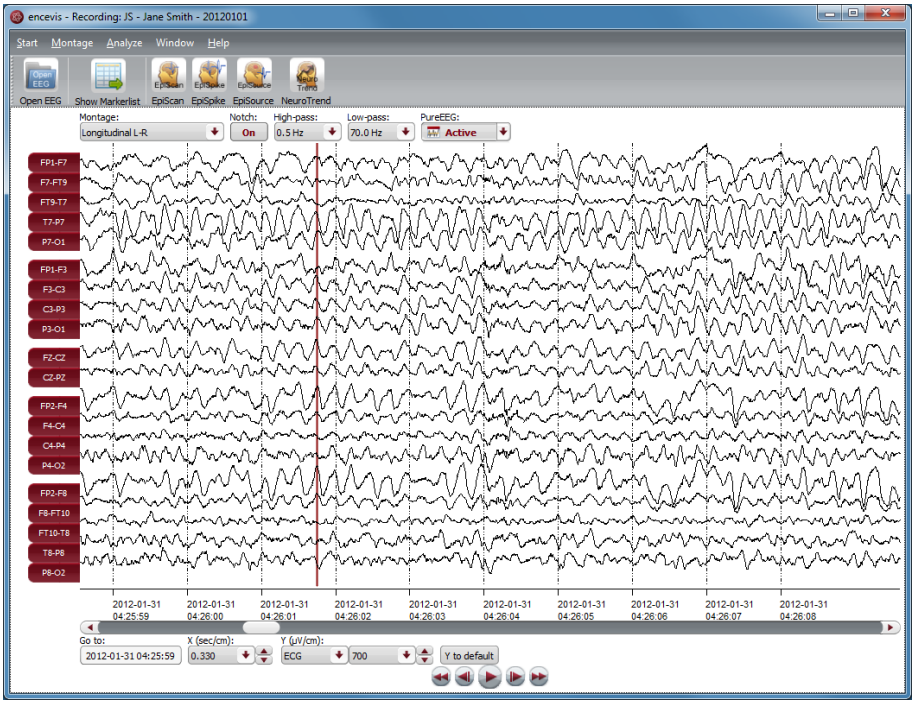
NeuroTrend



Start NeuroTrend and use all its functionalities:

- Find color coded detections of six different patterns.
- Read localization, frequency and amplitude of the detected patterns.
- Find burst suppressions and attenuations.
- See the amplitude-integrated EEG and the proportion of the frequencies as continuous measures.
- Read the heart rate based on the ECG.
- Navigate in time.
- Zoom in and zoom out using the mouse wheel.
- Synchronize with the EEG shown in the encevis viewer.
- Select or deselect patterns that you want to have shown or hidden.
- Switch on/off the traces you want to have displayed.

encevis EEG viewer



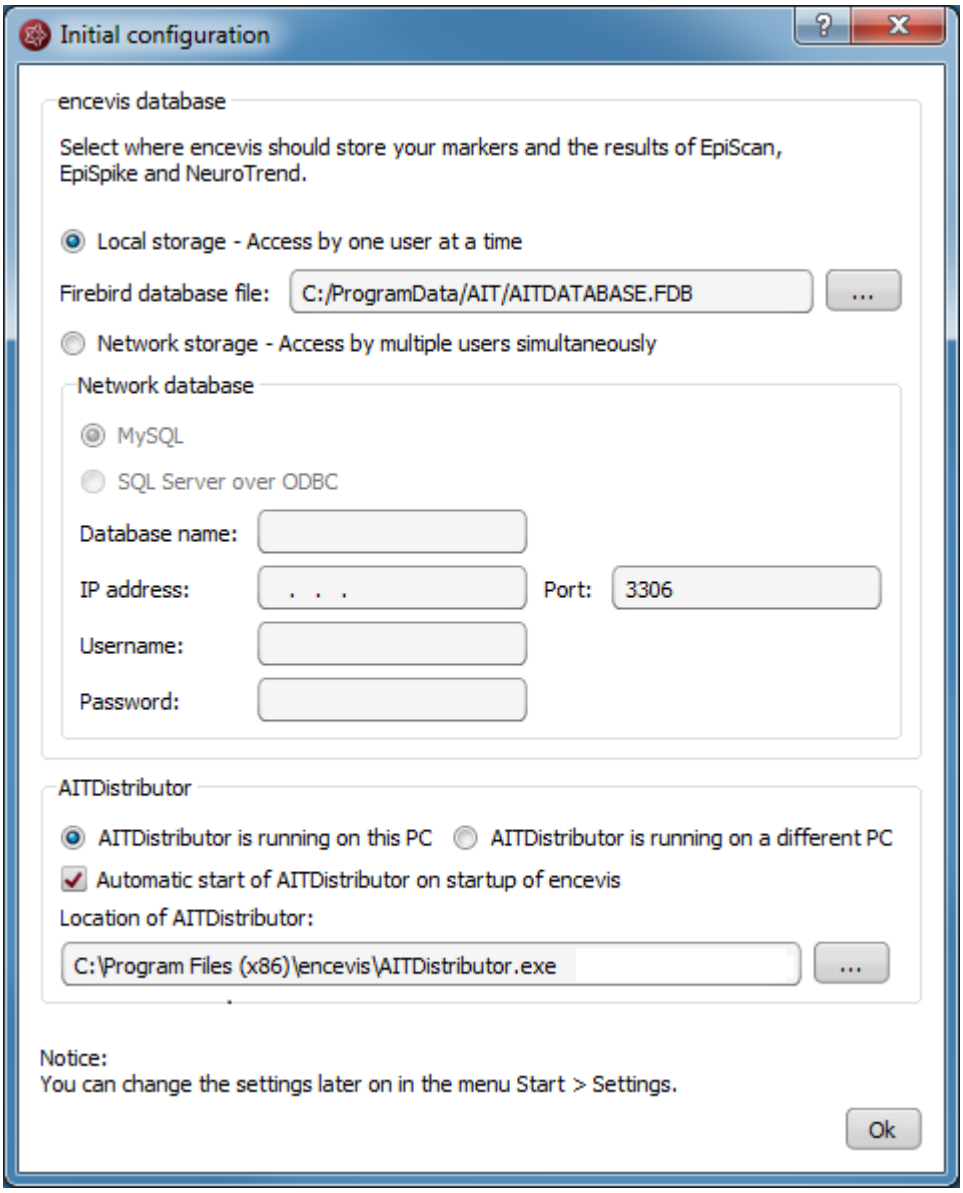
Overview

The encevis EEG viewer enables you to view your patients' EEG. It also helps you to have an overview of all your patients, their EEG recordings and the EEG files that correspond to them.

For more details on how to use the encevis EEG viewer see the following sections: Open EEG, View EEG, Markers, EpiScan, EpiSpike, EpiSource and NeuroTrend

Initial configuration

The first time you use encevis, you have the possibility to decide in which mode you want to use it.



encevis database

encevis stores your markers and the results of EpiScan, EpiSpike and NeuroTrend in one database. Select where encevis should store it:

Local storage - Access by one user at a time:

This is the best mode, when the results of your review with encevis should only be accessed from your PC. Only one user at a time can then access the results. You can leave the file name specified by default or select a personalized name.

Network storage - Access by multiple users simultaneously:

This is the best mode, when you want to access the results of your review with encevis from several PCs in your network. With this option several users can access the results at the same time. In this case, you need to specify a database where everybody has access to. It can be a MySQL database or a SQL server over ODBC.

Distributor

Select if the Distributor should run on your PC or on a different one. If the Distributor is running on another PC, you need to specify IP address and Port.

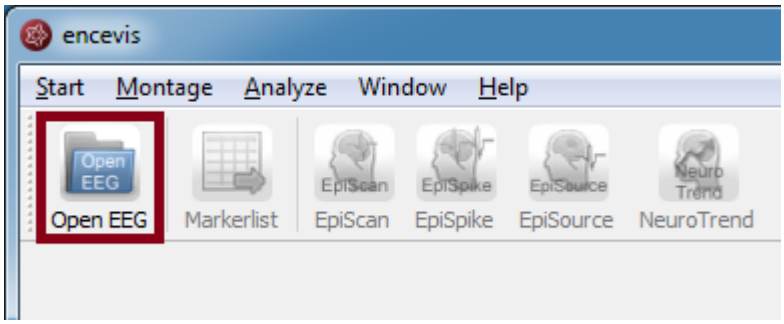
→ For more details, see section

→ Distributor.

These settings can be changed anytime under the sections *encevis database* and *Distributor* in the menu point *Start* > *Settings*. Whenever you change these settings, you need to restart encevis.

Open EEG

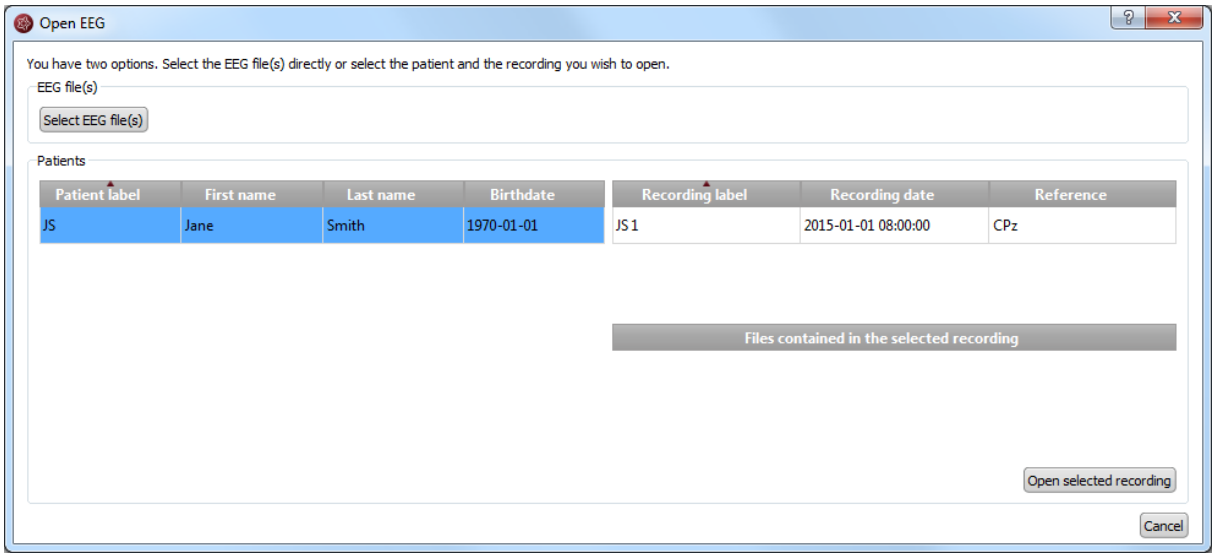
Click on the icon "Open EEG"



The “Open EEG dialogue” will open and show you the contents of the EEG File Management. The EEG File Management includes all the EEG files organized by recording and patient.

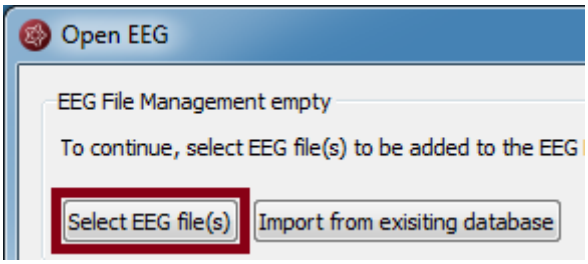
To open the EEG you want to review, you have two possibilities:

- Select EEG file(s) directly or
- Select an entry in the EEG File Management



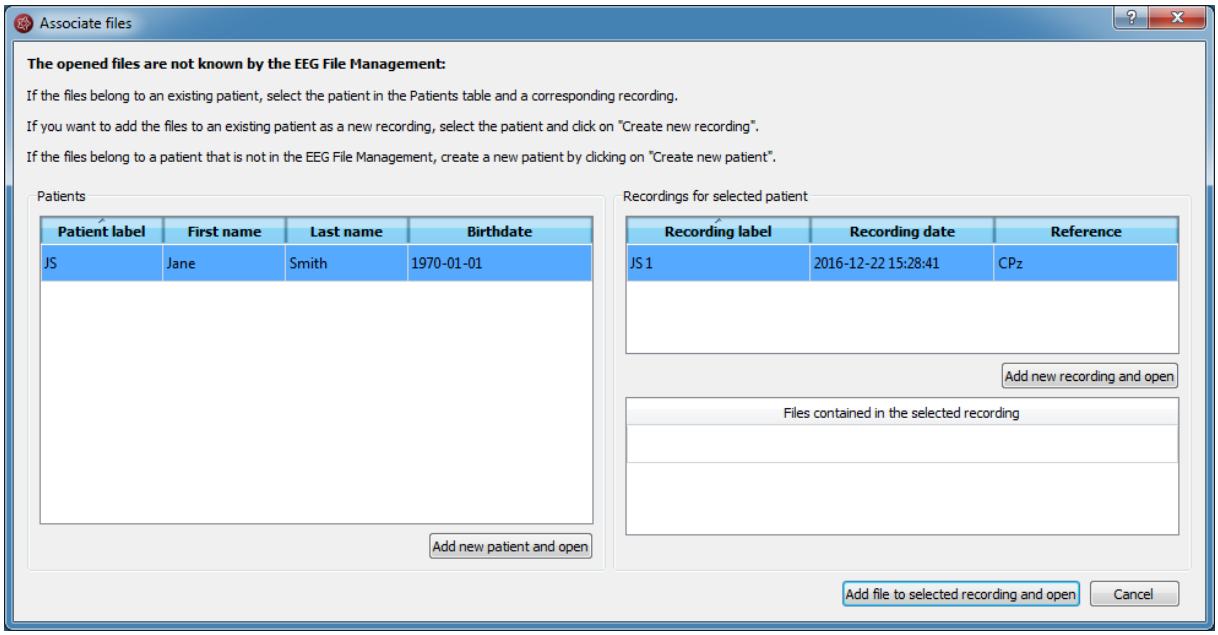
Select EEG file(s)

EEGs are stored in one or several EEG files as EEG recordings. If you want to open EEG files, click on the button “Select EEG file(s)”.



You may now select the EEG files.

- If the file(s) are already registered in the EEG File Management, they will be opened immediately.
- Otherwise, you will need to add them to the EEG File Management. In this case, the following window will open:

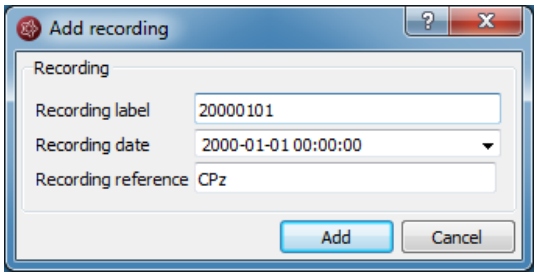


Add the file(s) to an existing recording:

1. Select the patient in the Patients list and the corresponding recording.
2. Click on "Add file to selected Recording and open".

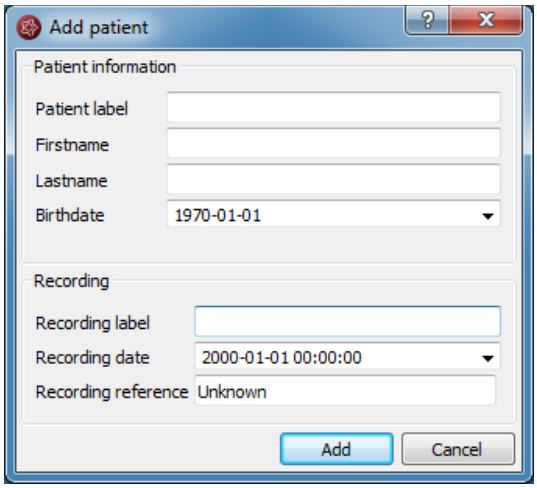
Add the file(s) to an existing patient as a new recording:

1. Select the patient in the Patient list.
2. Click on "Add new recording and open".
3. Fill in the recording label, date and reference.
4. Click on "Add".



Add the file(s) to a new patient:

1. Click on "Add new patient and open".



2. Fill in the fields of the "Patient information".
3. Fill in the recording label, date and reference.
4. Click on "Add".

EEG File Management

All information about the patients' EEG recordings and EEG files is stored in the EEG File Management. You can change the data in the EEG File Management anytime. For this, open the EEG File Management by selecting the menu point *Start > EEG File-Management*

You can easily change the entries by double clicking on the field you want to change.

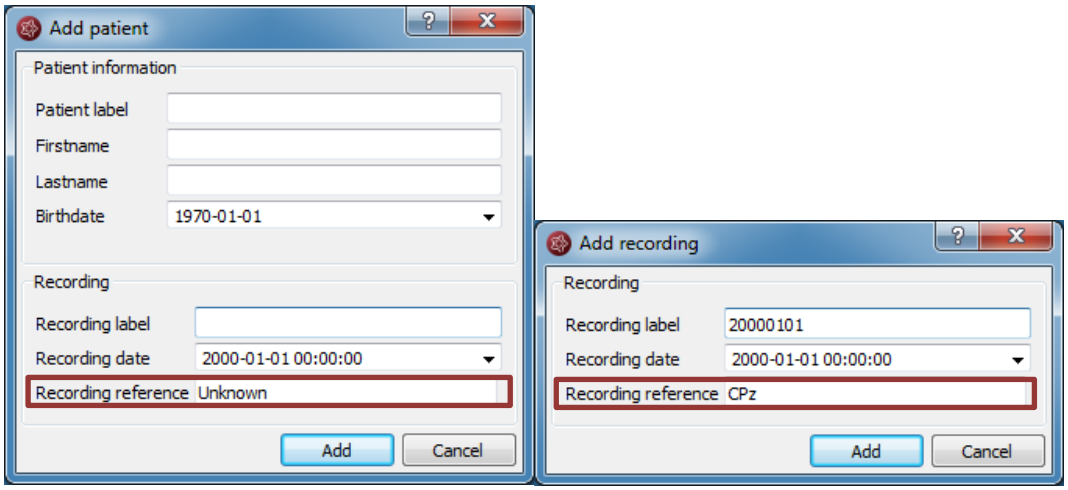
For more information on how to add patient and recording information, see the following chapters:

- Specify reference electrode
- Add a patient
- Add a recording
- Add file(s)

Specify reference electrode

- The location of the reference electrode that was used during the recording of the EEG (*Recording reference*) is used by several encevis components as PureEEG, EpiSpike and NeuroTrend. For the optimal functioning of these tools, it is recommended to fill out the reference correctly.

  You have the possibility to fill out this information in the process of opening the EEG (see Select EEG File(s), Add a patient and Add a recording).

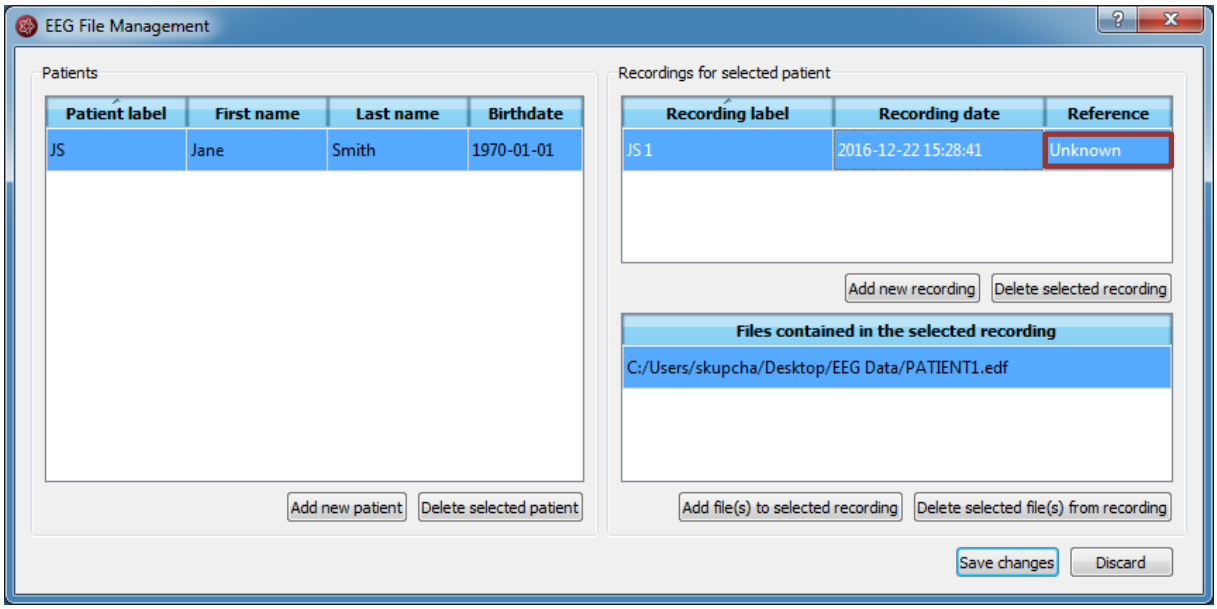


When the reference is stored in the file, encevis reads it out automatically and writes it in the field "Recording reference".

When the reference is not stored in the file, encevis writes "Unknown". You have then the possibility to correct this if you know the location. For this, type in an electrode label from the 10-20 standard.

→ If you don't have the information about the reference, leave it as "Unknown".

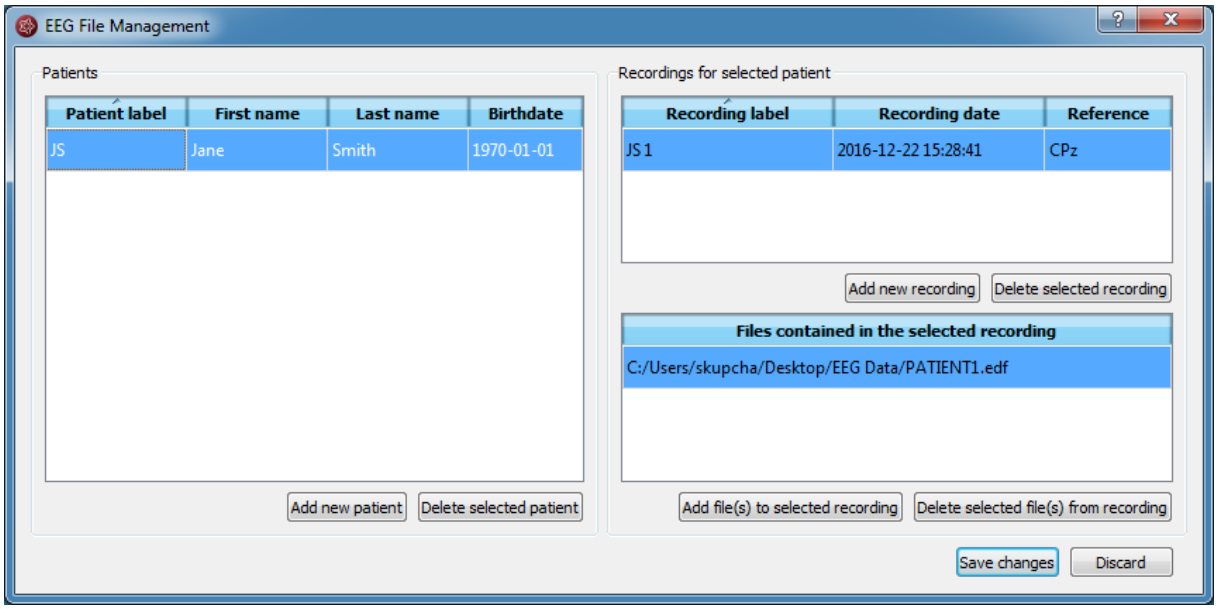
→ If you want to correct the reference later on, change the field in the EEG File Management.



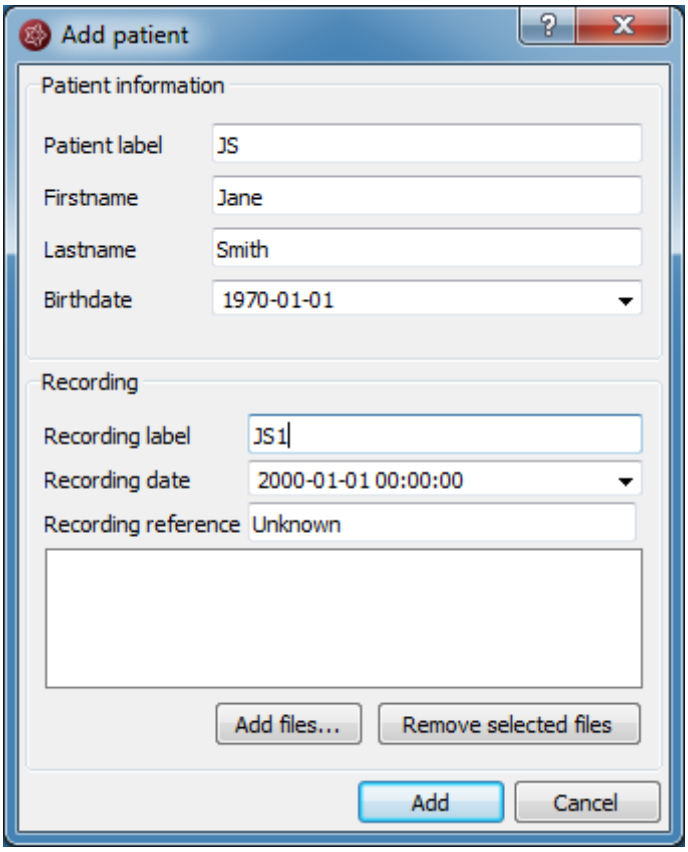
Add a patient

Follow these steps in order to add a new patient to the EEG File Management:

1. Select the menu point *Start* > *EEG File Management*. A window will open:



2. Click on "Add new patient". A form will open.
3. Fill in the fields of the "Patient information".

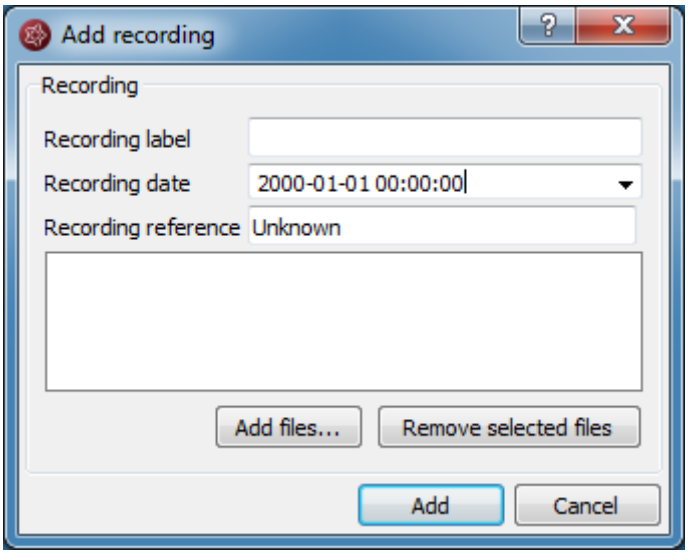


4. Fill in the recording label.
5. Select the recording date.
6. Correct the recording reference if it appears as "Unknown". If you don't know it, leave "Unknown". For more information on the recording reference see section Specify reference electrode.
7. Click on "Add files" and choose the files that belong to the recording.
8. Click on "Add".
9. Click on "Save changes".

Add a recording

If you would like to add a recording to the EEG File Management, select the menu point *Start > EEG File Management*.

1. Select the patient in the Patient list.
2. Click on "Add new recording". A form will open.



3. Fill in the recording label.
4. Select the recording date.
5. Type in the label of the electrode that was used as a reference during the recording. If you don't know it, leave "Unknown".
6. Click on "Add files" and select the files belonging to the recording.
7. Click on "Add".
8. If you need to add files to the recording once finished, then
9. Click on "Add file(s) to selected recording"
10. Choose the additional files that belong to the recording.
11. Click on "Save changes".

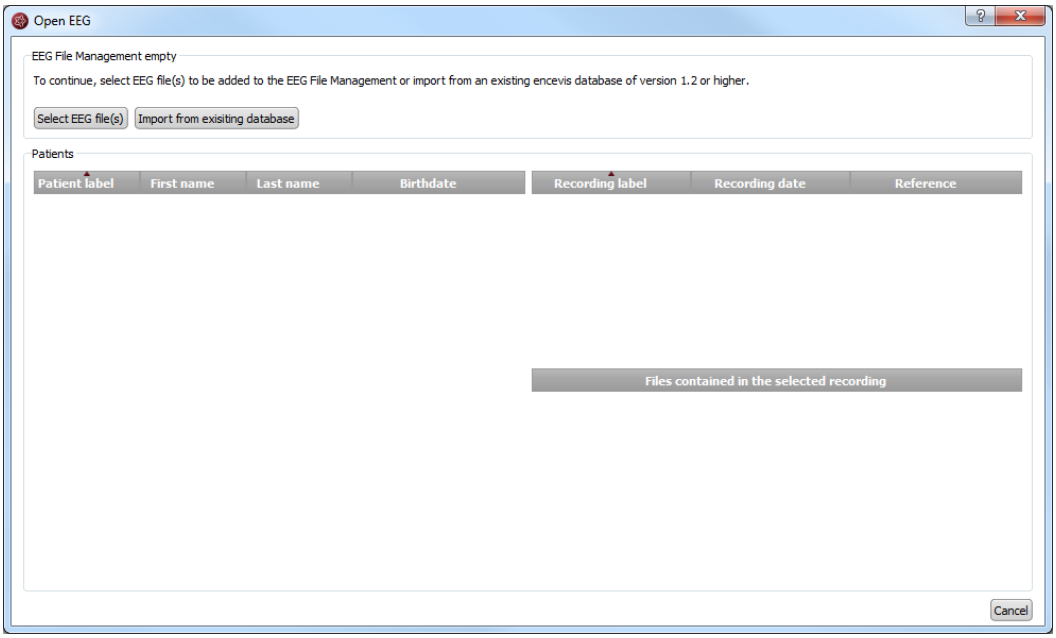
Add file(s)

In order to add new file(s) to the EEG File Management, select the menu point *Start > EEG File Management*.

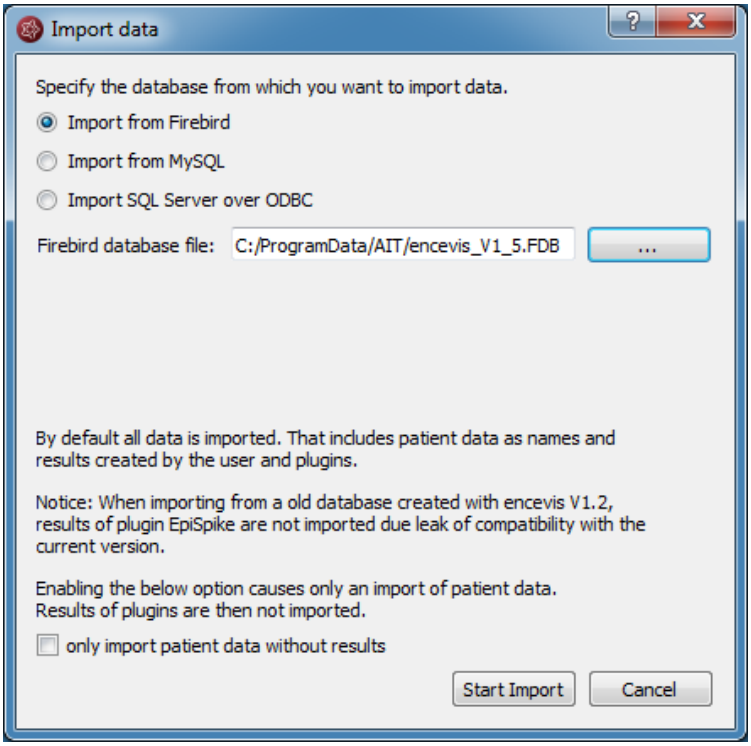
1. Select the patient in the Patient list.
2. Select the recording in the list of Recordings for the selected patient.
3. Click on "Add file(s) to selected recording".
4. Select the file(s) that belong to the recording.
5. Click on "Save changes".

Import from existing database

When the EEG File Management is empty, thus the first time you use a version of encevis or an encevis database, the following window will open:



1. If you want to start on an empty EEG File Management, click on the button "Select EEG file(s)". Further steps are explained in section Select EEG file(s).
2. If you want to reuse patient data saved in an EEG File Management you have used before, you can import it from an existing encevis database from versions 1.2 or higher. For this, click on "Import from existing database".



View EEG

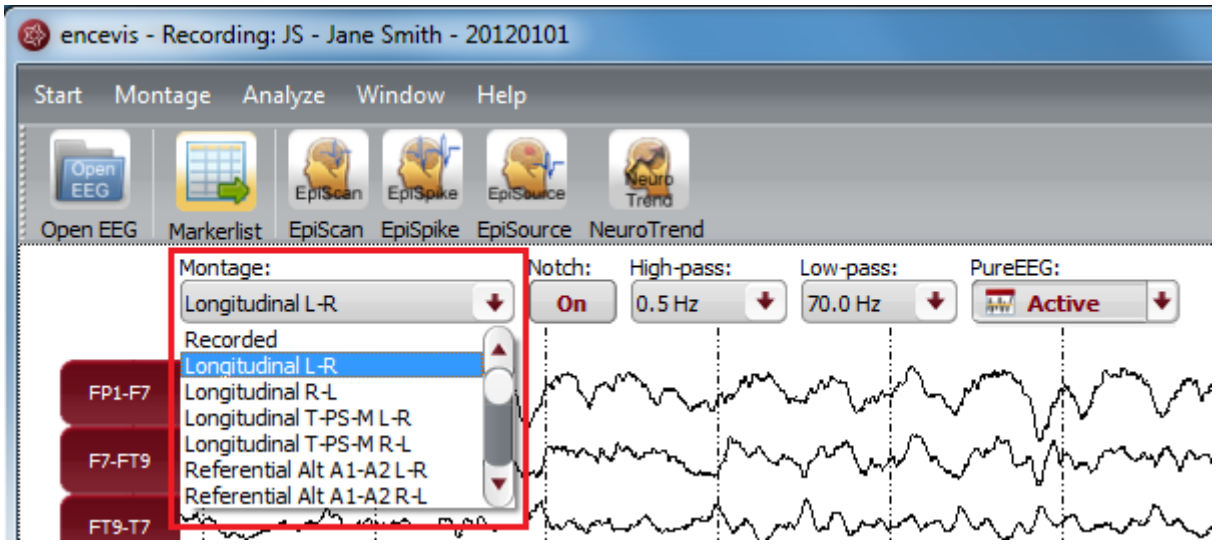
For a better review of the EEG, you have several possibilities:

- Change the montage and the way channels are displayed.
- Edit the montages.
- Navigate in time.
- Change the resolution in time and in voltage.
- Change the filters.
- Watch the EEG in two windows at the same time.
- Add and review markers

Channel and montage settings

Select a montage

The montage control is in the upper part of the viewer.

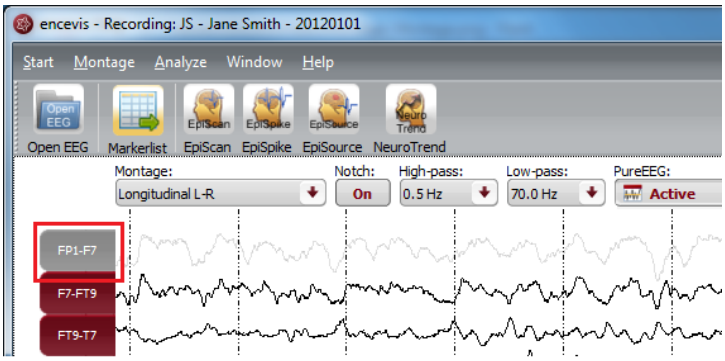


You can choose between a variety of montages. There is a default list of montages in encevis. The default list of montages includes referential, longitudinal and transverse montages with several references and order of the channels. You can find details about these montages as well as adapting and adding new ones in the Montage

editor. You can find details about these montages as well as adapting and adding new ones in the Montage editor.

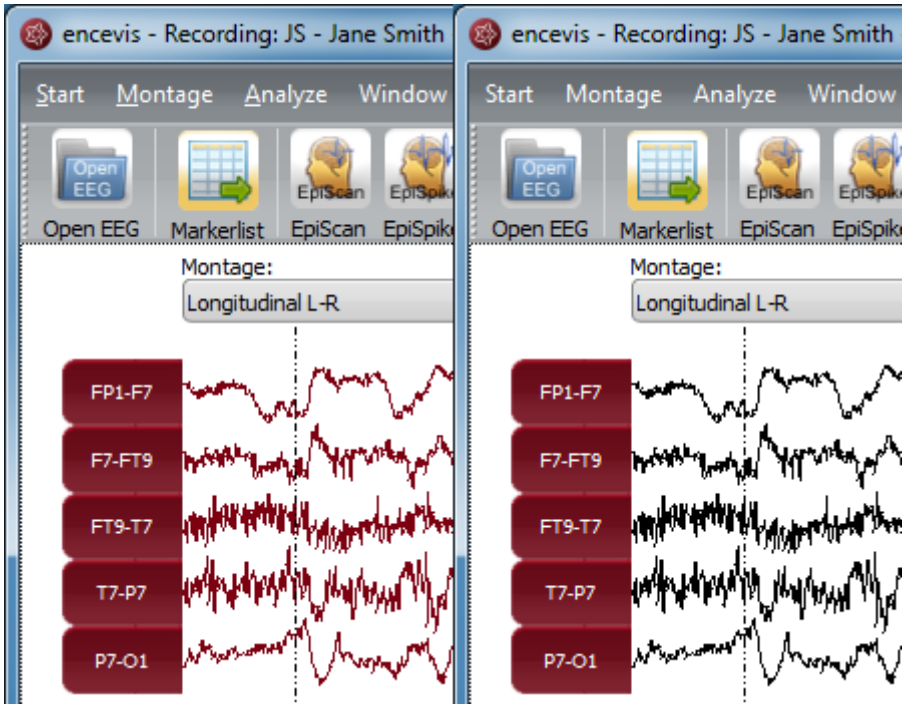
Select and unselect channels

Click on the red box on the left, where the channel name is shown in order to make the EEG of this channel visible or invisible.



Color of the curves

Select if you want to have the channels displayed in color or black

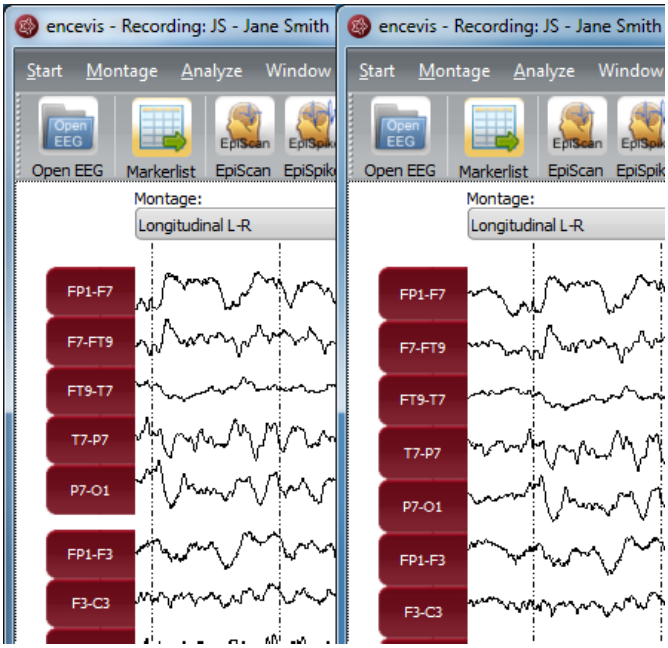


Click on the menu point *Montage* > *Colored curves* to show the channels in color or in black and white.

You can also select the exact color that you want for the curves in the Montage editor, see section Color.

Display the channels grouped

Right side and left side channels can be shown grouped.



Click on the menu point *Montage* > *Grouped curves* to switch on/off the grouping of the channels.

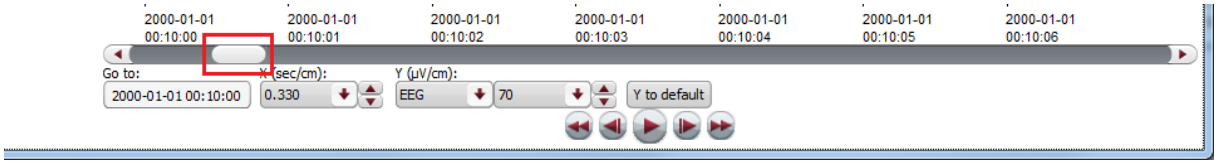
Time navigation

In order to navigate in time through the EEG, you have several possibilities. You can use your mouse wheel or the controls found in the lower part of the viewer.

Scroll in time with your mouse wheel

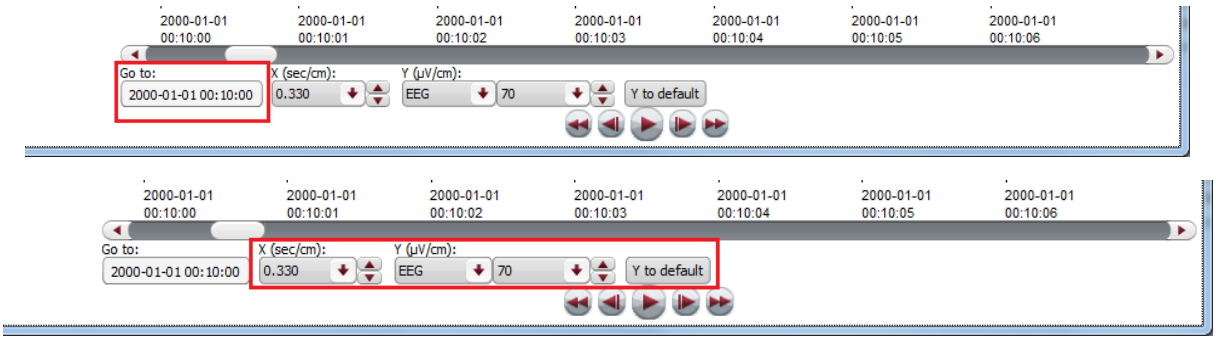
Click on the EEG and use your mouse wheel up and down to move back and forward in time.

Scroll in time with the slider



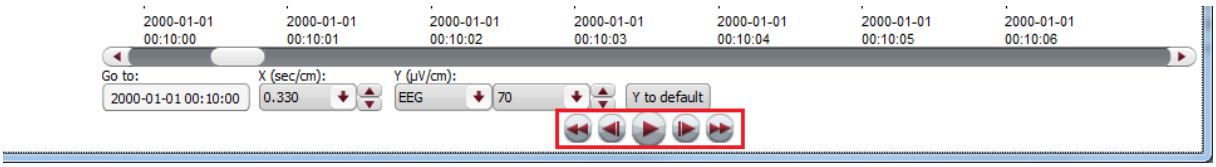
- Click on the slider and move it left and right to move back and forward in time.
- Alternatively use the back and forward arrows next to the slider to move back and forward in time.

Fill in the field "Go to:"



- Click in the field the field "Go to:" under the slider or
- Enter the date you want to start to view the EEG.

Use the video buttons

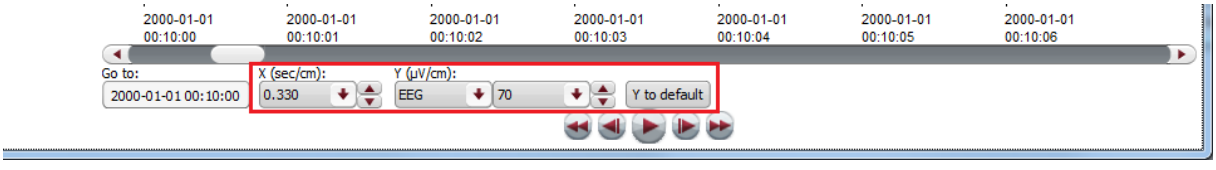


- Click on the forward or backward buttons next to the play button and the EEG will move by 1 seconds at a time.
- Click on the forward or backward button and the EEG will move by 5 seconds at a time.
- Click on the play button on the bottom of the viewer and the EEG will be shown as in a movie.
- Click on pause and the movie will pause.

Resolution

For a better review of the EEG, you have the possibility to change the resolution in time and in voltage.

The controls for this are found under lower part of the viewer.



Change time resolution

Click on the drop-down list "X:" on the bottom of the viewer and select the sensitivity you wish in sec/cm.

Change voltage resolution

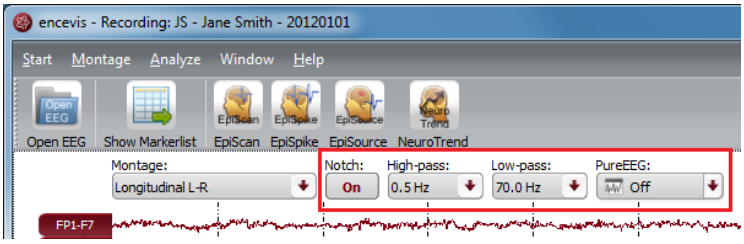
Click on the drop-down list "Y:" on the bottom of the viewer and select the sensitivity you wish in microVolt/cm.

Go back to the standard resolution

Click on the button "Y by default" to go back to the standard resolution of 70 microVolt/cm.

Filters

For a better review of the EEG, you have the possibility to use several filters. The controls for this are on the top of the viewer.



Notch filter

Click on the button "Notch:" to switch on/off the notch filter of 50Hz.

High-pass filter

Click on the drop-down list "High-pass" and select the frequency you want for the high-pass filter.

Low-pass filter

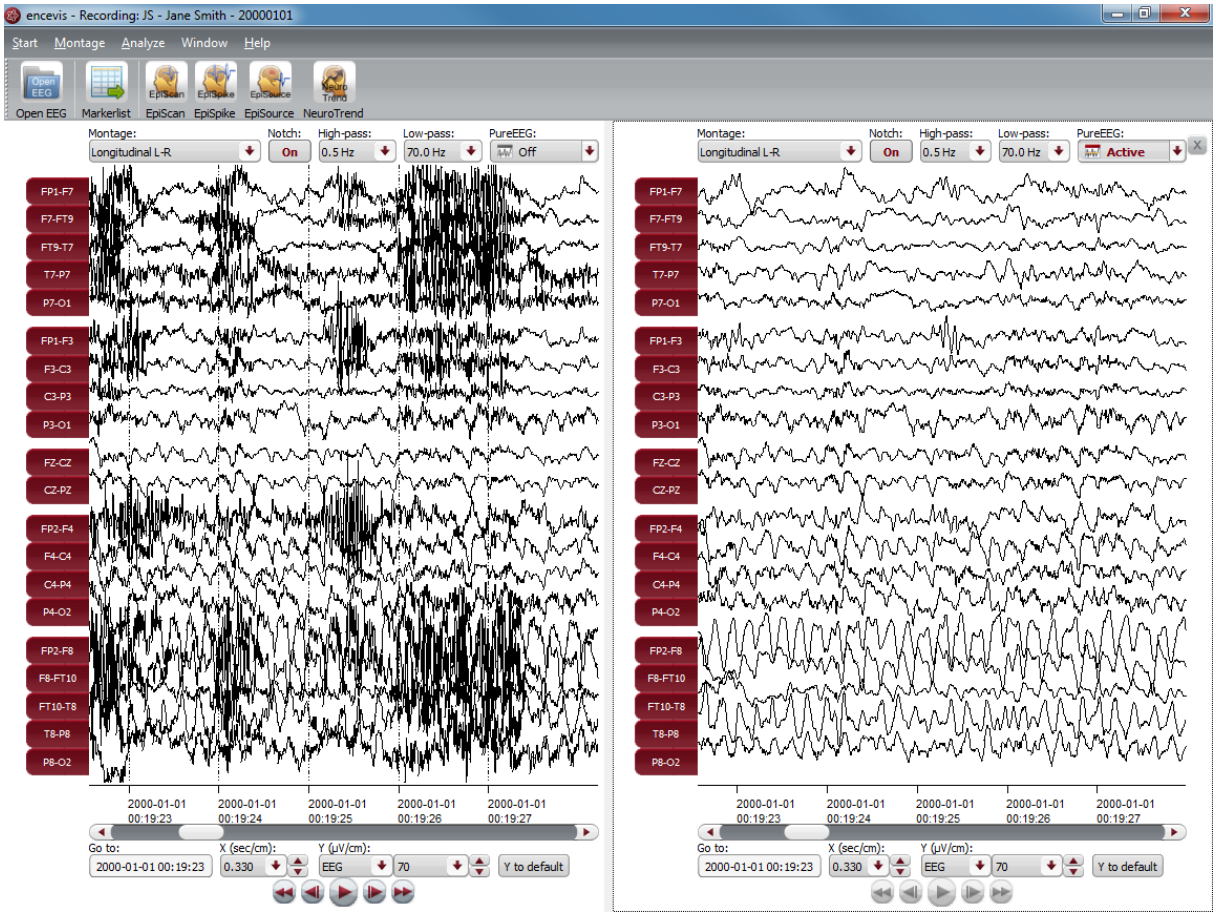
Click on the drop-down list "Low-pass" and select the frequency you want for the low-pass filter.

Artifact filter PureEEG

Click on the drop-down list "PureEEG" to switch on/off the artifact reduction filter PureEEG. For more details see PureEEG.

Split window

For a better review of the EEG, you have the possibility to watch your patient's EEG in two windows at the same time. You can use this mode in order to easily compare two different time segments or the EEG in two different settings.



Select the menu point *Window* > *Split window* and an additional EEG window will open. You can use this window in the same way as the original one.

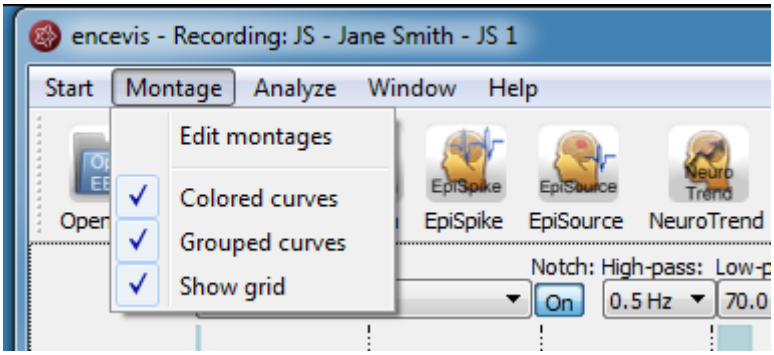
You can choose to navigate in time synchronously in both windows. In this mode, if you move the time cursor in one window, it will move automatically in the other. Select the menu point *Window* > *Synchronize windows* to switch on/off the synchronous mode.

If you want to close the additional plot, just click on the cross icon in the upper right corner of the window or select the menu point *Window* > *Split window*.

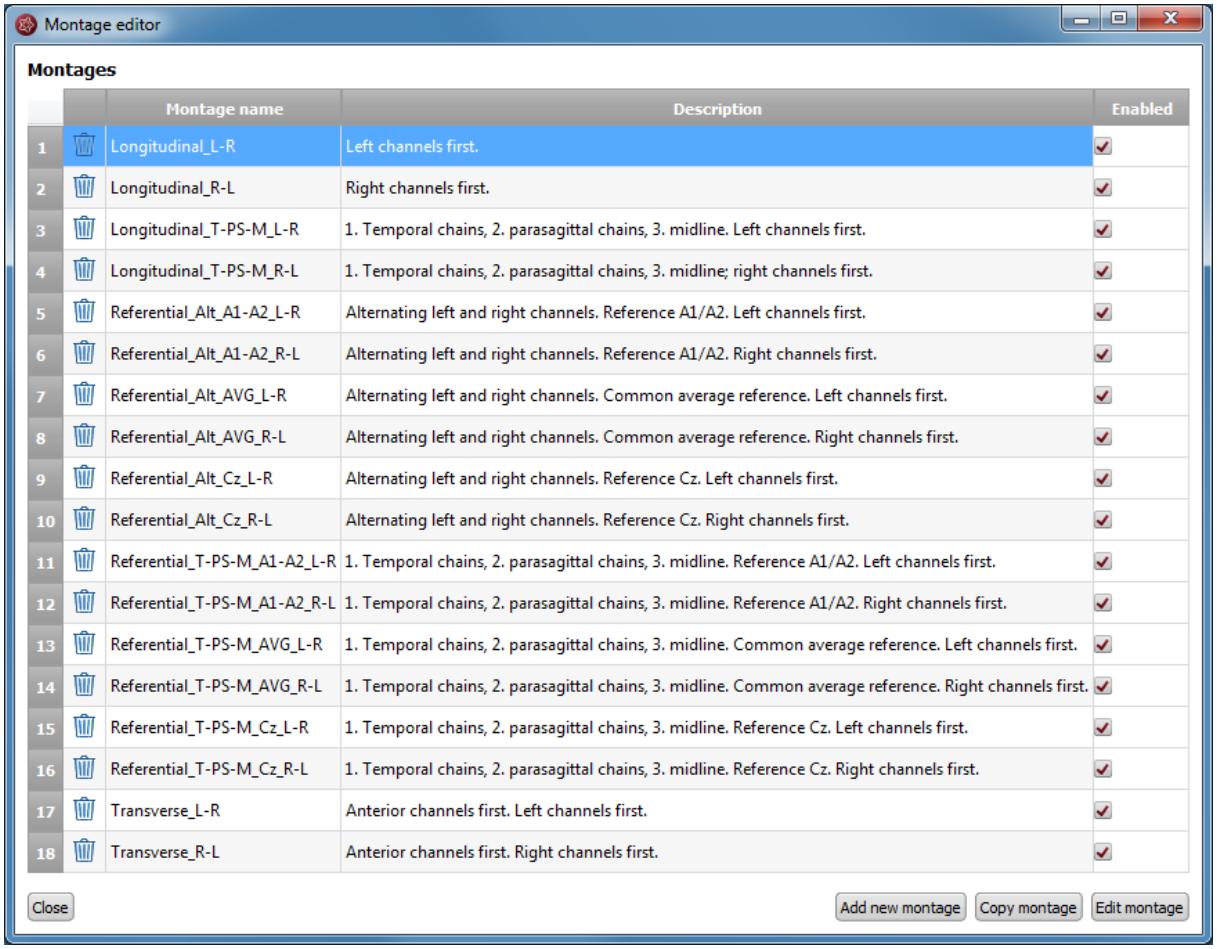
Montage editor

With the Montage editor you can change the montages that are used in the viewer. You can add new montages or edit the existing ones.

To open the montage editor select the menu point *Montage* > *Edit montages*.



The montage editor will open showing the list of montages:



	Montage name	Description	Enabled
1	Longitudinal_L-R	Left channels first.	☑
2	Longitudinal_R-L	Right channels first.	☑
3	Longitudinal_T-PS-M_L-R	1. Temporal chains, 2. parasagittal chains, 3. midline. Left channels first.	☑
4	Longitudinal_T-PS-M_R-L	1. Temporal chains, 2. parasagittal chains, 3. midline; right channels first.	☑
5	Referential_Alt_A1-A2_L-R	Alternating left and right channels. Reference A1/A2. Left channels first.	☑
6	Referential_Alt_A1-A2_R-L	Alternating left and right channels. Reference A1/A2. Right channels first.	☑
7	Referential_Alt_AVG_L-R	Alternating left and right channels. Common average reference. Left channels first.	☑
8	Referential_Alt_AVG_R-L	Alternating left and right channels. Common average reference. Right channels first.	☑
9	Referential_Alt_Cz_L-R	Alternating left and right channels. Reference Cz. Left channels first.	☑
10	Referential_Alt_Cz_R-L	Alternating left and right channels. Reference Cz. Right channels first.	☑
11	Referential_T-PS-M_A1-A2_L-R	1. Temporal chains, 2. parasagittal chains, 3. midline. Reference A1/A2. Left channels first.	☑
12	Referential_T-PS-M_A1-A2_R-L	1. Temporal chains, 2. parasagittal chains, 3. midline. Reference A1/A2. Right channels first.	☑
13	Referential_T-PS-M_AVG_L-R	1. Temporal chains, 2. parasagittal chains, 3. midline. Common average reference. Left channels first.	☑
14	Referential_T-PS-M_AVG_R-L	1. Temporal chains, 2. parasagittal chains, 3. midline. Common average reference. Right channels first.	☑
15	Referential_T-PS-M_Cz_L-R	1. Temporal chains, 2. parasagittal chains, 3. midline. Reference Cz. Left channels first.	☑
16	Referential_T-PS-M_Cz_R-L	1. Temporal chains, 2. parasagittal chains, 3. midline. Reference Cz. Right channels first.	☑
17	Transverse_L-R	Anterior channels first. Left channels first.	☑
18	Transverse_R-L	Anterior channels first. Right channels first.	☑

As you can see, a variety of default montages are already defined in the montage editor. They include montages with channels from the 10-20 system. There are

standard referential, longitudinal and transverse montages with several orders of the channels and references.

You can decide if you want to have the montages included in the montage drop-down list of the viewer, by selecting or deselecting the check box "Enabled".

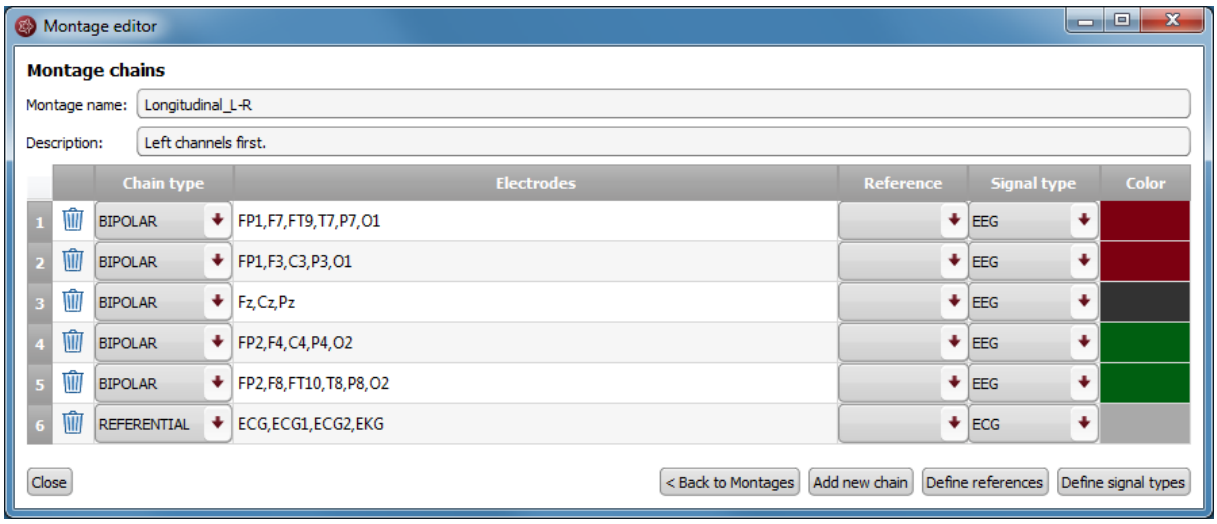
A montage is defined by a series of channels grouped to chains.

Select a montage in the montage editor and Click on "Edit montage" to see the chains included in it. More details on the montage chains are found in the following section.

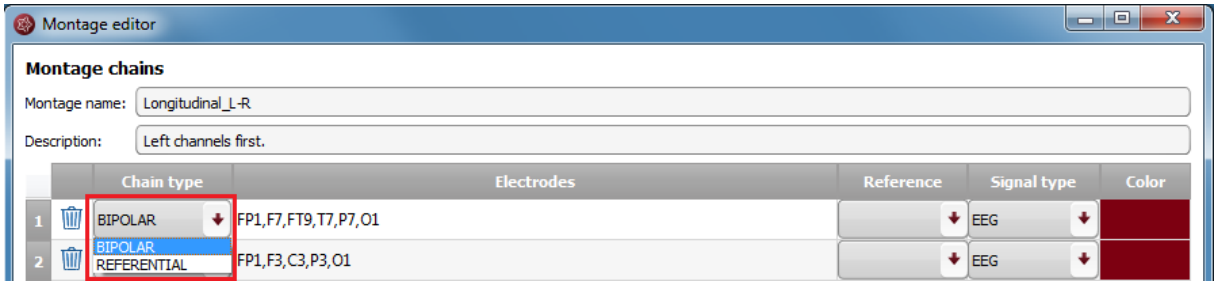
Montage chains

A montage is defined by a series of channels grouped to chains. By editing a montage you can see the chains that are defined in the selected montage.

→ Select a montage and Click on "Edit montage" to see the chains included in it.



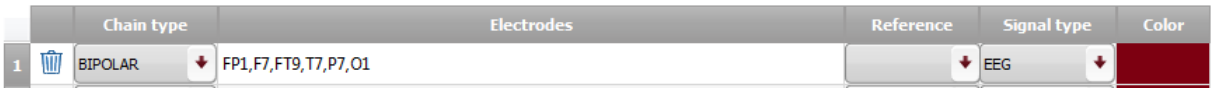
There are two types of chains: BIPOLAR and REFERENTIAL.



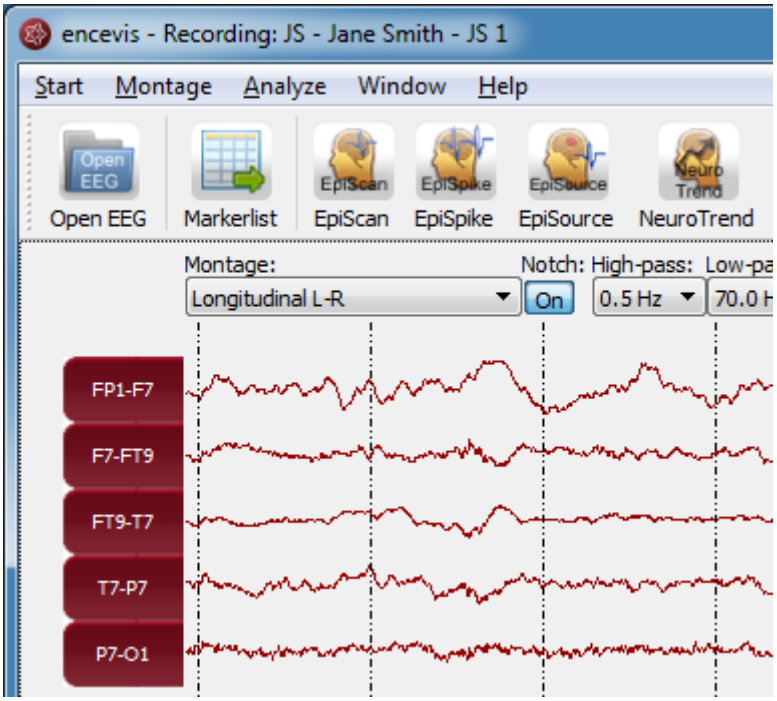
A BIPOLAR chain will result in a group of bipolar channels shown by the viewer.

In the field "Electrodes" are written the positive electrodes included in this group. For a BIPOLAR chain, the field "Reference" needs to be empty.

E.g. the chain including FP1,F7,FT9,T1,T7,P7,O1



will result in the group of channels FP1-F7, F7-FT9, FT9-T7,T7-P7 and P7-O1 when the montage is selected in the viewer.

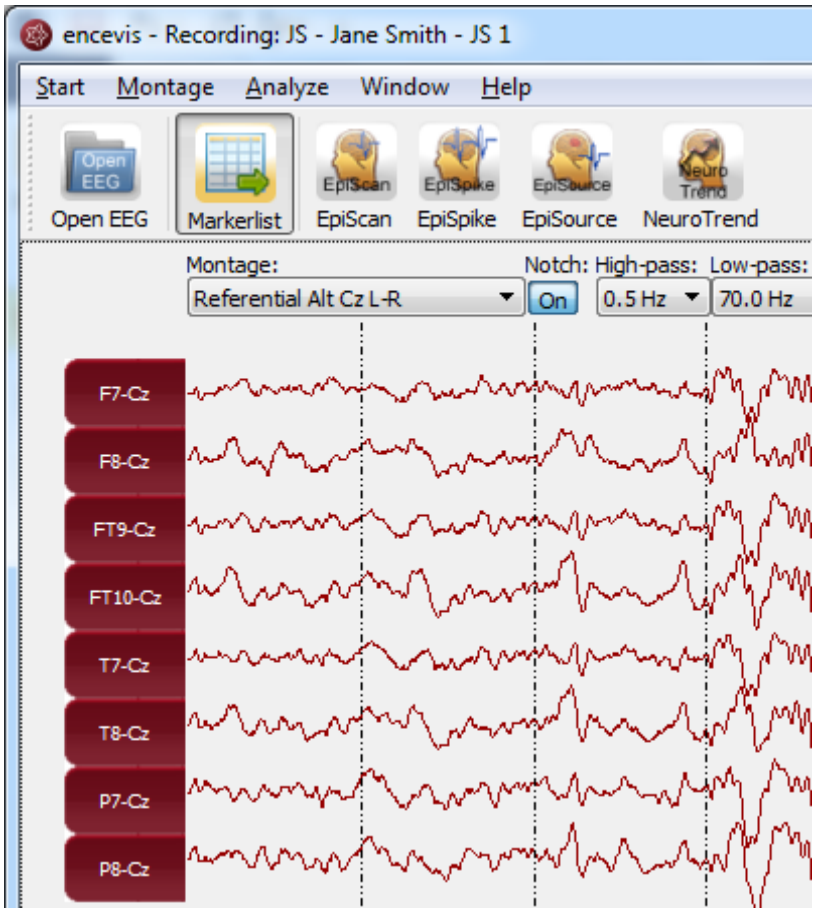


A REFERENTIAL chain will result in group of referential channels shown by the viewer.

In the field "Electrodes" are written the positive electrodes included in this group. For a REFERENTIAL chain, the field "Reference" needs to be filled. It should contain the reference that is whished for this group. On how to select the reference see References.

E.g. the chain including F7, F8, FT9, FT10, T7, T8, P7, P8 with Reference Cz

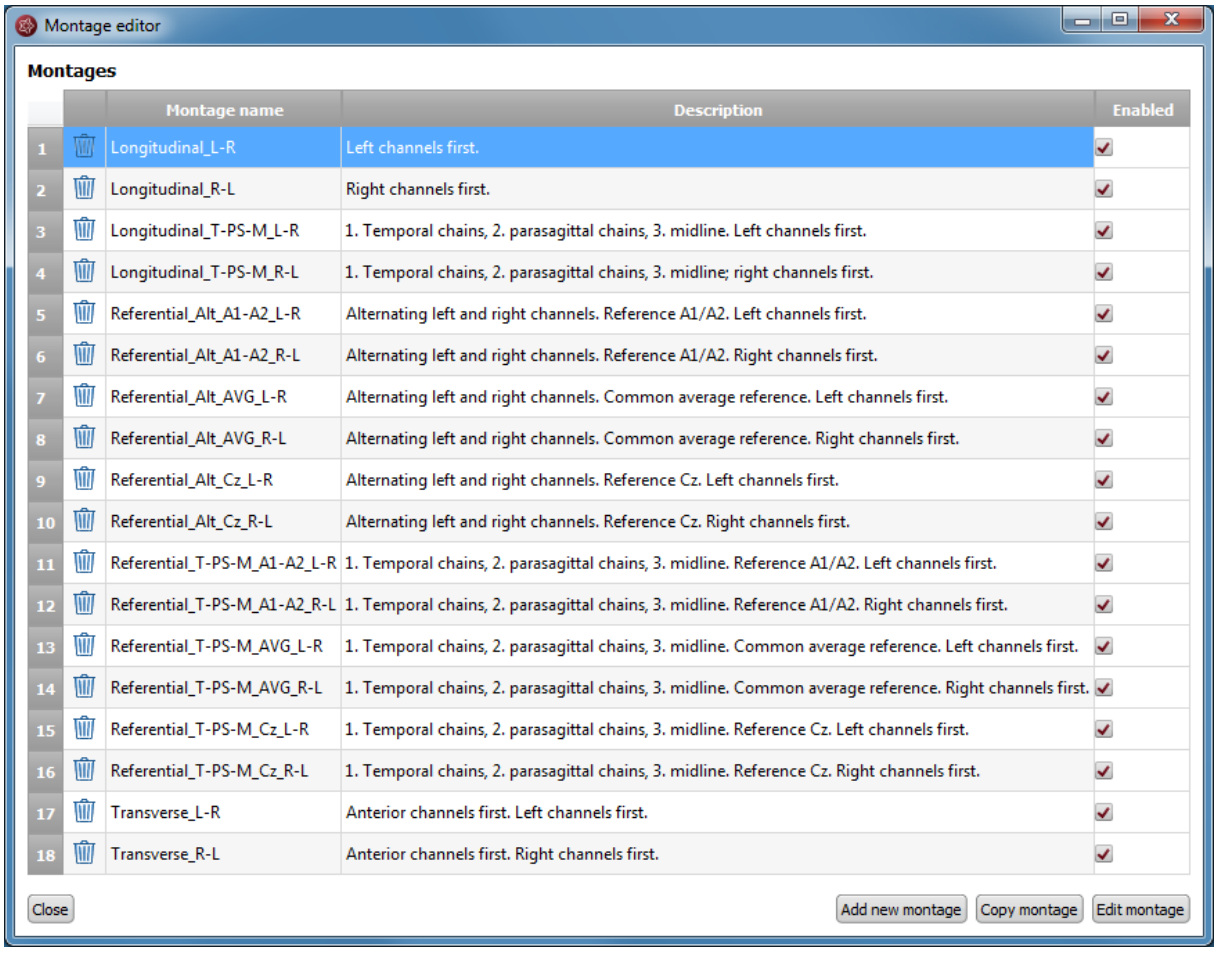
will result in the group of channels: F7-Cz, F8-Cz, FT9-Cz, FT10-Cz, T7-Cz, T8-Cz, P7-Cz, P8-Cz when the montage is selected in the viewer.



For more details on the other fields see the sections Chain references and Signal Types.

Add montage

If you want to add a new montage, first open the montage editor by selecting the menu point *Montage > Edit montages*



If you want to add a new montage to the existing ones you have two possibilities:

Add a completely new montage

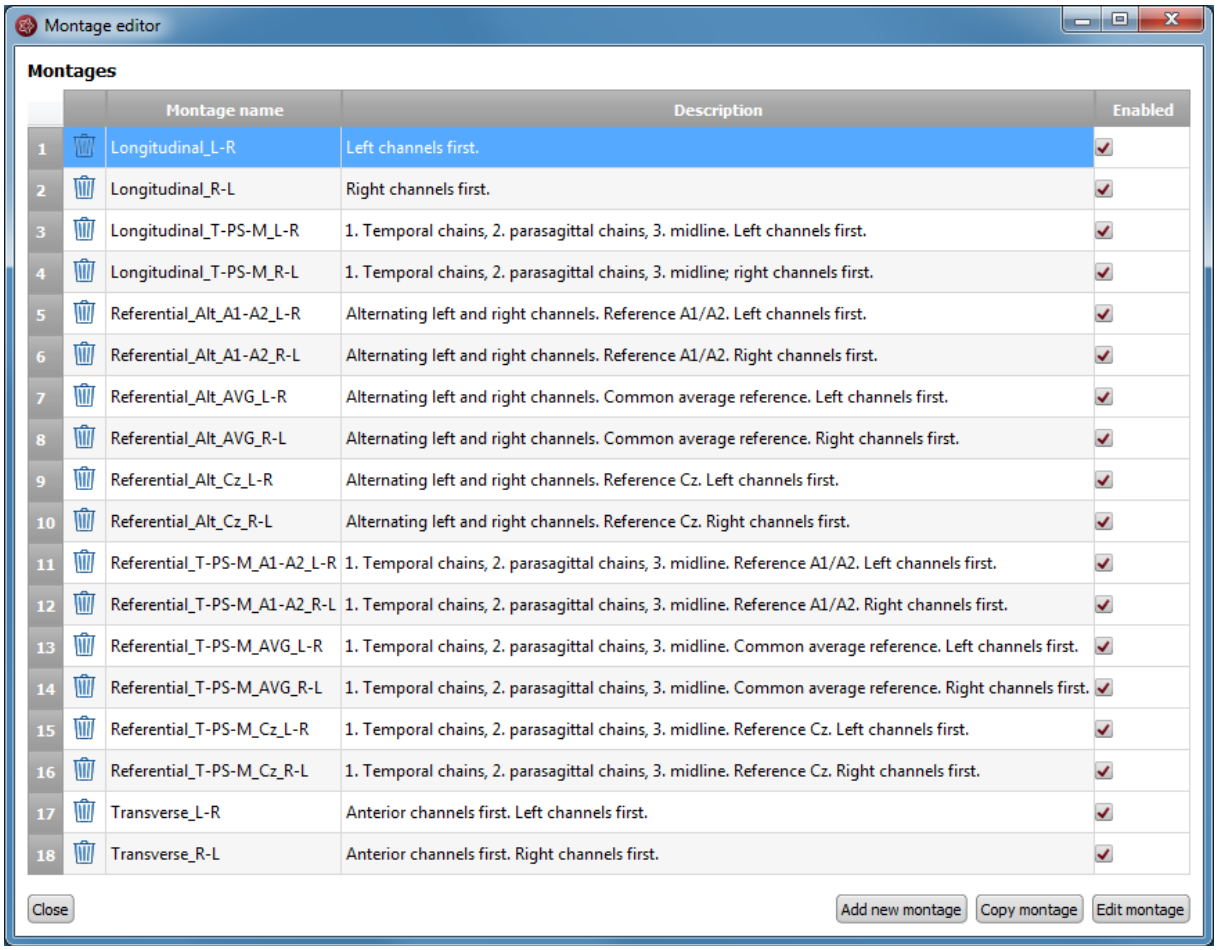
In this case you will need to add new montage chains too. Press the button "Add new montage", then edit the montage. For more details, see Montage chains and Edit montage chains.

Copy an existing montage and edit it

If you find an existing montage that it similar to the one that you want to add you may select and edit it. For this, select the montage and press the button "Copy montage". Then edit the montage. For more details see Edit Montage.

Edit montage

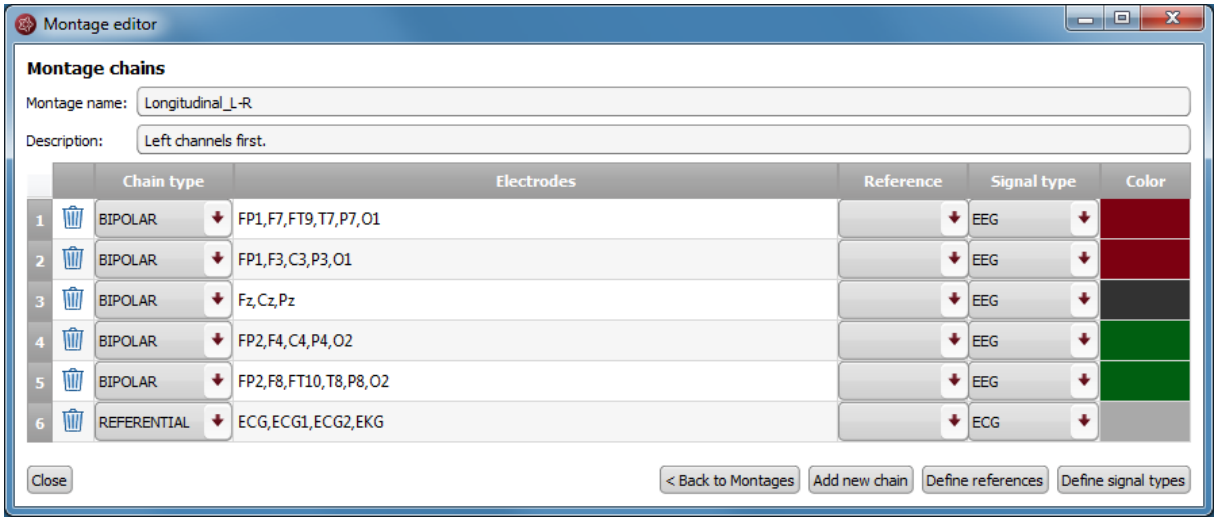
You may want to change an existing montage. For this, open the montage editor.



and select the montage you wish to change. Double click on it or click on the button "Edit montage". The window with the montage chains will open.

For details on the changes that can be made in the montage chains, see Edit montage chains and Montage chains.

Edit montage chains



The following changes can be made in the montage chains:

Montage name

Double click on the field "Montage name" and fill in the name you wish. This is the name that will appear in the drop-down menu Montage of the viewer.

Description

Double click on the field "Description" and fill in the description you wish. This field is for your personal information and not used elsewhere by the viewer.

Chain type

Click on the drop-down menu and select REFERENTIAL or BIPOLAR.

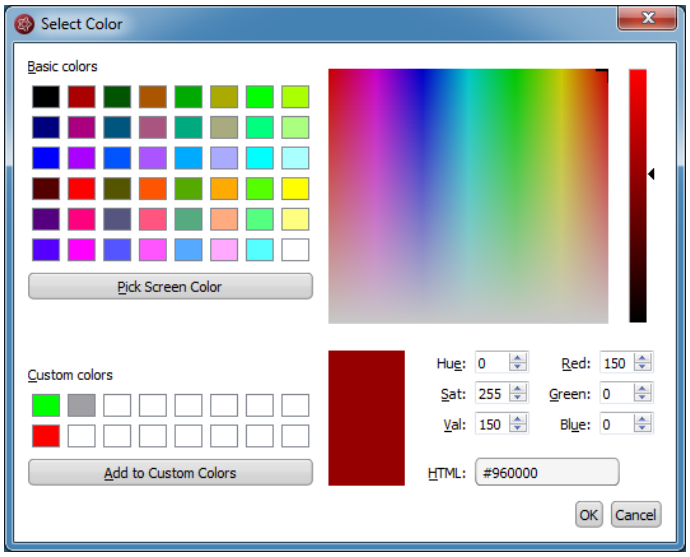
Electrodes

Double click on the field "Electrodes" and fill in the electrodes that should be included in the chain separated by commas.

- Reference: Click on the drop-down menu "Reference" and select an electrode in the list.
- Signal type: Click on the drop-down menu "Signal type" and select a type in the list.

Color

Double click on the field "Color". Select a color in the window and press "OK". This is the color displayed on the curves of the chains in the viewer.



Channel order

Change the order of the channels by changing the order of the electrodes in the field "Electrodes" or by clicking on the number for the chain and dragging and dropping the line where you wish to have it.

Add a new chain

Press the button "Add new chain" and edit the fields as described above.

For more information about the fields, see sections Chain references and Signal Types.

Order of the channels

The order of the channels in the montage chains corresponds to the order of the channels how they are displayed in the viewer when the montage is selected. To change the order of the channels you have two possibilities:

1. Change the order of the electrodes in the field "Electrodes".
2. Change the order of the chains by moving them in the list with drag and drop.

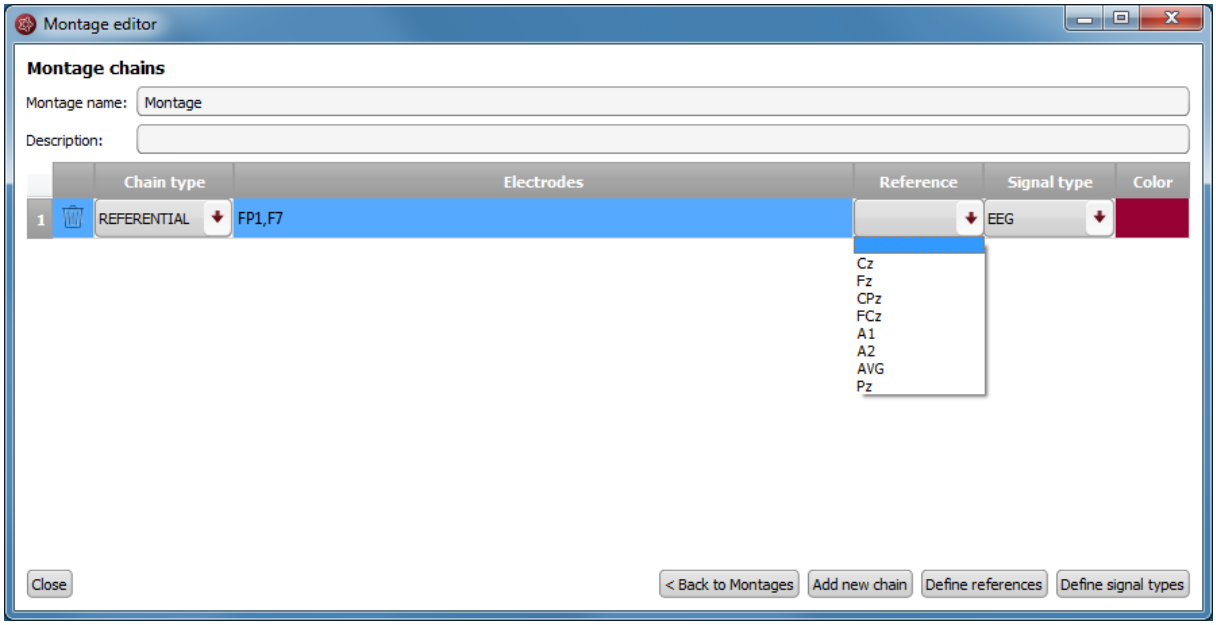
Chain references

A REFERENTIAL chain should always have the field "Reference" filled out.

	Chain type	Electrodes	Reference	Signal type	Color
1	REFERENTIAL	F7, F8, FT9, FT10, T7, T8, P7, P8	Cz	EEG	

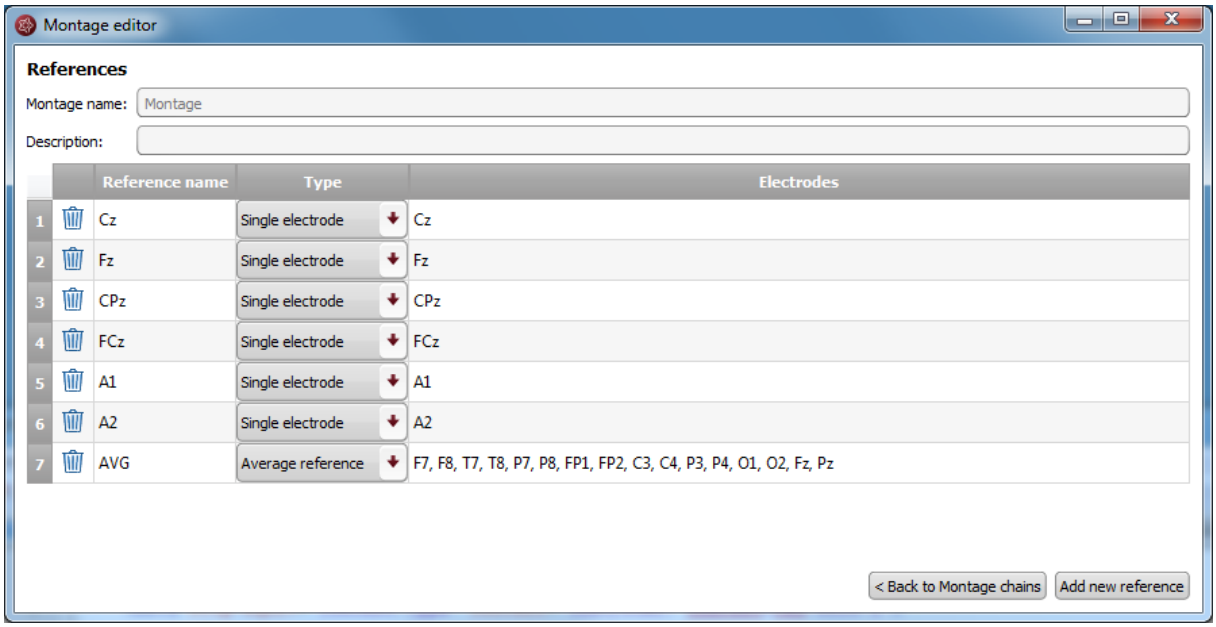
Fill in Reference

In order to fill in the Reference click on the drop-down menu and select an electrode in the list.

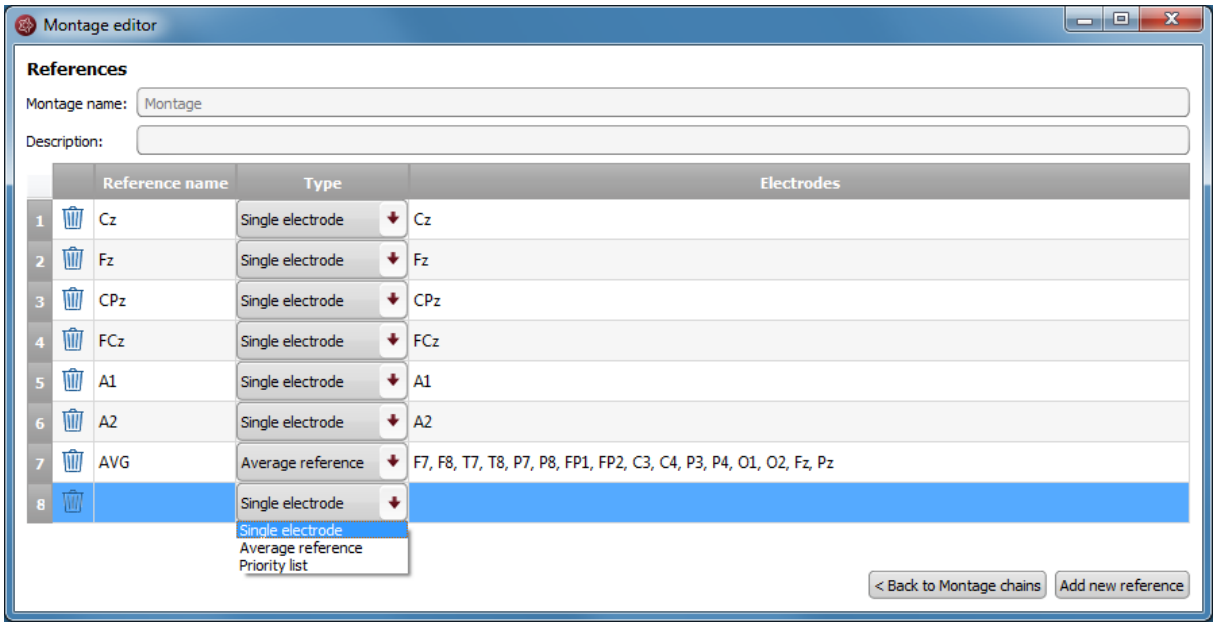


Define new reference

If the whished electrode is not in the list, it can be added by defining a new reference. For this, click on the button "Define references". The following window will open, showing the references already defined:



1. In order to add a new reference click on the button "Add new reference", a new line will be inserted:



2. Fill in the "Reference name".
3. Fill in the field "Type". For this:
    1. Select "Single electrode", when only one individual electrode should be the reference. Fill in the electrode label in the field "Electrodes".
    2. Select "Average reference", when the reference should be an average of several electrodes. Fill in the electrodes that should be included in this average in the field "Electrodes".
4. Click on the button "Back to Montage chains" to continue editing the chains.

Signal Types

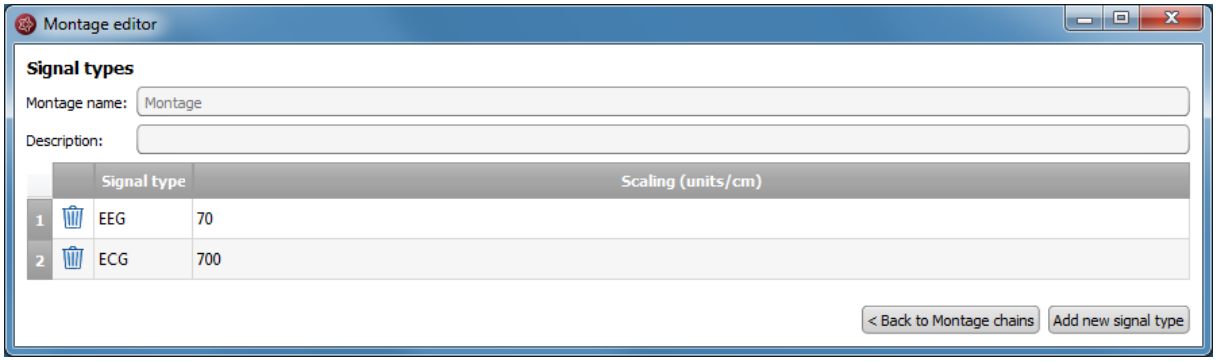
A chain should always have the field "Signal type" filled out.

Fill in signal type

In order to fill in the Signal type click on the drop-down menu and select a type in the list.

Define new signal type

If the whished signal type is not in the list, it can be added by defining a new signal type. For this, click on the button "Define signal types". The following window will open, showing the signal types already defined:



1. In order to add a new signal type click on the button "Add new signal type", a new line will be inserted.
2. Fill in the "Reference name".
3. Fill in the name of the signal type and the scaling in units/cm.
4. Click on the button "Back to Montage chains" to continue editing the chains.

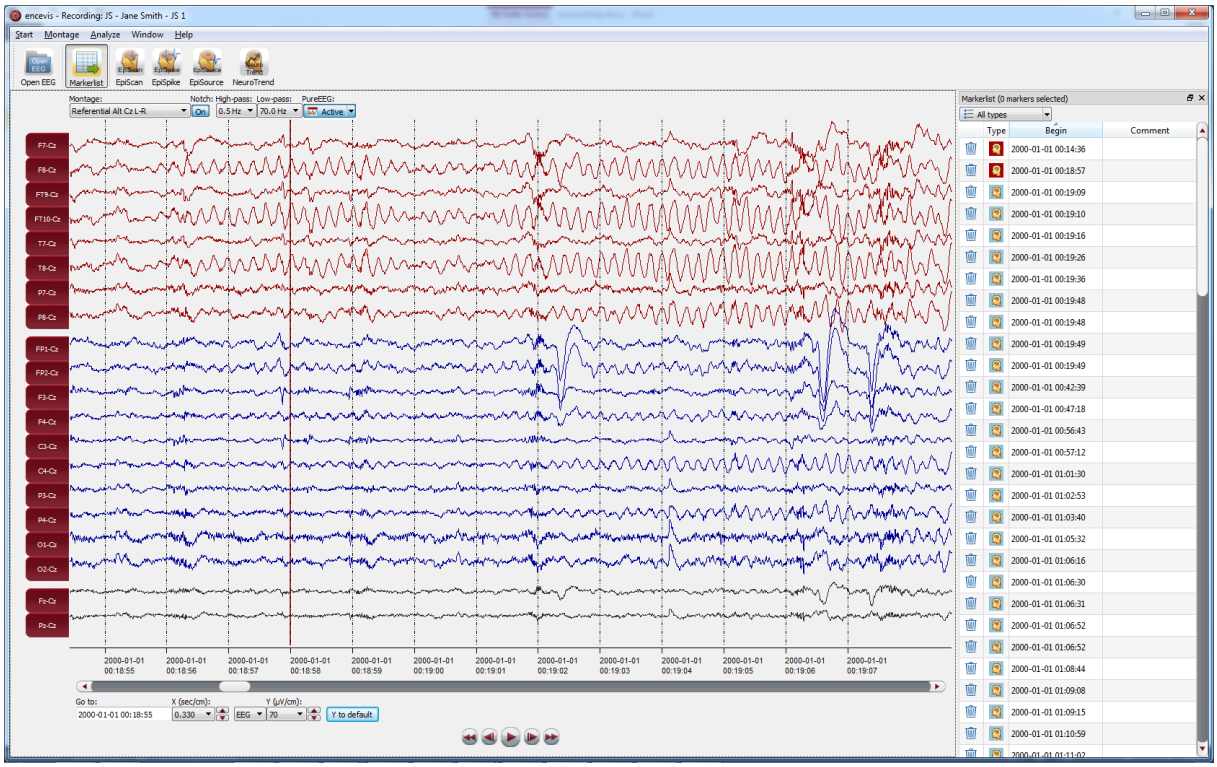
Markers

Special EEG events can be stored in the form of a marker. A marker includes the information:

- Type (see the different marker types)
- Begin
- End
- Comment

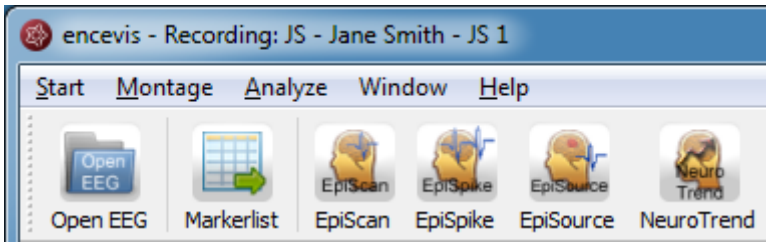
Markers are saved with the data in the marker list and can be viewed anytime.

In the viewer, the markers can be easily identified because they appear colored. More details on how to use the markers can be found in the following sections.



Markerlist

Click on the button "Markerlist" to open the Markerlist or select the menu point *Window > Markerlist*.

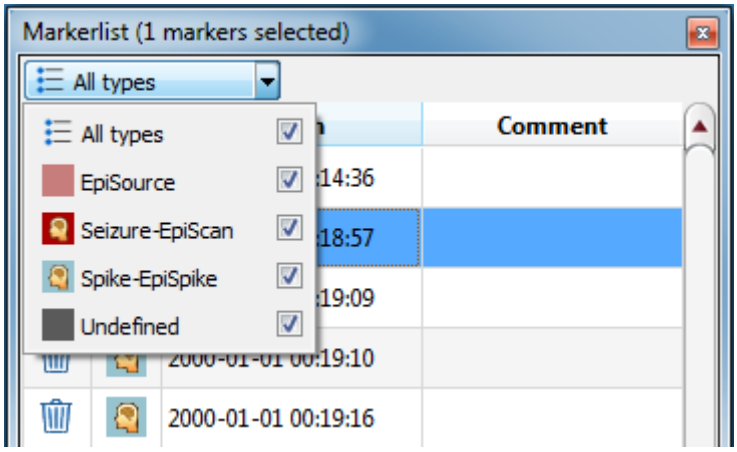


- Click on the button "Markerlist" to close the Markerlist when it is open.
- Click on a marker in the list. The EEG, starting with the begin of the marker, will be displayed in the viewer.

You can use the list in the following ways:

Select marker type

Select a marker type in the list "All types".



Navigate through the list

Use the keyboard arrows for going up and down the list.

Sort the list

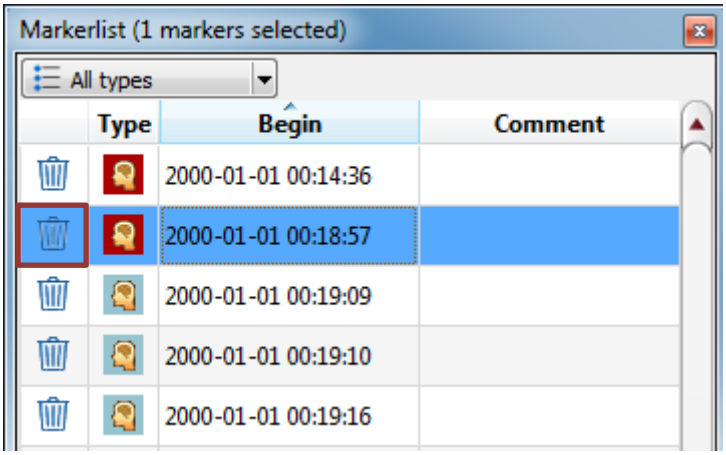
Click on the field you want to sort by.

Change the fields of a marker:

Double click on the marker in the Markerlist or right click on the marker on the screen and select “Edit marker”. Fill in the changes.

Delete marker(s) by moving them to the Recycle Bin:

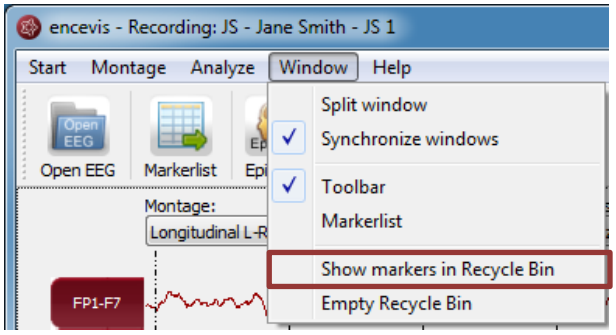
Click on the recycle bin icon on the left column of the marker or right click on the marker on the screen and select “Delete marker”.



Show/hide deleted markers in the list

You can choose to have the markers that were moved to the recycle bin shown in the Markerlist or hidden.

→ For this, select the menu point *Window* > *Show markers in Recycle Bin*.

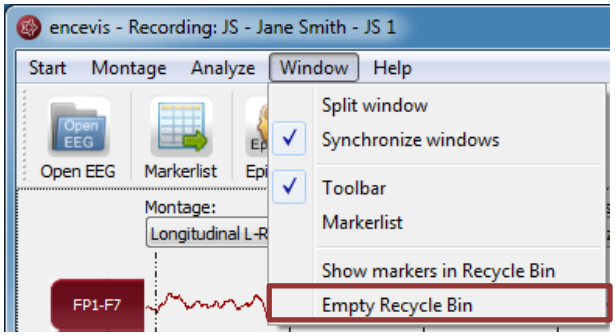


If you have chosen this setting, you can easily remove the marker from the recycle bin by clicking on the icon again.

Permanently delete marker(s)

You can choose to permanently delete markers by moving them to the Recycle Bin and emptying the Recycle Bin.

→ For this, select the menu point *Window* > *Empty Recycle Bin*.



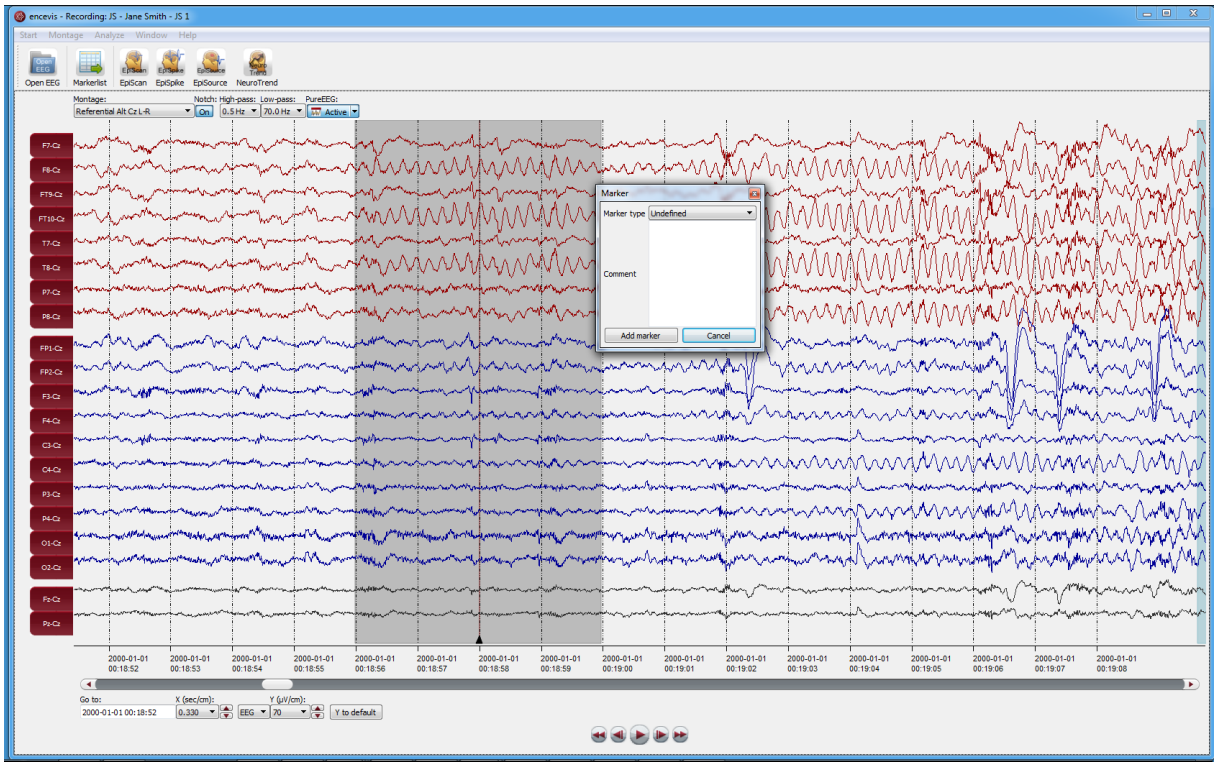
Add marker

Special EEG-events can be saved in the form of markers.

You can insert a marker in 2 different ways:

Add marker by clicking and dragging the mouse

1. Click on the EEG where the marker should start and leave the mouse pressed.
2. Move the mouse to select the time period for the marker (grey color).
3. Release the mouse and a window will pop-up.



In this window:

1. Select the Marker type.
2. Fill in the field "Comment" if necessary.
3. Click on "Add marker".

Add marker with right click

Right click on the EEG and select "Add Marker" or double click where the marker should start. A window will pop-up.

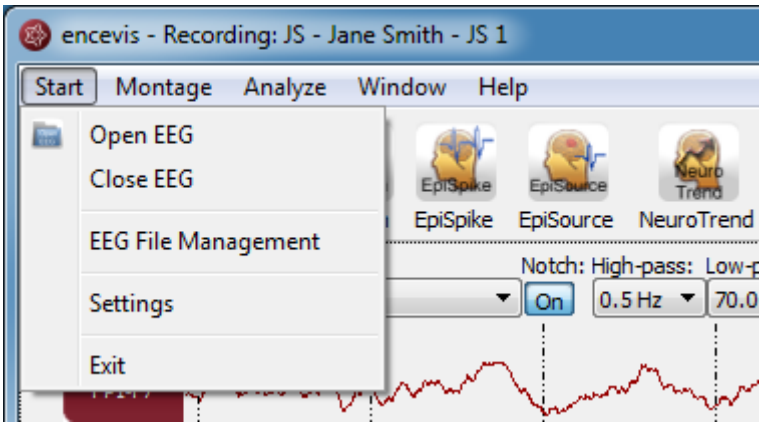
In this window:

1. Select the Marker type.

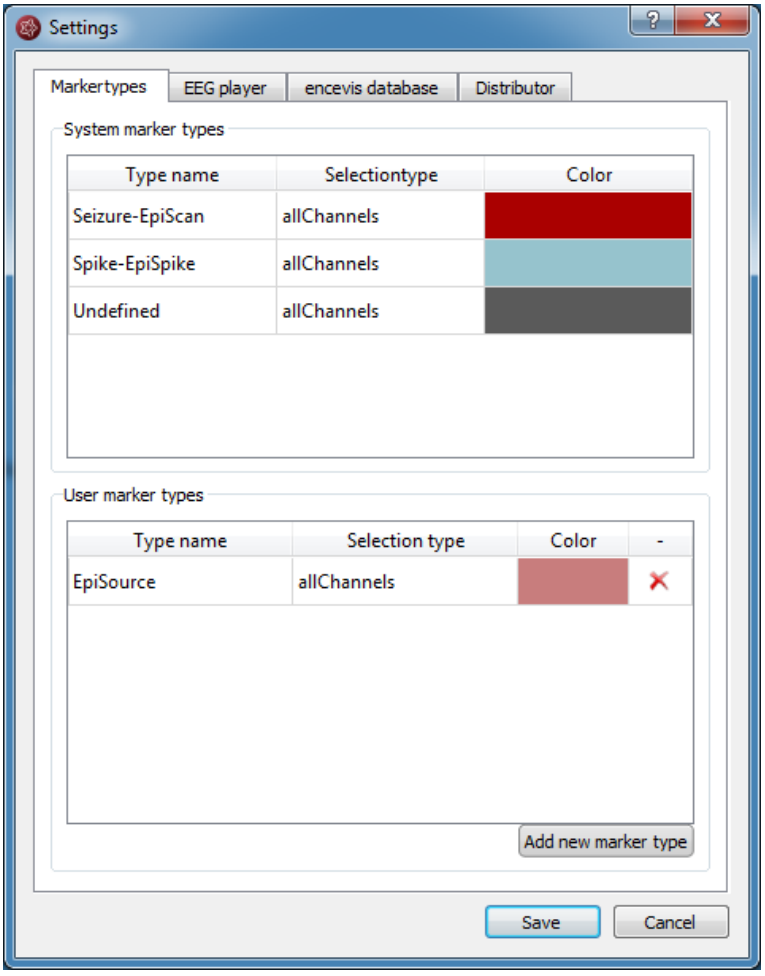
2. Fill in the field "Comment" if you wish.
3. Click on "Add marker".

Settings

Several settings can be defined in encevis. For this, select the menu point *Start* > *Settings*.



Settings Markertypes



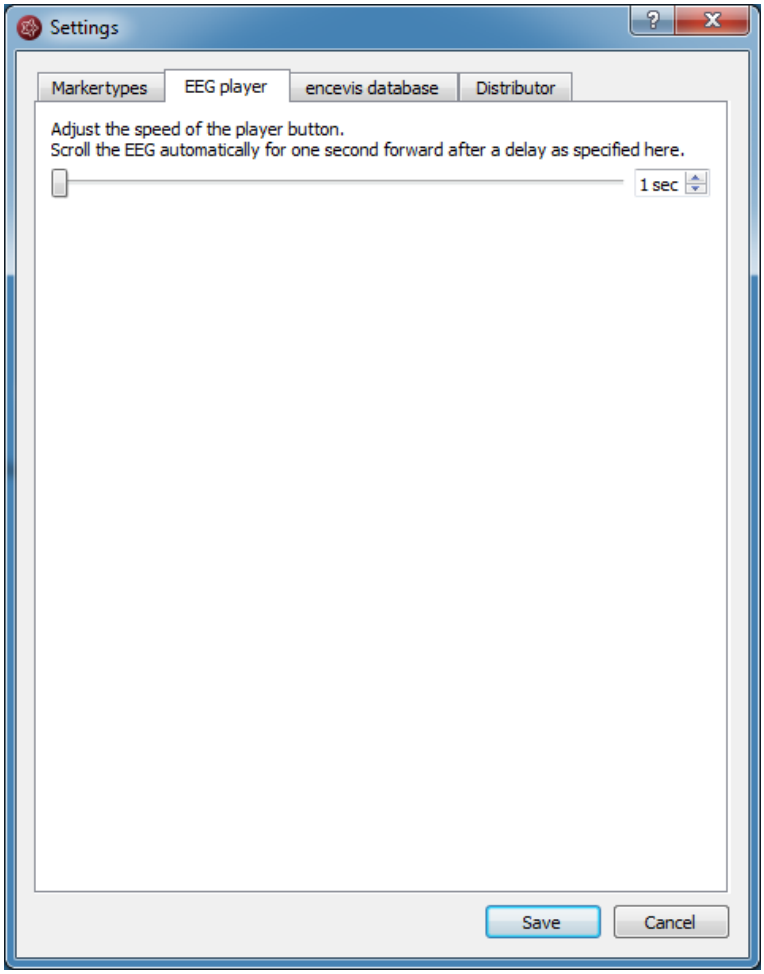
System marker types

System marker types are the default marker types of encevis. You can define their color by just double clicking on the field "Color".

User marker types

User marker types include marker types defined by the user. You can easily define new marker types. Press the button "Add new marker type" and choose a name and a color.

Settings EEG player



The play button in the viewer enables you to view the EEG as in a video. You have here the possibility to set the speed at which the EEG is shown.

Settings encevis database

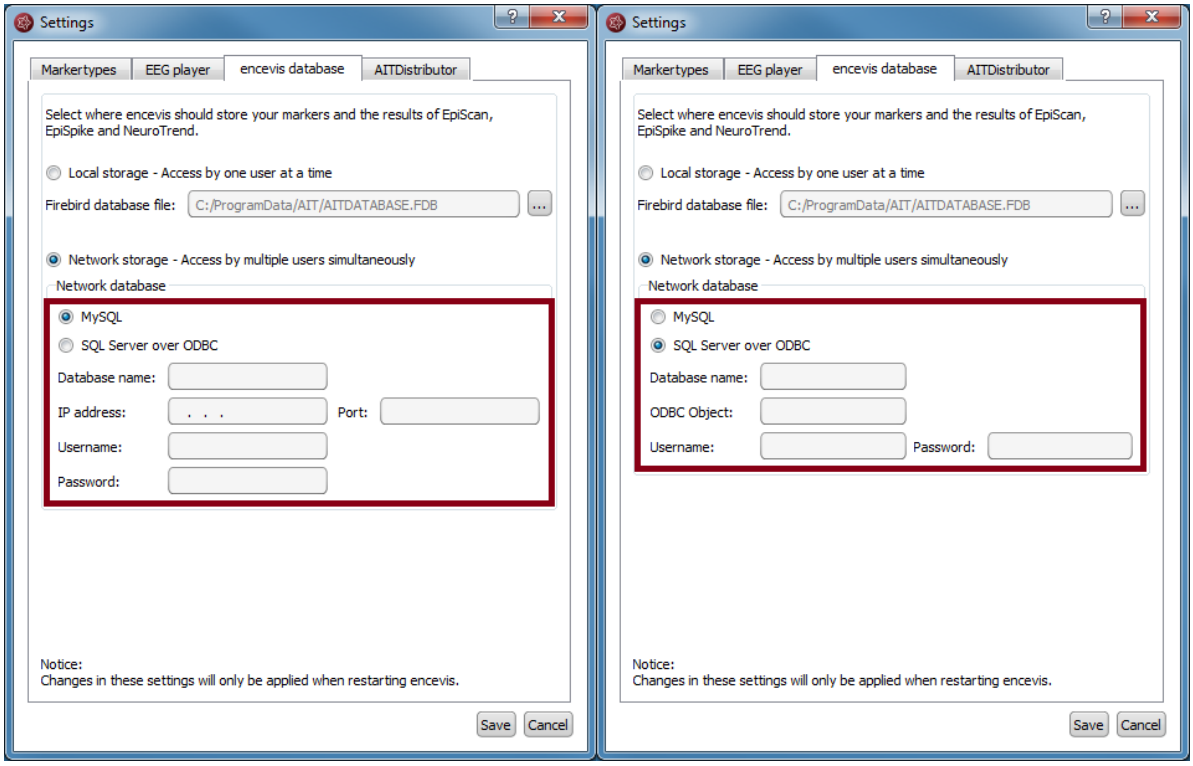
encevis stores your markers and the results of EpiScan, EpiSpike and NeuroTrend in one database. Select where encevis should store it:

Local storage - Access by one user at a time:

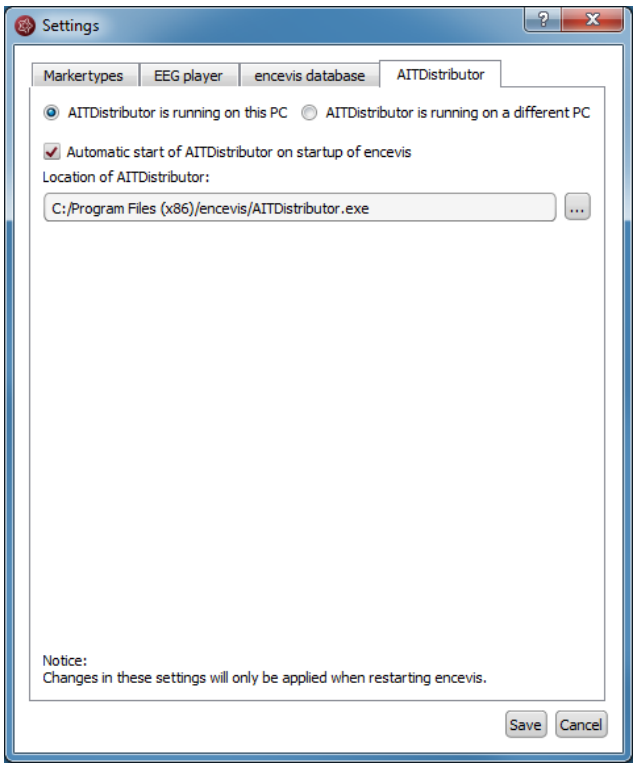
This is the best mode, when the results of your review with encevis should only be accessed from your PC. Only one user at at time can then access the results. You can leave the file name specified by default or select a personalized name.

Network storage - Access by multiple users simultaneously:

This is the best mode, when you want to access the results of your review with encevis from several PCs in your network. With this option several users can access the results at the same time. In this case, you need to specify a database where everybody has access to. This database can be MySQL or an SQL server over ODBC.

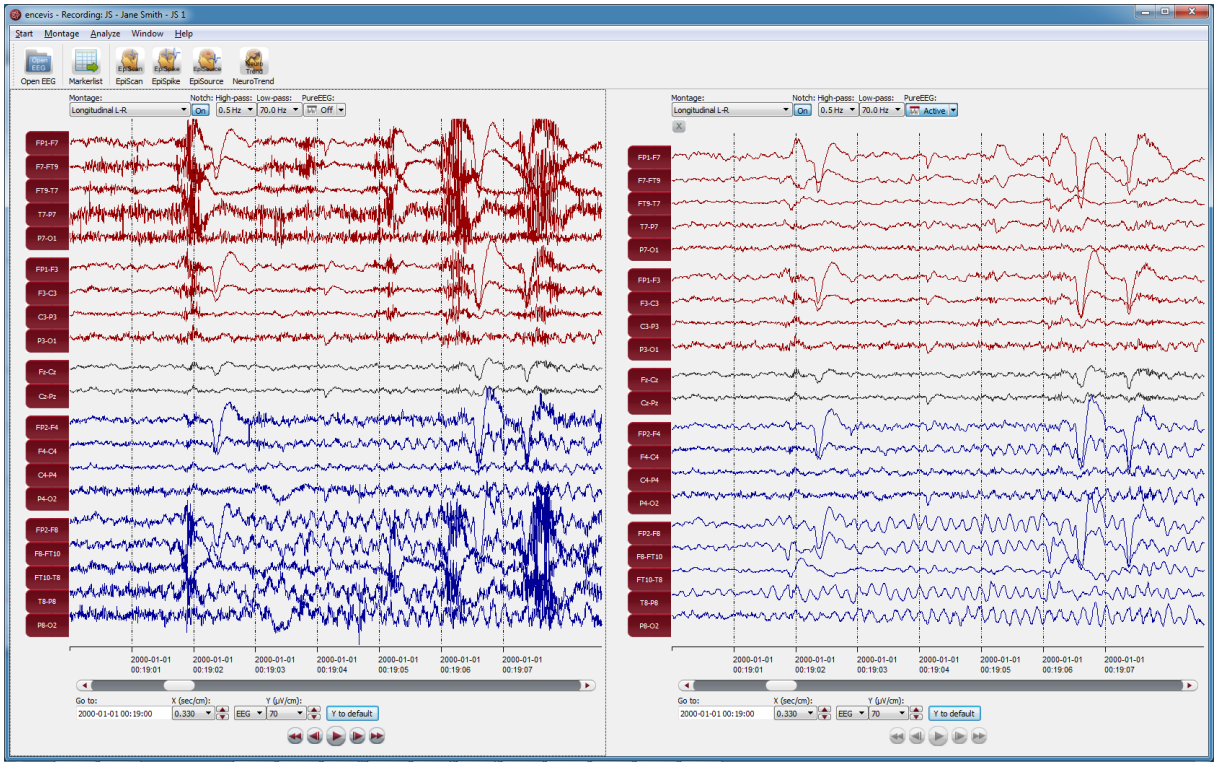


Settings Distributor



Select if the Distributor should run on your PC or on a different one. If the Distributor is running on another PC, you need to specify IP address and Port. For more details see the section Distributor.

PureEEG

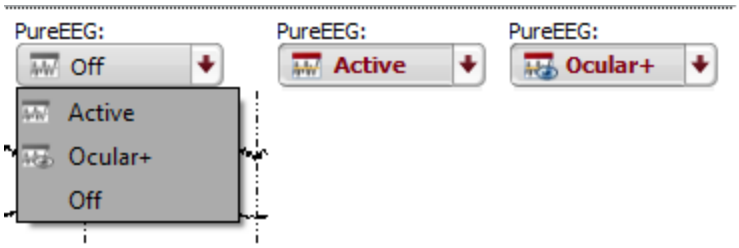


Overview

PureEEG is the automatic artifact reduction from encevis. It removes artifacts from your patient's EEG while the EEG coming from cerebral sources is left unchanged. You can choose to keep ocular artifacts or to remove them from the EEG.

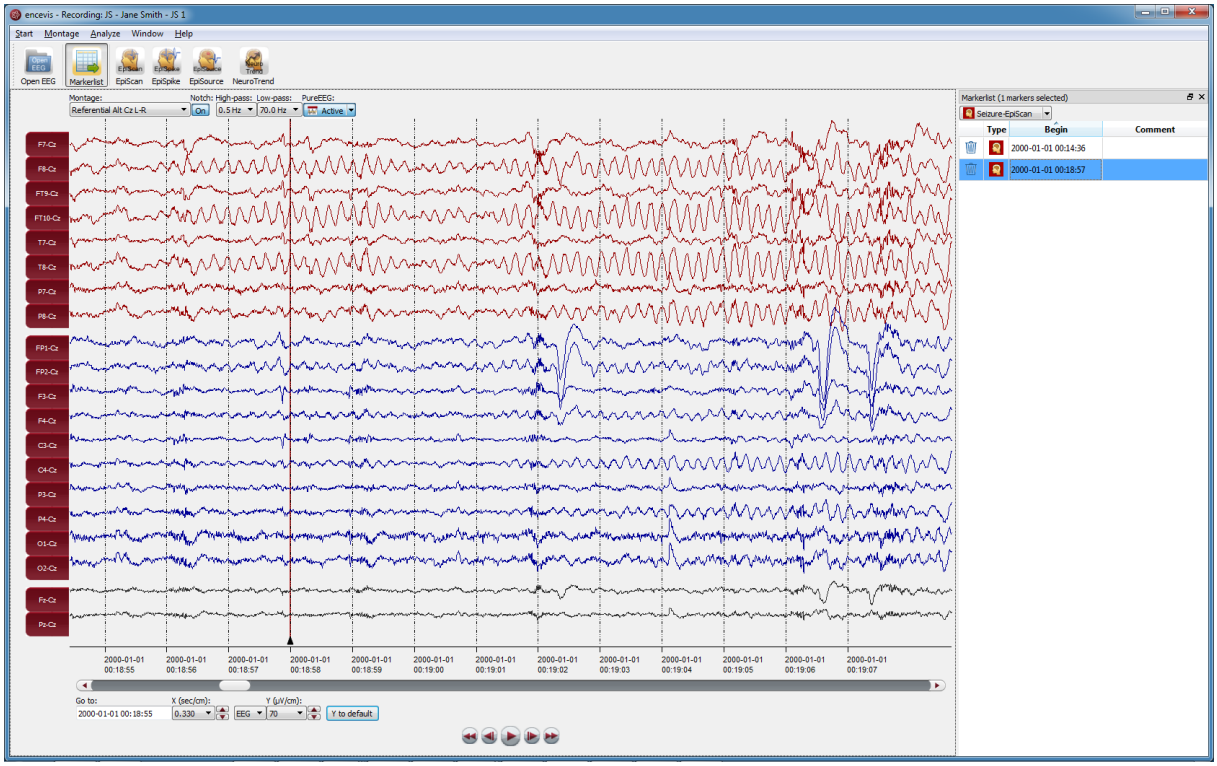
Use PureEEG

Simply click on the drop down list "PureEEG" to switch PureEEG on and off.



The location of the reference electrode used during the recording of the EEG (*Recording reference*) is used by PureEEG.
For the optimal functioning of PureEEG, it is recommended to fill out the reference correctly. For more details, see section Specify reference electrode.

EpiScan



Overview

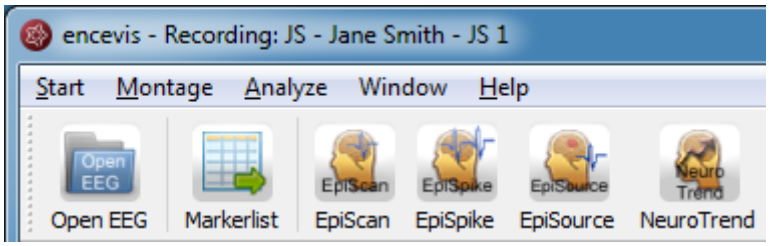
EpiScan is the automatic seizure detection from encevis. It enables to find seizures EEG-activity in your patient's recording. It creates a list of markers that can be easily reviewed. Markers are created and can be reviewed already during the calculation.

Start EpiScan

In order to start EpiScan you need to select the recording you want to analyze.

Follow these steps to start EpiScan:

1. Open the EEG that you want to analyze with EpiScan.
2. Click on the "EpiScan" icon under the menu to start the calculation.

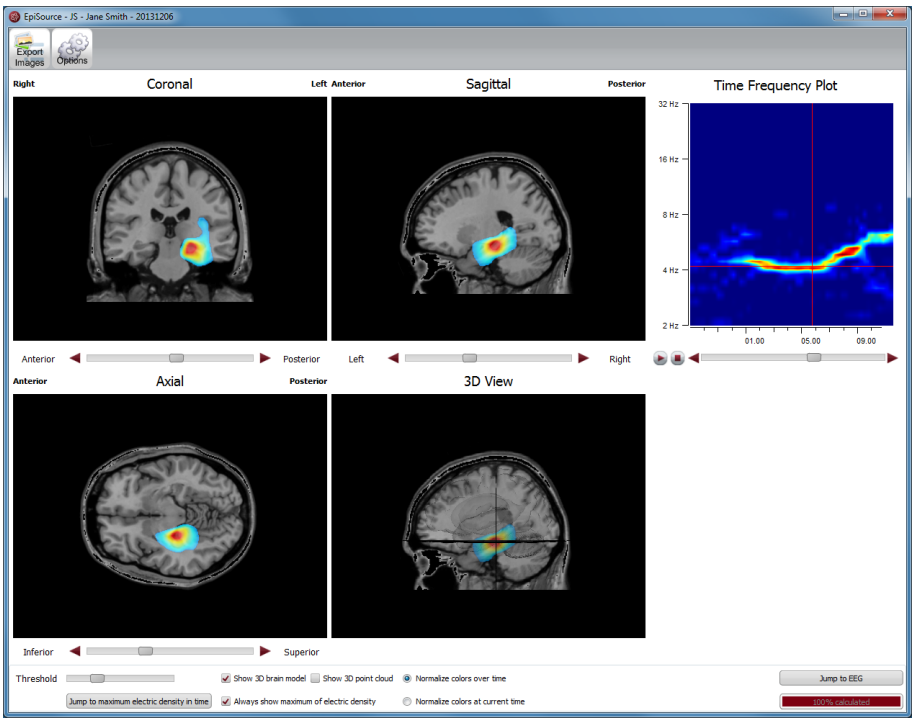


Once the calculation started, the progress will be shown under the icon.

During the calculation, if seizures have been detected, markers will be created and will appear automatically in the marker list.

You can easily view these seizure markers during the calculation. For more details on how to review markers see section Markerlist.

EpiSource



Overview

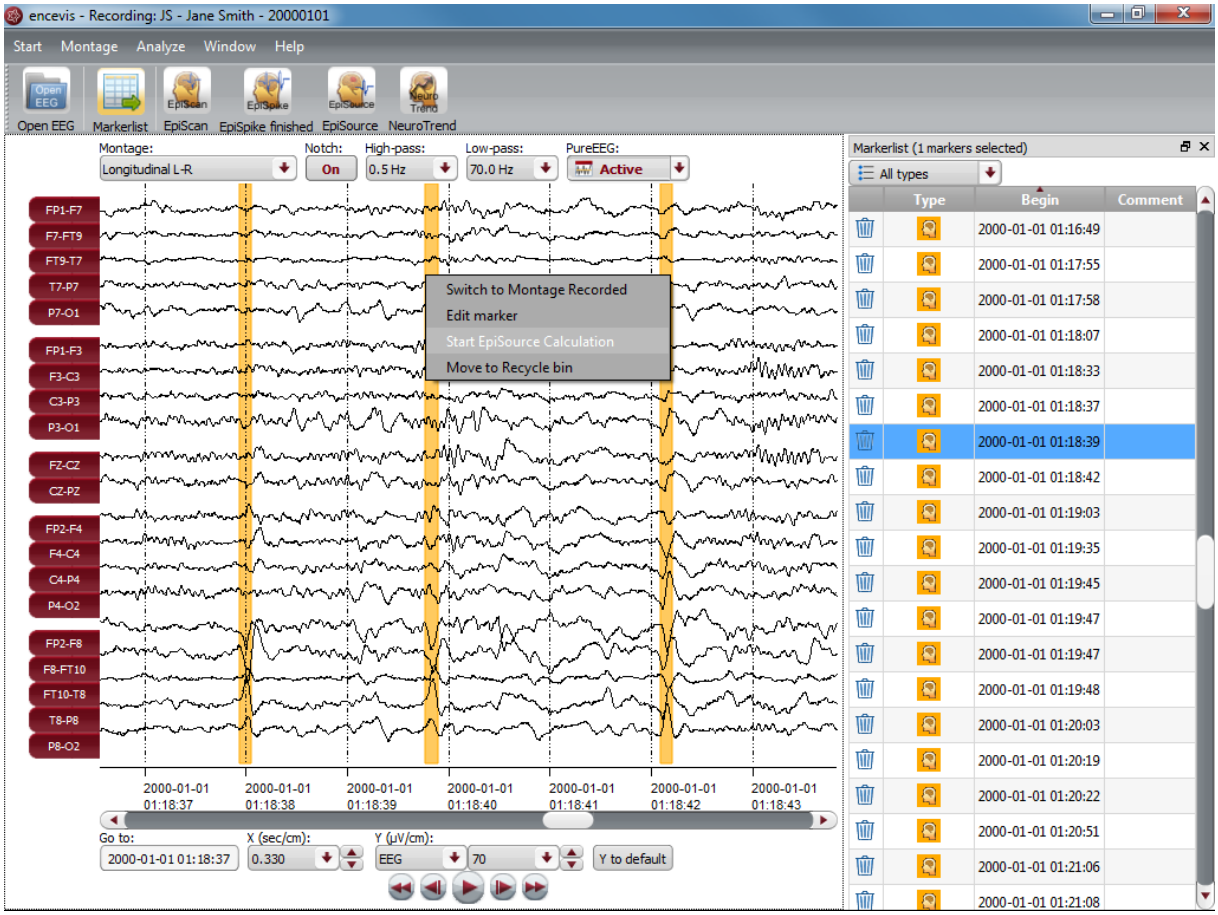
EpiSource is the 3D source localization from encevis. It enables to localize spikes and ictal EEG activity. EpiSource does not require any user-interaction. Instead, it is easy to use and parameter free. The result is a 3D visualization of the localized activity that can also run as a video.

Start EpiSource

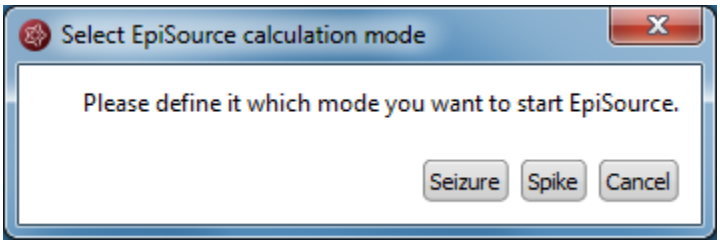
In order to start EpiSource you need to open in the viewer the marker you want to analyze. For instructions on how to insert a marker see section Add marker.

Follow these steps to start EpiSource:

1. Right click on the marker on the EEG screen.
2. Select "Start EpiSource Calculation".



3. If you have clicked on a marker that is not an EpiScan or EpiSpike marker, a window will pop up. You will be asked the following question:



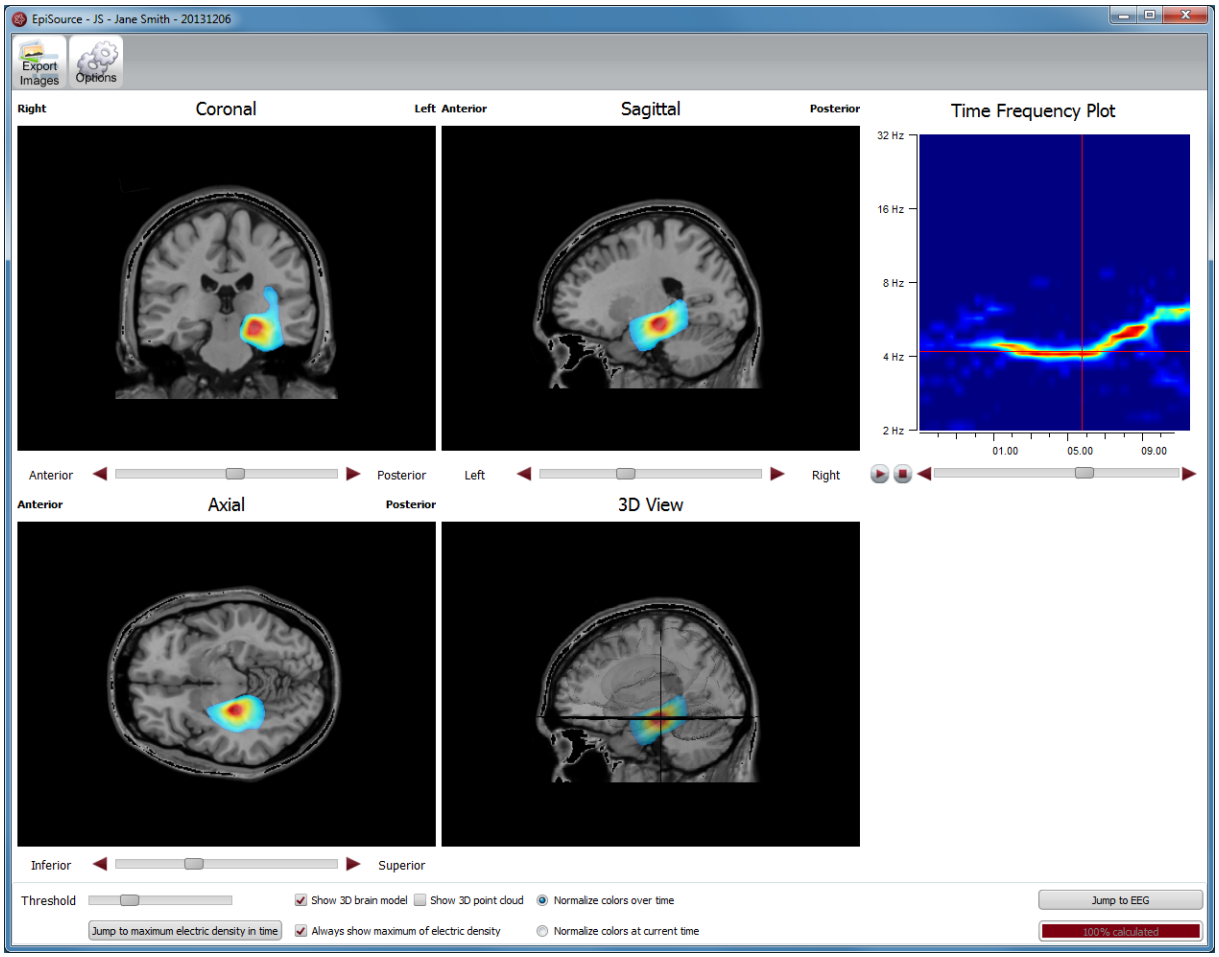
4. Click of "Seizure" if you want to localize seizure activity. For this the marker needs to be 1-300 sec long.
5. Click of "Spike" if you want to localize a spike. For this the marker needs to be 20-500 msec long.

The question regarding localization type is answered automatically if the marker you selected is of type EpiSpike or EpiScan.

The results of the localization will be shown on the EpiSource window that will pop-up immediately.

View EpiSource results for seizure localization

Once you have started EpiSource, the EpiSource window will open and the calculation will start.



Status of the calculation

On the lower right corner you will see the status on the calculation.

Results: Activity shown color coded in four images

Results shown in four images

Once the calculation is done, the results will be shown in three 2-dimensional images and one 3-dimensional:

- Coronal, Sagittal and Axial show 2-dimensional slices.
- 3D-View shows a 3-dimensional representation.

Results color coded

The activity is shown in all images as color coded overlay to the structural MRI.

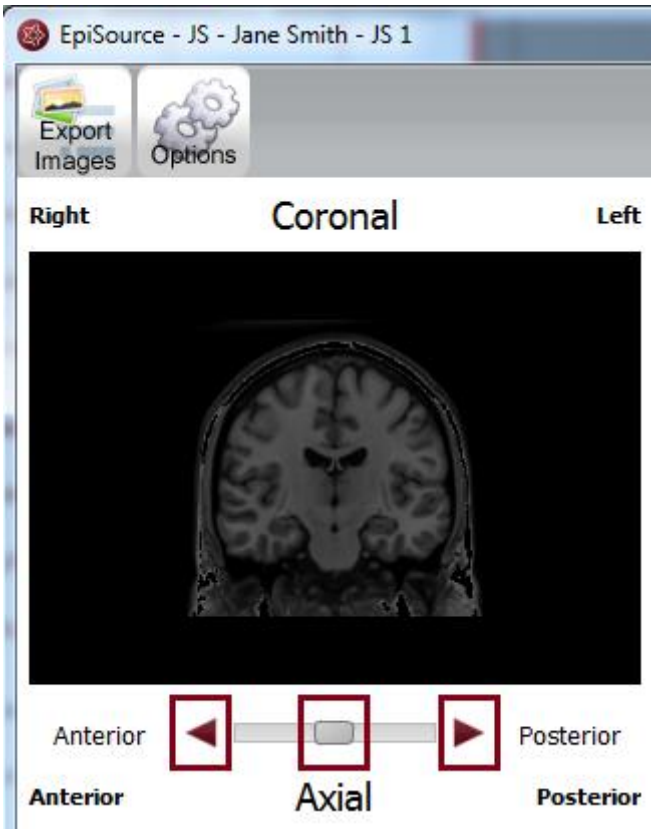
- High activity is red.
- Low activity is blue.

Navigation in the brain images

Navigate through the slices

You can navigate through the slices to see the distribution of the activity through the whole brain.

- Use the sliders under the respective image to navigate through the slices.



- Alternatively you can use the back- and forward buttons.
- Click on the image on a certain point and the slices corresponding to that point will appear in the other images.

Zoom in and out

You can easily zoom in in and out the images.

- Click on the image and scroll up and down with your mouse wheel.
- Zooming also works by pressing the right mouse button while moving the mouse for- and backward.

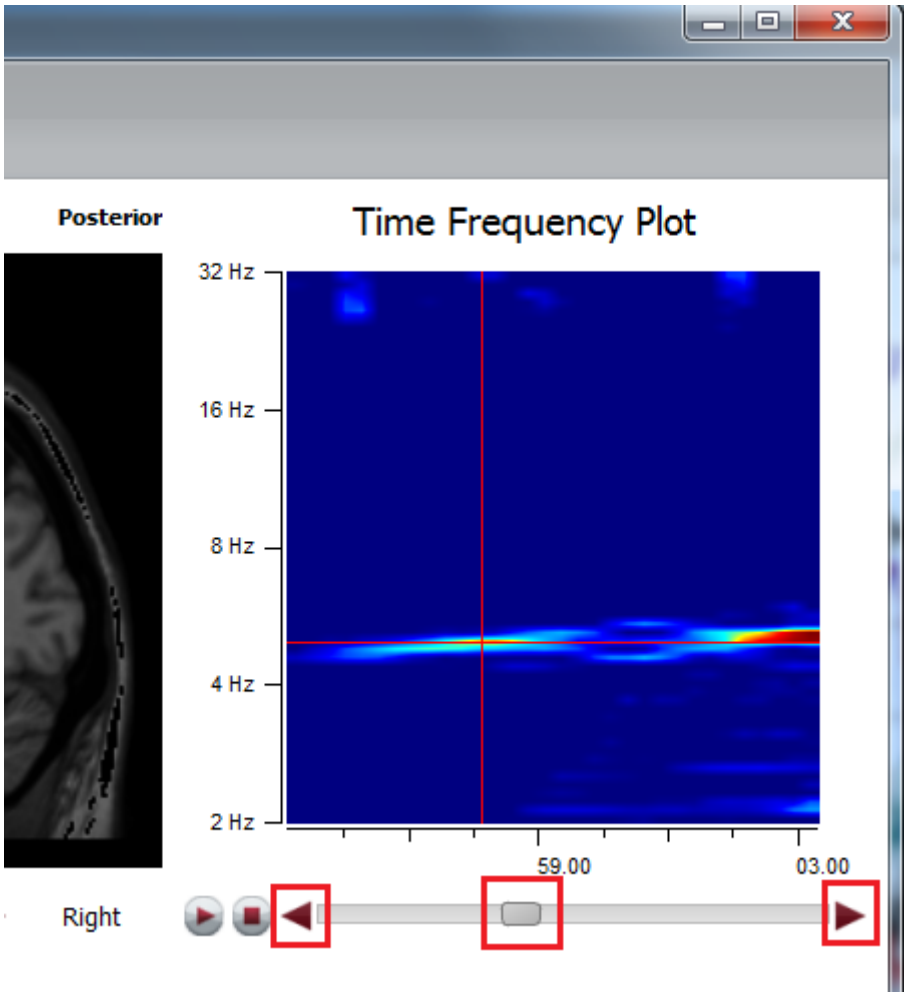
3D visualization

The fourth image shows a 3D visualization.

→ The 3D image can be rotated by pressing the left mouse button while moving the mouse.

Navigation in time

Here is the main difference to the spike mode. On the right side a time-frequency plot is shown.

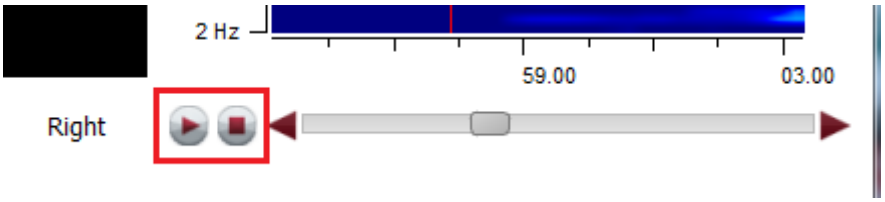


→ You can step through the time intervall by using the slider or the back and forward buttons under the time-frequency plot.

The dominant rhythmic pattern is chosen automatically for each time point and therefore the frequency in the time frequency plot is adjusted. This is shown with in the intersection of the red horizontal and vertical lines.

In parallel you can see in the viewer a red vertical line that highlights the center of the used EEG-segment which is the basis for the source localization calculation.

You can view the localization as a video.



1. Click on the play button on the left of the slider.
2. The video will show the localization results step by step.
3. The video will be shown on all images at the same time.

4. If you press play, the video will start from that time point.
5. If you press pause, the video will pause.
6. If you press stop, the video will stop and the slices will show from the starting point.

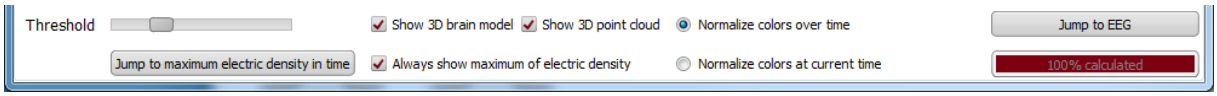
Jump to maximum electric density in time

You can always see the images, when and where the activity is the highest.

→ For this, click on "Jump to maximum electric density in time".

Controls

Several controls can be found on the lower part of the screen:



Threshold slider

You can hide the color coded overlay of brain regions with low activity.

→ Move the threshold slider in the lower left corner of the screen to do that

Check box "show 3D brain model"

A model of the inner brain structures can be faded in/out.

→ Click on the check box "show 3D brain model".

Check box "show 3D point cloud"

You can choose to show the EEG-activity in the 3D View with a point cloud.

→ Click on the check box "show 3D point cloud".

Buttons "normalize colors over time"/"normalize colors at current time"

A model of the inner brain structures can be faded in/out.

→ Selecting "normalize colors over time" will show a color distribution that you can use over the whole intervall.

→ Selecting "normalize colors at current time" will show the difference in activity for the current moment in more clarity.

Check box "always show maximum of electric density"

You can choose to always show the maximum EEG-activity in the 2-dimensional views. If you navigate in time, the images will automatically show the slices where the maximum activity was found.

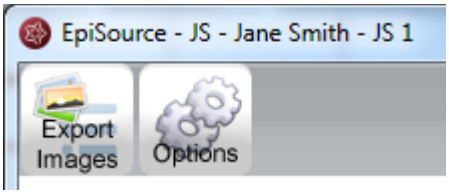
→ Click on the check box "always show maximum of electric density".

Button "Jump to maximum electric density in time"

You can see the images for the moment where the maximum activity was measured.

→ Click on "Jump to maximum electric density in time".

Menu



Export images

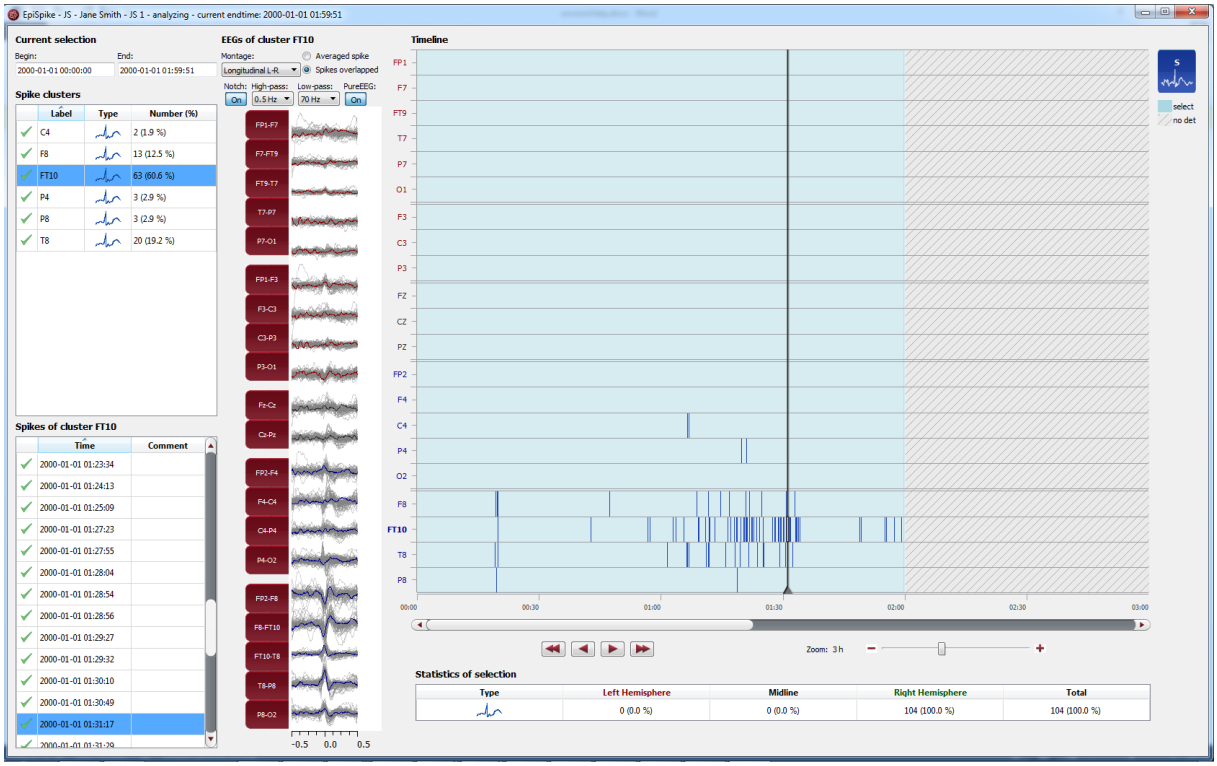
The images of the source localization results can be exported as png-figures.

→ Click on the button "Export Images" and select the folders, you want to have the images saved to.

Options

Here you can set the speed you want to watch the results as a video.

EpiSpike



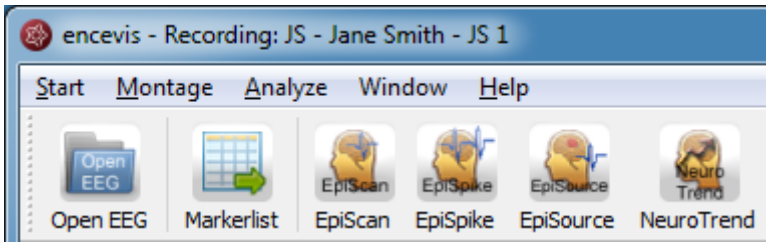
Overview

EpiSpike is the automatic spike detection from encevis. EpiSpike enables you to find spikes in your patient's recording. Markers are created and can be viewed already during the calculation. A graphical visualization enables you an easy and fast review of the results.

Start EpiSpike

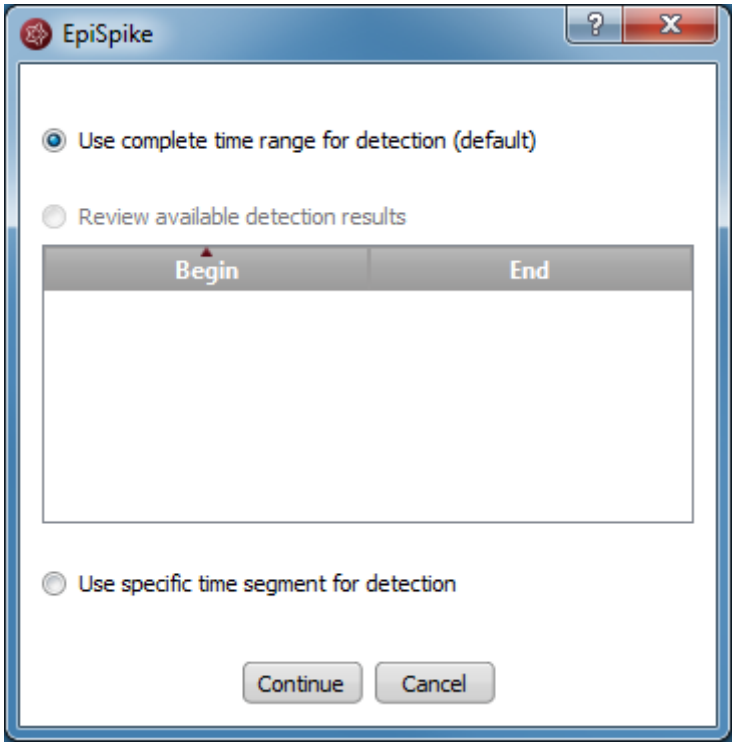
In order to start EpiSpike you need to select the recording you want to analyze. Follow these steps to start EpiSpike:

1. Open the EEG that you want to analyze with EpiSpike.
2. Click on the "EpiSpike" icon under the menu to start the calculation.



Starting EpiSpike for the first time

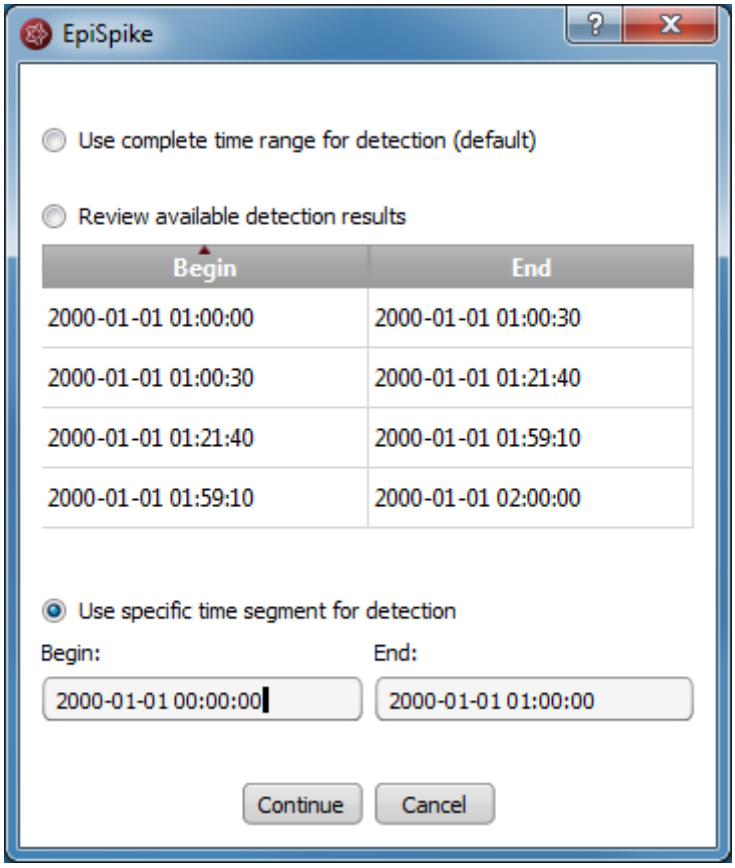
When you start EpiSpike the first time on a recording, the following window will pop-up:



→ Specify if you want to have the detection on the whole time range of the recording or just a segment.

Starting EpiSpike for the second time

When you start EpiSpike again after the first time and the detection was not completed, the following window will appear:

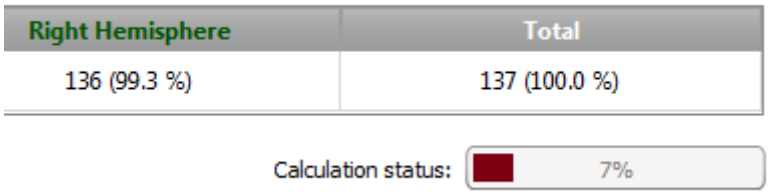


It shows you in which time ranges the detection is already a complete. You have the following possibilities here:

1. If you select *Use complete time range for detection*, EpiSpike will open and the detection will continue where it stopped before.
2. If you select *Review available results* , EpiSpike will open and show available detection results, but it will not start any new detections. This option is recommended, if you don't want any additional program running.
3. If you select *Use specific time range for detection,* EpiSpike will open and start the detection in the time range you specified. This option is recommended, if you are interested only in one specific time period and you want to access results faster.

EpiSpike calculations in progress

Once the calculation started, the progress will be shown lower right corner on the screen.



During the calculation, when spikes have been detected, markers will be created and will appear automatically on the EpiSpike screen.

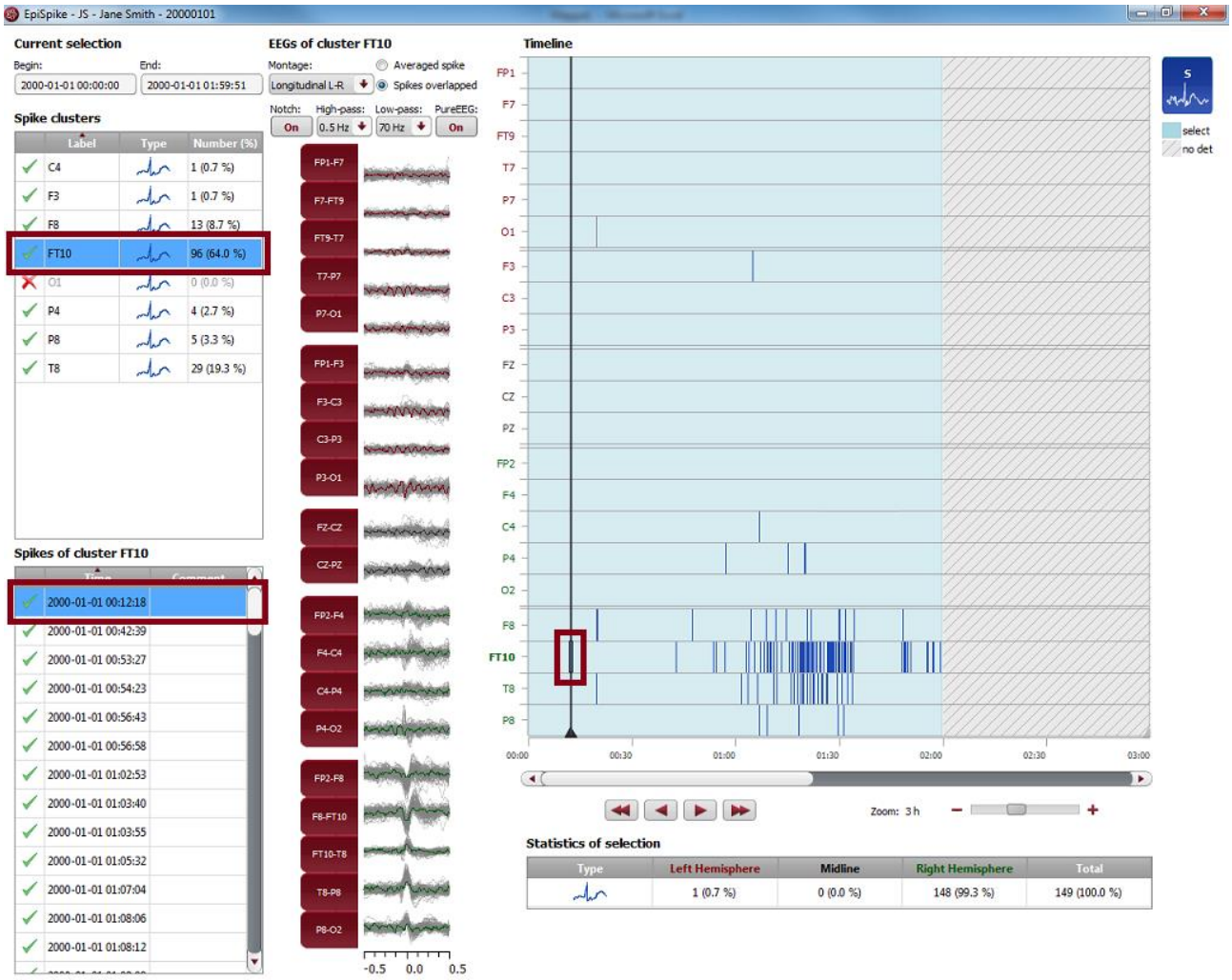
Additionally, the markers will appear automatically in the marker list of the viewer.

You can easily review these detections during the calculation.

- For more details on how to review the detections in the EpiSpike screen, see the section General description.
- For more details on how to review markers see the section Markerlist.

EpiSpike - General description

EpiSpike detects single spikes and groups them in spike clusters with respect to their localization. As localization the electrode label is defined, where the maximum of the spike has been detected. Once EpiSpike has been started, the EpiSpike screen opens and shows the results of the detections.



Timeline

Detections are shown as colored bars on the timeline (see right side of the screen). Each line of the timeline shows the detection within a cluster.

→ You can easily navigate through the results using the navigation controls, the zoom and the mouse.

→ The background can have different colors, see section Current selection for more details.

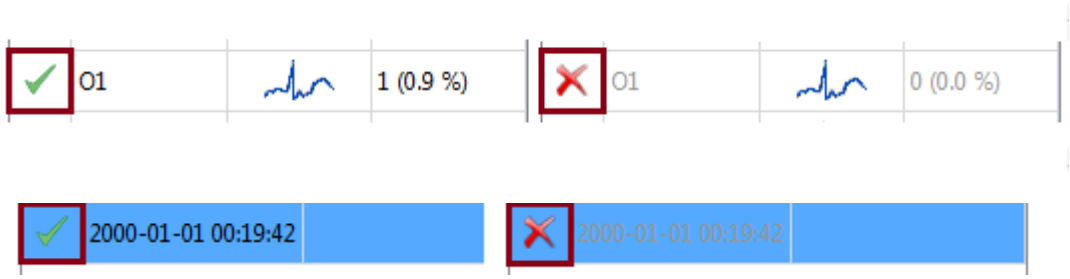
Cluster and spike lists

Additionally, the detections are shown in form of cluster and spike lists (see left side of the screen).

→ Click on a detection on the timeline. The spike and its cluster will be automatically selected in the cluster and spike lists and the EEG is shown (see middle of the screen).

You can delete single spikes or complete clusters.

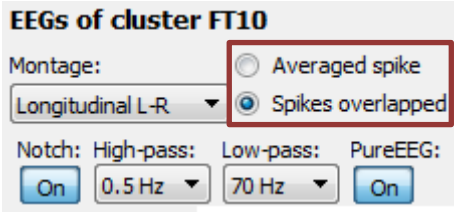
→ Clicking on the check symbol in the corresponding list. A cross will replace the check symbol and the spikes will then appear grey on the timeline.



EEG representation

When a spike is selected, the EEG of its cluster is shown (see middle of the screen).

There are two ways to show the EEG of the cluster:



1. By selecting *Averaged spike*, the EEG of all spikes within the cluster are averaged and the resulting averaged spike is displayed.
2. By selecting *Spikes overlapped*, the EEGs of all spikes are shown overlapped in grey. The EEG of the selected spike is shown in color.

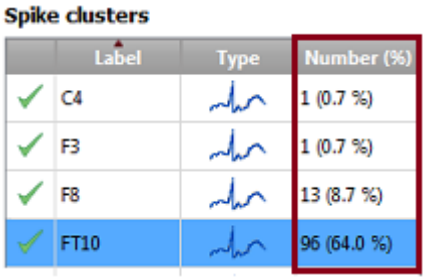
Montage and filters of the EEG can be changed independently of the setting chosen in the EEG viewer.

Synchronization with the EEG viewer

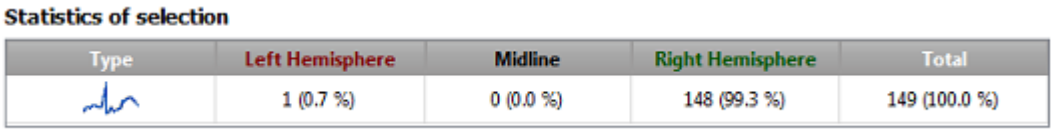
When a spike is selected on the EpiSpike screen, the EEG viewer shows automatically the spike on the main screen. In the same way, when you click on the spike marker in the EEG viewer, this spike will be automatically selected in the EpiSpike screen.

Counting of spikes and statistics

For each cluster, the spikes are counted. The numbers are shown in the spike list:



Additionally, statistics over all clusters are calculated. (see lower part of the screen).



Note that the counting is done in the current selection corresponding to the light blue area on the timeline.

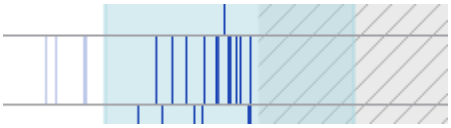
Current selection

The current selection is the time range that can be selected to have the spikes displayed and counted. It is shown in light blue on the time line.

The selection can be changed in two ways:

1. Using the mouse on the timeline. The edges of the light blue area, which marks the selection, can be dragged and moved as wanted. The detections that are not in the current selection are not counted and appear as grey bars on a white background.
2. Entering Begin and End (see upper left corner).

Depending on how the current selection is set, the background of the timeline can have different appearances:



White

White shows that the time range is not in the current selection, but detection results are available. Therefore, detections are not shown in the lists and appear on the timeline as grey bars on white background.

Light blue

Light blue shows that the time range part is part of the current selection and that detection results are available. Therefore, detections are shown in the lists and appear as blue bars on light blue background.

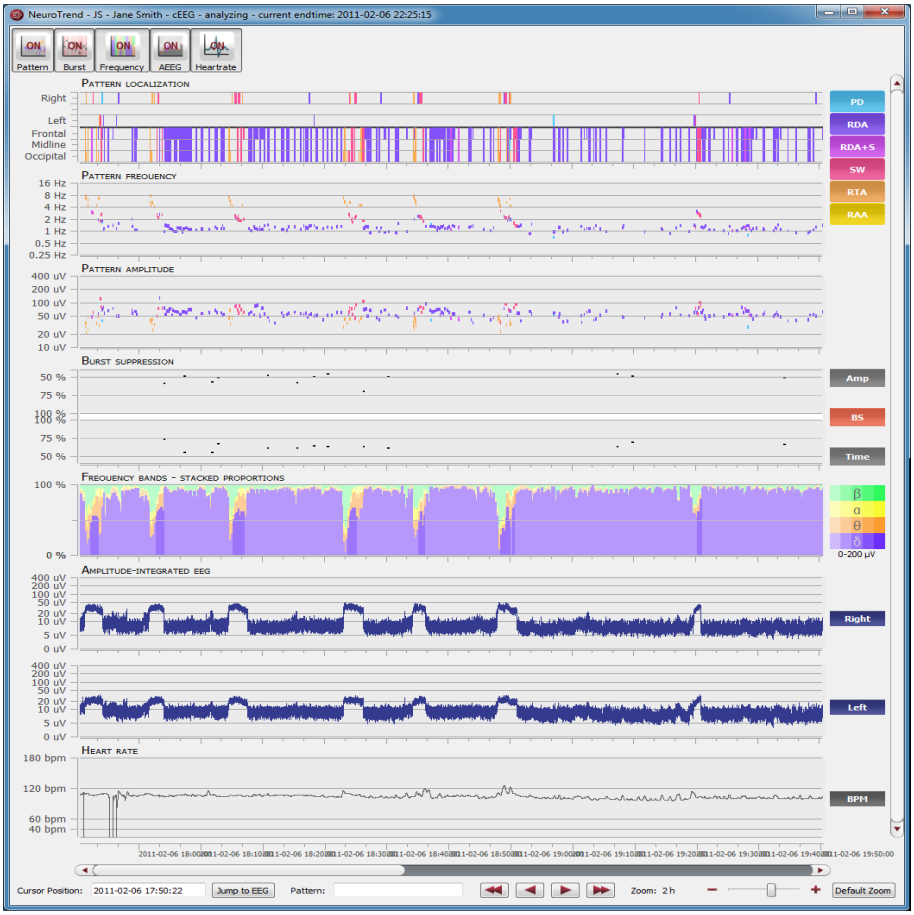
Light blue with hatching

Light blue with hatching shows that the time range is part of the current selection, but detection results are not available. This appears when the detection is not finished or when the time range has not been selected for review before starting EpiSpike.

Grey with hatching

Grey with hatching shows that the time range is not in the current selection and detection results are not available. This appears when the detection is not finished or when no EEG data is available in this time range.

NeuroTrend



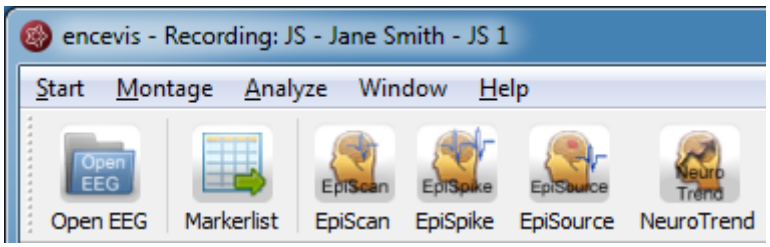
Overview

NeuroTrend is the encevis EEG trending software for the automatic analysis and trending of continuous EEG from critically ill patients at the ICU. NeuroTrend classifies epochs according to the ACNS's Standardized Critical Care EEG Terminology. It provides a condensed graphical representation based on the new standard that helps you assess all the information about trends in the functional state of your patient's brain within a very short time.

Start NeuroTrend

Follow these steps to start NeuroTrend:

1. Open the EEG that you want to analyze with NeuroTrend.
2. Click on the "NeuroTrend" icon under the menu to start the calculation.

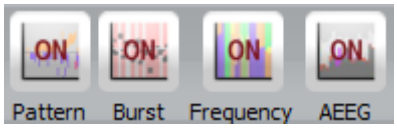


Once the calculation started, the progress will be shown under the icon.

The NeuroTrend screen will pop-up and show the results of the calculations.

NeuroTrend - Description

NeuroTrend includes six traces. The traces can be switched on and off in the button bar.



The first three traces show the detections of Traces “PATTERN” - rhythmic and periodic patterns based on the ACNS's Standardized Critical Care EEG Terminology. Detected patterns are shown as lines with a color code. The next trace shows detections of Trace „BURST SUPPRESSION“. The two last traces show the Trace „FREQUENCY BANDS- STACKED PROPORTIONS” and the Trace „AMPLITUDE-INTEGRATED EEG“.

How the screen can be read will be explained in the following.

Traces “PATTERN” - rhythmic and periodic patterns

The first three traces show the detections of rhythmic and periodic EEG patterns based on the ACNS's Standardized Critical Care EEG Terminology.

Detected patterns are shown as colored lines with the following color code:

PD — Periodic discharges

RDA — Rhythmic delta activity

RDA+S — Rhythmic delta activity + superimposed sharp waves

Sharply contoured rhythmic delta activity

SW — Rhythmic spike and wave

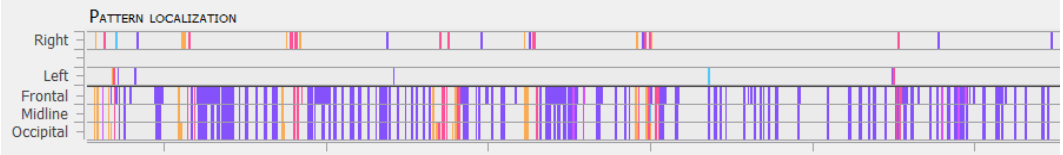
Rhythmic sharp and slow wave

Rhythmic polyspike and wave

RTA — Rhythmic theta activity

RAA — Rhythmic alpha activity

Trace „PATTERN LOCALIZATION”



In the first trace the localization of the patterns is displayed.

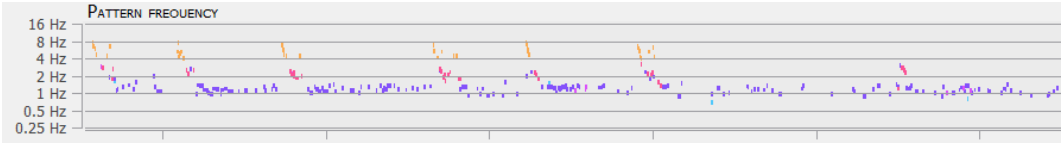
The upper part shows, when the pattern was lateralized:

- Right or
- Left

When no lateralization is recognized, then the lower part shows the dominance:

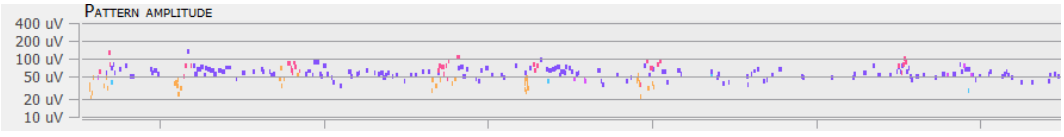
- Frontally predominant or
- Midline predominant or
- Occipitally predominant or
- Generalized, when the line covers Frontal, Midline and Occipital.

Trace „PATTERN FREQUENCY“



The frequency of detected patterns is shown on a logarithmic scale in the range: 0.25-16Hz.

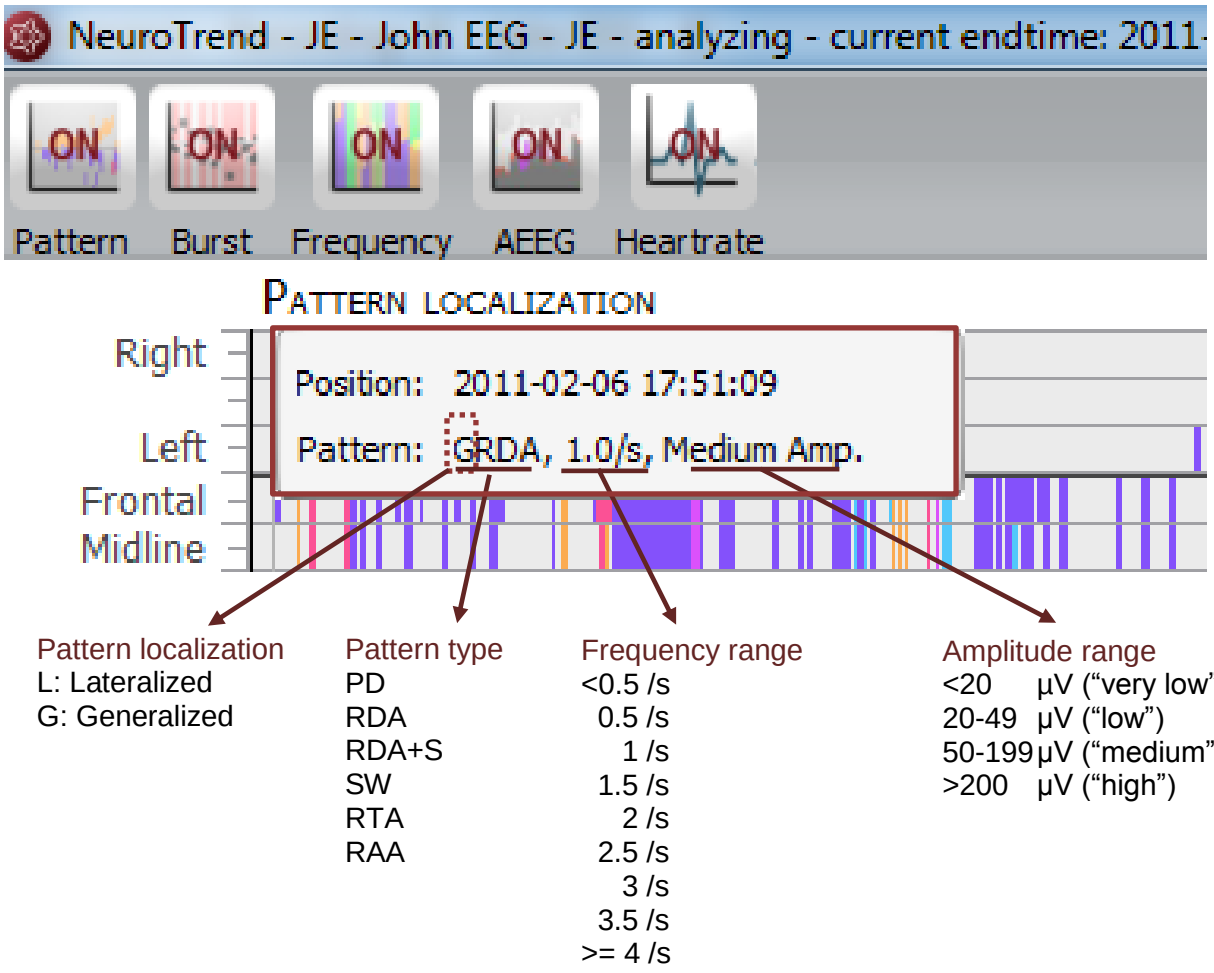
Trace “PATTERN AMPLITUDE”



The amplitude of detected patterns is shown on a logarithmic scale in the range: 10-400 uV.

Cursor text box

The cursor text box that appears when you move with the mouse includes the following summarized information:



Pattern localization
L: Lateralized
G: Generalized

Pattern type
PD
RDA
RDA+S
SW
RTA
RAA

Frequency range
<0.5 /s
0.5 /s
1 /s
1.5 /s
2 /s
2.5 /s
3 /s
3.5 /s
>= 4 /s

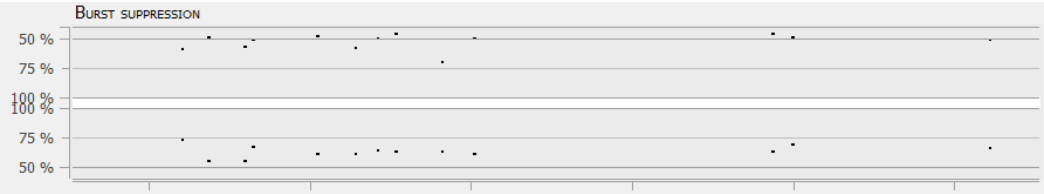
Amplitude range
<20 µV (“very low”)
20-49 µV (“low”)
50-199 µV (“medium”)
>200 µV (“high”)

Position: refers to the time point where the pattern was detected.

Pattern includes the summarized information on the pattern as described in the ACNS's Standardized Critical Care EEG Terminology

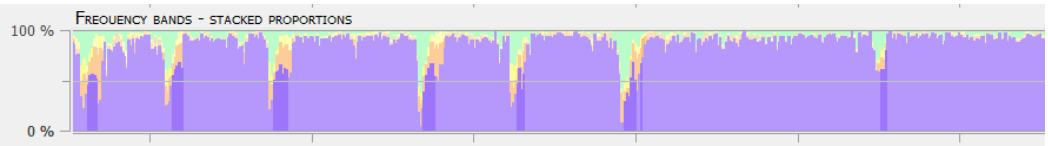
The Pattern information can also be found in the bottom of the screen:

Trace „BURST SUPPRESSION“



In this trace red lines show the detection of burst suppressions and black dots show burst attenuations.
In the upper part you can read off the relative amplitude attenuation and in the lower part the suppression time in the range 50-100%.

Trace „FREQUENCY BANDS- STACKED PROPORTIONS”



The proportions of the frequency bands are shown in the range: 0-100%.
The frequency bands are shown with a color code. The stronger the color, the higher the amplitude.

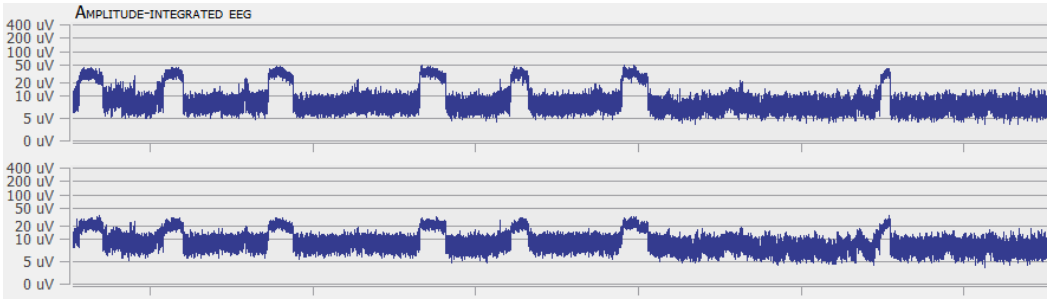
β Beta-Band

α Alpha-Band

θ Theta-Band

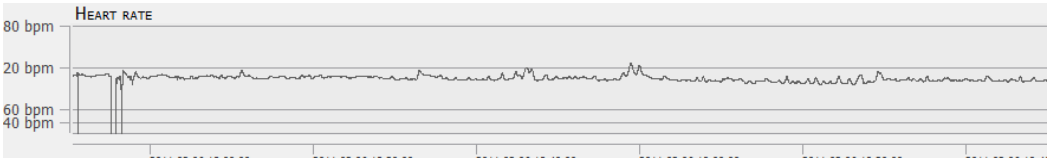
δ Delta-Band

Trace „AMPLITUDE-INTEGRATED EEG“



The amplitude integrated EEG is shown on two traces. The upper one shows the aEEG of the right hemisphere and the lower one the aEEG of the left hemisphere on a combined linear and logarithmic scale in the range: 0-400 uV.

Trace “HEART RATE”



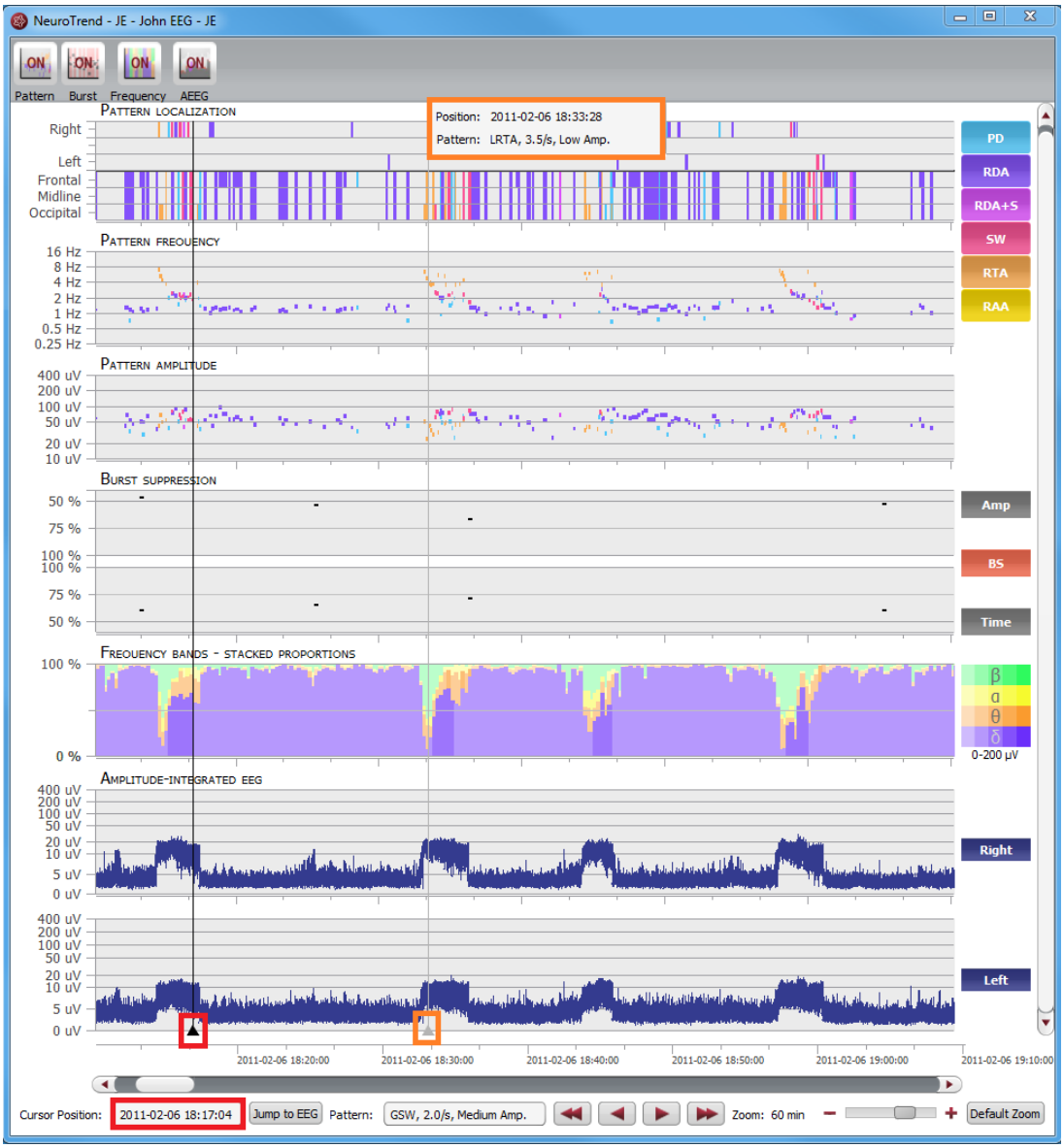
The heart rate is shown in beats per min (bpm) on a linear scale in the range 0-180bpm. The average heart rate is calculated based on the ECG signal and on a window of 10 seconds.

NeuroTrend – Navigation

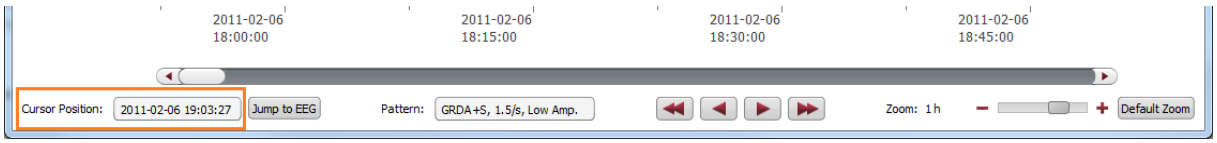
NeuroTrend provides a graphical user interface that makes navigation through the results very easy. The detection of the EEG patterns can be synchronized with the EEG at any time. You can navigate using your mouse and mouse wheel and by using the buttons on the bottom of the screen.

Cursor

- Move the mouse on the screen, a cursor will appear with a text box with the time position and the pattern detected (orange).
- Click on the screen and the cursor will be set on that position (red). On the bottom of the screen you will find the related Cursor Position and Pattern.

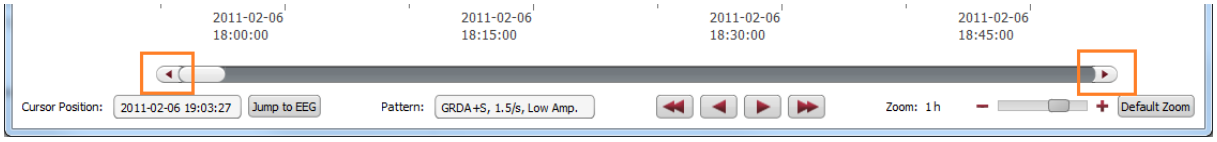


- Type in the exact time in the field "Cursor position"

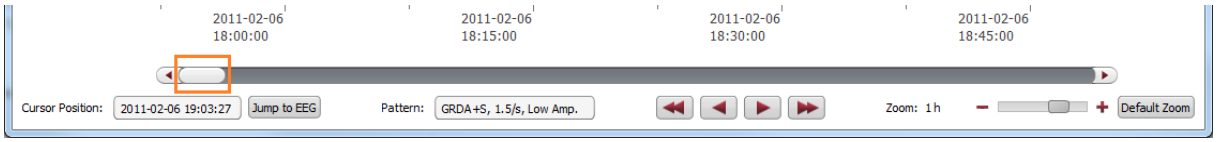


Move forward and backwards in time

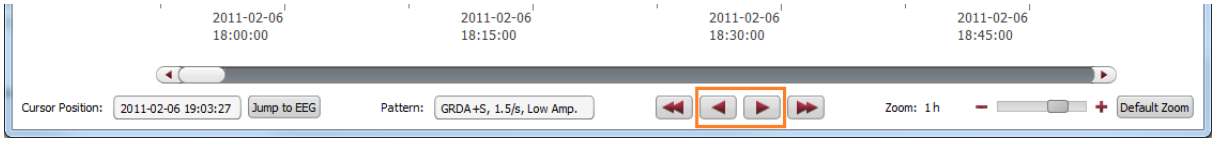
Click on the arrows of the scroll bar,



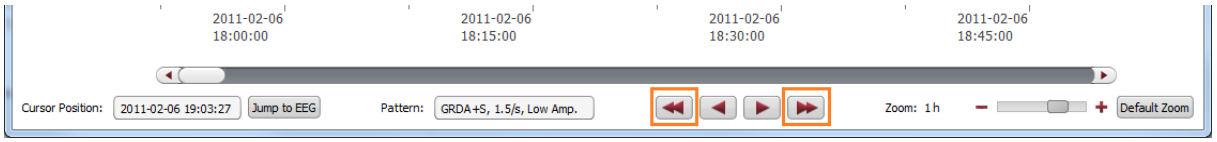
or use the slider,



or click on the simple buttons to move stepwise,



or click on the double buttons to move pagewise.



Zoom

You can zoom in and out and thus show more or less results on one screen.

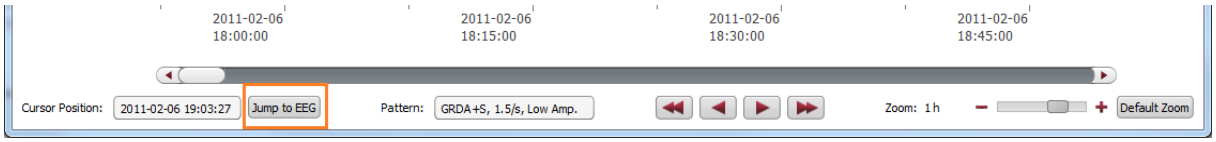
1. The easiest way to zoom is by clicking on the NeuroTrend screen and scrolling the mouse wheel.
2. You can also click on the symbols - and +. The resolution shows which time range is shown on the screen.

3. Clicking on "Default Zoom" gets you back to the initial zoom of 3h per screen.

Synchronize with EEG

The NeuroTrend screen can always be synchronized with the EEG viewer. You have two possibilities for that:

1. Click with the mouse on the screen, the EEG on the selected time point will be shown in the EEG viewer.
2. Click on the button „Jump to EEG", the EEG where the cursor is set will be automatically shown.



The synchronization works both ways. Additionally, when you click with on the screen of the EEG viewer, the cursor will automatically be set on that time point in the NeuroTrend screen.

Select pattern types

You can select and deselect patterns that will be displayed on the screen

→ Click on the icon on the upper right side of the screen

Distributor

Overview

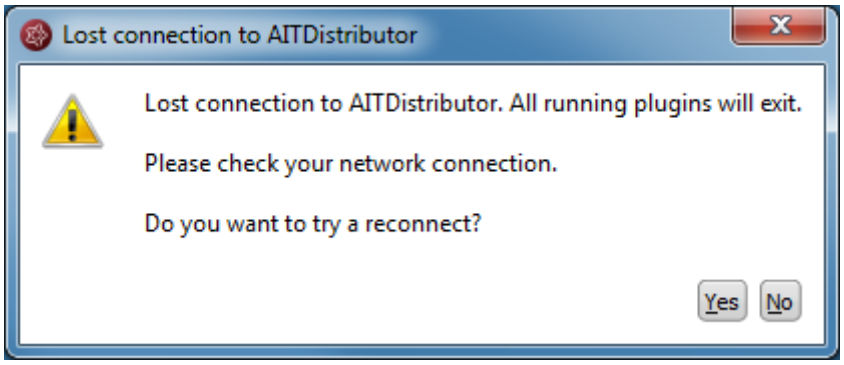
The Distributor is the tool that connects the EEG analysis tools as encevis EpiScan, EpiSpike, EpiSource and NeuroTrend to the encevis viewer. The Distributor needs to be running and connected, if you want to use the analysis tools.

Automatic start of Distributor

Usually, encevis starts automatically the Distributor when it is opened. This setting can be changed under the menu point *Start* > *Settings* > *Distributor*.

Manual start of Distributor

If you get the following error message when starting the plug-in:



→ Start the executable *Distributor.exe* and connect to the Distributor again.

Moberg Interface

Overview

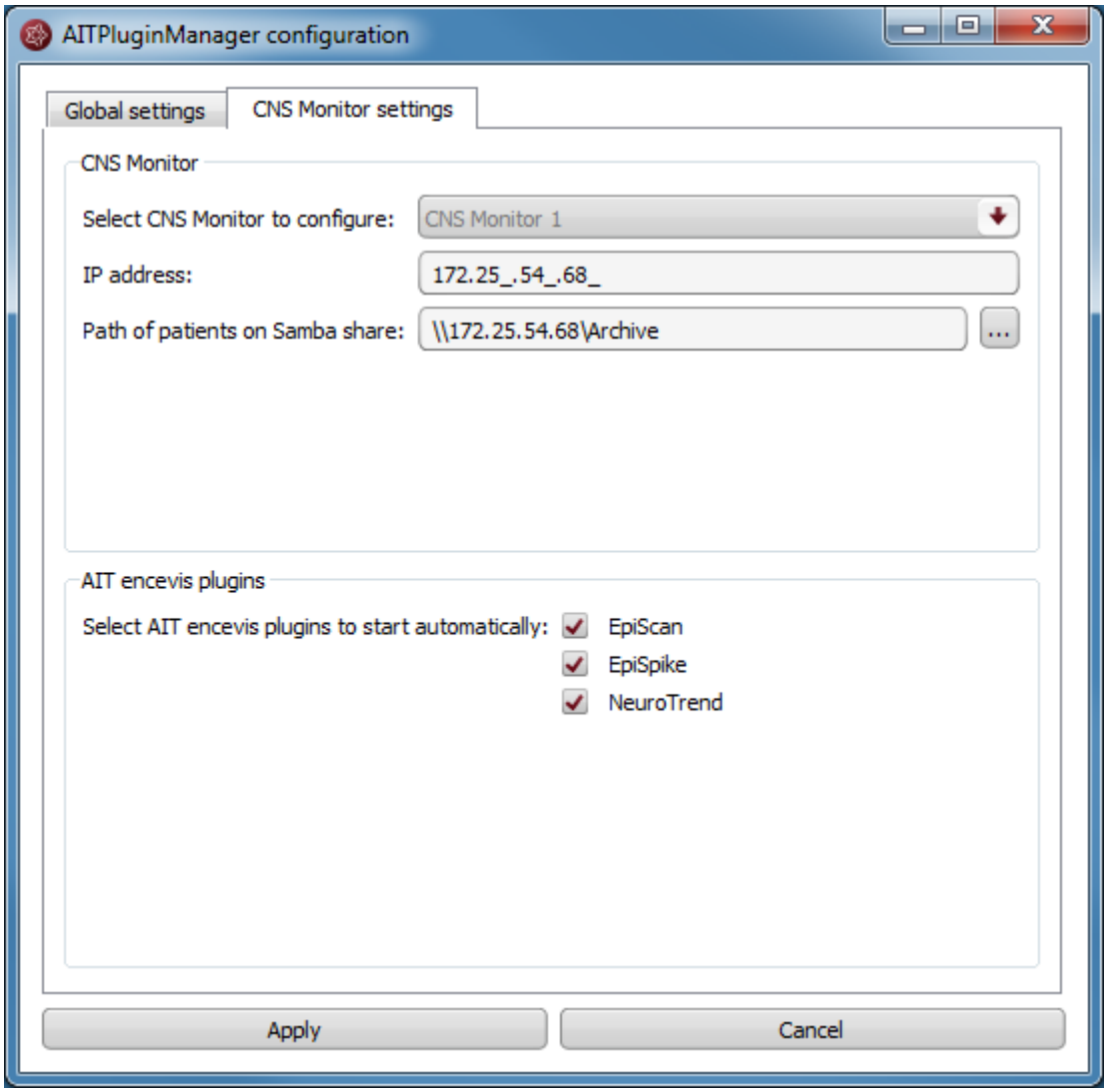
The Moberg interface enables you to use encevis in an "online" mode, together with the Moberg CNS Monitor. You can have the plugins EpiScan, EpiSpike and NeuroTrend running and processing data while you are recording an EEG with a CNS Monitor. Once set up, the Moberg interface scans automatically if an EEG recording is being performed with the CNS Monitor and starts the plugins that you want. When an EEG recording of a new patient is started, the Moberg interface adds the patient's data automatically in the encevis EEG File Management. The calculation results of the plugins can then be reviewed.

Moberg interface configuration

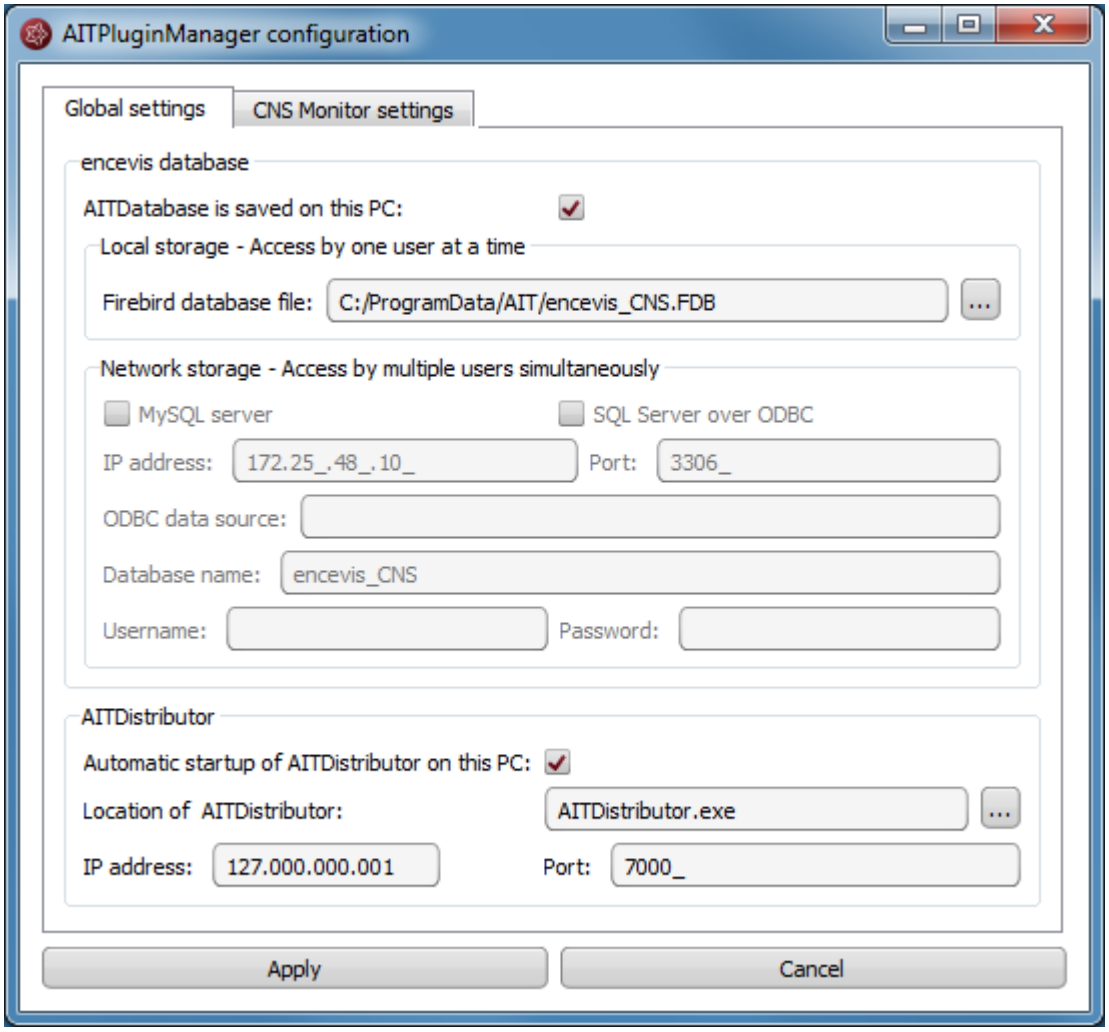
Start the executable *MobergInterface.exe*, the configuration will open.

Section *CNS Monitor settings*

- Fill out the IP address of the CNS Monitor and the path where the patients' data are stored.
- Select the plugins that should be started automatically. EpiScan, EpiSpike and NeuroTrend can run at the same time.
- Click on "Apply".



Section *Global settings*



Fill out the fields of *encevis database*

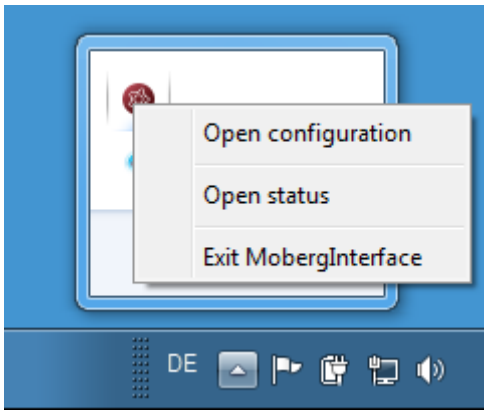
- Local storage - Access by one user at a time:
  This is the best mode, when the results of your review with encevis should only be accessed from your PC. Only one user at at time can then access the results. You can leave the file name specified by default or select a personalized name.
- Network storage - Access by multiple users simultaneously:
  This is the best mode, when you want to access the results of your review with encevis from several PCs in your network. With this option several users can access the results at the same time. In this case, you need to specify a database where everybody has access to. This database can be MySQL or an SQL server over ODBC.

Fill out the fields of *Distributor*

- Select if the Distributor should run on your PC or on a different one. If the Distributor is running on another PC, you need to specify IP address and Port. For more details on the Distributor see Distributor.
- Click on "Apply".

Access Moberg interface

Once it has been started, the AITPluginManager runs in the background. You can access it by clicking on the tray in the lower right corner of your screen and right clicking on the encevis icon.



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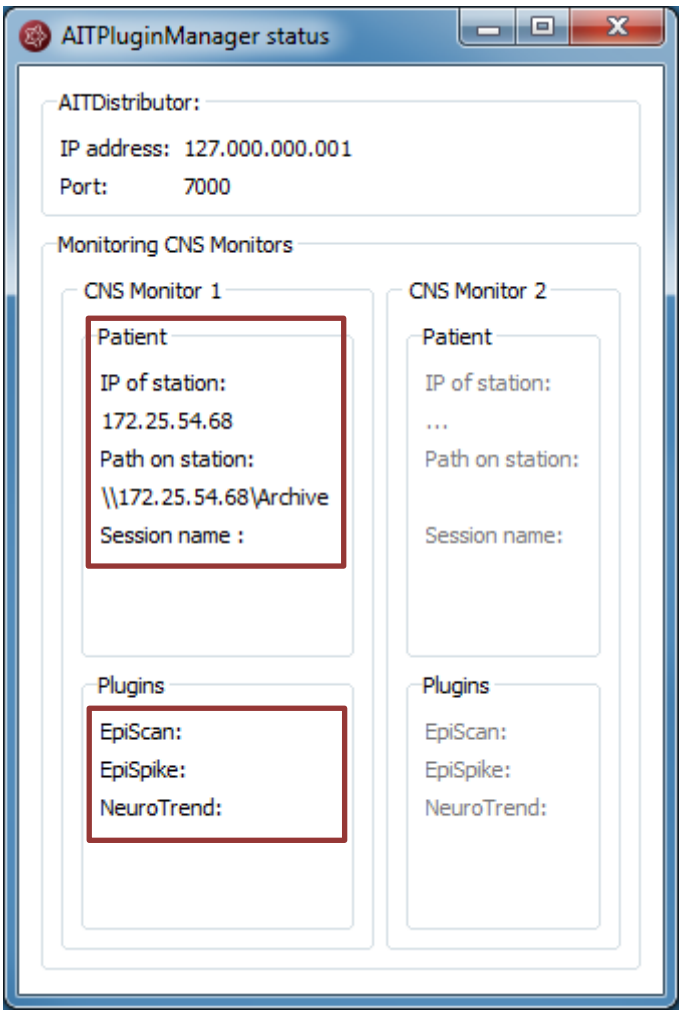
Moberg Interface status

No EEG data is being recorded

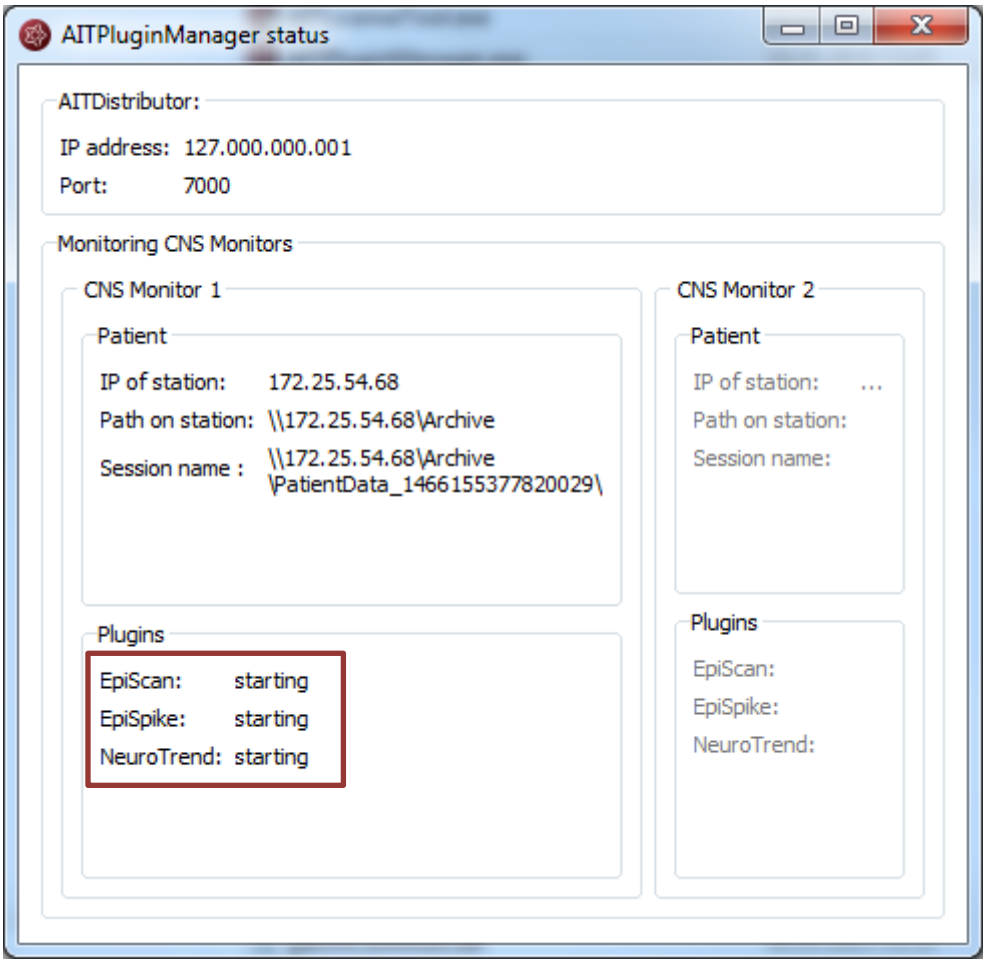
When no EEG data is being recorded by the CNS monitor, this is shown in the status window:



EEG recording starting in CNS Monitor

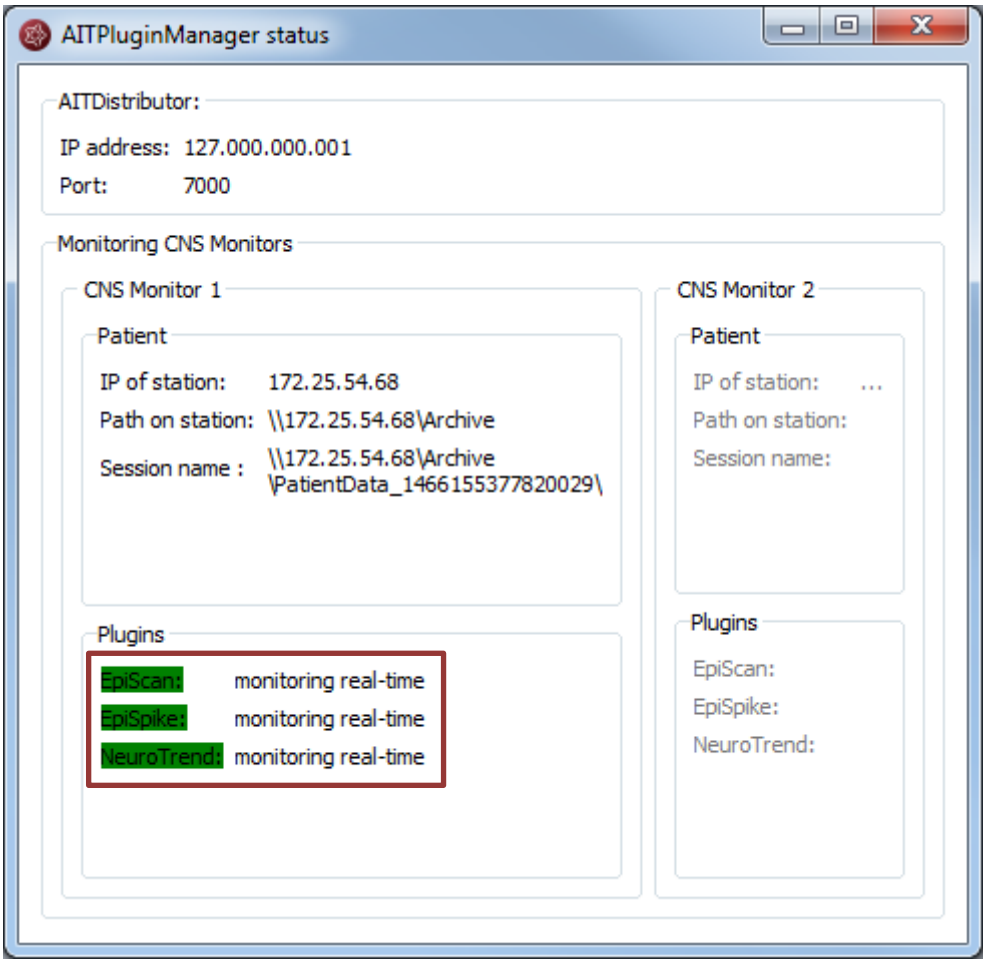
Start a recording with the CNS Monitor. Note, that In order to use EpiScan, you should make sure, that the Pz electrode is being used.

When a recording is being started in the CNS Monitor, this is shown in the status window:



EEG recording running in the CNS Monitor

When an EEG is being recorded with the CNS Monitor, this is shown in the status window:



The following color code can be read on the screen:

- green: everything is well, monitoring is done in real time.
- yellow: attention, monitoring is not in real time anymore.
- red: error.

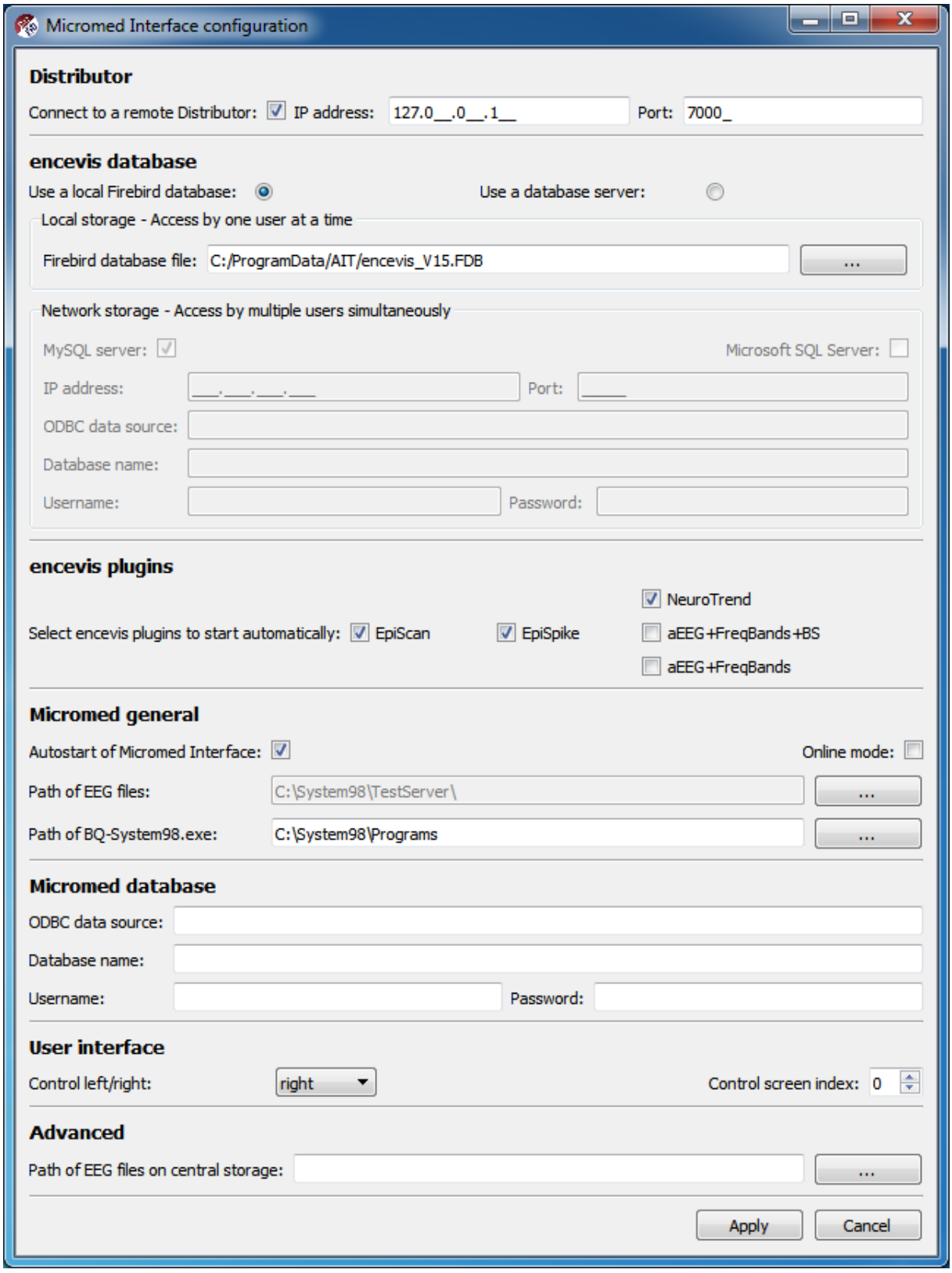
Micromed Interface

Overview

The Micromed interface enables you to use encevis close together with Micromed SystemEvolution Plus. New recordings started in Micromed SystemEvolution Plus can be automatically analyzed by the encevis tools EpiScan, EpiSpike and NeuroTrend. The results can be then reviewed and synchronized with the EEG in the Micromed SystemEvolution Plus EEG viewer.

Configuration

After the installation of encevis, you can start by configuring the Micromed interface.



The configuration window is opened when the Micromed interface is started for the first time. Additionally it can be opened by clicking on the settings icon in the Status window.

Distributor

This option is mainly relevant when you set up the Micromed interface on your acquisition PC. You may select to connect to a remote Distributor if you would like to reduce the calculation load on the computer. For this, enter the IP address and the Port of the server, where the Distributor should be running.

encevis database

encevis stores your markers and the results of EpiScan, EpiSpike and NeuroTrend in one database. Select where encevis should store it:

Local storage - Access by one user at a time:

This is the best mode, when the results of your review with encevis should only be accessed from your PC. Only one user at at time can then access the results. You can leave the file name specified by default or select a personalized name.

Network storage - Access by multiple users simultaneously:

This is the best mode, when you want to access the results of your review with encevis from several PCs in your network. With this option several users can access the results at the same time. In this case, you need to specify a database where everybody has access to. It can be a MySQL database or a SQL server over ODBC.

encevis plugins

In this part, you selected which encevis tools should be started automatically with the Micromed interface.

1. EpiScan – seizure detection
2. EpiSpike – spike detection
3. NeuroTrend.or aEEG+FreqBands+BS or aEEG+FreqBands - trends

Micromed general

In this part, you are able to configure the following settings:

Autostart of Micromed interface

You can choose to have the Micromed interface always started when the computer is started. When the Micromed interface is running and Micromed SystemEvolution Plus, then the control will always be visible. From this control it is always possible to

access the status window of the Micromed interface For more details on the control and the status window see Status window.

Online mode

Selecting the online mode enables the Micromed interface to identify if a new recording is being started with Micromed System Plus Evolution. As soon as a new recording is started, the status window will pop up and give information on the status of the calculations. If the online mode is not selected then it is possible to review the results of encevis of already recorded data.

Path of EEG Files

Please enter path where the EEG files are stored from Micromed.

Path of BQ-System98.exe

Here you should enter the path of BrainQuick. You may leave the default path.

Micromed database

Here you should specify the database used by Micromed for storing patient related data. This database may be locally stored in a Microsoft Access file or on a MSSQL Server.

ODBC data source

In case of local storage the ODBC data source should be “MS Access Database”.

In case that a MSSQL Server is used, a valid ODBC data source must be configured on the PC and its name must be entered here.

Database name

In case of local storage, the field Database name should contain the path and file name to the local Microsoft Access database file.

In case that a MSSQL Server is used, the Database name should be then the database schema name on the MSSQL server.

Username and Password

If a username and password is required on the MSSQL Server, these should be entered here.

User interface

Here you can specify if the Control should be located on the left edge or the right edge of the screen. Further you can select the screen on which the Control should be displayed by changing the Control screen index.

Advanced

This field should be filled out, when the files from the acquisition computer are automatically moved from the local storage on the acquisition station to a central storage or file server. The Micromed interface will then make sure, that the files and the calculation results are mapped and will enable you to review the results.

Online mode

The Micromed interface enables to have the analysis tools EpiScan, EpiSpike and NeuroTrend started as soon as a new recording is started. This is possible when the online mode was selected in the configuration see section Configuration Online mode.

Note that the Micromed interface in online mode can only detect the start of a new recording. If a recording is already running, no calculations will be started. Once a new recording has been started and the analysis tools are running, the status of the calculations can be monitored.

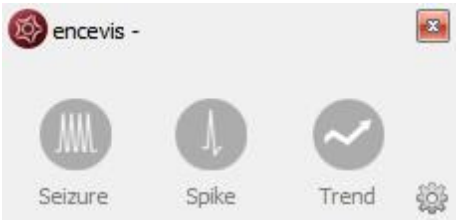
Status window

Access status window

The status window opens automatically when a new recording is started. It can also be opened by clicking on the control as in the following picture:

The status windows shows the three analysis tools that can be running:

Seizure (EpiScan), Spike (EpiSpike) and Trend (NeuroTrend).



When the icon is shown in grey, it means that the analysis tool has not been selected to be automatically started. Otherwise the icon is shown in color:

Status Start

When "Start" is written over the icon, it means that calculations are getting started for the current recording (exam).

Status Active

When “Active” is written over the icon, then the calculations are running correctly and in time.

Status Slow

When “Slow” is written over the icon and the background is shown yellow, then it means that the connection to the data is slow and results may not be shown in real time.

Status Wait

When a calculation is not receiving new data for more ten seconds, the text above the icon goes to "Wait". This indicates that the calculations are waiting for new data. This may happen because the current recording was paused or ended by the user. The calculations are waiting for a maximum of three hours for new data. After that time period the calculations are exited.

Status Error

When “Error” is written over the icon with a warning sign and the background is shown red, then an error has occurred and the calculations are not running. Get more information by clicking on the warning sign.

An error identified by a warning sign can also be seen in the control:

Database loss

In case of database loss, a corresponding symbol is shown on the right side of the status window. This means that calculation results cannot be saved. For more information click on the corresponding symbol.

Distributor loss

In case the connection to the distributor is lost, a corresponding symbol is shown on the right side of the status window. This means that calculations are not running. You may have to restart the distributor. For more information click on the corresponding symbol.

Offline review mode

The Micromed interface can be used after the recording has been finished. This is possible when the online mode was unselected in the configuration, see section Online mode. This enables you to review the results and to synchronize and compare them with the EEG in your EEG viewer Micromed SystemEvolution Plus.

Start offline review mode

In order to review the results you may start the MicromedInterface. This will automatically start Micromed SystemEvolution Plus as well.

The status control and the status window will appear on your screen.

1. Click on “Seizure” and access all results of the seizure detection EpiScan.
2. Click on “Spike” and access all results of the spike detection EpiSpike.
3. Click on “Trend” and access the results of the trends that you selected to have calculated. This could be NeuroTrend or the reduced EEG+FreqBands+BS or aEEG+FreqBands.

Note:The results will be available for the tools that you have previously selected to have calculated automatically, see section encevis plugins.

→ The results can all be viewed and will be automatically synchronized with the EEG viewer Micromed SystemEvolution Plus.