Data Acquisition Software Release 6.0

User's Manual

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MEGIN

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- US6876196 (Head position determination)
- US7463024 (Signal Space Separation)
- US7502720 (Signal Space Separation)
- US7649351 (Interference suppression)
- US7933727 (Interference suppression)
- US8229540 (Ac and dc signal separation)
- US8838225 (Signal space separation)
- US9642554 (Signal space separation)
- US20140343882 (Signal space separation)

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CONTENTS

1. INTRODUCTION

1.1. Overview

The Data Acquisition Software is used to control MEG measurement system and to acquire data with it. This manual covers performing measurements with a system that has been installed, configured and tuned. Software installation and basic configuration have been explained in document NM24013A-* *Data Acquisition Software Release 6.0 Installation Guide*. Tuning has been described in document NM24011A-* *Sensor Tuner User's Manual*.

This manual applies only to Data Acquisition Software Release 6.0. The software allows both evoked response measurements and recording of continuous raw data. It also supports Internal Active Shielding (IAS) noise reduction system, and provides continuous head position tracking capabilities when used with MaxFilter™ software. The software release 6.0 runs on Linux workstations and requires a TRIUX™/TRIUX™ neo system.

1.2. Typographical conventions

The following typographical conventions are used in this manual.

`commands`

Typed commands and text as well as messages on non-graphical screens or windows are shown in typewriter font. For example, commands to be given to the Linux shell are written in this font:

```
show_fiff -v online.fif
```

These commands should be typed exactly as shown, including spaces, underscores, hyphens, slashes, punctuation etc. only omitting the constructions denoting parameters (see below). When using the graphical user interface, it is necessary to open a terminal window first in order to type the commands.

buttons and messages

The textual items of the graphical user interface are denoted with bold Helvetica. The names of buttons, menus and menu items and messages appearing on graphical windows are shown in this font. For example:

> Select **Save averages...** from **File** menu.

means using the mouse or arrow keys to point and activate the menu labeled as “File”, and then moving the pointer to an item in this menu reading “Save averages...” and selecting it.

names and parameters

Text in italics indicates the name of an application program, manual, or other specific term. Italics is also used to introduce new concepts and to emphasize words.

Parameters are marked with italicized text enclosed in angle brackets (<,>). The whole construction, including the angle brackets, should be replaced by the value of the parameter. For example, in the shell command described as

> `show_fiff -v` <*data file*>

the string <*data file*> is substituted with a real file name. Optional parameters or arguments are enclosed in square brackets.

1.3. Software safety

This product has been designed for the following intended use:

The TRIUX™/TRIUX™ neo systems are magnetoencephalographic (MEG) devices which non-invasively detect and display biomagnetic signals produced by electrically active nerve tissue in the brain. When interpreted by a trained clinician, the data enhances the diagnostic capability by providing useful information about the location relative to brain anatomy of active nerve tissue responsible for critical brain functions.

Warning: MEG data can be inherently explained by many different source distributions, and measurements often contain various kinds of artefacts. Data used for clinical purposes must be interpreted by a trained clinician who is capable of judging the relevance and quality of the data.

Warning: Do not use the system without also carefully reading *TRIUX User’s Manual* or *TRIUX™ neo Instructions for Use*.

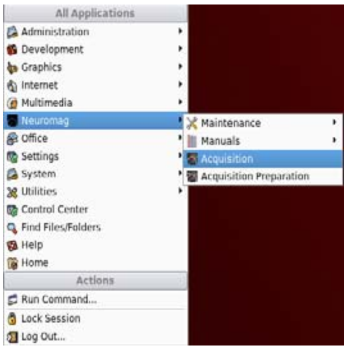
2. GETTING STARTED

2.1. Hardware checklist

Before starting a measurement:

1. Check that you have a set of at least three HPI coils available.
2. Check that the evoked-response stimulation hardware is properly set up, if needed.
3. Check that the necessary electrodes, paste, and other related items are available for recording electric signals.

2.2. Starting the software



All the Data Analysis and MEGIN Data Acquisition software programs are started by clicking the corresponding icon in the **Neuromag** application folder within the desktop’s application menu.

The data acquisition control program (*megacq*) is started by selecting the **Acquisition** icon. In addition to the main window (see page 4), the raw data display appears (see Section 5.3. on page 34).

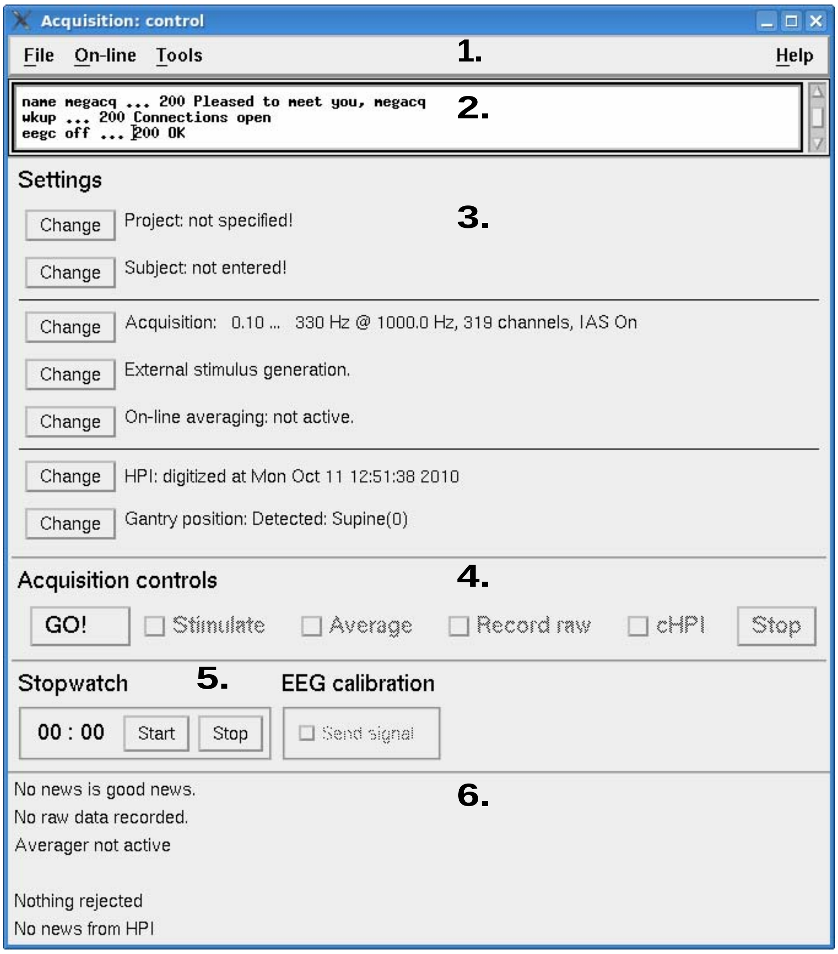
On start-up, *megacq* checks the integrity of the data connections from the data acquisition system to the workstation. If connections are faulty, an error dialog indicating the failure pops up. Should this happen, check first that the front-end electronics is switched on (see *TRIUX User’s Manual* or *TRIUX™ neo Instructions for Use*). Further guidance for resolving possible problems can be found in Section 7. on page 45.

Here we assume that the system is tuned and that SSP vectors used in suppression of external artefacts have been set. For details see *Sensor Tuner User’s Manual* and Section 8. “Using signal space projection” on page 46.

Before proceeding it is advisable to check the available disk space on data volumes from **Disk space…** in the **Tools** menu.

2.3. Components of the control program

The main window of *megacq* consists of:



```
name megacq ... 200 Pleased to meet you, megacq
wkup ... 200 Connections open
eegc off ... 200 OK
```

Project: not specified!

Subject: not entered!

Acquisition: 0.10 ... 330 Hz @ 1000.0 Hz, 319 channels, IAS On

External stimulus generation.

On-line averaging: not active.

HPI: digitized at Mon Oct 11 12:51:38 2010

Gantry position: Detected: Supine(0)

No news is good news.
No raw data recorded.
Averager not active

Nothing rejected
No news from HPI

1. The menubar with **File**, **On-line**, **Tools**, and **Help** menus.
2. A log window for informational messages.
3. The setup buttons with a synopsis of the setup state indicated next to each button.
4. Acquisition control buttons, which are enabled and disabled according to the state of the acquisition process.
5. A stopwatch for measuring time and a toggle for sending EEG calibration signals during measurement.
6. Five or more status message lines indicating the state of the acquisition. There is one Averager line for each set of 16 averaging categories.

2.3.1. The menus

The items in the **File** menu store and recall measurement parameters from files, thus facilitating setting up for a measurement. See Section 3.8. “Saving and restoring settings” on page 27 and Section 4. “Experiment preparation” on page 28 for the details of the items in this menu. Finally, there is **Quit** for exiting the acquisition system.

The **On-line** menu contains functions which control the on-line averager and the on-line average display during a measurement. See Section 5.4. “On-line averaging” on page 39 for a description of this menu.

Most of the functions in the **Tools** menu control the magnetometer probe:

Reset channels

Resets the MEG and EEG channels. To ensure fast settling of the signals after resetting the electronics the digital high-pass filter is automatically switched to a high corner frequency for a couple of seconds and then back to the setup value.

A reset is applied automatically when a measurements starts, so this function is intended for recovering channels in the rare case of system malfunction.

Tuner...

Invokes the automatic sensor tuner. For details see *Sensor Tuner User's Manual.*

Helium level...

Shows the liquid Helium level history and estimated zero-level time. This can be done also by clicking the **Helium** icon in the **Neuromag -> Maintenance** folder.

Disk space...

Shows the available disk space on all mounted volumes.

Phantom...

Opens up the phantom measurement control tool. See Section 9. "Phantom measurement" on page 49 for details.

2.4. Closing the software

When the measurements are completed and all the necessary data saved, the acquisition system user interface can be closed to release computer resources for other tasks. To close the acquisition programs select **Quit** in the **File** menu of *megacq*. You will be asked for a confirmation.

All the child applications of *megacq* (raw data display, average response display etc.) will close automatically.

The state of *megacq* is not automatically saved when closing it. Thus, you have to explicitly use the procedures explained in Section 3.8. “Saving and restoring settings” on page 27 if you want to continue using the same parameters.

Note that exiting *megacq* only closes the user interface of the data acquisition system, while the system remains powered and the system’s server software remain running. These should be shut down only as part of service operations. It is preferable to keep the electronics on between measurement sessions; the system requires considerable time to completely stabilize after a power-up.

The restarting procedure is described in detail in Section 7. “Restarting the software” on page 45. The power-up and power-down procedures of the MEG system are described in both *TRIUX User’s Manual* and *TRIUX*™ *neo Instructions for Use*.

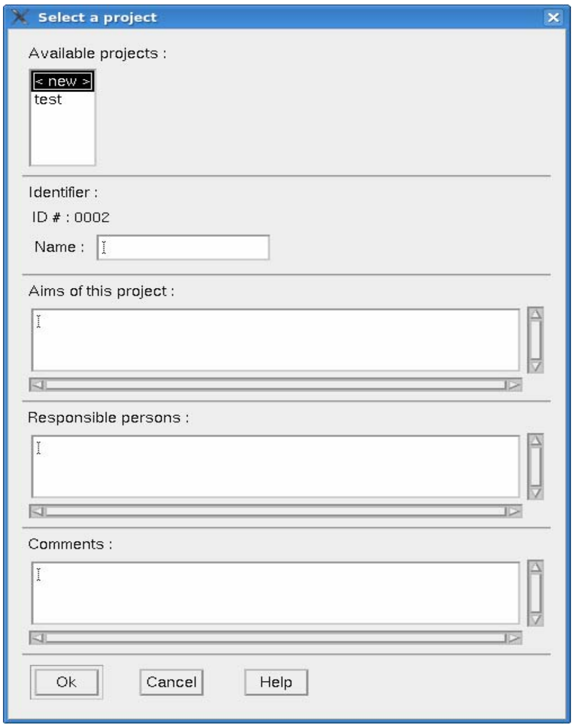
3. SETTING UP

This section describes the setup tasks to be performed before starting the acquisition. If the personal data of the subject are available, the setup can be completed before the subject arrives. See “Experiment preparation” on page 28 for more information.

3.1. Project

The measured data are grouped into projects according to the conventions at each site. For example, one project might correspond to a group of patients with common symptoms or patients investigated by one clinician.

The project is selected from the project dialog which appears when the project setup button is pressed.



If you are collecting data to an already existing project, just select the project name from the list and press **OK** or double click the project name.

If you are defining a new project, select the item **<new>** from the list and enter the project name and other reference information in the text entry areas. The project name may consist of lowercase letters and the underscore character. In addition to the project name, aims, and names of responsible persons are required for the definition of a new project.

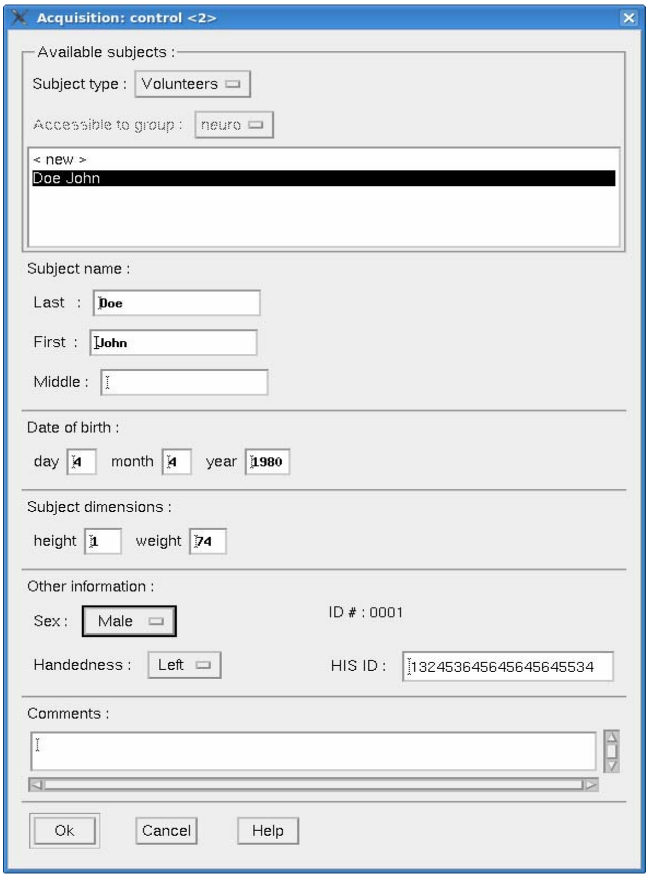
If you want to close the project dialog without changing anything press **Cancel**.

There are two useful keyboard shortcuts in the project list. First, you can go to the **<new>** item by pressing the home key with control down. Second, you can browse the list alphabetically by clicking any of the items and then pressing a letter key. The list will move to the first project name beginning with this letter.

3.2. Subject

3.2.1. Subject list

The names of defined subjects are listed alphabetically at the top of the dialog.



Acquisition: control <2>

Available subjects :

Subject type : Volunteers

Accessible to group : neuro

< new >
Doe John

Subject name :

Last : Doe

First : John

Middle :

Date of birth :

day 4 month 4 year 1980

Subject dimensions :

height 1 weight 74

Other information :

Sex : Male

ID # : 0001

Handedness : Left

HIS ID : 132453645645645645534

Comments :

If you are collecting data from an already defined subject, just select the subject name from the list and press **OK** or double click the subject name.

To define a new subject, select the item **<new>** from the list, enter the information to the text fields, select the appropriate choices, and press **OK**. You are required to enter the first and the last name, and the date of birth. Do not to define the same subject twice as a double-entry may confuse the MEG/MRI subject matching in the analysis programs.

Weight and height are optional whereas handedness and sex are always taken from the corresponding option menus. Hospital Information System (HIS) ID is intended for a hospital-wide patient code, such as social security number, which uniquely identifies the subject. HIS ID is stored with each data file and it can be used as a path name component for the saved files.

If you want to close the subject dialog without changing anything press **Cancel**.

The keyboard shortcuts in the subject list are identical to those in the project list.

3.2.2. Volunteers and patients

Sites studying patients would often like to protect patient information from unauthorized access. megacq provides a grouping of persons to be studied to 'volunteers' and 'patients'.

Volunteers are healthy subjects participating in the MEG studies. When a person is classified as volunteer, megacq applies no special protection on the data:

1. The personal data of a volunteer can be read by any user in megacq. All personal information is included with the measured data.
2. The data will be saved - by default - in directories

   <volume>/<project>/<last name>_<first name>/<date>,

   as discussed in Section 6.1. on page 43. All directories on the path are accessible to any user.

For a person classified as a patient, the following protective measures are taken:

1. Only the patient id number will be written to the data files. The data files will contain case as the patient's first name and the id number as the last name. Therefore, if you list the person's name from a data file it will be something like `case_567`.
2. The data will be saved - by default - in directories

   *<volume>/<project>/*case_*<id>/<date>*.
3. The creator of the patient chooses the access restrictions which apply to the personal data of the patient entered and to the MEG and EEG data saved.

   In the strict access mode, the data are only readable by the creator of the patient.

   In the group access mode, read, and write access to the patient data is additionally granted to a designated group of users.

The choice between volunteers and patients is made in the option menu at the top of the subject definition dialog. When the menu is set to **Volunteers**, all volunteers are listed.

Available subjects :

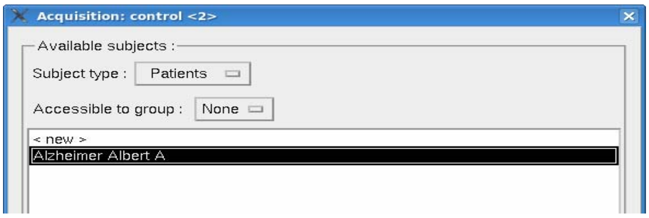
Subject type : Volunteers

Accessible to group : neuro

< new >
Doe John

Subject name :

When the menu is set to **Patients** all patients accessible to the current user are listed.



Acquisition: control <2>

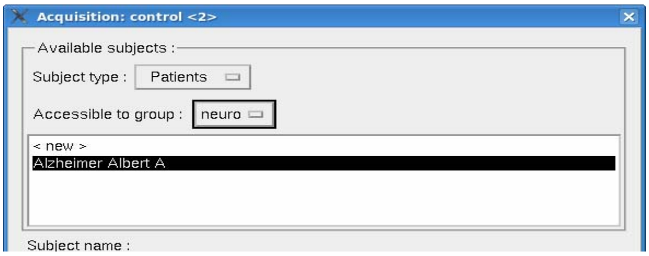
Available subjects :

Subject type : Patients

Accessible to group : None

< new >
Alzheimer Albert A

If you have created the patient, the **Accessible to group:** option menu becomes enabled.

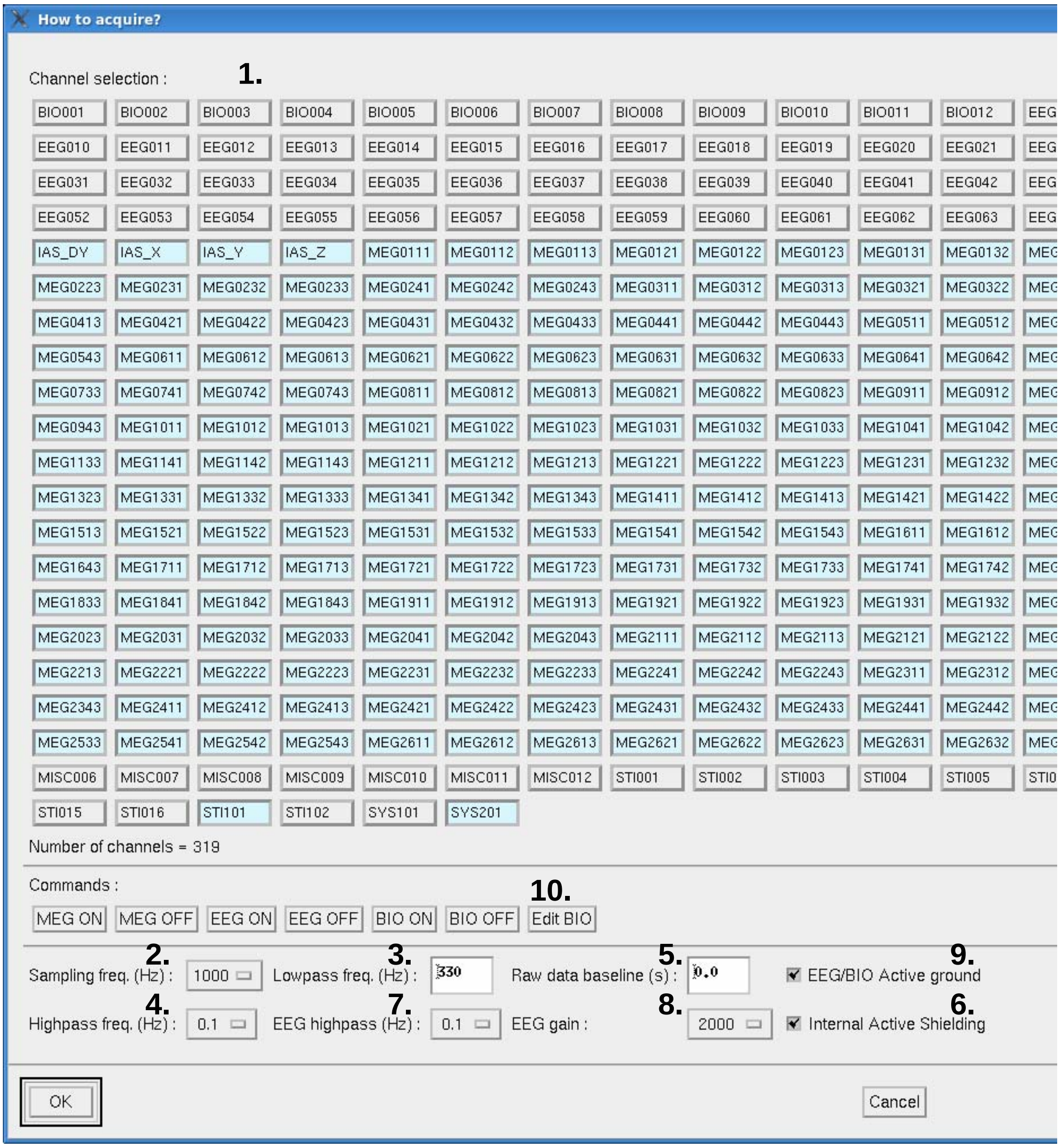


If the choice is **None** the data of this patient are only accessible to you (the user currently logged in). If you select a group of users, the data become accessible to this group as well. Please consult your system administrator if you need a new group of users. The number of groups should be kept as small as possible.

Note: If you have restarted the acquisition software as described in Section 7, you can reuse earlier HPI data when *megacq* is restarted. However, you can change the subject only once (from **No subject** to some available subject) without losing the HPI data.

3.3. Acquisition

The acquisition setup dialog, which appears when the acquisition setup button is pressed, adjusts the following:



Number of channels = 319

Sampling freq. (Hz) : 1000

Lowpass freq. (Hz) : 330

Raw data baseline (s) : 0.0

☑ EEG/BIO Active ground

Highpass freq. (Hz) : 0.1

EEG highpass (Hz) : 0.1

EEG gain : 2000

☑ Internal Active Shielding

1. The selection of channels to be acquired.

   The channels are switched on and off from the corresponding buttons in the upper part of the dialog.

Note: All MEG channels are selected by default. Switching any of them off should be done with caution. It is better to ignore malfunctioning channels in the analysis software instead of not recording them at all. This enables, e.g., checking if artefacts on other channels are due to malfunctioning channel. In addition, some third party analysis tools may assume that all channels be present in the data file.

The number of EEG input channels is system specific.

Each of the bioamplifier channels can be denoted either as an unspecified BIO input, or as a specified EOG, EMG, or ECG input. The type and other attributes of each bioamplifier channel can be changed in the BIO channels editor (see description of the **Edit BIO** button). The change of the input type affects the channel name. This is often useful in the artefact rejection and later stages of data analysis. For example, *xplotter*, the plotting program, may be set up to lay out the EOG channels in a particular position. Also, the scales of various bioamplifier channel types can be separately set in *xplotter* and in the raw data display.

Channels labeled with STI are stimulus channels whose usage is described in more detail in Section 3.4. on page 14.

Channels labeled with MISC are auxiliary electrical input channels.

Channels labeled with SYS are digital system state channels whose usage is described in Section 3.5. “On-line averaging” on page 17.

Channels labeled with IAS are Internal Active Shielding system’s channels.

Channel labeled with EXCI is used internally in tuning. See Section 5.3.4. “XY display” on page 38 for more details.

2. The sampling frequency.

   The sampling frequency, f_s, is set with an option menu below the channel selectors. It is the same for all channels.

   The sampling rate cannot be set lower than 3 times the highest HPI coil frequency.

   The actual sampling rate may slightly differ from the selected one because of limitations in the hardware. However, the real sampling rate is reported in the data files and in the information window on top of the main acquisition window.

3. Low-pass filter

   The low-pass filter corner frequency, f_a, is set with a text field to the right of the sampling frequency. It applies to MEG, EEG, MISC and IAS channels. The BIO channels have their own low-pass filter corner settings (see list item 10).

   The actual filter corner may differ somewhat from this setting. The real corner frequency is saved into data files and reported in the information window. For more detailed low-pass filter specifications consult the *TRIUX™/TRIUX™ neo Technical Manual*.

   According to the Nyqvist criterion, the sampling frequency should be at least twice the highest frequency component in the analog signal, $f_s > 2f_a$ to avoid aliasing. Since analog filters cannot have an infinitely steep transition at the corner frequency, *megacq* adds a safety margin and only allows $f_s > 3f_a$.

4. High-pass filter

   The corner frequency of the MEG channels’ high-pass filter can be set in steps. The available corner frequencies can be selected from an option menu. The EEG and BIO channels have their own high-pass filter corner settings (see list items 7 and 10).

5. Raw data baseline

   With this option, it is possible to define the amount of data to be saved preceding the time when raw data saving was switched on. The length of this ‘baseline’ will be at least the indicated amount. The maximum length is 15 seconds. This feature allows keeping the raw data saving off until something interesting happens. When saving is activated, the event noticed can be saved, even though it has already gone.

6. Internal Active Shielding

   This option is present only in systems having Internal Active Shielding. The toggle button is used to activate or deactivate the internal feedback system. See *Internal Active Shielding User’s Manual*.

7. EEG high-pass filter

The corner frequency of the EEG channels' high-pass filter can be set in steps. The available corner frequencies can be selected from an option menu.

8. EEG gain

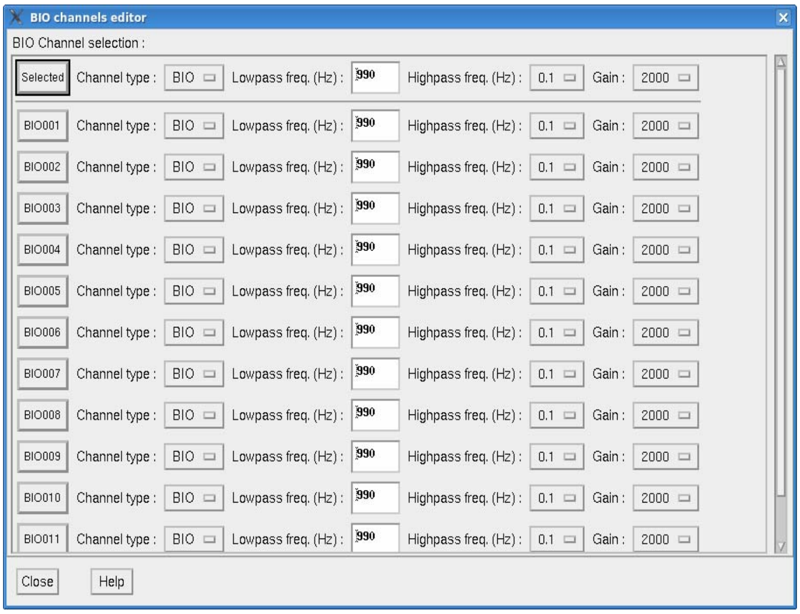
   The total gain of the EEG input circuitry (applies to all EEG channels) can be selected in steps with this. The available gain settings are shown in an option menu.

9. EEG/BIO Active ground

   Selecting this will refer EEG and BIO channels to an active ground, otherwise the EEG electronics isolated ground is used. See *TRIUX User's Manual* or *TRIUX™ neo Instructions for Use*.

10. **Edit BIO** button

    This button pops up the BIO channels editor, which is used to configure the BIO channels individually. The editor is shown in the following figure.



BIO channels editor

BIO Channel selection :

Selected Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO001 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO002 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO003 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO004 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO005 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO006 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO007 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO008 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO009 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO010 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000
BIO011 Channel type : BIO Lowpass freq. (Hz) : 990 Highpass freq. (Hz) : 0.1 Gain : 2000

The buttons of the top row will apply the particular settings to all BIO channels.

The button in the first column allows to switch the BIO channel on and off. The selection state is automatically copied to the acquisition setup dialog and vice versa.

The option menu in the second column allows to specify the channel's type as either BIO, EOG, EMG or ECG. The channel's selection buttons (in this dialog and in the acquisition setup dialog) are renamed accordingly.

Rest of the columns allow to set the channel's low-pass and high-pass filter corner frequencies and the channel gain. Note that low-pass fields (in this dialog and in the acquisition setup dialog) are automatically set to the maximum allowed value when the sampling frequency is changed.

3.4. Stimuli and triggers

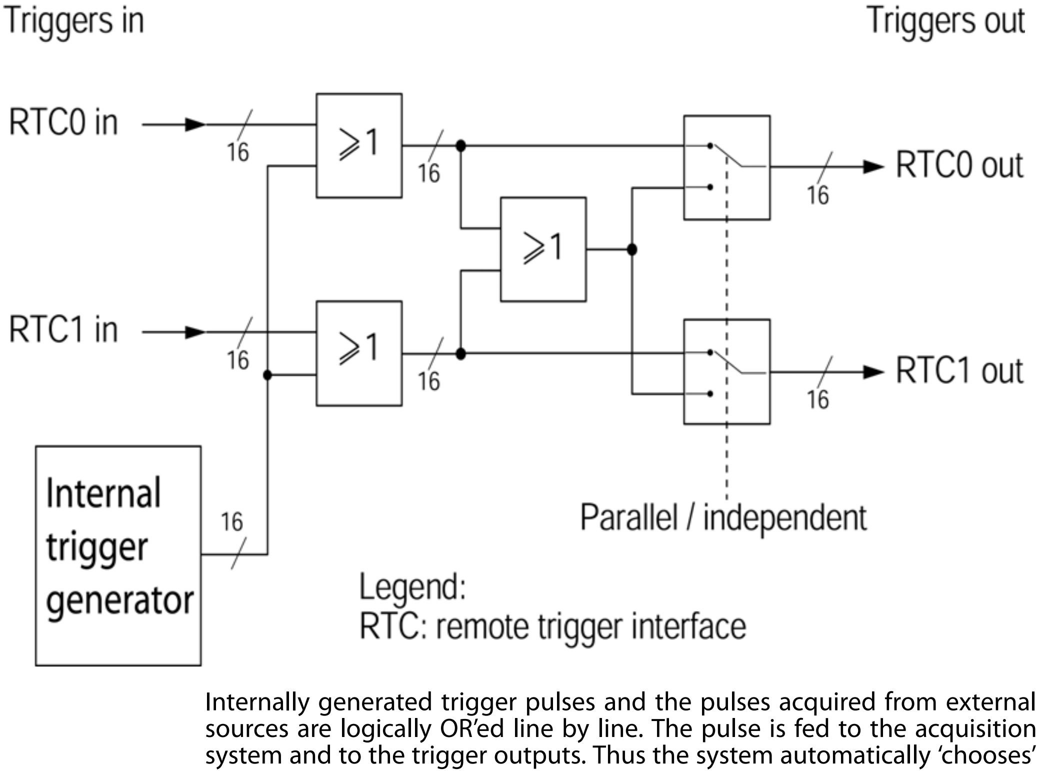
The electrical stimulus *triggers,* that mark events for the acquisition software, can be provided either by the data acquisition unit or by an external stimulation system. The acquisition software processes the trigger signals exactly in the same way, independent of their origin. This section describes the trigger system and generation of triggers.

3.4.1. Trigger interfaces and triggering modes

The electric interface of the trigger signals is called a *Stimulus Trigger Interface Unit*, which is connected to the *System Control Card (SCC)* housed in the data acquisition system cabinet. TRIUX™/TRIUX™ neo systems include two such interface units, which by default operate in parallel, i.e. input #1 and output #1 on both interface units correspond to trigger line #1 on the combination trigger channel (STI101) associated with the 1st interface unit. However, the two interfaces can also be treated separately by turning on (selecting for acquisition) the trigger channel (STI102) associated with the 2nd interface unit. This is done using the acquisition setup dialog.

For details about the Stimulus Trigger Interface Unit and for electrical specifications of the trigger pulses, see *TRIUX User's Manual* or *TRIUX™ neo Instructions for Use*, as well as *TRIUX™/TRIUX™ neo Technical Manual.*

The SCC manages both internal and external triggers. Irrespective of the triggering mode (internal/external) the trigger pulses *always* appear at the corresponding trigger outputs of *both* interface units. The principle is shown in the following figure.



Internally generated trigger pulses and the pulses acquired from external sources are logically OR'ed line by line. The pulse is fed to the acquisition system and to the trigger outputs. Thus the system automatically 'chooses' the right source for each trigger channel provided that a trigger channel is not receiving pulses both from internal and external sources at the same time. Should this happen, pulses from those two or three sources will be intermixed and indistinguishable at further processing stages.

Typically the trigger event is associated with the rising edge of trigger pulse, however, the analysis tools can be configured to also monitor the falling edge. Note that the timing of the falling edge does not accurately reflect any physical event in systems which incorporate circuitry that fixes the pulse length. See Section 3.5.3. “Events” on page 18 for more details.

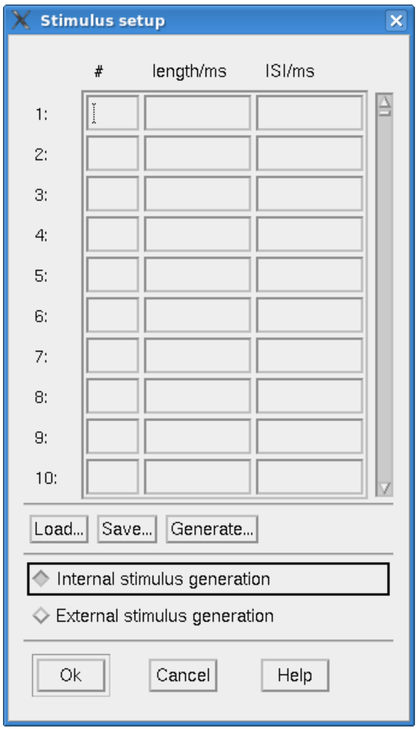
The stimulus setup dialog shown below selects the trigger source from the software point of view: if internal triggering is selected, you are allowed to define a stimulus sequence.

If you prefer external triggering, turn the switch to the external position and connect a TTL level trigger pulse output from your stimulation system to the trigger input.

Note: Both internal and external triggers can be used in the same session.

3.4.2. Stimulus sequence

The stimulus setup dialog appears when you press the stimulus setup button.



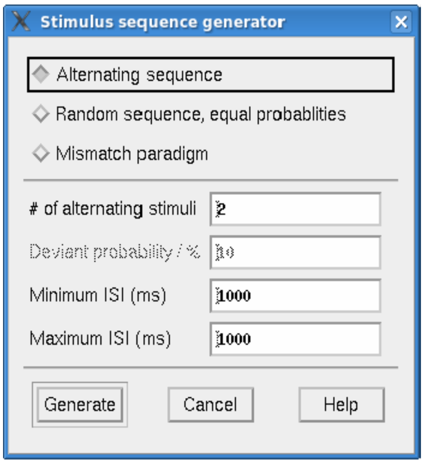
Each item in the internal stimulus sequence is defined by the trigger number (1 – 16), the length of the trigger pulse (ms), and the length of the interval from the start of the trigger to the next. This period is often called the inter-stimulus interval (ISI).

The maximum length of the sequence is 500 stimuli. The minimum pulse length is 5 ms and the minimum ISI is 50 ms. There must be at least 40 ms from the end of the trigger to the next.

The stimulus sequence can be either entered manually, generated with help of the sequence generator, or loaded from a file.

3.4.3. Sequence generator

The sequence generator utility is accessed trough the **Generate** button in the stimulus definition dialog.



◆ Alternating sequence
◇ Random sequence, equal probablities
◇ Mismatch paradigm

# of alternating stimuli: 2
Deviant probability / %: 10
Minimum ISI (ms): 1000
Maximum ISI (ms): 1000

You can create several kinds of sequences:

1. An alternating sequence

   Given number of stimuli, *n*, are repeated sequentially: 1,2,…,*n*,1,2,…,*n*,… If the ISI limits are equal, the ISI remains constant; if they are different, the ISI's are random within the interval with a uniform probability density.

2. Random sequence

   The given number of stimuli have an equal probability to occur in the random sequence. The handling of ISI's is the same as in the alternating sequence.

3. Mismatch sequence

   Rare (deviant) stimuli occur randomly with given probability in a monotonous sequence of standard stimuli. If the deviant probability is less than 15 percent, two deviant stimuli will never occur sequentially. Normally stimulus 1 is the standard and stimulus 2 the deviant. If the deviant probability is set to higher than 85 percent, the roles of the stimuli are reversed.

Once you click **Generate**, the sequence is generated and the values are entered into the stimulus sequence table.

3.4.4. Loading and saving sequences

You can load stimulus sequences from text files and save existing sequences for future retrieval. By default, the stimulus-sequence files are stored in the directory /neuro/dacq/stim.

You can also generate sequence files yourself either with a text editor or with a program. The sequence file simply replicates the sequence table:

<trigger #1> <length 1/ms> <ISI 1/ms>
<trigger #2> <length 2/ms> <ISI 2/ms>
…

Space, tab, and newline are allowed as separator characters between the numbers.

3.5. On-line averaging

3.5.1. Basics

The most complex part of the acquisition setup concerns on-line averaging. For the discussion to follow we need to define a few relevant concepts first.

Trigger channel

An electric impulse carrying solely timing information and occurring on a single digital line is called a trigger. A trigger could be used to drive a stimulator to produce a stimulus, or it could reflect subject's behavioral response. Triggers are generated by the system described in Section 3.4.1. The output of that system controls the on-line averager.

The system has several trigger channels for recording trigger pulses. STI1 to STI16 contain analog-like signal of a single trigger line and are provided for backwards compatibility. STI101 and STI102 carry bit combinations describing state of the two interface units. Each bit corresponds to one of the trigger lines of the boxes. SYS101 and SYS201 carry bit combinations for triggers generated by internal events, like HPI and phantom.

Event

A transition from an inactive to active state or vice versa on one or more trigger lines is an *event*. The source of an event can be either a stimulus trigger or a trigger associated with an action performed by the subject, such as a button press.

To avoid misinterpretations of the trigger combinations due to race conditions, the following procedure is implemented in the on-line averager. Assume sample k with all trigger lines inactive followed by sample $k + 1$ having one or more active trigger lines. Sample $k + 1$ is used as the timing reference, but the trigger line combination is determined from sample $k + 2$. This allows a slight asynchrony between the on-sets of the trigger lines.

Epoch

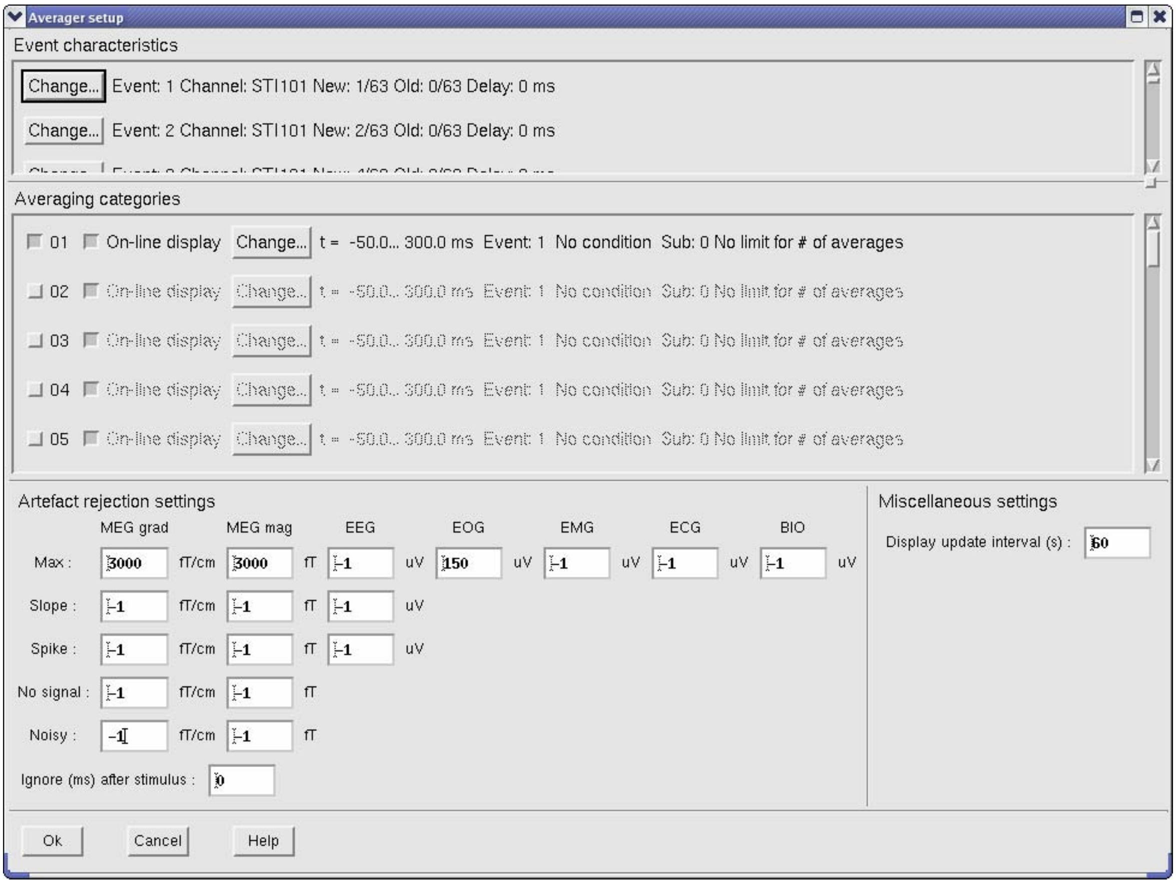
An *epoch* is a section of the incoming continuous data, defined by the occurrence of an event and the time limits t_{min} and t_{max} with respect to that event. We will call the event determining the zero time of an epoch a trigger event.

Category

A *category* defines the epoch to be averaged, any additional conditions to averaging, and the processing of epochs during averaging. For example, some categories may be set up to produce, in addition to the standard average, several subaverages of, say, eight consecutive epochs each.

3.5.2. On-line averaging dialog

The on-line averaging dialog appears when you press the on-line averaging button. The events are defined in the top part as described in Section 3.5.3. The categories are defined in the middle part as described in Section 3.5.4. The artefact rejection and miscellaneous settings are defined in the bottom part as described in Section 3.5.5, Section 3.5.6, and Section 3.5.7.



Event characteristics

Event: 1 Channel: STI101 New: 1/63 Old: 0/63 Delay: 0 ms

Event: 2 Channel: STI101 New: 2/63 Old: 0/63 Delay: 0 ms

Averaging categories

☑ 01 ☑ On-line display Change... t = -50.0... 300.0 ms Event: 1 No condition Sub: 0 No limit for # of averages

☐ 02 ☑ On-line display Change... t = -50.0... 300.0 ms Event: 1 No condition Sub: 0 No limit for # of averages

☐ 03 ☑ On-line display Change... t = -50.0... 300.0 ms Event: 1 No condition Sub: 0 No limit for # of averages

☐ 04 ☑ On-line display Change... t = -50.0... 300.0 ms Event: 1 No condition Sub: 0 No limit for # of averages

☐ 05 ☑ On-line display Change... t = -50.0... 300.0 ms Event: 1 No condition Sub: 0 No limit for # of averages

Artefact rejection settings

	MEG grad		MEG mag		EEG		EOG		EMG		ECG		BIO	
Max :	3000	fT/cm	3000	fT	-1	uV	150	uV	-1	uV	-1	uV	-1	uV
Slope :	-1	fT/cm	-1	fT	-1	uV								
Spike :	-1	fT/cm	-1	fT	-1	uV								
No signal :	-1	fT/cm	-1	fT										
Noisy :	-1	fT/cm	-1	fT										

Ignore (ms) after stimulus : 0

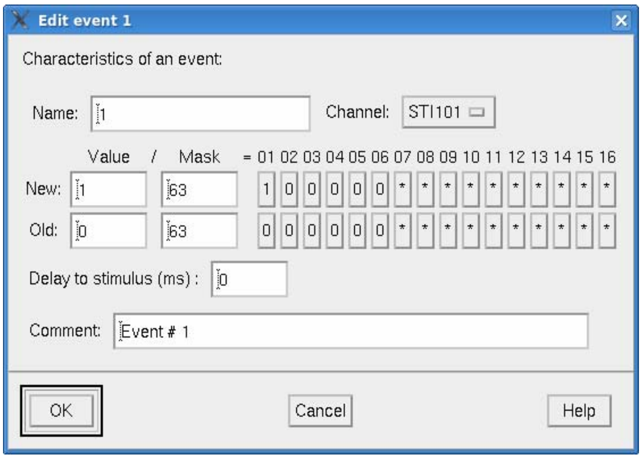
Miscellaneous settings

Display update interval (s) : 60

3.5.3. Events

The **Event characteristics** section in the top part of the on-line averaging dialog is used to define the events used in averaging. There are 32 event lines, each of which contains a **Change...** button and a description of the event properties.

The dialog appearing from the **Change...** button contains the following controls.



Characteristics of an event:

Name: 1

Channel: STI101

Value / Mask = 01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16

New: 1 / 63 = 1 0 0 0 0 0 * * * * * * * * * *

Old: 0 / 63 = 0 0 0 0 0 0 * * * * * * * * * *

Delay to stimulus (ms) : 0

Comment: Event # 1

Name:

A text field to enter a descriptive name for the event. Spaces are not allowed.

Channel:

An option menu to select a combination trigger channel.

Old Value/Mask and **New Value/Mask:**

These fields define the trigger channel state transition that is mapped to this event. The **Old** fields define the state of the triggers before the transition, and the **New** fields define the state after the transition.

First Old Value and previous bit combination are logically anded with Old Mask. If the resulting values are equal, then New Value and next bit combination are logically ANDed with New Mask. If the resulting values are again equal, then transition is considered to have taken place.

Bit 01 corresponds to trigger line 1 and so on. Each Value/Mask pair can be entered directly as two decimal bit combination values. Alternatively each bit can be toggled separately such that '0' changes to '1', '1' to '*', and '*' back to '0'. Asterisk stands for 'do not care' and is added to Mask.

Delay to stimulus:

A text field used to enter a delay (in ms) from the trigger state transition to the actual stimulus. For example, if you have plastic tubes with known transmission delays leading auditory stimuli to the subject's ears, enter the delay here to set the time scale of the responses correctly. The delay must be defined positive if the stimulus occurs after the trigger and negative if it occurs before the trigger.

Name:

A text field to assign a comment to the event.

For backwards compatibility, the default definitions of the events correspond to the transitions on the trigger lines as follows (Old Value/Mask is set to 0/63 and New Mask is set to 63):

Event #	Trigger lines to activate
1	1
2	2
3	3
4	4
5	5
6	6
7	1 & 2
8	1 & 3
9	2 & 3

10	1 & 2 & 3
11	1 & 4
12	2 & 4
13	1 & 2 & 4
14	3 & 4
15	1 & 3 & 4
16	2 & 3 & 4
17	1 & 2 & 3 & 4

Note: As described in Section 3.5.1, event numbers do not directly relate to category numbers. For example, event # 1 may be used as a trigger in several categories, not necessarily including category # 1. Therefore, if you adjust the delays of some events, keep in mind that event # 5 is not always triggering category # 5.

3.5.4. Categories

The **Averaging categories** section in the middle part of the on-line averaging dialog is used to define the categories to be averaged. There are 32 category lines, each of which contains the following items:

On-off toggle

A toggle button to activate and deactivate a category. You can often define all categories you need in a study consisting of several consecutive acquisitions and then just switch the categories on and off as needed.

Display on-off toggle

This toggle button sets the on-line display state of a category. The states of these buttons define the initial selection of categories displayed in the xplotter window during averaging. The selection of displayed data can be modified during acquisition as discussed in Section 5.4.4. However, when the acquisition is finished, the final results from any categories which have one or more epochs averaged will be displayed regardless of the on-line display selection. Note also that any changes made to the on-line display selection during the data collection will remain in effect for the subsequent acquisitions.

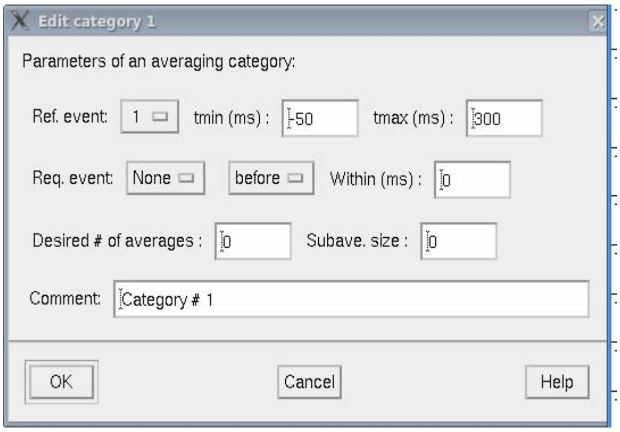
Change…

This button invokes a dialog to define the characteristics of a category.

Description

A text describing the properties currently selected for this category from the category definition dialog.

The dialog appearing from the **Change…** button contains the following controls:



Parameters of an averaging category:

Ref. event: 1 tmin (ms) : -50 tmax (ms) : 300

Req. event: None before Within (ms) : 0

Desired # of averages : 0 Subave. size : 0

Comment: Category # 1

Ref. event:

An option menu to select the trigger event. The event is considered as the zero-time point, with the optional stimulus delay compensation taken into account (see the previous subsection on Events). The event name list reflects the defined events in the top part of the on-line averager window.

tmin:

The start time of the averaging window with respect to the reference event. This value can be negative (prior to the occurrence of the reference event) or positive (after the occurrence of the reference event).

tmax:

The end time of the averaging window with respect to the reference event.

Req. event:

An option menu to select the condition event. If None is selected, there is no condition.

When:

An option menu to select **Before** or **After**. If **Before** is selected, the condition event must occur before the trigger event. In case of **After**, the condition event must occur after the trigger event.

Within:

The time range within which the condition event must occur in order for an epoch to match this category.

Desired # of averages:

If this number is zero or negative, the number of epochs averaged is controlled manually, see Section 5.1. on page 30.

If the setting is positive, averaging is automatically suspended when the desired number of averages is reached. You can then either continue averaging manually or stop the measurement.

If several categories have the desired number of averages set, the first one to reach the limit causes the averaging to be suspended. Other limits not satisfied remain active. Therefore, if you continue averaging manually, the averaging will be again suspended if some other category reaches the limit.

Subave. size:

If this number is set to $M > 0$ both normal and alternating subaverages are computed consisting of M epochs. If we denote the epochs by $e_k(t)$, the jth normal and alternating subaverages are

$$\bar{e}_j(t) = \sum_{k = 1 + (j-1)M}^{jM} e_k(t) \text{ and}$$

$$\tilde{e}_j(t) = \sum_{k = 1 + (j-1)M}^{jM} (-1)^{k+1} e_k(t) \,,$$

respectively.

Note: M should be an even number to get proper alternating sub-averages.

Comment:

A text entry field to annotate a category with a comment. The comment is shown when new data are loaded for plotting and source modeling.

3.5.5. Artefact rejection

There are three kinds of artefact rejection criteria available for MEG and EEG channels. Each of these can be turned off by entering a negative number into their control field.

Amplitude (Max)

The peak-to-peak amplitude within an epoch must not exceed this value. Typical value is 3000 fT/cm for gradiometers and 3000 fT for magnetometers. This criterion depends on the residual noise within the magnetically shielded room.

Slope

The epoch is subdivided into four equally long pieces. The averages over each piece is calculated. None of the three differences between subsequent partial averages must not exceed this value. By default, this criterion is not in use.

Spike

The absolute value of the difference between any sampled value in an epoch and the average of 20 previous values must not be larger than this. By default, this criterion is not in use.

The above criteria are applied to all MEG and EEG channels. If a channel not meeting the criteria throughout the epoch is found, the epoch is rejected. Some channels can be excluded from the artefact rejection during acquisition, see Section 5.4.3.

BIO, EOG, EMG, and ECG rejection is only possible on the basis of the amplitude criterion.

In addition to the above criteria, an epoch up to a given time interval after the reference event can be excluded from the rejection (**Ignore (ms) after stim**). This is useful if a strong stimulus artefact is expected.

3.5.6. Noisy and silent channels

It sometimes happens that few MEG channels are either showing no signal or are very noisy. There are two additional parameters to check these channels: **MEG no signal** and **MEG noisy**.

If the peak-to-peak amplitude of a channel is less than the **MEG no signal limit** or larger than the **MEG noisy limit**, the channel will be omitted from further artefact checking during the current and all subsequent epochs. The noisy and silent channels so detected will be marked 'bad' in the resulting evoked-response data files.

The signals of "noisy" or "silent" channels are stored in the very same way as those of any other channels; the automatic detection only affects rejection checking.

3.5.7. On-line display updates

During on-line averaging the progress is displayed by showing data averaged so far in the standard plotting program (*xplotter*).

By default this display is updated every 15 seconds. You may want to set this value higher in order to work with the data between updates. It is also advisable to set the update interval higher if the ISI is small (< 500 ms), if the sampling rate is high (> 1 kHz), the epochs are long (> 2 s), or if many categories are selected to the on-line display. If the updates are too frequent, the on-line averaging may not proceed in real-time and, consequently, you may have to wait at the end of the acquisition for on-line averaging to complete.

3.6. Head digitization

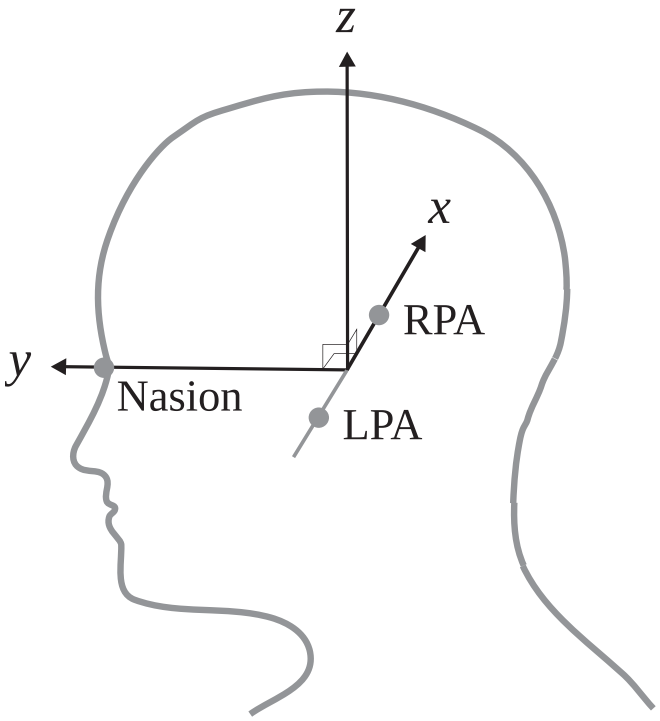
In order to be able to locate signal sources relative to the head, one must know the position of the head within the probe. For this purpose we use a head position indicator (HPI) system. Before the measurement, one attaches small coils to the head and digitizes their locations on the head. These coils are then used during the measurement to measure the location of the head. Following sections describe the coordinate systems used and how the digitization is performed.

3.6.1. Coordinate frames

The TRIUX™ systems internally use *device coordinate system*. The recorded signals represent field components at fixed sensor locations in the device coordinate system. The origin of this coordinate system is located at the center of the posterior spherical part of the helmet with *x*-axis from left to right, *y*-axis pointing from back to front, and *z*-axis pointing up. Thus the position of subject's head in respect to the measurement probe does not affect the way the signals are recorded.

The results of source modeling calculations are presented in a more relevant coordinate system, namely the *head coordinate system* (also called the *anatomical coordinate system*). This is essential in order to integrate the source model into an anatomical image, *e.g.* magnetic resonance image.

The head coordinate system is defined as follows: The *x*-axis passes through the preauricular points with positive values on the right, the *y*-axis will be perpendicular to the *x*-axis, passing through the nasion and the positive axis pointing towards the nose, and the *z*-axis will point up, perpendicular to the *xy*-plane. This is illustrated in figure below. LPA and RPA stand for the left and right peri- or preauricular points, respectively. LPA, RPA and nasion are called the *anatomical landmarks* or *cardinal points*.



To establish the coordinate transformation between the head coordinate system and the device coordinate system the anatomical landmarks have to be expressed in the device coordinate system. This is done indirectly by using HPI coils whose locations can be measured with respect to the anatomical system and also with respect to the device coordinate system. The former measurement is called *Head digitization* and the latter *HPI measurement*. The combination of these two measurements results in a coordinate transformation between device coordinate system and head coordinate system.

3.6.2. Digitization

The final task before starting the measurement is the digitization of the anatomical landmarks on the head and the position of the HPI coils with respect to them.

When you click the HPI **Change** button, *megacq* connects to and initializes the 3D digitizer used for this purpose. Digitizer initialization takes a few seconds. You are informed about this in a dialog. Once the initialization is complete the HPI dialog appears.

The left section of the dialog contains the controls for the tasks which are necessary to complete the HPI procedure. The lower right section (**Additional data**) contains controls for optional items. The label above the dialog buttons will dynamically indicate the task to be performed next.

The operation of the digitizer, and how to attach HPI coils are described in more detail in *TRIUX User's Manual* as well as in *TRIUX™ neo Instructions for Use*.

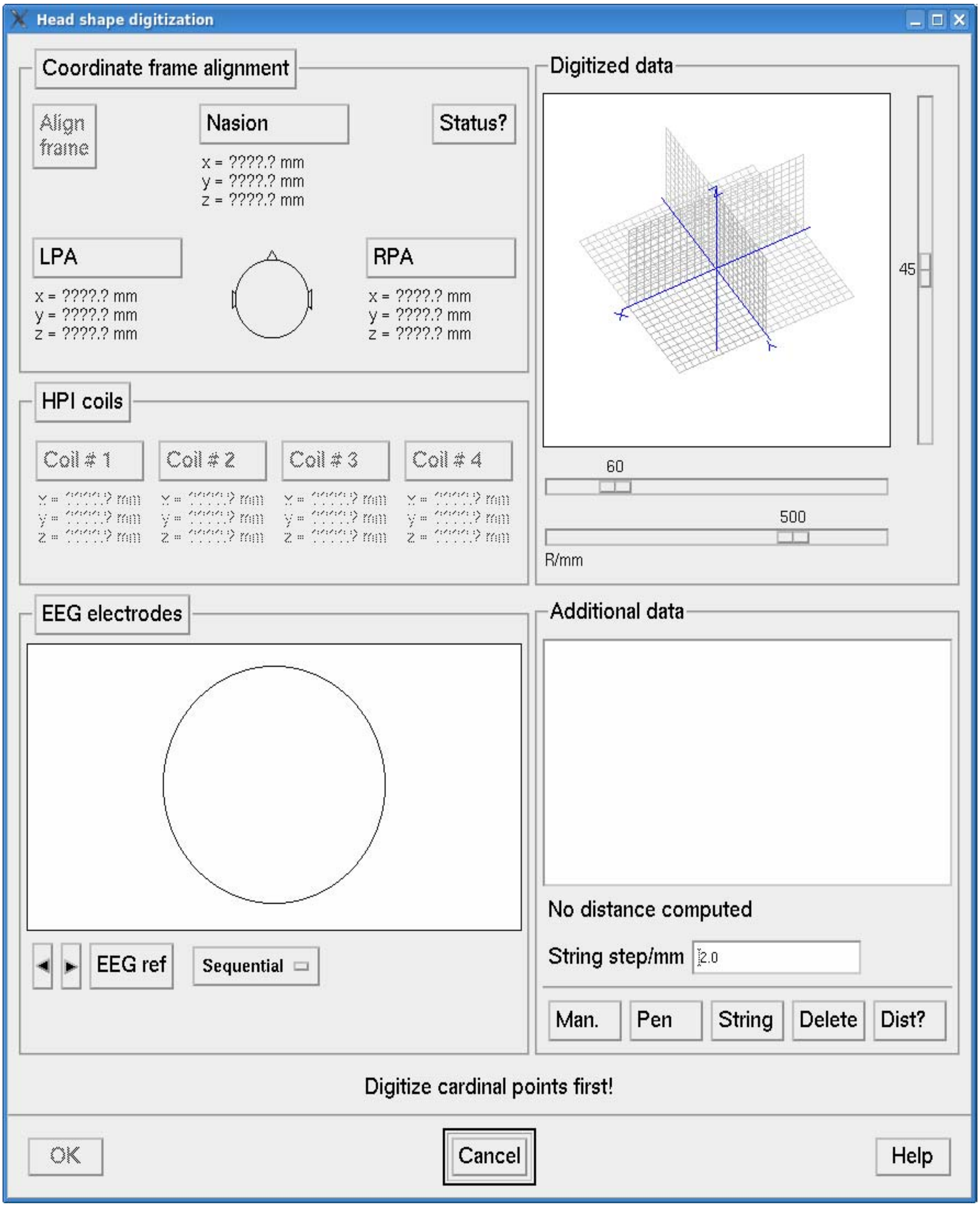
Proceed as follows with the digitization:

1. Attach the HPI coils on the head. Typically the coils are placed so that two are behind the ears as high as possible without being on the hair, and two on the forehead well separated but not on the hair. The coil locations must be covered by the MEG sensor array and they must not move relative to the head during the measurement. The coils should not be directly under the IAS reference channels, i.e. they should not be in the middle of forehead, on the inion or near pre-auricular points.

   The most precise HPI information is obtained when the coils are as far apart as possible but still within the sensor helmet. Try avoiding situation where coils form a nearly perfect square.
2. The digitization system is equipped with goggles which track head movements during the digitization. Place the goggles firmly on the subject's head and tighten the strap. Check that nasion and the coil centers are still accessible with the digitizer stylus.
3. Make sure the digitization chair is sufficiently far (over 1.5 m) from large metal objects as they severely distort the digitizer and compromise its accuracy. Tell the subject to avoid excessive head movement.
4. Digitize the anatomical landmarks which define the head coordinate system: the nasion and the two auricular points. Depending on your preferences you may use either peri-auricular or pre-auricular points. Be sure to record which points were used to be able to correctly identify them later on the anatomical MR images.

   To digitize, position the tip of the 3D digitizer stylus at the desired point and click the corresponding button in the HPI dialog. It is best to have two people available for the digitization: one to position the stylus and another to operate the program. Alternatively, the stylus button can be used for the digitization: click the **Coordinate frame alignment** button to start the "single operator" mode. Then digitize the landmarks in any order; the system will automatically associate the points with proper landmarks.

   The coordinates next to each button indicate the digitized position in a coordinate frame tied to the signal source of the digitizer behind the chair. The results are averages of three sequential readings taken from the digitizer. If they differ from each other by more than 2 mm, an error message telling to keep the pointer steady appears and you can re-digitize the point.



Nasion
x = ????.? mm
y = ????.? mm
z = ????.? mm

LPA
x = ????.? mm
y = ????.? mm
z = ????.? mm

RPA
x = ????.? mm
y = ????.? mm
z = ????.? mm

Coil # 1
x = ????.? mm
y = ????.? mm
z = ????.? mm

Coil # 2
x = ????.? mm
y = ????.? mm
z = ????.? mm

Coil # 3
x = ????.? mm
y = ????.? mm
z = ????.? mm

Coil # 4
x = ????.? mm
y = ????.? mm
z = ????.? mm

No distance computed

String step/mm 2.0

Digitize cardinal points first!

5. When the digitization of the cardinal points is complete, press the **Align frame** button (the alignment is done automatically when operating with the stylus button and all three landmarks are digitized). The coordinates of subsequent readings will be given in the head coordinate frame, tied to the cardinal landmarks.

   When **Align frame** is pressed, the coordinates of the cardinal locations will change to the head frame. Notice that the *z* coordinates of all three points are zero. The *y* coordinates of the auricular points are zero with a positive *x* coordinate on the right and a negative on the left auricular point, respectively. The nasion has a zero *x* coordinate and its *y* coordinate is positive. The auricular points are usually rather symmetrically located: their *x* coordinates are opposite and about of equal magnitude. This serves as an additional check that the digitized values are reasonable.

6. Digitize the HPI coils (order does not matter).
7. If scalp EEG channels are selected for acquisition, the program moves on to digitize the EEG electrode locations. Alternative electrode digitization sequences for different EEG caps can be configured by editing text file /neuro/dacq/setup/eeg_digit_maps. A sequence is specified on one line and contains a name, a colon, and a colon separated list of electrode numbers (where 0 stands for the mandatory reference electrode). The sequences which contain K+1 electrode numbers (where K equals number of selected EEG channels in the acquisition setup dialog) are available for selection in the EEG digitization quadrant of the window. The option menu also contains one generated sequence, called **Sequential**, which contains electrode numbers from 0 to K, in ascending order.
8. You can digitize additional points to obtain information about the head shape, which allows more accurate alignment with the anatomical MR images. Press **Man** to digitize the location of the stylus in the "two operator" mode or **Pen** to use the stylus button. Click **String** (enabled separately) to digitize continuous runs of the digitizer pen (see "String digitization (sweep mode)" on page 26 for more details of the usage). Select one or more of the digitized extra points from the list and press **Delete** to remove any unneeded entries. Select two points in the list and press **Dist?** to find out the distance between the selected points. The coordinates of the additional points will be saved into the measurement files. Once you have completed the digitization, press **OK**.

The digitization procedure and other pre-measurement setups can be performed also on a workstation other than the acquisition workstation even when there is a measurement in progress. See "Experiment preparation" on page 28 for more information.

Note: If you press **Cancel** in the dialog you will loose all the digitized data. A warning dialog will appear to confirm this.

3.6.3. Using less than five coils

By default systems are configured to have five coils. If you only digitize the first three or four coils, the system will then use only those coils.

3.6.4. String digitization (sweep mode)

The string digitization mode allows one to sweep the pen freely, e.g. across the subject's head, and automatically digitize points along the movement. The digitization starts right away when you click on the **String** button, so position the pen first to the start point of the sweep and then click the **String** button. Subsequently, all movement of the stylus will be digitized until either the stylus button is clicked to pause digitization or the **Done** button is clicked on the dialog window to finish the sweep mode digitization. When paused, the digitization can be continued again by clicking the stylus button again. The digitized points are displayed on the screen after finishing the digitization with the **Done** button on the dialog. By clicking **Abort**, the strings digitized will be forfeited.

Use the **String step/mm** setting to control the point density of the digitization (default 2.0 mm).

The string digitization support is turned on by setting variable `DEFisotrakStrokes` in file `/neuro/dacq/setup/megacq.defs.local` to value of 1.

3.7. Gantry position

Before starting a measurement, one should make sure that **Gantry position** in the *megacq* main window reflects the current dewar position. The adjacent gantry position setup button can be used to automatically detect the current position. If this fails, a dialog pops up and allows you to manually change the position to **Upright 68** degrees**, Upright 60** degrees or **Supine**. The gantry position is also automatically detected when the **Start** button is pressed.

Correct gantry position is required for proper operation of IAS and SSP. See "Using signal space projection" on page 46.

Note: Do not change the gantry position when a measurement is running. The system is not able to detect the change of the gantry position after the acquisition has been started, and the file format allows saving only one gantry position per measurement. Incorrect gantry position in the measurement file can reduce the quality of the analysis results. If IAS is used, the quality of raw data may also be reduced significantly or the system may become inoperational. If you have accidentially left the acquisition running when changing the gantry position, stop the measurement and don't save the data if the data collection was on.

3.8. Saving and restoring settings

All of the above settings apart from the project and subject data can be saved between sessions. Settings are saved specifically for each project. Therefore, you cannot save or load settings prior to selecting a project.

Settings are saved and loaded with the **Save settings…** and **Load settings…** items in the **File** menu. When you save settings you must provide a descriptive name for the setup. This name is shown in the list of available settings when you load the settings back later.

The settings are also included with the measured data. By choosing **Load measurement settings…** from the **File** menu you can locate a data file and load the settings from that. This option is useful if

1. You would like to replicate a measurement with identical settings.
2. You would like to check the actual settings used afterwards.

Note that the Head digitization data (see Section 3.6. on page 23) are not stored in the settings nor can they be loaded from a data file. On the contrary, subject preparation information includes everything that is in the settings as well as the digitization data. You can create a preparation from the current setup and digitization by choosing **Save preparation** from the **File** menu and recall it later by choosing **Load preparation...** in the same menu. See Section 4. on page 28 for more details.

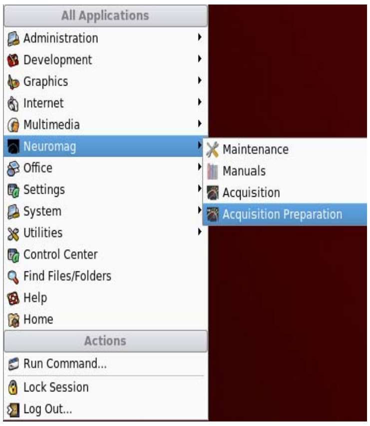
Note: Using settings or preparations which are copied from some other system is not supported. Loading such files can alter the configuration of the system so that it no longer matches the hardware of the system.

4. EXPERIMENT PREPARATION

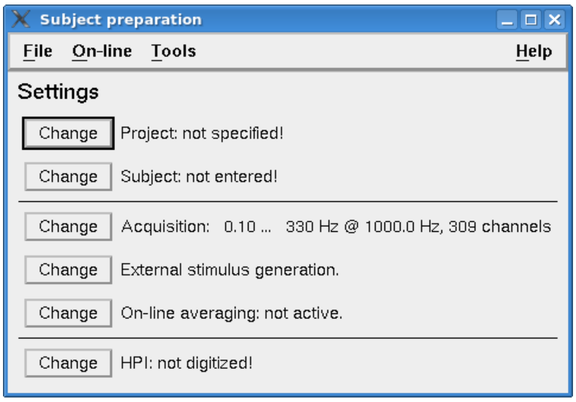
As discussed in Section 3.8, the acquisition and averaging parameters can be saved between sessions using the **Save settings...** and **Load settings...** items in the **File** menu. Therefore, a given experimental paradigm can be easily repeated.

It is often beneficial to save all measurement parameters, including the project and subject selections, all acquisition and averaging parameters, and the head digitization data for subsequent use. This complete set of information is called a *preparation*.

4.1. Restricted *megacq*



An experiment can be prepared either from the standard *megacq* or from its restricted version. The restricted version is started by double clicking the **Acquisition Preparation** icon in the **Neuromag** folder.



Project: not specified!

Subject: not entered!

Acquisition: 0.10 ... 330 Hz @ 1000.0 Hz, 309 channels

External stimulus generation.

On-line averaging: not active.

HPI: not digitized!

The *restricted megacq* does not communicate with the acquisition hardware (only certain software modules), and the acquisition control buttons (see Section 5.1) are absent. A new experiment can be prepared from another workstation while data are being collected at the acquisition workstation. The experiment preparation workstation has to be located near the digitizer for feasible digitization.

Note: You can also use the restricted *megacq* to check information about a subject or a project during off-line analysis without disturbing the measurement.

4.2. Saving a preparation

Before you can save a preparation, you will have to complete the following steps:

1. Select a project
2. Select a subject
3. Enter the acquisition, stimulus, and averaging parameters or load one of the settings available for the selected project.
4. Perform the head digitization.

With all the above data complete you can save the preparation by selecting **Save preparation** from the **File** menu. If some of the required data is missing an error dialog will appear. If all data is present, the preparation will be saved. You will be informed about the name given to the preparation. The name is of the form

<project name> / <subject name> / <date> <time>.

A saved preparation will be kept for 24 hours from its creation time. Whenever *megacq* or its restricted version is started, the preparation database is checked for old preparations which are automatically discarded.

Note: Using the head digitization data from the preparation is only meaningful if the HPI coils are kept attached on the subjects head from the preparation time to the actual measurement.

4.3. Loading a saved preparation

When **Load preparation...** is selected from the **File** menu, a list of available experiment preparations will appear. You can easily identify the desired one from the descriptive name. Please be careful to select the correct one. There is no way for the program to check that the subject to be measured is the one you claim him/her to be.

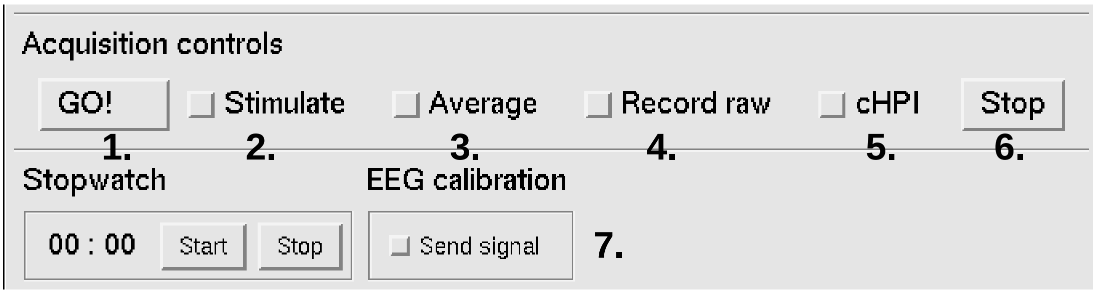
If necessary, you can override any of the data in the preparation simply by redoing the relevant parts of the settings. For example, you can redo the head digitization, if there is any doubt that the HPI coils are not at the same positions as they were at the time of the preparation.

5. ACQUISITION

Once the setup is complete, subject is seated under the magnetometer, the HPI coils and EEG electrodes have been connected as described in the hardware manual, and the shielded room door is closed, you can start the actual acquisition.

5.1. Acquisition controls

The acquisition control buttons are:



1. **GO!/Restart**

   Press **GO!** to Start the acquisition. If the parameters have been changed or if this is your first acquisition, the acquisition system is informed about the new parameters first. Thereafter, the magnetometer electronics is set to the correct state including analog filter settings.

   Depending on the changes needed this procedure may take about 5 - 10 seconds. The log window shows messages about the conversation with the data collection server. Once the setup is complete, a **New measurement is starting...** message appears on the first message line below the acquisition control buttons.

   When data collection is started, this button changes to **Restart**. You can then restart the acquisition by clicking this button. All raw data and on-line averages collected will be discarded and you can also redo the head position measurement (see Section 6.2).

2. **Stimulate**

   When using internal triggering, this button becomes enabled when the data collection is started. You can then engage the internal triggers with this button. This button does not apply when using external triggering.

3. **Average**

   With at least one active category, the button is enabled when data collection is started. You can then switch on-line averaging on and off by clicking this button. If there are no active averaging categories, this button remains dimmed.

4. **Record raw**

   Recording of raw (spontaneous) data is independent of on-line averaging. You can switch the raw data recording on and off at will during the acquisition. The amount of data collected in seconds and megabytes as well as the space remaining on the acquisition hard disk is displayed on the second message line of *megacq*.

5. **cHPI**

   This button is enabled when a normal HPI is done. You can then switch continuous HPI on and off by clicking this button. If HPI is not digitized or you have decided to omit HPI localization, this button remains dimmed. See also “Continuous HPI” on page 33.

6. **Stop**

   Press to finish the acquisition, see Section 5.7.

7. **EEG Calibration signal**

   This toggle button creates a rectangular 1 Hz signal to EEG and BIO channels. The signal can be used to check the EEG system operation at the start and end of a measurement. This cannot be activated simultaneously with EEG impedance measurement.

Sometimes it might be necessary to reset the MEG and EEG channels after an excessively strong magnetic or electric disturbance. This can be done while a measurement is in progress by selecting **Reset channels** from the **Tools** menu. On-line averaging and raw data recording should be turned off before doing reset and they should be kept off until all the channels have settled again. Otherwise the data could be spoiled by the huge signals involved in the reset operation.

5.2. Head position indicator

If you have digitized the HPI coil locations as described in Section 3.6.2, you can localize subject's head with respect to the neuro-magnetometer. Normal HPI measures the head position at the beginning of the measurement. The result is saved into the data file. Continuous HPI allows determining the head position during the measurement. This requires extra processing of the data file after the measurement is completed.

5.2.1. Normal HPI acquisition

If the HPI coils have been digitized, the system automatically pops up an HPI measurement dialog when data collection is started. This dialog gives you the following choices:

Measure

Measure the magnetic field generated by current fed into the HPI coils and determine the location of each coil. During the measurement you will see messages on the last message line of the *megacq* main window. If no signals are seen or if they are considered too noisy, you will get an error message. Should this happen, check that the coils are properly connected and that the coils are working properly by rechecking them with the HPI coil tester.

Once the measurement is complete, the positions are fitted. When the fit completes, the results are reported as described in Section 5.2.2 below.

The HPI procedure takes usually less than 10 seconds.

Reuse

If you have performed a successful HPI measurement within this session and you have not re-digitized the head, you can reuse the previous head position. Use this option with caution. If you have any doubt that the head has moved since the last HPI measurement, use the **Measure** choice instead.

Omit

Do not perform HPI localization at all.

5.2.2. HPI fitting

When the HPI signals have been acquired, a fitting program is started to find out the locations of the coils. HPI fitting takes from three to ten seconds. When the fitting is complete, you will see a dialog with the following information:

1. Locations of the HPI coils in the device coordinates (see Section 3.6.1 for the definition).
2. The goodness-of-fit value for each coil with an indication of acceptance.
3. Distances between the coils as measured by the digitizer.
4. Distances between the coils from the fitting procedure.
5. A list of discrepancies between the distances measured by the digitizer and calculated from the fitting procedure. Distances larger than 5 mm are indicated, suggesting a need to redo the HPI measurement.
6. Location of the head coordinate system origin in device coordinates.
7. Suggestion from the fitting program to accept or reject this result.

With the buttons at the bottom of the dialog, you can either accept the HPI data, redo the measurement, or omit HPI localization.

Note: If you stop the acquisition and you have neither accepted nor discarded the HPI result, no HPI data will be available in the files produced when you save the data.

5.2.3. Continuous HPI

The system also supports recordings with continuous HPI (cHPI). Using continuous HPI requires that a normal HPI measurement is performed at the beginning of the measurement. When this has been done, the cHPI button becomes available, and the user can activate the HPI coils. This will lead to a measurement which contains both the brain signals and the cHPI signals.

In order to judge the data quality during the cHPI measurement, a low-pass filter should be used in the raw data display. By setting the filter corner frequency suitably, the cHPI signals can be filtered out from the data being displayed.

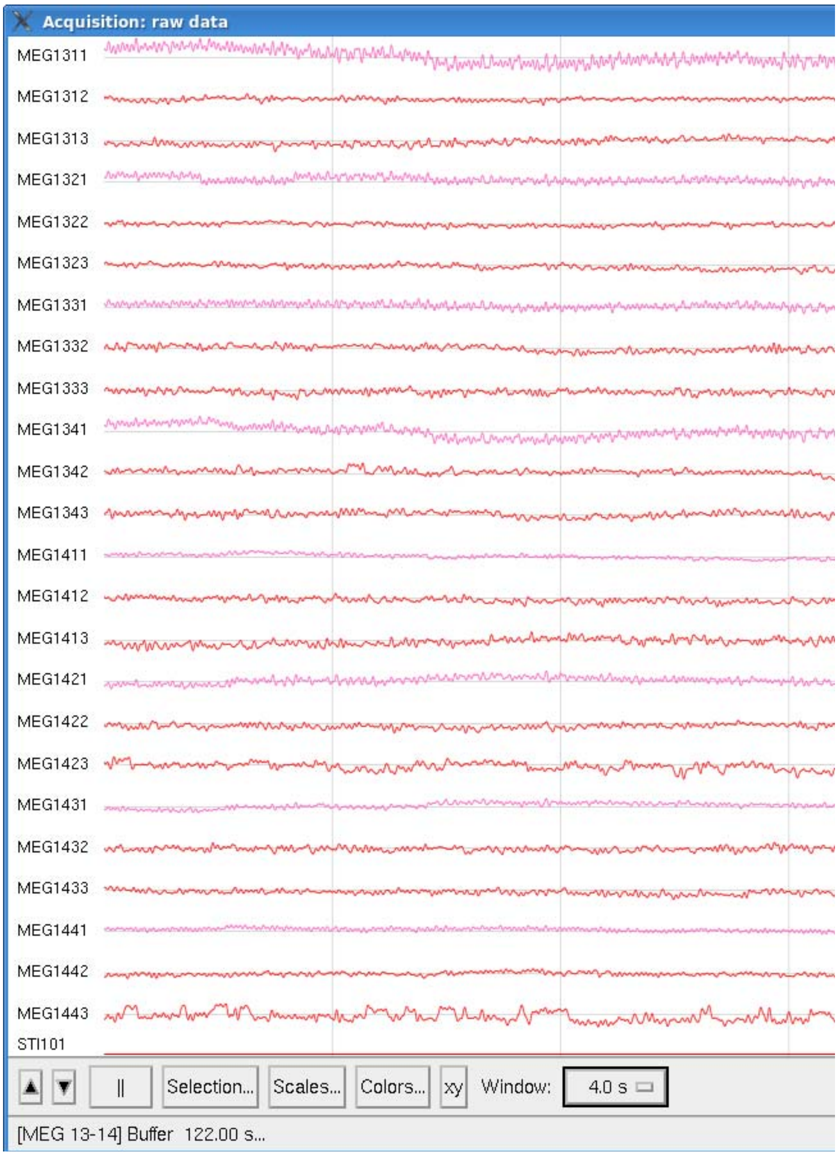
On-line averaging can in principle be performed during a cHPI measurement, but currently there are problems which limit its feasibility. The strong cHPI signals render artefact rejection almost useless and, with the limited time span available, filtering out the cHPI signals from the average is not as effective as with continuous data.

The cHPI data is post-processed using MaxFilter™ Software to extract the head position as a function of time and to remove the cHPI signals. MaxFilter™ also provides an off-line averager similar to the on-line averager.

For details, see document *MaxFilter™ User's Guide*. This system requires MaxFilter™ release 2.2 or higher.

5.3. Raw data display (real-time display)

During acquisition the incoming data are displayed in a window positioned to the right of *megacq* by default.



Window: 4.0 s

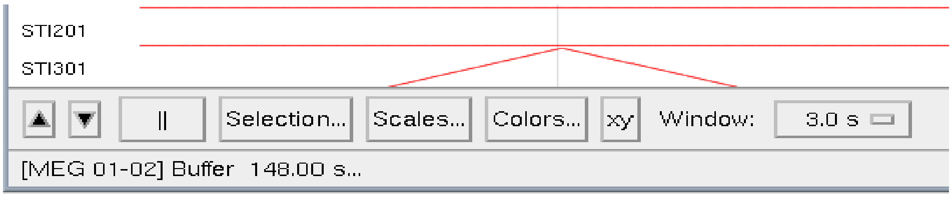
[MEG 13-14] Buffer 122.00 s...

The length of the displayed raw data segment can be set to various predefined lengths.

The name of each channel shown is indicated to the left of each trace. Vertical lines are shown at a selectable spacing for time reference. The events detected on the stimulus input channels are also shown by yellow vertical lines if any of the stimulus input channels are selected to the display.

5.3.1. Controls

The following controls are located at the bottom of the window:



[MEG 01-02] Buffer 148.00 s...

1. Channel selection buttons.

   When you press the left or right arrow buttons the display shows the previous or next set of channels, respectively. Channel selections are discussed in detail in Section 5.3.2.

2. **Pause (||)**

   The raw data display is frozen, but the acquisition still continues. When the raw data display is frozen you can still move through the channels with the channel selection buttons.

3. **Selection...**

   This button invokes a dialog showing the currently selected MEG channels in graphical form. The shortcut buttons to go to a desired selection are also located here.

4. **Scales...**

   When you press this button a dialog appears to change the scales of various channel types and the spacing between vertical time markers.

5. **Colors...**

   When you press this, a color definition dialog is shown to change the colors of the components of the display.

6. **xy**

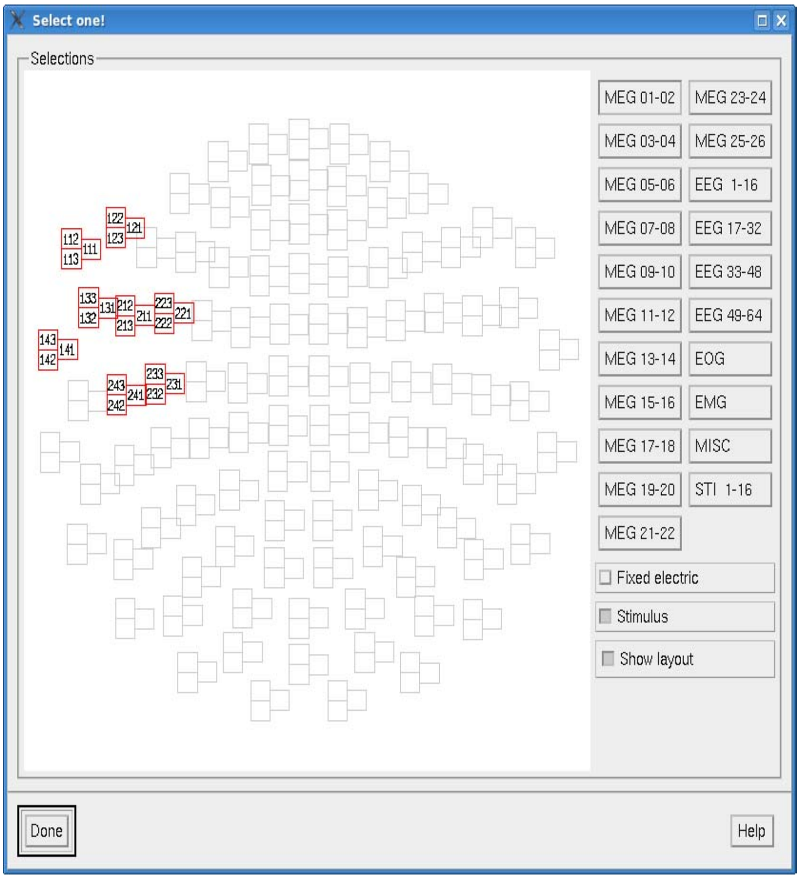
   An oscilloscope-like display for sensor tuning pops up with this button.

7. **Window**

   An option menu for selecting the time span of the displayed raw data trace in seconds. The choices are 1, 3, 5, 8 and 10 seconds.

5.3.2. Channel selections

When you press the **Selection…** button in the raw data display controls the window shown below appears.



The graphical display on the left indicates the currently selected channels. The buttons on the right list the available selections with descriptive names. There are two add-on selections available to include additional channels to each selection:

Fixed electric

The first two electric (BIO, EEG, EOG, EMG, or ECG) channels are shown after the currently selected channels.

Stimulus

Switch on/off displaying of stimulus trigger channels (signals labelled as STI...).

Show layout

The channel layout on the left can be hidden with this function to make the selection window smaller.

You can customize the standard selections in the following way:

1. Copy `/neuro/dacq/setup/rawdisp.sel` to the directory `.meg_analysis` under your home directory

   ```
   cp /neuro/dacq/setup/rawdisp.sel ~/.meg_analysis/
   ```

2. Edit file `~/.meg_analysis/rawdisp.sel` with a text editor.

   Each line in this file corresponds to a selection. The format of each line is:

   <selection name>:<ch name 1>|<ch name 2>|…

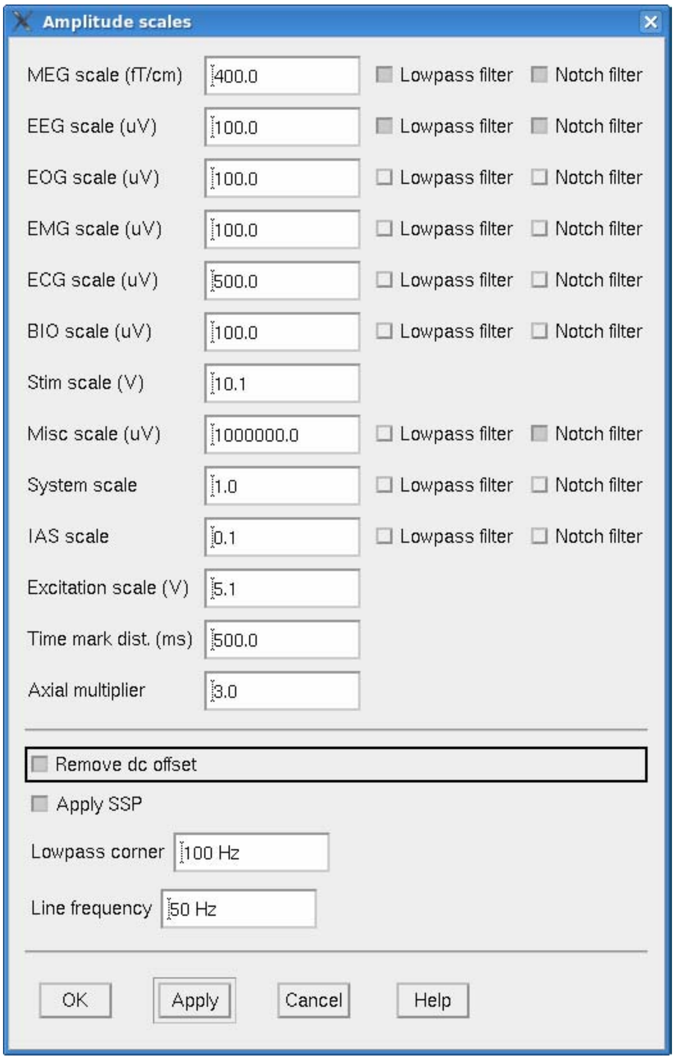
   For example:

`My selection:MEG0111|MEG0112|MEG0113`

The channel names are identical to those listed in the channel selection dialog, see Section 3.3. on page 11.

5.3.3. Scales

The vertical scales of the real-time display are fully configurable with the means of the **Scales...** dialog whereas the time span of the raw data display is determined by the window selection only. However, the time marks can be set to appear at user specified intervals by the **Scales...** dialog. The default scales can be configured by qualified service personnel.



Amplitude scales

MEG scale (fT/cm) 400.0 ☑ Lowpass filter ☑ Notch filter
EEG scale (uV) 100.0 ☑ Lowpass filter ☑ Notch filter
EOG scale (uV) 100.0 ☐ Lowpass filter ☐ Notch filter
EMG scale (uV) 100.0 ☐ Lowpass filter ☐ Notch filter
ECG scale (uV) 500.0 ☐ Lowpass filter ☐ Notch filter
BIO scale (uV) 100.0 ☐ Lowpass filter ☐ Notch filter
Stim scale (V) 10.1
Misc scale (uV) 1000000.0 ☐ Lowpass filter ☑ Notch filter
System scale 1.0 ☐ Lowpass filter ☐ Notch filter
IAS scale 0.1 ☐ Lowpass filter ☐ Notch filter
Excitation scale (V) 5.1
Time mark dist. (ms) 500.0
Axial multiplier 3.0

☑ Remove dc offset
☑ Apply SSP
Lowpass corner 100 Hz
Line frequency 50 Hz

Magnetometer and axial gradiometer channels typically require wider display scales than planar gradiometer channels. The axial sensor scale multiplier (**Axial Multiplier**) multiplies the **MEG scale** figure to set the vertical scale for axial gradiometer and magnetometer channels.

By default, raw data display subtracts the average signal amplitude calculated over the display time span from each sample thus keeping the signal traces on the display even when strong low frequency signal components are present. This behavior can be switched on and off by toggling **Remove dc offset** button. This affects only the display and not the raw data recorded to a file.

If an on-line signal space projection operator (see Section 8) is used, the noise suppression for the display can be controlled by the **Apply SSP** button. Note that this does not have any effect on the raw data recording itself.

Use of display low-pass filtering can be controlled by the **Lowpass filter** buttons. The low-pass corner frequency can also be specified. The low-pass filtering can be toggled on or off for each channel type individually.

Use of display notch filtering can be controlled by the **Notch filter** buttons. If turned on, the specified line frequency and its first two harmonics (e.g. 50 Hz, 100 Hz, and 150 Hz) are filtered out. The notch filter can also be toggled on or off for each channel type individually.

5.3.4. XY display

The tuning of the SQUID sensors can be done without the tuner program by using the XY display incorporated in the raw data display. The XY display shows the signal from one channel at a time; the Y (vertical) deflection is driven by the output of the selected channel whereas the X (horizontal) deflection is driven by the excitation signal fed to the SQUIDs in the tune mode.

The XY display works in conjunction with the **Squiddler** program so that selecting a channel in **Squiddler** automatically selects the same channel for the XY display. In addition, the arrow buttons can be used to select any individual channel. You can also choose from three different scales.

Tuning is described in more detail in document *Sensor Tuner User's Manual*.

Note: The XY display is functional only if you have selected the EXCI channel in the acquisition setup dialog. See Section 3.3. "Acquisition" on page 11.

5.4. On-line averaging

5.4.1. Messages

As mentioned in Section 5.1, on-line averaging is switched on and off from the **Average** control button. The number of responses averaged into each category is listed on the third message line. If an epoch is rejected from the average, a message indicating this is displayed on the fourth message line. The **Epoch rejected** message will remain for a while even if subsequent epochs are again accepted. Reasons for the rejections (and the pertaining channels) are listed in the log message area at the top of the main control window.

5.4.2. Adjusting on-line averaging

You will notice that the on-line averaging setup button remains active even during acquisition. Therefore, you can change the on-line averaging parameters during acquisition. If you accept the changes, all existing averages are cleared and the averaging is started from beginning. Changes to the on-line averaging parameters do not affect the raw data collection.

5.4.3. Marking channels as “bad”

You can set channels to be ignored from the on-line artefact rejection procedure from the dialog that appears when you select **Set bad channels...** from **On-line** menu. If some channels are causing rejections and you would like to continue without rectifying the problem, check the corresponding channels in the bad channels dialog. The ignored channels will be marked ‘bad’ in the resulting evoked-response output files but their signals will nevertheless be present in both average and raw data files unlike those channels that are turned off.

5.4.4. On-line average display

During averaging, partial results are displayed at selectable intervals in the standard plotting program, *xplotter*, as discussed in Section 3.5.7. You can manipulate the display of responses (filtering, baselines, scales, etc.) in the *xplotter* window during acquisition.

If you would like to update the averages without waiting for the selected time interval to elapse, select **Update average display** from the **On-line** menu. When you schedule a display update manually, the display update timer will be reset and the next update will be scheduled to occur after the regular interval from the manual display update.

5.4.5. Select displayed categories

The categories displayed on-line are initially selected from the averaging parameters dialog. You modify the selection of displayed categories and on-line display update rate from **Select displayed categories...** in the **On-line** menu. The choices are kept between acquisitions, *i.e.*, any changes made here are equivalent to modifying the standard averaging parameter dialog with the exception that the on-line averaging is *not* restarted from the beginning when you activate the changes from the **OK** button.

When on-line averaging completes, all categories averaged are *always* displayed, regardless of the currently active display selection.

If on-line averaging is not active, selecting displayed categories gives an error message.

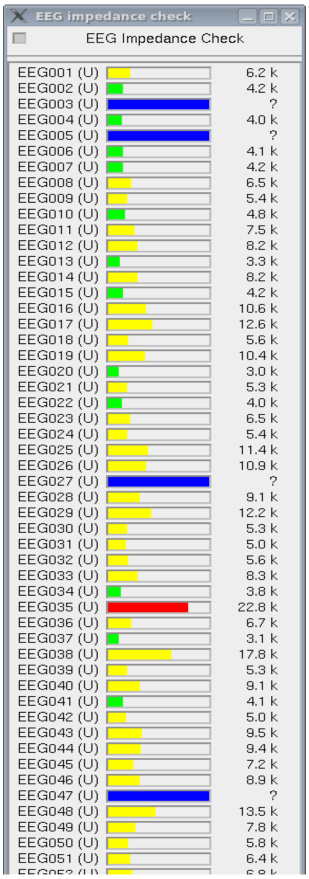
5.5. Raw data recording

While the measurement is running you can start recording raw data by using the **Record raw** button in the acquisition controls. If you switch recording on and off several times during one measurement, the separate segments of raw data will be concatenated into the same raw data file. Since all the segments will have time tags referring to the actual measurement time, the different segments can be identified at the analysis phase.

When raw data is being recorded, the amount of data recorded as well as the amount of free disk space are displayed on the second message line of *megacq*.

5.6. EEG impedance measurements

The acquisition system allows measurement of EEG electrode impedances. When electric (BIO, EEG, EOG, EMG, or ECG) channels have been activated, the EEG impedance display pops up automatically when a measurement is started.



EEG001 (U)	🟨	6.2 k
EEG002 (U)	🟩	4.2 k
EEG003 (U)	🟦	?
EEG004 (U)	🟩	4.0 k
EEG005 (U)	🟦	?
EEG006 (U)	🟩	4.1 k
EEG007 (U)	🟩	4.2 k
EEG008 (U)	🟨	6.5 k
EEG009 (U)	🟨	5.4 k
EEG010 (U)	🟩	4.8 k
EEG011 (U)	🟨	7.5 k
EEG012 (U)	🟨	8.2 k
EEG013 (U)	🟩	3.3 k
EEG014 (U)	🟨	8.2 k
EEG015 (U)	🟩	4.2 k
EEG016 (U)	🟨	10.6 k
EEG017 (U)	🟨	12.6 k
EEG018 (U)	🟨	5.6 k
EEG019 (U)	🟨	10.4 k
EEG020 (U)	🟩	3.0 k
EEG021 (U)	🟨	5.3 k
EEG022 (U)	🟩	4.0 k
EEG023 (U)	🟨	6.5 k
EEG024 (U)	🟨	5.4 k
EEG025 (U)	🟨	11.4 k
EEG026 (U)	🟨	10.9 k
EEG027 (U)	🟦	?
EEG028 (U)	🟨	9.1 k
EEG029 (U)	🟨	12.2 k
EEG030 (U)	🟨	5.3 k
EEG031 (U)	🟨	5.0 k
EEG032 (U)	🟨	5.6 k
EEG033 (U)	🟨	8.3 k
EEG034 (U)	🟩	3.8 k
EEG035 (U)	🟥	22.8 k
EEG036 (U)	🟨	6.7 k
EEG037 (U)	🟩	3.1 k
EEG038 (U)	🟨	17.8 k
EEG039 (U)	🟨	5.3 k
EEG040 (U)	🟨	9.1 k
EEG041 (U)	🟩	4.1 k
EEG042 (U)	🟨	5.0 k
EEG043 (U)	🟨	9.5 k
EEG044 (U)	🟨	9.4 k
EEG045 (U)	🟨	7.2 k
EEG046 (U)	🟨	8.9 k
EEG047 (U)	🟦	?
EEG048 (U)	🟨	13.5 k
EEG049 (U)	🟨	7.8 k
EEG050 (U)	🟨	5.8 k
EEG051 (U)	🟨	6.4 k

The impedance measurement is started and stopped by clicking on the check-box at the left upper corner of the dialog. When the impedance measurement is started EEG system starts feeding probe currents to the electrodes and measures the resulting voltages. The amplitudes of the voltages are then converted to impedance values and shown on the dialog.

The display uses color coding to indicate the resistance as high = red, intermediate = yellow, low = green, and unrecognized behavior is indicated in blue. By default, low resistance is below 5 kOhm for unipolar EEG channels and below 75 kOhm for the bipolar ones. High resistance is over 20 kOhm for unipolar EEG channels and over 100 kOhm for bipolar ones.

Note: Currents are fed to the electrodes during the impedance measurement. This prevents making normal EEG measurements while the impedance measurement is on.

5.7. Stopping the acquisition

When you have collected the desired number of responses into the averages and you have collected all necessary raw data, press **Stop** to finish the acquisition. If on-line evoked-response averaging was requested, the save dialog for evoked-response data will appear automatically once all data have been processed. After the evoked-response data are stored, a dialog prompting for the raw data file name will appear if any raw data were collected.

If you choose not to save either data, the system will emit a “last chance” message when starting a new measurement which would destroy these data.

See Section 6.2. “Saving averages and raw data” on page 43 for details about saving your data.

6. SAVING DATA

6.1. Data volumes

Acquired data are saved to one of the predefined data volumes. Under the volume top level directory, the data files will be stored in

<project>/<last name>_<first name>/<date>,

if you are studying a volunteer, or

<project>/case_*<id>*/*<date>*

if your subject is a patient, as explained in Section 3.2.2.

If no subject name has been selected, the subject part of the path will be no_name.

The saving paths can be tailored according to local needs by MEGIN Customer Care.

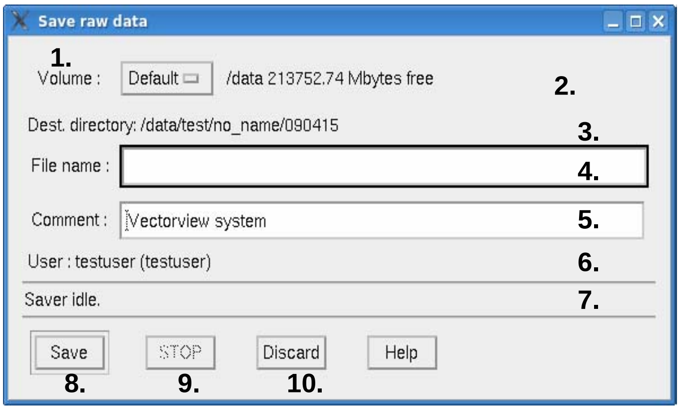
6.2. Saving averages and raw data

If any on-line averages were computed or raw data was recorded, a saving dialog appears automatically. The user is first prompted for saving averages, if any. In this case the dialog is titled **Save evoked responses**. The user is then prompted for saving raw data, if any. In this case the dialog is (re)titled **Save raw data**.

Saving is done in background. Therefore, you can continue with the next acquisition while saving of previously acquired raw data is still in progress. You can iconify the data saving window.

If the recorded raw data file size becomes larger than a predefined value (in normal configuration 2GB minus 100MB), the data file is closed and a new continuation file is created. The exact size of the file can vary somewhat depending on how the internal blocks exceed the limit. When this kind of a split measurement is saved, the first segment is given the name which user writes into the saving dialog. Rest of the segments have the same name with a dash and a running number appended (numbering starts from one).

6.3. The saving dialog


Save raw data

Volume : Default /data 213752.74 Mbytes free

Dest. directory: /data/test/no_name/090415

File name :

Comment : Vectorview system

User : testuser (testuser)

Saver idle.

The saving dialog has the following components:

1. An option menu to select the destination volume.
2. The root pathname of the selected volume and the amount of free space on the volume.
3. The destination directory for the data.
4. A text field to enter the destination file name. Use only letters, numbers and the underscore character in the file name. The suffix .fif is appended automatically.
5. A text field to enter a comment to go with the data.
6. Real and login name of the current user, which are saved with the data.
7. Status line indicating the state of saving.
8. **Save** button to start saving.
9. **Stop** button to interrupt saving.
10. **Discard** button to discard the averages or raw data.

6.4. Rescuing data after a crash

If you have collected data but *megacq* has ceased to work after you pressed **Stop**, you can rescue your data by selecting the **Rescue Data** icon in the **Maintenance** folder.

If there is data that can be saved, you will first see a confirmation dialog that you would really like to proceed, as shown below:

This command should only be used after the acquisition program has crashed. The acquisition should not be restarted until this command has completed.

There are 2 evoked data file(s).
There are 1 raw data file(s).

Should we continue?

Thereafter, a standard *megacq* saving dialog (see Section 6.3) will appear. Note that the rescued data will be saved under the project directory called unknown if the real project name could not be retrieved.

7. RESTARTING THE SOFTWARE

7.1. When to restart

The data acquisition may under some circumstances either stop prematurely or freeze with the following symptoms:

1. *Megacq* becomes non-responsive for a long time. When windows covering *megacq* are moved, the exposed areas are not repainted.
2. When *megacq* is started it fails to contact the data server.

Most common reasons for this are networking problems. You can recover the system by restarting the acquisition software modules.

If the front-end DSP boards hang up, a complete power cycle is not normally required. It is enough to stop the acquisition program (*megacq*), reset the DPS boards, and restart the acquisition program again. The DSP boards are reset by pressing the Reset button on the SCC board panel and waiting until all DSP boards boot-up to green Run-status.

7.2. Restarting procedure

1. Open the **Maintenance** folder under **Neuromag** folder in the desktop's applications menu to see the available actions.
2. Select the **Restart Acquisition Programs** icon.
3. Confirm that you really want to proceed by answering y to the question appearing in the **Restart Acquisition Programs** terminal window.
4. Observe the messages in the window during the restarting. Should the restart operation fail, verify all physical power and data connections as well as network connections.
5. Wait until the message

   ```
   Restart complete. Press <Enter> to close the window
   ```

   appears and press <Enter>.
6. If you had collected data and *megacq* ceased to work after you pressed **Stop**, you can rescue your data by double-clicking the **Rescue Data** icon in the **Maintenance** folder.

   If there is some data to be saved, you will first see a dialog to confirm that you would really like to proceed. Thereafter, a standard *megacq* saving dialog (see Section 6.3) will appear. Note that the rescued data will be saved under the project directory called unknown if the real project name could not be retrieved.
7. Restart *megacq* by selecting the **Acquisition** icon in the **Neuromag** folder.
8. If you have completed the HPI digitization, you will be given a chance to use the HPI data again. Alternatively, you can use **Load preparation** in the **File** menu which allows quick restoration of the previous setup of the acquisition software.
9. Reload the SQUID tuning file (with Tuner) if the power-up tuning settings are not optimal.

8. USING SIGNAL SPACE PROJECTION

8.1. Background

External magnetic disturbances which have fairly uniform distribution but varying amplitudes can be suppressed by the signal space projection (SSP) technique.

The measured signals span a signal space whose dimension equals the number of channels *n* being measured. Thus, at each sampling point in time, the signals can be described as a vector in the signal space. For a given distribution or field topology the signal vector points to the same direction but its length varies as the amplitudes of the signals change. Once the distribution(s) corresponding to a disturbance are known a suppressing SSP operator can be constructed from the distributions. The operator projects each sample vector in the signal space so that the disturbance becomes orthogonal to the *n*-1 dimensional hyperplane in the signal space and thus disappears. The drawback is losing one degree of freedom, *i.e.*, one independent measurement, and the slight deformation of response patterns if viewed without a subsequent reconstruction.

Since the topology of external disturbances at a particular site is typically constant to a good approximation, it is not necessary to define the SSP operator individually for each measurement, if the magnetometer probe is at a fixed location and orientation. The system selects automatically the SSP operator from a predefined set of operators depending on the gantry position and whether internal active shielding is being used.

The data are always stored intact, but the operator is included in the data files, so that various data viewers and analysis programs can take it into account, or at request, show the non-projected original data. Note however, that if MaxFilter™ is applied to the data files, it removes the SSP vectors from the resulting filtered data files, as the SSS processing (by MaxFilter™) and applying SSP vectors are complementary methods for artifact removal.

8.2. SSP and the on-line averager

Since averaging and projection are both linear operations and thus commute, projection can also be done to the final average. The on-line averager attaches the SSP operator to the output average file but leaves the actual signal intact, i.e., un-projected. The visualization software is responsible for applying the SSP operator to the data.

The rejection checking of the on-line averager, however, uses SSP-filtered data.

8.3. Creating SSP operators

8.3.1. Locations of the SSP files

The SSP operator used by the system is defined in a FIFF file. Exactly which file is used depends on the gantry position angle (0 for supine, 60 for semi-upright, 68 for upright), and whether Internal Active Shielding (IAS) is being used. The SSP operators are loaded from

`/neuro/dacq/setup/ssp/online_0.fif`,
`/neuro/dacq/setup/ssp/online_60.fif`, or
`/neuro/dacq/setup/ssp/online_68.fif`,
when the system does not have IAS or it is turned off, or from
`/neuro/dacq/setup/ssp/online_0_ias.fif`,
`/neuro/dacq/setup/ssp/online_60_ias.fif`, or
`/neuro/dacq/setup/ssp/online_68_ias.fif`,

when IAS is turned on.

If that file does not exist or if it does not contain an SSP operator, the on-line SSP is silently turned off.

8.3.2. Pre-requisites

The following procedure requires Data Analysis software, which must be installed to the workstations where the SSP files are generated.

8.3.3. Procedure

1. Tune all the channels. Make a note of extremely noisy or nonfunctional channels.
2. Do a set of “empty room” measurements. Use 1000 Hz sampling frequency, 330 Hz low-pass and 0.1 Hz high-pass filtering. Record raw data for about two minutes in all gantry positions (separately both with Internal Active Shielding turned off and on). Save the raw data files with names like `empty_room_0.fif` and `empty_room_0_ias.fif`, where the gantry angle 0 is replaced with 60 or 68 depending on the gantry position.
3. Start the Signal processor (graph) program. Load or create a Graph setup, which includes at least the ssp and pca packages in addition to the basic setup. These additional modules can be loaded by the lisp commands

   ```
   (require "pca")
   (require "ssp")
   (require "std-selections")
   ```

   Create and connect the widgets as follows (the *type* of the widget is in parenthesis and the name you should give to the widget is before the parenthesis):

   file(diskfile) > buffer(ringbuffer) > meg(pick) >

   ssp(suppressor) > pick(pick) > display(plotter)

   Change the buffer size of ssp widget by double-clicking its icon: Enter 20000 (the default is 2000, which is too low). Increase also the buffer size of the buffer widget to 1000000 to speed up the processing.
4. To calculate the SSP operator for gradiometers, change the **names** resource of the meg widget to `MEG*` and **ignore** to `MEG*1`. This retains the original order of the gradiometer channels in the data file.

   Open the raw data file

   `empty_room_0.fif`

   Add the bad channels, if any, as ignored channels so that they won't spread the noise to the good channels via the SSP. Use **Selections** menu to display and browse through the channel sets of interest. You may want to enable the **superpose** function of the display widget for a better view.

   Enter the lisp command

   ```
   (pca-on-widget 'meg 0 120)
   ```

   to calculate the principal components for the time span 0 …120 seconds since the beginning of the file. Once the PCA calculation is complete, select **SSP dialog...** from the **Commands** menu. In SSP dialog select **Add PCA fields** from the **Actions** menu, then select **8 vectors**. You should get an entry like PCA[204,8] in the vector pool. Select it by clicking it and do **Explode** from the **Edit** menu. Now you can apply the vectors one at a time by first selecting the vector (start from PCA-v1 as it is the one corresponding to the largest singular value) and then clicking the right arrow, which copies the vector to the SSP vector panel. The suppressor automatically turns on once there is at least one vector assigned for it. You should see a decreasing noise level on the display as you keep on adding vectors.

Once you have decided how many and which vectors you need, delete the rest ALSO from the vector pool! Then select **Save** from **File** menu and specify file name

```
/neuro/dacq/setup/ssp/grad_ssp_0.fif
```

Generally, 5 vectors for magnetometers seem to be enough in most cases, and 0 … 3 vectors for gradiometers. Using more vectors, of course, make the raw data look better but they unnecessarily attenuate brain signals as well and complicate analysis. So, do not use more vectors than necessary.

Select a short time span (less than one second) of raw data on the display with the right mouse button. Select **Make evoked file** from **File** menu and specify file name

```
/neuro/dacq/setup/ssp/grad_names_0.fif
```

5. Open a terminal window. Do

```
cd /neuro/dacq/setup/ssp
```

```
/neuro/bin/util/add_proj_namelist -f
    grad_names_0.fif grad_ssp_0.fif
```

This operation adds the channel names to the SSP vectors. The second command is a single command line, though it is here divided on two line.

6. You may now repeat steps 4. and 5. for magnetometers. Of course, delete the previous SSP vectors both from the pool and SSP panels. Set **names** resource of the meg widget to `MEG*1` and remove `MEG*1` from **ignore** before doing the PCA for the magnetometers. Save the results to files

```
/neuro/dacq/setup/ssp/mag_ssp_0.fif
```

```
/neuro/dacq/setup/ssp/mag_names_0.fif
```

7. Combine the gradiometer and magnetometer SSP operators in the Source modelling program (xfit).

Open an evoked response file which has data from all channels (both magnetometers and gradiometers if you are going to do the operator for both types of sensors.) Open the **Projection** window and use **Load** in **File** menu to load your newly created

```
/neuro/dacq/setup/ssp/grad_ssp_0.fif
```

and

```
/neuro/dacq/setup/ssp/mag_ssp_0.fif
```

Check the **Allow measurement ID mismatch** before loading the above files.

Select all the SSP vectors in the projection list. Select **Save** from **File** menu and specify file name

```
/neuro/dacq/setup/ssp/online_0.fif
```

8. Change the file permissions

```
cd /neuro/dacq/setup/ssp
```

```
chmod 644 online_0.fif
```

9. Test the new SSP operator by starting the acquisition such that the gantry angle and the IAS state match the file created in step 7. Checking the signals on the raw data display with the **Apply SSP** button in the **Scales** window on and off. If the button is insensitive (i.e. you cannot click it), the SSP vectors were not found or were unreadable.
10. Repeat the steps 4. through 9. with the raw data file `empty_room_0_ias` (same gantry position and IAS turned on). Remember to replace `_0` with `_0_ias` also in the other file names.
11. Repeat the steps 4. through 10. with the raw data from the other gantry positions. Remember to replace the gantry angle 0 with 60 for semi-upright and 68 for upright in the file names.

9. PHANTOM MEASUREMENT

9.1. Introduction

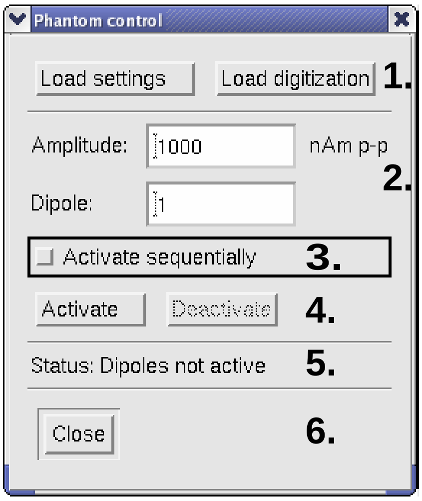
The basic operation of the system is typically easily verified by running a phantom test. The default configuration of the Data Acquisition Software Release 6.0 includes phantom test setup files for standard Phantom (Art. no. NM24058N). If another phantom is used, the process may be customized for the particularities with the instructions in Section 9.5.

The automated phantom protocol switches on the dipoles inside the phantom sequentially and records the resulting signal. The resulting file must then be analyzed to establish that the system has functioned as expected. This chapter does not discuss the details of this analysis, see e.g. documents *TRIUX User's Manual* or *TRIUX™ neo Instructions for Use* for full details.

The automated phantom protocol can be used for the following two purposes: (1) verifying the operation of the full system, or (2) verifying the operation of the magnetometer probe only.

9.2. Phantom control tool user interface

The user interface parts are shown and described below:



Amplitude: 1000 nAm p-p

Dipole: 1

☐ Activate sequentially

Status: Dipoles not active

The dialog contains the following items:

1. Buttons for loading the measurement settings for the phantom protocol, and loading up a pre-digitization of the phantom head.
2. Text fields for specifying the dipole amplitude and the starting dipole of the sequence.
3. A checkbox for selecting automatic dipole changing sequence or no sequence (one individual dipole activated only).
4. Activate and deactivate buttons for the dipole operation.
5. A message line containing the phantom's current status.
6. A close button for closing the phantom control dialog.

9.3. Procedure for system verification

1. Start the **Acquisition** control software from **Neuromag** folder in the desktop's applications menu.
2. Select a suitable project (e.g. Verification tests).
3. Select a suitable subject (e.g. Phantom)

4. Select **Phantom...** in the **Tools** menu.
5. Click on **Load settings** in the phantom control tool.
6. Verify that the amplitude is the desired (the default 1000 nAm pp is used in the Phantom test protocol)
7. Select **Change** in the acquisition control software to start and perform the head digitization in a normal fashion. Finally close the head digitization.
8. Click on **GO!** to start measuring.
9. Click on **Measure** in the HPI measurement dialog.
10. Check the HPI coil locations in the HPI results dialog and, if the HPI fitting was successful, click on **Accept** and proceed to next step. Otherwise click on **Try again** and redo this step.
11. Back at the phantom control tool, specify the first dipole to fire, if 1 is not suitable.
12. Select **Activate sequentially.**
13. Click on **Activate**.
14. Select **Average** in the acquisition control software.
15. Observe the progress of the phantom measurement in signal trace curves in the raw data display window and also the averaging progress on the acquisition control software's status lines.
16. The phantom measurement deactivates automatically at the end of the defined sequence, or you can click on **Deactivate** to stop it prematurely.
17. Click on **Stop** in the acquisition control software.
18. Save the resulting files to a suitable location.
19. Analyze the resulting files according to the phantom analysis instructions given in *TRIUX User's Manual* or in *TRIUX™ neo Instructions for Use*.

9.4. Procedure for probe verification

Follow the procedure described above for full system verification otherwise but at step 5, also click on **Load digitization** in the phantom control tool. Also skip step 7, the head digitization, altogether. This way you will use the pre-made digitization files and are able to quickly determine the functioning of the magnetometer probe.

9.5. Customizing the phantom measurement

The measurement settings for a phantom measurement are loaded from `phantom.set` file in `/neuro/dacq/setup/phantom`. The head digitization file is loaded from `phantom.iso` in the same directory. These two files can be modified to adapt the phantom sequence to the phantom hardware used.

The `phantom.set` file contains a subset of the settings found in a standard settings file saved with acquisition control software's **Save settings** feature. Only the settings beginning with ERF prefix from such a regular settings file should be included in the `phantom.set` file.

The head digitization file is easily created by digitizing the phantom in a normal fashion and then copying the resulting digitization file from `/neuro/dacq/meas_info` into `/neuro/dacq/setup/phantom` directory and then re-linking the `phantom.iso` symbolic link to point to this digitization file.

Depending on your phantom hardware you should also set the *phantomCal* value in `/neuro/dacq/setup/collector/conf/collector.defs`. See the commentary in that file for details on how to determine this value.

APPENDIX A Error messages

This appendix gives descriptions for the error messages that can be expected to be delivered by the software. It is possible that other messages are also given if there are design errors or the software is otherwise brought to a state that is not anticipated by the designers. Please consider contacting MEGIN Customer Care if such error messages occur.

The messages are given in two tables below. The first one provides the error messages given by the data acquisition control module. The second one provides the errors messages produced by the measurement front end. The messages in the latter ones are often referenced in the messages given in the first table.

Variable parts of the messages are denoted by text enclosed by < and > characters. For example <*number*> means, that there is some number in the message at this point. The menu and dialog items are separated by **>** characters. For example menu entry **File > Save settings** means **Save settings** -button in the **File** menu.

Table 1:

Context	Error message	Description	Actions
Any time	<program_name> (pid = <number>) died due to signal <number>) [core dumped]	A software component has stopped unexpectedly. The <number> after 'pid =' is the process number in the system and the signal number is the reason why the program was terminated. These errors usually mean that something unexpected has happened.	If the error repeats, please contact MEGIN Customer Care.
Any time	<program_name> (pid = <number>) terminated with <number>.	A software component has stopped on purpose or unexpectedly. The <number> after 'pid =' is the process number in the system and the signal number is the reason why the program was terminated. These errors usually mean that something unexpected has happened.	If the unexpected termination repeats, please contact MEGIN Customer Care.
Any time	<program_name> (pid = <number>) terminated unexpectedly	A software component has stopped unexpectedly. The <number> after 'pid =' is the process number in the system and the signal number is the reason why the program was terminated. These errors usually mean that something unexpected has happened.	If the error repeats, please contact MEGIN Customer Care.
Any time	Tried to send to a closed connection	System is not up properly, some software components are not running.	Please restart the acquisition system.
Any time	Collector not connected!	System is not up properly, some software components are not running.	Please restart the acquisition system.
Any time	Collector conversation failed: <error>!	Collector communication failed.	Check that collector is running.
Any time	Get collector status command failed: <error>	Collector communication failed.	Check that collector is running.
Any time	Could not get collector status: <error>	Collector returned an invalid status response.	Contact MEGIN Customer Care.
Any time	xplotter command <command> failed in <context>: <error>	Xplotter communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.

Table 1:

Context	Error message	Description	Actions
Starting acquisition program	Opening <path>/licenses.neuromag: <system error>	License file cannot be loaded.	Please contact the local administrator.
Starting acquisition program	There is no license for you. Sorry.	There is no license to run this version of acquisition program.	Please contact MEGIN Customer Care to obtain necessary licenses.
Starting acquisition program	<name>.vars: <system error>	Variable definitions file cannot be loaded.	Please contact MEGIN Customer Care.
Starting acquisition program	<name>.defs: <system error>	Variable settings file cannot be loaded.	Please contact MEGIN Customer Care.
Starting acquisition program	NM_DEVICE is not set	Internal error in configuration of the system.	Please contact MEGIN Customer Care.
Starting acquisition program	NM_DEVICE is unknown: <device_name>	Internal error in configuration of the system.	Please contact MEGIN Customer Care.
Starting acquisition program	<path>/prepared/index: <system_error>	Preparations database cannot be updated.	Please contact MEGIN Customer Care.
Starting acquisition program	Could not get collector host.	Internal error in configuration of the system	Please contact MEGIN Customer Care.
Starting acquisition program	Could not contact collector.	The front end of the system has probably not been started or has terminated.	Restart acquisition programs. If this does not help, please contact MEGIN Customer Care.
Starting acquisition program	Could not login to collector.	Internal error in configuration of the system.	Please contact MEGIN Customer Care.
Starting acquisition program	Could not connect to data server!	Internal error in configuration of the system.	Please contact MEGIN Customer Care.
Starting acquisition program	Could not initialize acquisition.	Possible reasons: out of resources, collector communication failed, invalid or missing configuration variable. More detailed error message can be found in megacq.log file.	Restart acquisition programs. If this does not help, reboot the workstation. If this does not help, please contact MEGIN Customer Care.
Starting acquisition program	Could not initialize averaging.	Possible reasons: out of resources, invalid or missing configuration variable. More detailed error message can be found in megacq.log file.	Restart acquisition programs. If this does not help, reboot the workstation. If this does not help, please contact MEGIN Customer Care.
Starting acquisition program	Could not read Isotrak: <error>	Internal error. Cannot access digitization data.	Check that /neuro/dacq/meas_info does not contain file isotrak that is owned by some unexpected owner.
Main window > Change project	<path>/projects/index: <system error>	Projects database cannot be loaded.	Please contact MEGIN Customer Care.
Main window > Change subject button	<path>/subjects/index: <system error>	Subjects database cannot be loaded.	Please contact MEGIN Customer Care.

Table 1:

Context	Error message	Description	Actions
Main window > Change acquisition	Changing the states of the electric channels may invalidate the digitization of the EEG electrode locations.	Digitization of the electrodes is made according to the EEG channel selections. If you change this setup after digitization, the settings may become incompatible with the digitization!	Either do not change the EEG settings or redo the digitization.
Main window > Change HPI button	Isotrak hemisphere definition variable not set!	System configuration is invalid.	Please contact MEGIN Customer Care.
Main window > Change HPI button	Illegal Isotrak hemisphere definition: <HEMI>	System has invalid configuration.	Please contact MEGIN Customer Care.
Main window > Change gantry button	Get gantry position command failed: <error>	Collector communication failed.	Check that collector is running.
Main window > Change gantry button	Could not get gantry position: <response>	Collector returned an error response.	Check that all cables are connected. Contact MEGIN Customer Care.
Menu 'File > Save preparation	'Please select project first.	Preparations are stored per project. To save the preparation some project must be set.	Please select a project and then retry.
Menu 'File > Save preparation	'<name>.set: <system error>	The contained settings file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Menu 'File > Save preparation	'<name>.sti: <system error>	The contained stimulus file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Menu 'File > Save preparation	'Could not store project data (status=<exit code>).	The contained project file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Menu 'File > Save preparation	'Could not store subject data (status=<exit code>).	The contained subject file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Menu 'File > Save preparation	'Could not store Isotrak data (status=<exit code>).	The contained isotrak file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Menu 'File > Save preparation	'<path>/prepared/index: <system error>	Preparations database cannot be updated.	Please contact MEGIN Customer Care.
Menu 'File > Load settings	'Please select project first.	Settings are stored per project. To save the settings, some project must be set.	Please select a project and then retry.
Menu 'File > Load settings	'<path>/settings/index: <system error>	Settings database cannot be loaded.	Please contact MEGIN Customer Care.

Table 1:

Context	Error message	Description	Actions
Menu 'File > Load settings	'No settings available [for this project]	Settings database does not contain any entries for current project.	If no settings have been saved so far, you can ignore this message. Otherwise contact MEGIN Customer Care.
Menu 'File > Load preparations	'<path>/prepared/index: <system error>	Preparations database cannot be loaded.	Please contact MEGIN Customer Care.
Menu 'File > Load preparations	'No normal preparations available	Preparations database does not contain any entries.	If no preparations have been saved so far, you can ignore this message. Otherwise contact MEGIN Customer Care.
Menu 'File > Save settings	'Please select project first.	Settings are stored per project. To load settings, some project must be set.	Please select a project and then retry.
Menu 'File > Quit	There are <number> files being saved in background. Cannot quit yet!	Some measurement data has not yet been saved.	Please wait for savers to complete (or cancel them).
Menu 'Help > On version	'Warning! This is a beta-test version of the data acquisition...	This acquisition program has not been officially released.	Do not use this software for clinical purposes.
Menu 'Online > Update average display	'to_averager: <error>	Averager communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Load preparations dialog	Cannot load preparation when measurement is running.	Cannot change measurement settings whilst measurement is running.	Stop the measurement and load the new settings.
Load preparations dialog	Nothing selected	Selection field is empty.	Select preparation to be loaded.
Load preparations dialog	<name>.set: <system error>	The contained settings file cannot be loaded. The system error message <system error> provides more information about the underlying reason.	Check that the preparation file exists and is readable by you.
Load preparations dialog	Cannot get stimuli file from variable.	Settings file does not contain name of stimulus file.	Please contact MEGIN Customer Care.
Load preparations dialog	<name>.sti: <system error>	The contained stimulus file cannot be loaded.	Check that the directory /neuro/dacq/settings exists and is readable by you.
Load preparations dialog	Illegal data in stimulus file!	Stimulus file is of wrong format.	Please contact MEGIN Customer Care.
Load preparations dialog	<name>.proj: <system error>	The contained project file cannot be loaded.	Check that the file exists and is readable by you.
Load preparations dialog	No project id in <name>.proj	Project file does not contain project id tag.	Please contact MEGIN Customer Care.
Load preparations dialog	<name>.subj: <system error>	The contained subject file cannot be loaded.	Please contact MEGIN Customer Care.

Table 1:

Context	Error message	Description	Actions
Load preparations dialog	No subject id in <name>.subj	Subject file does not contain subject id tag.	Please contact MEGIN Customer Care.
Load preparations dialog	Subject mode cannot be determined	Subject file attributes cannot be used to determine whether subject is patient or volunteer.	Please contact MEGIN Customer Care.
Load preparations dialog	Could not restore Isotrak data (status=<exit code>)	The contained isotrak file cannot be loaded.	Check that the file exists and is readable by you.
Load preparations dialog	Could not read Isotrak: <error>	Isotrak file does not contain isotrak information.	Please contact MEGIN Customer Care.
Load preparations dialog	Could not restore hpi_meas data (status=<exit code>)	The contained HPI measurement file cannot be loaded	Please contact MEGIN Customer Care.
Load preparations dialog	Could not restore hpi_result data (status=<exit code>)	The contained HPI measurement file cannot be loaded	Please contact MEGIN Customer Care.
Load settings dialog > Apply	Nothing selected	Selection field is empty.	Select settings to be loaded.
Load settings dialog > Apply	<name>.set: <system error>	Settings file cannot be loaded.	Check that the file exists and is readable by you.
Load settings dialog > Apply	Cannot get stimuli file from variable.	Settings file does not contain name of stimulus file.	Please contact MEGIN Customer Care.
Load settings dialog > Apply	<name>.sti: <system error>	Stimulus file cannot be loaded.	Check that the file exists and is readable by you.
Load settings dialog > Apply	Illegal data in stimulus file!	Stimulus file is of wrong format.	Please contact MEGIN Customer Care.
Load settings dialog > Delete	Nothing selected	Selection field is empty.	Select settings to be deleted.
Load settings dialog > Delete	<path>/settings/index: <system error>	Settings database cannot be updated.	Check that the file exists and is writable by you.
Load settings dialog > Delete	No settings available [for this project]	Settings database no longer contains any entries for current project.	Informative, not actions needed.
Save settings dialog > Save	Settings name is empty.	Name field is empty.	Enter the name of the settings file.
Save settings dialog > Save	<name>.set: <system error>	Settings file cannot be created. Invalid system configuration or out of resources.	Check that the directory /neuro/dacq/settings exists and is writable by you.
Save settings dialog > Save	<name>.sti: <system error>	Stimulus file cannot be created. Invalid system configuration or out of resources.	Check that the directory /neuro/dacq/settings exists and is writable by you.
Save settings dialog > Save	<path>/settings/index: <system error>	Settings database cannot be updated.	Check that the directory /neuro/dacq/settings exists and is writable by you. Check that the index is writable.

Table 1:

Context	Error message	Description	Actions
Load measurement settings dialog > OK	Load file not specified.	Selection field is empty or ends with '/'.	Enter the name of a data file.
Load measurement settings dialog > OK	Selection is <not valid | a directory | a special file>.	Selection field should contain a valid existing filename.	Enter name of a proper data file.
Load measurement settings dialog > OK	<name>.fif: <system error>	Selected file cannot be loaded.	Check that the file exists and is readable by you.
Load measurement settings dialog > OK	No settings available here	Selected file does not contain settings tag.	Please contact MEGIN Customer Care.
Load measurement settings dialog > OK	<name>.set: <system error>	Temporary settings file cannot be created. Invalid system configuration or out of resources.	Check that the directory /neuro/dacq/settings exists and is writable by you.
Load measurement settings dialog > OK	Cannot get stimuli file from variable.	Settings file does not contain name of stimulus file.	Please contact MEGIN Customer Care.
Load measurement settings dialog > OK	<name>.sti: <system error>	Temporary stimulus file cannot be created. Invalid system configuration or out of resources.	Check that the directory /neuro/dacq/settings exists and is writable by you.
Load measurement settings dialog > OK	Illegal data in stimulus file!	Stimulus file is of wrong format.	Please contact MEGIN Customer Care.
Set bad channels dialog > OK	<path>/tmp/erf.evp: <system error>	Averaging parameter file cannot be created. Invalid system configuration or out of resources.	Check that the directory <path>/tmp exists and is writable by you.
Set bad channels dialog > OK	to_averager: <error>	Averager communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Select categories dialog > OK	<path>/tmp/erf.evp: <system error>	Averaging parameter file cannot be created. Invalid system configuration or out of resources.	Check that the directory <path>/tmp exists and is writable by you.
Select categories dialog > OK	to_averager: <error>	Averager communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Phantom dialog > Load settings	<path>/phantom/phantom.set: <system error>	Phantom settings file cannot be loaded.	Check that the file exists and is readable by you.
Phantom dialog > Load digitization	Could not restore Isotrak data (status=<exit code>)	Phantom isotrak file cannot be loaded.	Please enter a valid amplitude

Table 1:

Context	Error message	Description	Actions
Phantom dialog > Load digitization	Could not read Isotrak: <error>	Isotrak file does not contain isotrak information.	Please enter a valid amplitude
Phantom dialog > Activate	Amplitude is not a valid floating point value!	Invalid value was given.	Please enter a valid amplitude
Phantom dialog > Activate	Amplitude is not in range 5.0 .. 10000.0!	Invalid value was given.	Please enter a valid amplitude
Phantom dialog > Activate	Dipole number is not a valid integer value!	Invalid value was given.	Please enter a valid dipole number
Phantom dialog > Activate	Dipole number is not in range 1 .. 32!	Invalid value was given.	Please enter a valid amplitude
Phantom dialog > Activate	Send activate phantom failed: <error>	Collector communication failed.	Check that collector is running.
Phantom dialog > Activate	Bad activate phantom response: <response>	Collector returned an error response.	Please enter a valid amplitude
Phantom dialog > Deactivate or Close	Send deactivate phantom failed: <error>	Collector communication failed.	Check that collector is running.
Phantom dialog > Deactivate or Close	Bad deactivate phantom response: <response>	Collector returned an error response.	Please enter a valid amplitude
Project dialog > Existing project selected	<name>.proj: <system error>	Project file cannot be loaded.	Check that the file exists and is readable by you.
Project dialog > OK	Current project is not valid	Error occurred when this project was selected for editing.	Check that the project name is correct.
Project dialog > OK	<name>.proj: <system error>	Project file cannot be created. Invalid system configuration or out of resources.	Please contact MEGIN Customer Care.
Project dialog > OK	<path>/projects/index: <system error>	Projects database cannot be updated.	Check that the file exists and is writable by you.
Subject dialog > Subject type selected	<path>/subjects/index: <system error>	Subjects database cannot be loaded.	Check that the file exists and is writable by you.
Subject dialog > Existing subject selected	stat: <system error>	Subject file does not exist.	Please contact MEGIN Customer Care.
Subject dialog > Existing subject selected	Subject mode cannot be determined	Subject file attributes cannot be used to determine whether subject is patient or volunteer.	Please contact MEGIN Customer Care.
Subject dialog > Existing subject selected	<name>.subj: <system error>	Subject file cannot be loaded.	Check that the file exists and is readable by you.
Subject dialog > OK	Current subject is not valid	Error occurred when this subject was selected for editing.	Check that the subject name is correct.

Table 1:

Context	Error message	Description	Actions
Subject dialog > OK	We can study only persons born in or after year 1900	For technical reasons the birth date is limited to years after 1900.	Check that the birth date is correct.
Subject dialog > OK	There are only 12 months in a year!	The month value is invalid. Please enter a valid one.	Check that the birth date is correct.
Subject dialog > OK	Illegal day of month!	The day value is invalid. Please enter a valid date.	Check that the birth date is correct.
Subject dialog > OK	Julian date is too big!	This error can occur if the date is unreasonable, very long in the future or the past.	Check that the birth date is correct.
Subject dialog > OK	<name>.subj: <system error>	Subject file cannot be created. Invalid system configuration or out of resources.	Check that the directory /neuro/databases/subjects exists and is writable by you.
Subject dialog > OK	<path>/subjects/index: <system error>	Subjects database cannot be updated.	Check that the file exists and is writable by you.
Stimulus load dialog > OK	Internal stimulus not selected.	Stimulus kind was changed to External after this dialog was launched.	If usage of external stimulus is intentional, no actions are needed. Otherwise change the stimulus kind to 'Internal' and load the stimulus settings again.
Stimulus load dialog > OK	Load file not specified.	Selection field is empty or ends with '/'.	Please enter the name of the stimulus file.
Stimulus load dialog > OK	Selection is <not valid | a directory | a special file>.	Selection field should contain a valid existing filename.	Please enter name of a valid stimulus file.
Stimulus load dialog > OK	<name>.sti: <system error>	Stimulus file cannot be loaded.	Check that the file exists and is readable by you.
Stimulus load dialog > OK	Illegal data in stimulus file!	Stimulus file is of wrong format.	Please enter name of a valid stimulus file.
Stimulus save dialog > OK	Internal stimulus not selected.	Stimulus kind was changed to External after this dialog was launched.	Change stimulus kind back to 'Internal' and try to save again.
Stimulus save dialog > OK	Save file not specified.	Selection field is empty or ends with '/'.	Please enter the name of the stimulus file.
Stimulus save dialog > OK	Selection is <not valid | a directory | a special file>.	Selection field should contain a valid filename.	Please enter name of a valid stimulus file.
Stimulus save dialog > OK	<name>.sti: <system error>	Stimulus file cannot be created. Permission denied or out of resources.	Check that the directory /neuro/dacq/stim exists and is writable by you.
Averaging editor > OK	<path>/tmp/erf.evp: <system error>	Averaging parameter file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Averaging editor > OK	to_averager: <error>	Averager communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.

Table 1:

Context	Error message	Description	Actions
Digitizing	Head digitization was cancelled.	Digitization was cancelled.	Informative, no actions needed.
Digitizing	Could not restore Isotrak data (status=<exit code>)	The created isotrak file cannot be loaded.	Please contact MEGIN Customer Care.
Digitizing	Could not read Isotrak: <error>	Isotrak file does not contain isotrak information.	
Starting measurement	Data saving is pending, waiting for timeout	Saving data from previous measurement is blocking the start of a new measurement.	Please wait until evoked responses file and all raw data files from the previous measurement have been handed over to a saver program.
Starting measurement	Data saving is pending, waiting for evoked!	Saving data from previous measurement is blocking the start of a new measurement.	Please wait until evoked responses file and all raw data files from the previous measurement have been handed over to a saver program.
Starting measurement	Data saving is pending, waiting for raw data!	Saving data from previous measurement is blocking the start of a new measurement.	Please wait until evoked responses file and all raw data files from the previous measurement have been handed over to a saver program.
Starting measurement	Project name undefined!	Many operations are project related, and the project must be set before a measurement can be performed.	Please select a project and then retry.
Starting measurement	No selected channels!	Cannot make a measurement where no channels are measured.	Please select some channels and then retry.
Starting measurement	Get gantry position command failed: <error>	Collector communication failed.	Check that collector is running.
Starting measurement	Could not get gantry position: <response>	Collector returned an error response.	Check that all cables are connected. Contact MEGIN Customer Care.
Starting measurement	<name>.set: <system error>	The contained settings file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Starting measurement	<name>.sti: <system error>	The contained Stimulus file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Starting measurement	Could not store project data (status=<exit code>).	The contained project file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Starting measurement	Could not store subject data (status=<exit code>).	The contained subject file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.

Table 1:

Context	Error message	Description	Actions
Starting measurement	Could not store Isotrak data (status=<exit code>).	The contained isotrak file cannot be created. Invalid system configuration or out of resources.	Check that the disk is not full.
Starting measurement	<path>/prepared/index: <system error>	Preparations database cannot be updated.	Check that /neuro/dacq/prepared/index is accessible.
Starting measurement	<ftok | semget>: <system error>	Internal system error. Semaphores are not configured properly.	Reboot the system. If the error repeats, please contact MEGIN Customer Care.
Starting measurement	Tuning in progress!	Tuner is running.	Please stop the tuner first and then start the measurement.
Starting measurement	Previous measurement is still running!	A measurement is running while trying to start new one. This probably indicates that there is some external measurement tool being used..	Stop any tools making measurements.
Starting measurement	Could not set up parameters!	Could not send parameter values to collector.	Check that collector is running.
Starting measurement	Could not set up stimuli!	Could not send stimulus sequences to collector.	Check that collector is running.
Starting measurement	Could not set up collector completely! Some functionality is missing.	Collector setup failed in manner that enables the system to run, but some functionality is missing.	Check that all acquisition hardware components are up and running.
Starting measurement	Could not set up data collector!	Could not setup collector.	Check that collector is running.
Starting measurement	The old HPI program is still running.	System is in unexpected state.	Please restart the acquisition software. If problem continues, contact MEGIN Customer Care.
Starting measurement	Cannot do HPI : No HPI coils in Isotrak file!	Internal system error. Corrupted digitization data.	Please contact MEGIN Customer Care.
Starting measurement	Cannot do HPI : failed to find out DAC amplitude!	Invalid or missing configuration variable.	Please contact MEGIN Customer Care.
Starting measurement	The old averager program is still running.	System is in unexpected state.	Please restart the acquisition software. If problem continues, contact MEGIN Customer Care.
Starting measurement	<path>/tmp/erf.evp: <system error>	Averaging parameter file cannot be created. Invalid system configuration or out of resources.	Check that the directory <path>/tmp exists and is writable by you, or that the disk is not full.
Starting measurement	Timeout when waiting for the started programs to get connected to the data server.	Internal system error: some program component failed to start or was too slow.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Starting measurement	Measurement could not be started: <response>	Measurement could not be started. The response details the reason.	

Table 1:

Context	Error message	Description	Actions
During measurement	Only <number MB of space remaining. Measurement will soon stop automatically.	Disk space has run out and the measurement is stopped automatically.	Informative, not actions needed.
During measurement	<Collector error message>	Collector generated error message. See Table Collector errors for details.	See Table Collector errors for details.
Starting HPI measurement	HPI was not properly started or died unexpectedly!	Cannot start HPI measurement because HPI program is not running.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Starting HPI measurement	to_hpi: <error>	HPI communication failed.	Stop the measurement and try to start it again. Please contact MEGIN Customer Care if this error repeats.
Starting HPI fitting	Cannot do HPI fit: <variable> not specified!	Invalid or missing configuration variable.	Please contact MEGIN Customer Care.
HPI measurement	error: Timed out when waiting for trigger	The trigger channel indicating HPI activation status was not found or the status is not properly recognized.	Check that STI201 has been included in measurement, trigger configurations, and the trigger box connections.
HPI measurement	error: Too many vectors in the new subspace!	The SSP operator removed almost all signals leaving too few to do calculations any further.	Reset channels, if not sufficient check MSR door closure, noise levels and correct problems.
HPI measurement	error: Failure in detecting signals! (Details: amplitude fitting failed)	HPI coil signals could not be detected reliably.	Check coil cabling, coil positioning within helmet and feed-through boards in the cabinet. Retry.
HPI measurement	error: Weak HPI coil signals. (Details: poor correlations)	HPI coil signals could not be detected reliably.	Check coil cabling, and coil positioning within helmet. Retry.
HPI measurement	error: No sufficient signal in any coil! Check cabling.	None of the HPI coil signals could be distinguished reliably from the background noise.	Check coil cabling, EEG rack connections, and coil positioning within helmet. Retry.
HPI measurement	error: Some coil signals are weak.	One or more of the HPI coil signals could not be distinguished reliably from the background noise.	Check coil cabling, and coil positioning within helmet. If only one is weak, you can continue with others.
HPI measurement	error: Not enough good coils	At least three sufficiently reliably detected HPI coils are needed for position detection.	Check coil cabling, and coil positioning within helmet. Retry.
HPI measurement	error: Adjusting weights failed for coil <NUMBER>.	Too few sensors contribute to the detection of the indicated HPI coil.	Check coil cabling and coil positioning within helmet. Retry.

Table 1:

Context	Error message	Description	Actions
HPI measurement	error: Adjust: Only <NUMBER> signals larger than limit, problems are expected!	Too few sensors contribute to the detection of the indicated HPI coil.	Check coil positioning within helmet. Avoid being outside of the helmet closure volume, but also avoid being too close to the helmet plastic. Continue, if results are otherwise good for all other coils, or retry.
Showing HPI results	error: hpifit (pid=<number>) exited with code 1: Bad parameters	HPI fit encountered an unexpected system parameter.	Please contact MEGIN Customer Care.
Showing HPI results	error: hpifit (pid=<number>) exited with code 2: Bad HPI amplitudes. Maybe some coils are broken	No sufficient signal in any coil.	Check the HPI coils are connected to the side panel and that none of the wires is broken.
Showing HPI results	error: hpifit (pid=<number>) exited with code 3: Bad coil order. Check the coil connections	Automatic matching of coils failed.	Check the cabling.
Showing HPI results	error: hpifit (pid=<number>) exited with code 4: File error	HPI fit failed to load or create some file.	Please contact MEGIN Customer Care.
Showing HPI results	error: hpifit (pid=<number>) exited with code 5: Misc error	HPI fit failed to process the data.	Please contact MEGIN Customer Care.
Showing HPI results	error: hpifit (pid=<number>) exited with code 6: Could not create transformation. Check coil placement	HPI fit failed to create transformation.	Try redoing the HPI measurement. If the measurement fails systematically, please contact MEGIN Customer Care.
Showing HPI results	error: hpifit (pid=<number>) exited with code <number>: <explanation>. HPI fitting results access failed	Internal system error. The HPI results file is not readable.	Please contact MEGIN Customer Care.
Showing HPI results	error: hpifit (pid=<number>) exited with code <number>: <explanation>. HPI fitting results read failed: <error>	Internal system error. The isotrak or HPI results file is invalid.	Please contact MEGIN Customer Care.
Showing HPI results	warning: hpifit (pid=<number>) exited with code 7: Goodness-of-fit too low. Maybe you should try to place the coils higher. <HPI fitting results>	HPI fit suggests that HPI should be redone.	Redo the measurement. If it still fails, check that the MEG channels are giving proper signal, that the HPI coils are in proper places and that the coil cables are not broken.
Showing HPI results	warning: hpifit (pid=<number>) exited with code 8: Too large discrepancy between Isotrak and coil fitting. Maybe you should try to place the coils higher. <HPI fitting results>	HPI fit suggests that HPI should be redone.	Redo the measurement. If it still fails, check that the MEG channels are giving proper signal, that the HPI coils are in proper places and that the coil cables are not broken.

Table 1:

Context	Error message	Description	Actions
Restarting measurement	Could not restart acquisition!	Something unexpected happened while restarting the ongoing measurement.	Please contact MEGIN Customer Care.
Activating stimulation	Could not start stimulation!	Something unexpected happened when toggling the stimulation on.	Please check log for more information.
Deactivating stimulation	Could not stop stimulation!	Some unexpected error occurred when toggling the stimulation off.	Please check log for more information.
Activating averaging	to_averager: <error>	Averager communication failed. Stop the measurement and try to start it again.	Please contact MEGIN Customer Care if this error repeats.
Deactivating averaging	to_averager: <error>	Averager communication failed. Stop the measurement and try to start it again.	Please contact MEGIN Customer Care if this error repeats.
Activating recording	Could not start recording!	Something unexpected happened when activating recording. Check log for more information.	Please check log for more information.
Deactivating recording	Could not stop recording!	Something unexpected happened when deactivating recording. Check log for more information.	Please check log for more information.
Activating continuous HPI	to_hpi: <error>	HPI communication failed. Stop the measurement and try to start it again.	Please contact MEGIN Customer Care if this error repeats.
Deactivating continuous HPI	to_hpi: <error>	HPI communication failed. Stop the measurement and try to start it again.	Please contact MEGIN Customer Care if this error repeats.
Activating calibration signal	Could not start eeg calibration signal!	Something unexpected happened when activating the EEG calibration signal. Please check log for more information.	Please check log for more information.
Deactivating calibration signal	Could not stop eeg calibration signal!	Something unexpected happened when deactivating the EEG calibration signal.	Please check log for more information.

Table 2:

Context	Message	Description	Actions
Powering up system	Could not initialize EEG electronics	EEG electronics did not behave fully as expected during bringing up the system.	Check opto-cabling to EEG rack, powering of EEG rack, EEG board insertion snugness, EEG board id configuration. Do a RAP after correcting errors.
Powering up system	Could not initialize MEG electronics	MEG electronics did not behave fully as expected during bringing up the system.	Check opto-cabling to MEG preamplifiers, powering of the MEG preamplifier bus, MEG board insertion snugness, MEG board id configuration. Do a RAP after correcting errors.
Powering up system	Connection to FEC failed! Cannot do anything.	The operating of the connection gateway to all front-end electronics failed. This is typically due to network connectivity problems, e.g. due to changes in network infrastructure, network configurations, IP addresses, or plainly irregular system reset.	Reset FEC, wait for boot-up and do a RAP.
Any time	Select socket timed out	An ethernet connection has abruptly terminated, or the other end is not responding.	Check ethernet connections, firewall.
Any time	Janitor-MEG: Command '<COMMAND>' causes: <PROBLEM>	Prefix to deeper error messages.	See description for <PROBLEM>.
Any time	Janitor-EEG: Command '<COMMAND>' causes: <PROBLEM>	Prefix to deeper error messages.	See description for <PROBLEM>.
Any time	Janitor-MEG gave an empty reply	Generic fatal error in the servers, possibly due to complete unresponsiveness due to other ongoing activities (probably faulting).	You need to close down and take a RAP and retry.
Starting Megacq	No connection to the data server	The acquisition application and data server cannot communicate due to the data server having crashed, or being fully busy with e.g. timeouting from non-existing connections.	Do a RAP. If not helpful, check connections, firewall and finally do a RAP.

Table 2:

Context	Message	Description	Actions
Starting Megacq	400 Connection failed: <DSP NAME>	The acquisition application could not communicate to all configured DSP boards.	Check a) ethernet cabling, b) The Run-status of all DSP boards inside electronics cabinet and reset if needed, c) IP address configuration on the workstation, d) Firewall settings. Do a RAP after fixing connections.
Starting Megacq	Data server does not want to listen to us	The server process exists, is reachable and responds but is configured not to interoperate.	Check IP addresses and hostnames.
Loading setups	500 Recalling old setups is not supported with this system	You have tried to load measurement settings from an earlier software release that is not compatible.	Create the set up anew.
Starting measurement	410 Could not setup all sources: <DSP NAME>	Some DSP boards could not be configured without problems. Most likely data from that DSP will not come in at all, or will not be processed fully according to requested settings.	Typically due to typos in the DSP parameter scripts, or channel definitions for collector. Check also firewall settings.
Starting measurement	402 Problems while switching to meas mode: <PROBLEM>	Prefix to deeper error messages.	See description for <PROBLEM>.
Starting measurement	Previously disconnected	The acquisition application has lost communication to one or more DSP boards, usually due to DSP board malfunction.	Reset the particular DSP boards and do a RAP.
Starting measurement	Channel <EEG CHANNEL>: Cannot find a calibration for the current gain (<NUMBER>, available <NUMBER>)	The EEG channel could not be set up for correct gain, thus the values of that channel may not be correct.	Check EEG calibration file for typos, or do a RAP to restart a tangled EEG system.
Starting measurement	The SQUID loop rate deviates too much with the selected sampling rate - please adjust it	The data sampling loop rate cannot realize all 'non-round' values but attempts the nearest possible value.	Use a different sampling rate, preferably a round number.
Starting measurement	Low-pass filter corner too low for HPI, should be at least <NUMBER> Hz	The low-pass filter cannot be set lower than the highest HPI frequency in order not to lose that HPI signal. This restriction unfortunately applies even though no HPI would actually be used.	Use higher low-pass frequency and possibly higher sampling frequency too.
Starting measurement	Invalid gantry position information (<code>)	Gantry position value is invalid.	Check gantry sensors, their adjustments within filter cabinet and cabling. Compare to gantry 'traffic lights'.

Table 2:

Context	Message	Description	Actions
Starting measurement	Taking too much time, bailing out.	The EEG system took too long time in the offset calibration process. As a result, the EEG system has been set up properly for use only up to the point when time limit was exceeded. Typically the EEG/ BIO connectors were wrongly connected or a failure in the EEG electronics.	Investigate and correct electrode connections. Restart measurement.
Starting measurement	EEG control failed right away! Bailing out.	The EEG system was completely unresponsive and, as a result, it has not been set up properly for measurement.	Check control connections, powers. Reattempt the measurement.
Starting measurement	Channel <name>: Offset too high. Possibly an open input?	Some EEG channels failed to calibrate their offsets. Other EEG channels are ok, unless the timeout problem ensued as a result of this.	If single channel problem, note this and the use can be continued. Otherwise investigate and correct electrode connections.
Starting measurement	Channel <name>: Offset calibration failed.	Some EEG channels failed to calibrate their offsets. Other EEG channels are ok, unless the timeout problem ensued as a result of this.	If single channel problem, note this and the use can be continued. Otherwise investigate and correct electrode connections.
Starting measurement	Gantry position has not been defined manually!	The gantry position signal path has failed and this situation has not been manually overridden.	Check gantry position cabling, the traffic-lights, feed-through boards to correct the automatic detection, or, enter the gantry angle manually from acquisition application main window.
Starting measurement	403 MaxShield state unknown - cannot measure. Turn MaxShield on or off	The system could not command the IAS (MaxShield) subsystem fully. Thus its operation cannot be guaranteed and thus data validity is compromised. Measurement will be prohibited until corrected.	Retry measurement but if persists, verify that all DSP participating in the IAS are fully operational, possibly resetting the DSP boards and taking a RAP, or minimally, issue manually command 'ias off' to collector.
EEG impedances	Switch off calibration signal first.	The calibration signal is still turned on while trying to engage EEG impedance measurement.	Toggle off the EEG Calibration signal from the check box on the Megacq.
EEG impedances	Could not setup oscillator!	The oscillator that is used for EEG impedance measurement failed to start.	Check the cabling of the EEG rack. Take a RAP, and retry.
During measurement	Data no longer available! Acquisition workstation is probably overloaded.	The MEG signal data has been lost due to excessive lagging in data processing on the workstation. Thus the workstation is no longer capable of staying in real-time status.	Check ethernet connections and ethernet infrastructure loads. Also ensure that workstation is not excessively stressed during measurement. Stop acquisition and retry.

Table 2:

Context	Message	Description	Actions
During measurement	Large gap in source data!	The MEG signal data is missing altogether for some period of time in the middle of measurement. Expect data gaps during analysis. Other data most likely fully valid.	Check ethernet connections and ethernet infrastructure loads. Also ensure that workstation is not excessively stressed during measurement. Analyze the data with additional care.
Stopping measurement	401 Acquisition did not stop gracefully: Sampling clock was turned off but ODP thread did not exit	Typically ensues after other root problems during measurement. Typically a recoverable situation, but indicates presence of other problems during measurement.	Check for prior error messages, otherwise the system use can be continued.
Stopping measurement	ERROR: These data sources dropped out in the middle of the measurement: <DSP NAMES>	The listed DSP boards stopped supplying MEG data in the middle of the measurement. The data up to that point may exist and is most likely valid, but afterwards is probably flat.	This can be due to ethernet cabling failure, ethernet software bug, or excessive ethernet load. Check administration interface of the ethernet switches too for collisions or other physical faults. Otherwise reset the particular DSP and restart Megacq.