NICA

User Manual

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1 Introduction

NICA (short for **N**ear **I**nfrared spectroscopy **C**alculations and **A**nalysis) is a MATLAB-based Graphical User Interface (GUI) to analyse functional Near-Infrared Spectroscopy (fNIRS) measurement data recorded with the *NIRScout* device.

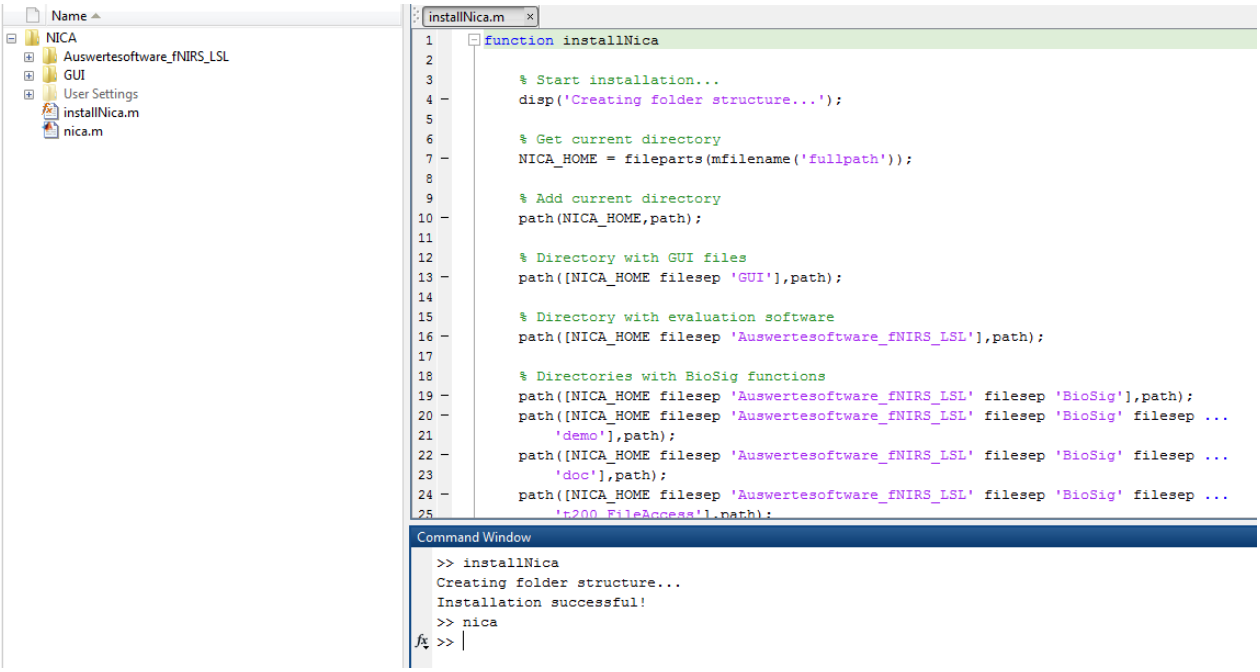
The measurement data consists of an HDR- and an XDF-file for each measurement. The HDR-file provides basic information about the measurement setup (filename, date, number of sources and detectors, etc.); the XDF-file includes information about the recorded signals (fNIRS, ECG, heart rate, blood pressure, and respiratory frequency).

For a complete analysis, the signal is pre-processed, biological and technical artefacts are removed, the concentration change of oxy- and deoxyhaemoglobin is calculated and various output-files and figures are generated.

The GUI included already existing MATLAB-files, which were developed and adapted by Günther Bauernfeind and Dominik Bachmaier, as well as analysis-functions (*BioSig, EEGlab*), which are used at the Graz University of Technology.

2 Installation

To install NICA you have to run the file *installNica.m***,** which can be found in the main folder. The installation creates the folder structure for all the necessary functions and files for the GUI. After a successful installation the command window displays the message *Installation successful!*



NICA can now be started at any time (also after restarting Matlab) from the command window by simply typing the command *nica*.

3 Surface

In the top left corner of the GUI you can find a menu bar, including the following options:

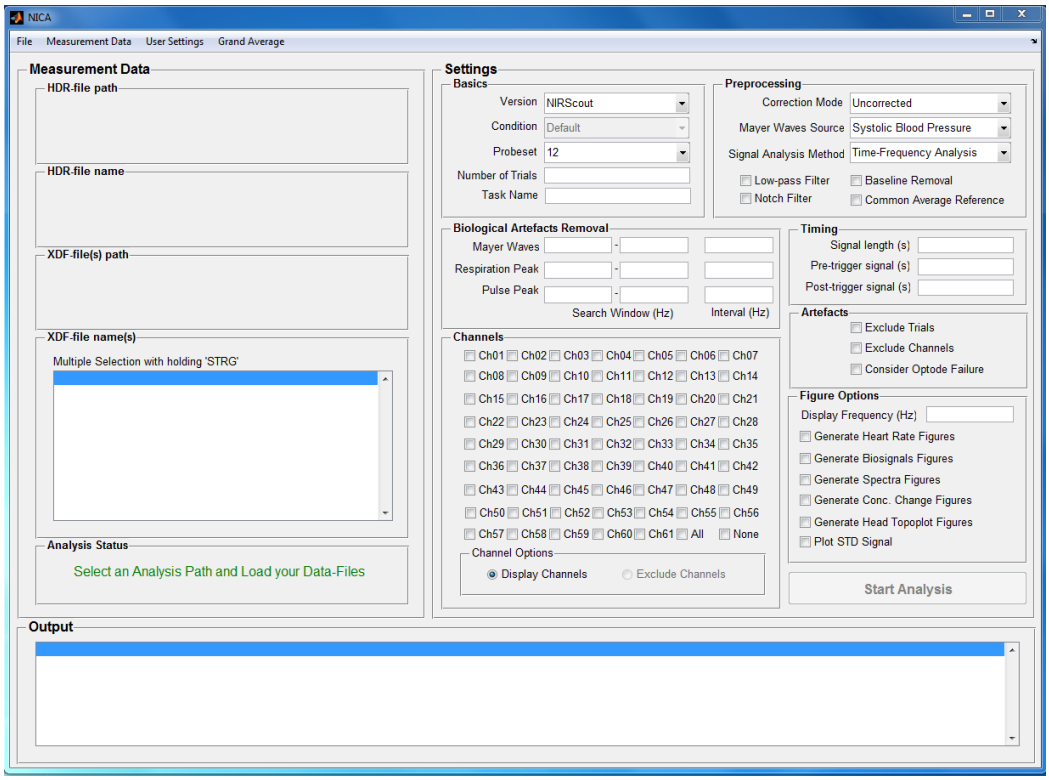
- *File*
- *Measurement Data*
- *User Settings*
- *Grand Average*

The main part of the surface is divided into 4 areas, so called panels:

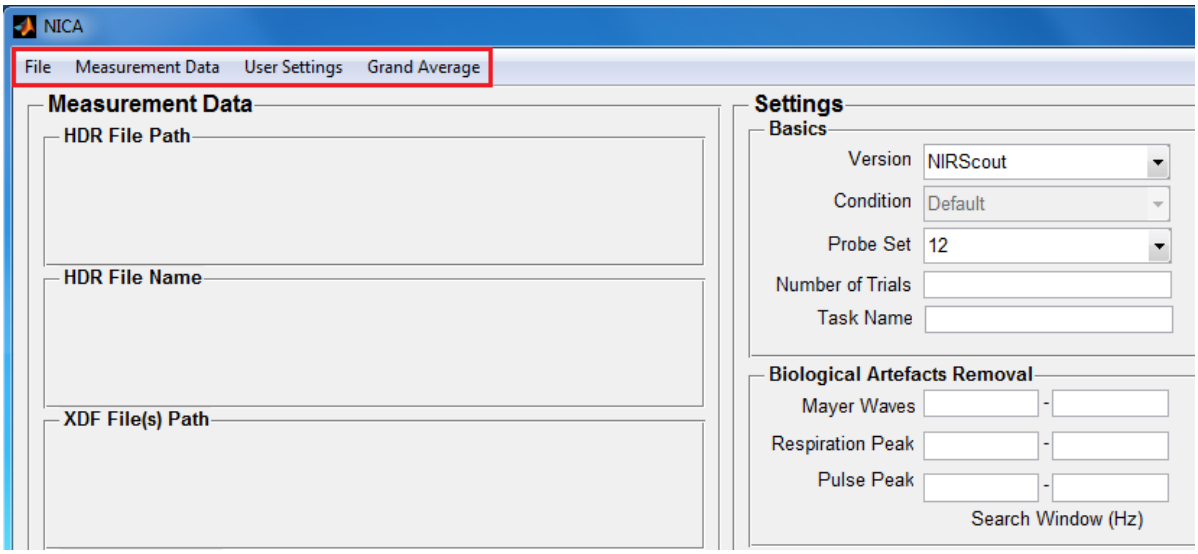
- *Measurement Data*
- *Settings*
- *Analysis Status*
- *Output*

In the bottom right corner at the panel *Settings* you find the pushbutton *Start Analysis*, which starts the analysis after correctly entering the required settings.

Under the panel *Measurement Data* you can find the panel *Analysis Status*, which provides information about the current state of analysis.



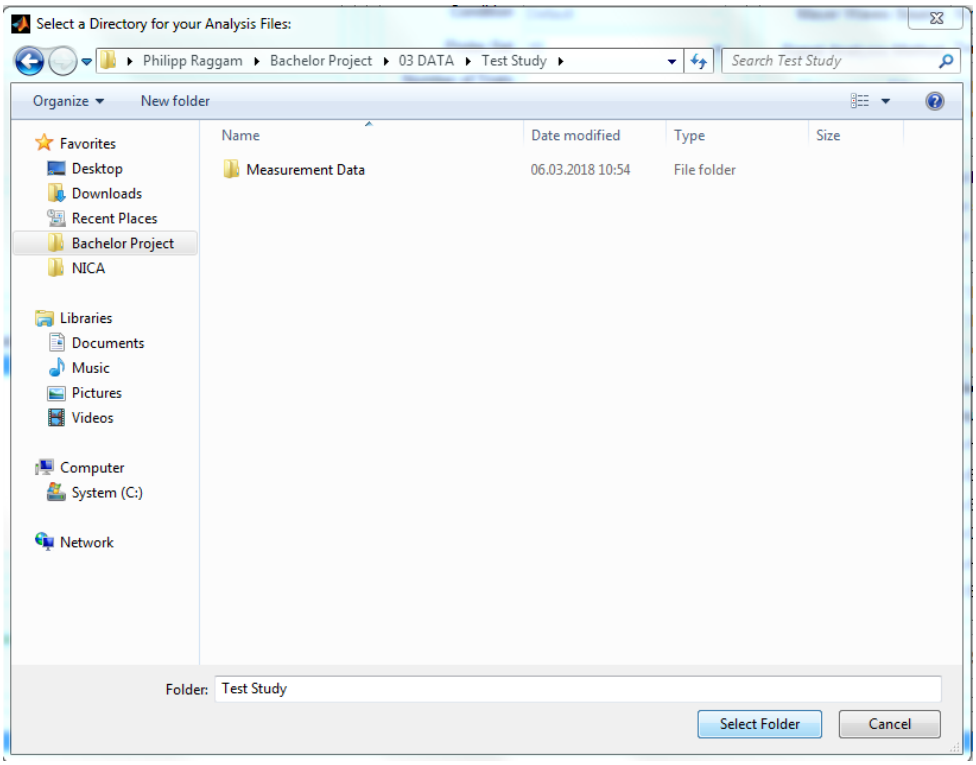
4 Menu Bar



4.1 File

4.1.1 Select Analysis Path

Before you can start an analysis, you have to select a directory where your output-files will be saved. In order to do this, a file selection dialog box opens where you can choose your preferred directory. It is recommended, to use the directory of your measurement data.



4.1.2 Open Analysis Path

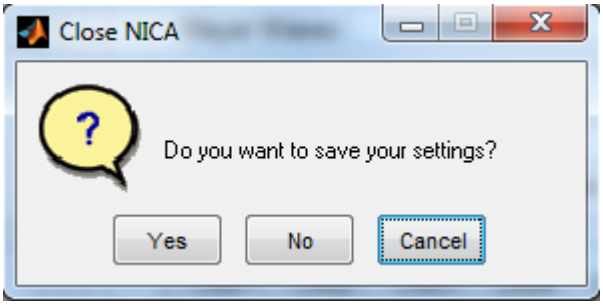
After an analysis, you can open the directory where your current output-files are saved.

4.1.2 Close all Figures

During an analysis, several figures are generated and displayed. With this option, you can close all figures at once.

4.1.3 Close GUI

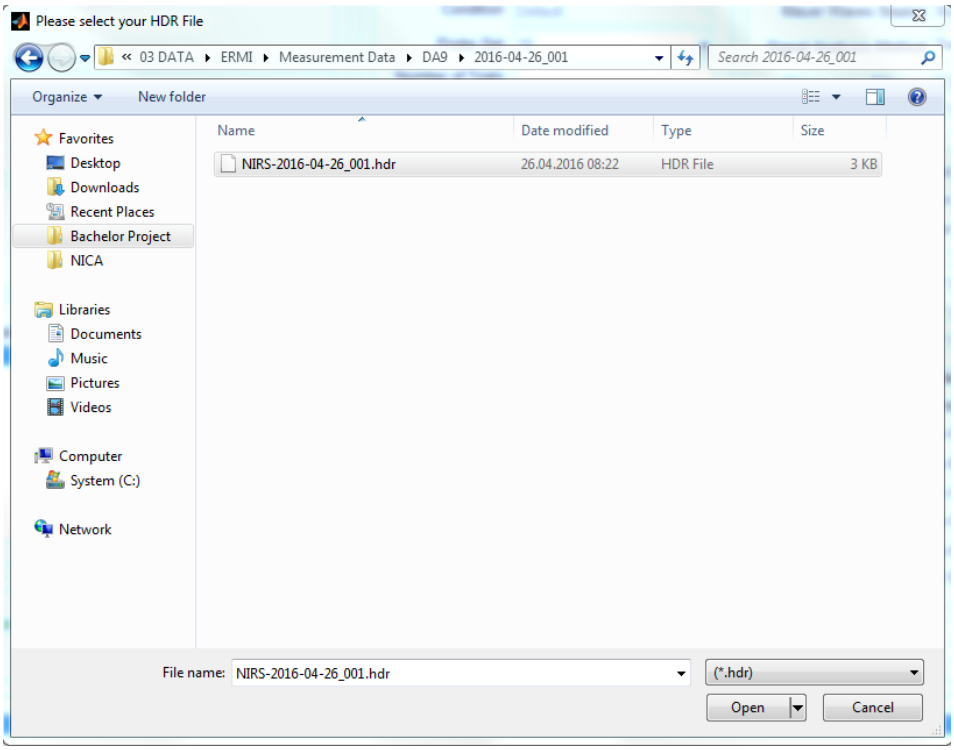
Closes the GUI and asks whether you want to save your settings.



4.2 Measurement Data

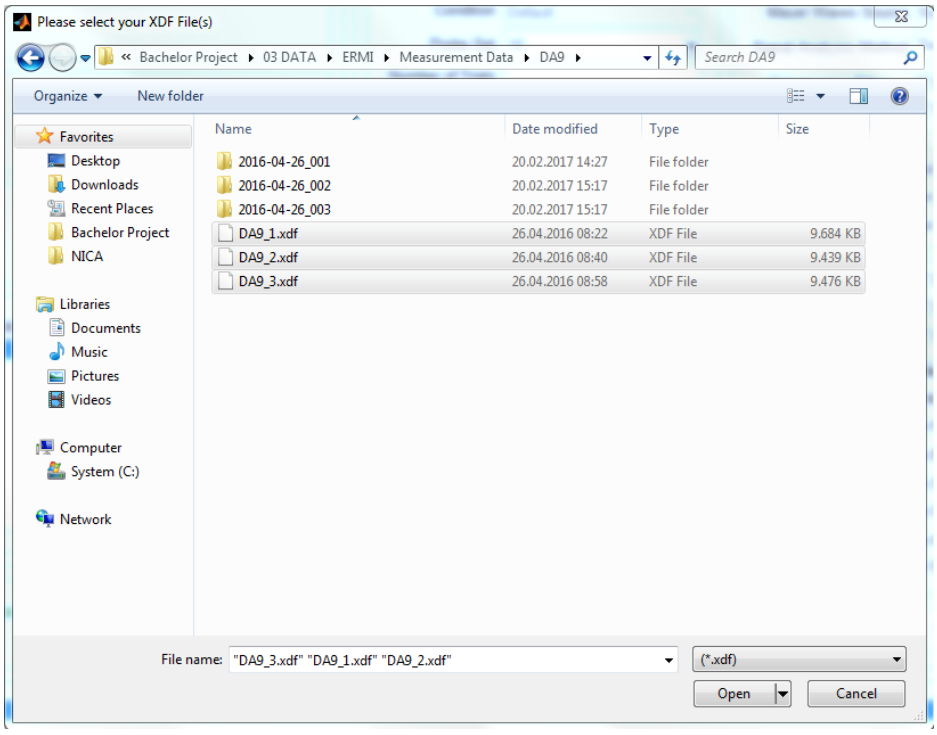
4.2.1 Load HDR File

This option opens a file selection dialog box to load the HDR-file. When you have measured more than 1 run (i.e. more than 1 existing XDF-file) from the same subject, you still have to load only 1 HDR-file.



4.2.2 Load XDF File(s)

With this option, you can load your XDF-file(s), again with a file selection dialog box. If you have measured more than 1 run for the same subject, you can load all your XDF-files at once. Multiple selections can be done by holding the CTRL/STRG-key.

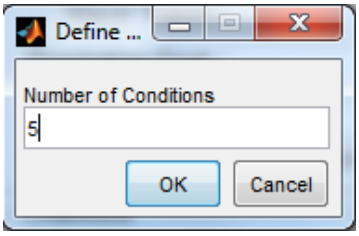


4.2.3 Clear Data

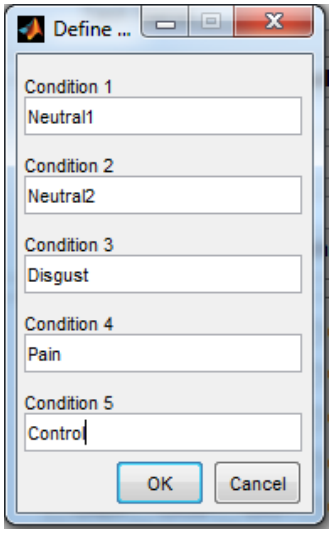
When you have done all the analyses for a subject and you want to continue with the next subject, you can remove your data-files. If you don't choose this option, the new data-files will be added to the old ones. To maintain a clear structure it is recommended, to remove your data after every subject.

4.2.4 Define Conditions

If you have different conditions during a single run, you have to define them in advance. After selecting this option, an input dialog box opens, where you have to enter the number of your conditions (e.g. 5):



After pressing *OK*, a second input dialog box appears, where you have to enter the names of your conditions. IMPORTANT: The order must be the same as during your measurements, otherwise it is not possible to find the right triggers.



After pressing *OK*, the conditions can be selected under *Settings*/*Basics*/*Condition*.

4.3 User Settings

4.3.1 Save

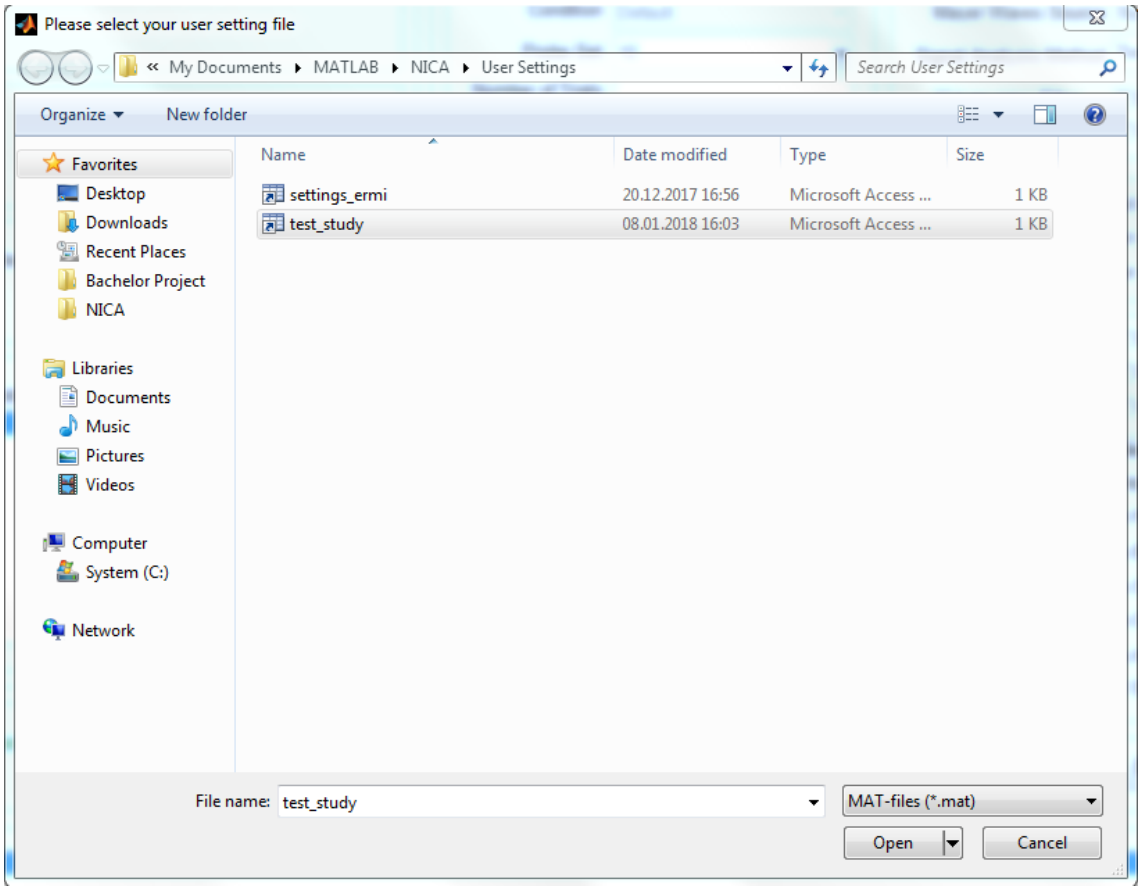
Selecting this option, you can save your settings to a file. If you save your settings for the first time, a window pops up, asking for the filename. After that, your settings always will be saved to the same file.

4.3.2 Save As

If you have to make changes to your settings and you want to save them to a different file, you can choose this option.

4.3.3 Load

Loads the settings-file and applies the settings to the GUI.



4.4 Grand Average

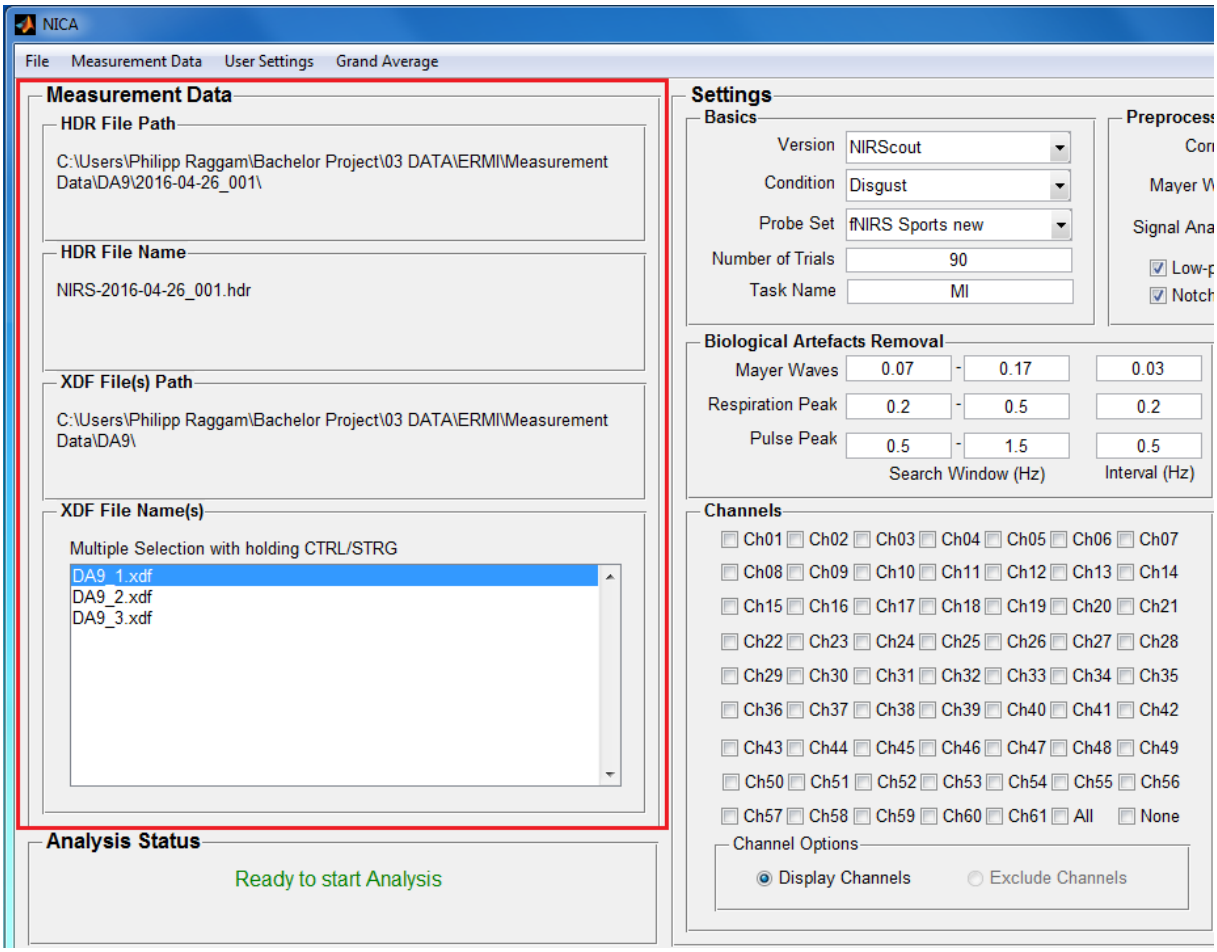
4.4.1 Start

This option enables the *Grand Average* for your analysis-files. The pushbutton *Start Analysis* changes its name to *Start Grand Average*. Further details are explained at section 8.2.

4.4.2 Stop

This option disables the *Grand Average.* The pushbutton changes its name back to *Start Analysis.*

5 Measurement Data



5.1 HDR File Path

This panel displays the directory path of the location of the HDR-file you are using for this analysis.

5.2 HDR File Name

Here you can see the name of the current HDR-file.

5.3 XDF File(s) Path

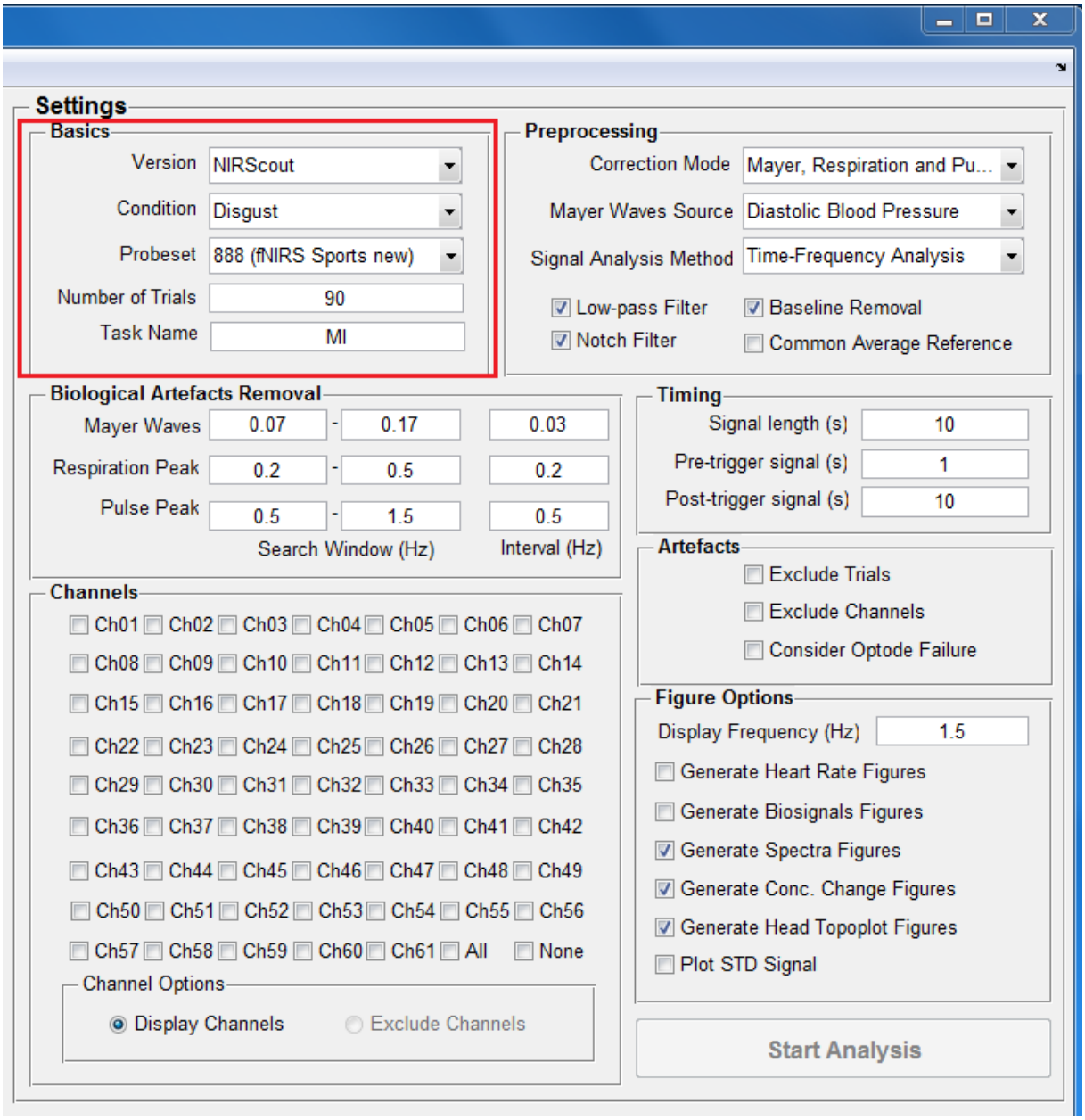
This panel displays the directory path of the location of the XDF-file(s) you are using for this analysis.

5.4 XDF File Name(s)

Here you can see the name(s) of the current XDF-file(s). If you want to use multiple XDF-files for your analysis you have to hold the STRG/CTRL-key and then select the files with a left mouse click.

6 Settings

6.2 Basics



6.2.1 Version

Here you have to choose the platform, with which the measurement data have been recorded. By default, the version *NIRScout* is selected. If you have recorded your measurement data with a different platform, you have to select the option *other*.

6.1.2 Condition

If you have defined different conditions (see section 4.2.4) you can select your current condition from a popup menu. If you have not defined your conditions, the setting simply says *Default.*

6.1.3 Probe Set

You have to select the probe set you were using for the recording of your measurement data. At the popup menu, some options are named after their used number of channels (*12, 24, 38, 47* and *50)*; the others use standard electrode setups, which are usually applied for recording fNIRS data (*Laboratory new, fNIRS Sports old* and *fNIRS Sports new).*

You have to be careful to select the right probe set (i.e. the correct number of channels); otherwise the plots of your output-files will be incorrect.

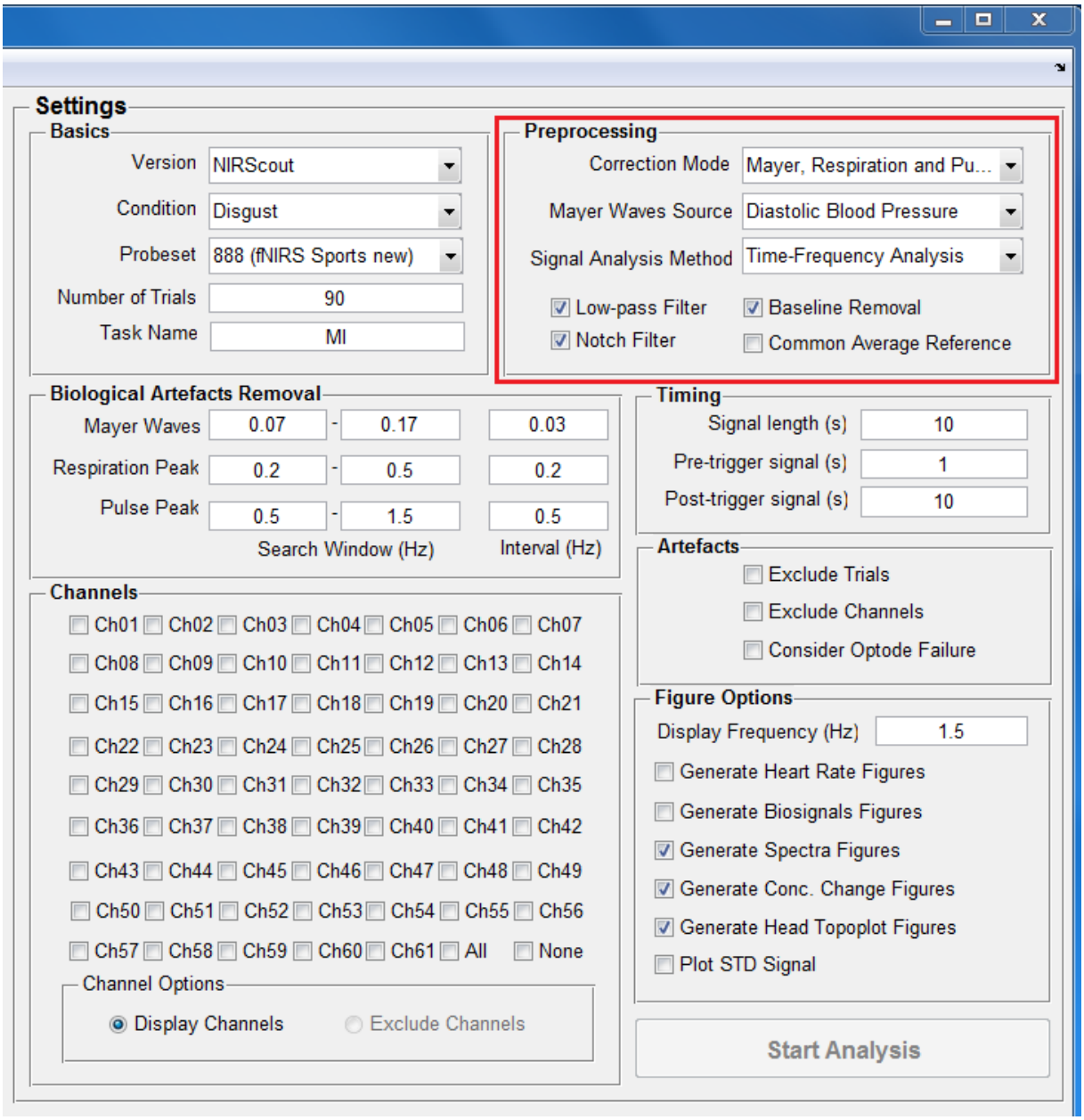
6.1.4 Number of Trials

Here you have to enter the total number of all your recorded trials.

6.1.5 Task Name

The task name will be included in the name of the output-files.

6.2 Preprocessing



6.2.1 Correction Mode

One of the main benefits of *NICA* is that you can remove the following biological artefacts:

- *Mayer Waves:* cyclic changes or waves in arterial blood pressure
- *Respiration peak:* rhythmic movements of the thorax due to breathing
- *Pulse peak:* influence of the heartbeat

You can select the correction of a single biological artefact (*Respiration*, *Mayer Waves* or *Only Adaptive Pulse)* a combination of them (*Mayer and Respiration* or *Mayer, Respiration and Pulse),* or no correction at all (*Uncorrected).*

NOTE: You can only remove the biological artefacts, if you have recorded them in addition to your fNIRS data.

6.2.2 Mayer Waves Source

You can select *Systolic Blood Pressure*, *Diastolic Blood Pressure* or *Heart Rate* as a source for detecting the Mayer Waves.

6.2.3 Signal Analysis Method

You can choose between two methods to remove the biological artefacts of your measurement data:

- *Time-Frequency Analysis*
- *Independent Component Analysis*

6.2.4 Baseline Removal

A filter removes the baseline drift (filter settings: band-stop between 0.005 and 0.1 Hz).

6.2.5 Notch Filter

This band-stop filter removes the 50 Hz power line frequency.

6.2.6 Common Average Reference (CAR)

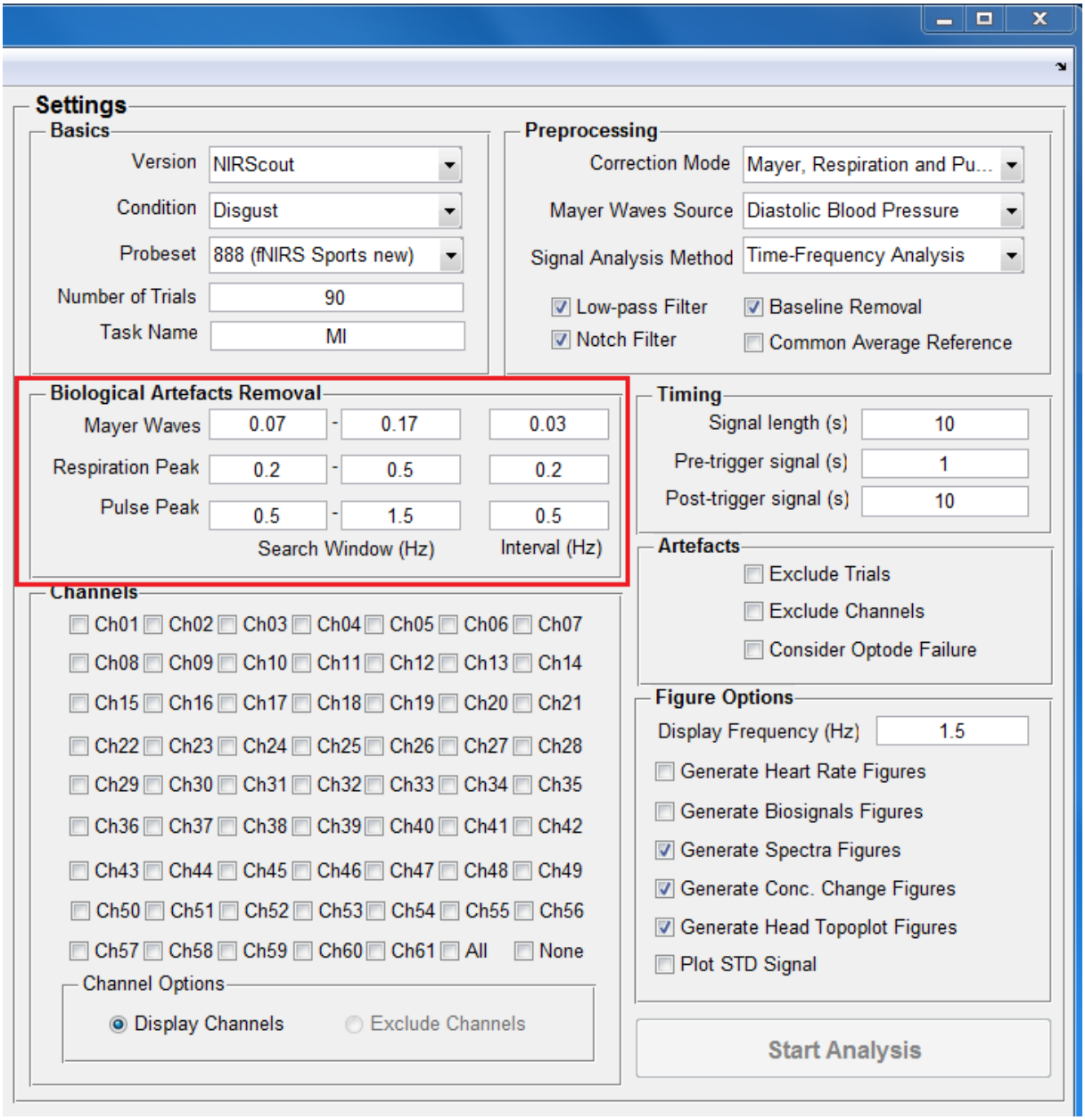
This spatial filter subtracts the average of the signals of all channels from the signal of the current channel.

NOTE: If you have an artefact at one of your channels, this artefact will influence the signal at every electrode used in your probe set.

6.3 Biological Artefacts Removal

With this option, you can define the search windows (*Search Window)* and the length of the segments (*Interval*) you want to remove (operations take place in the frequency domain).

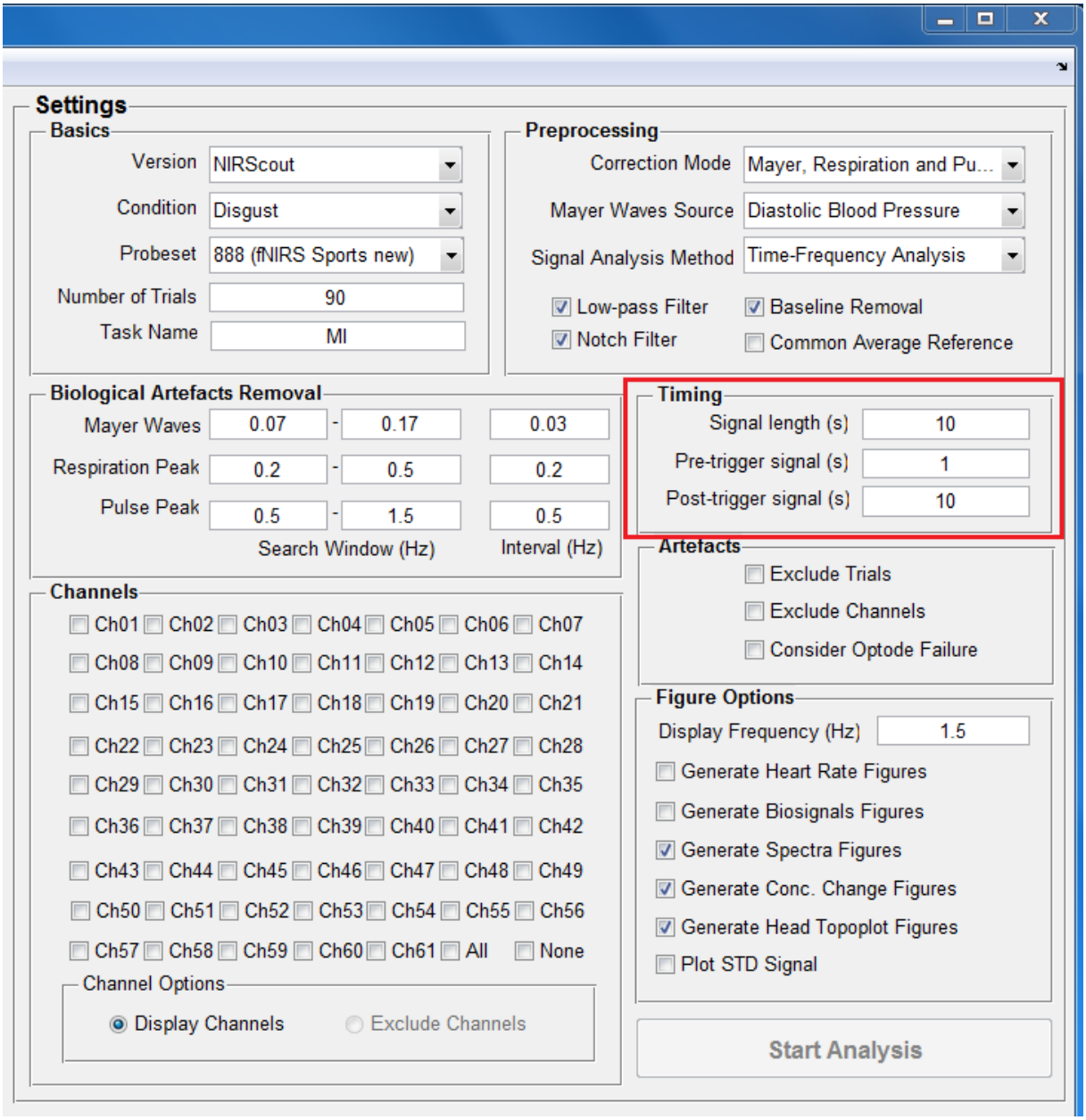
At this figure you can see the standard frequency intervals of the biological artefacts.



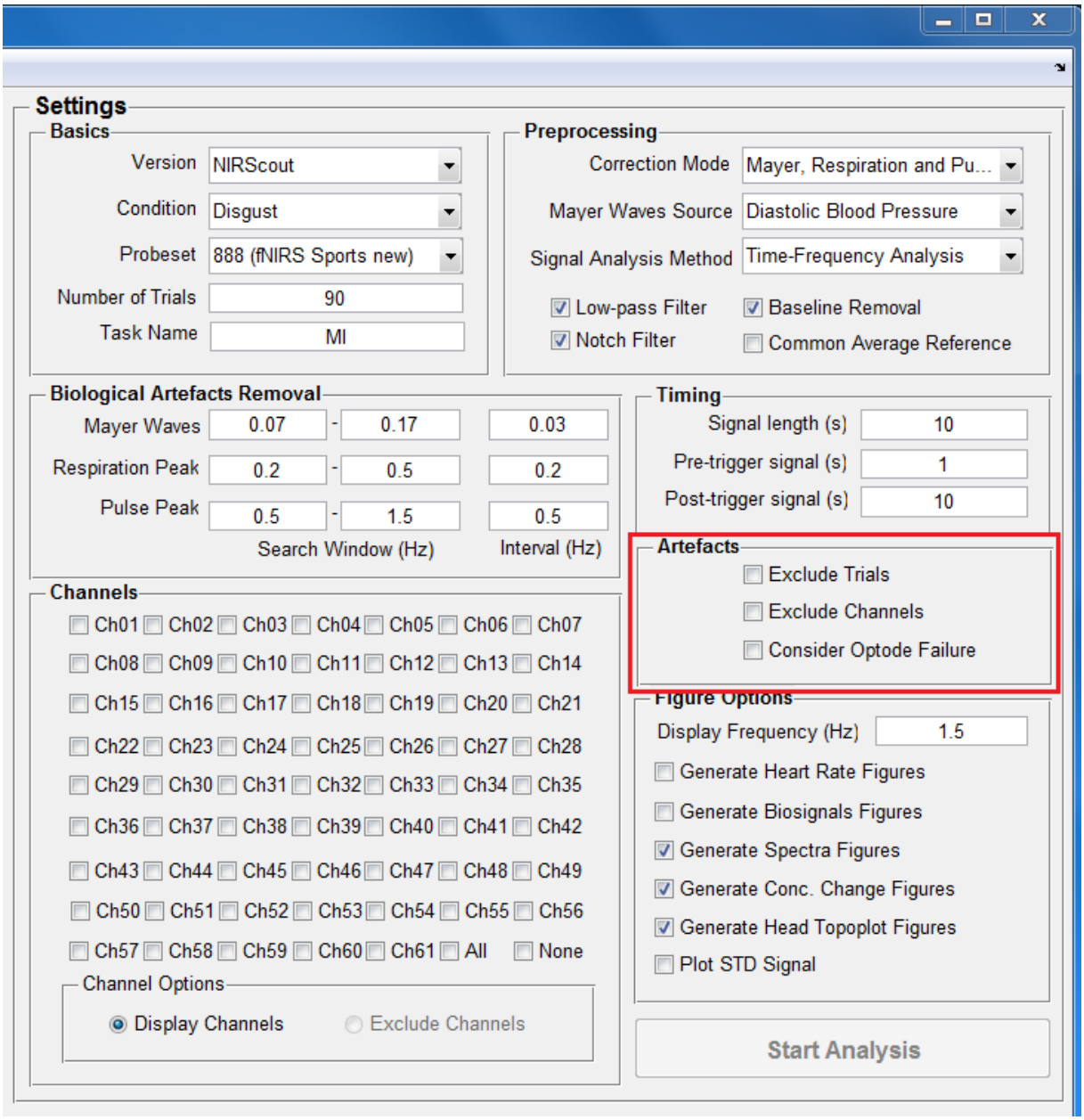
6.4 Timing

The timing settings determine the time axis at the figures of the concentration change of oxy- and deoxyhaemoglobin. In this example, 1 second before the start of the task (*Pre-trigger*

signal), the task duration of 10 seconds (*Signal length*), and 10 seconds after the task (*Post-trigger* signal) will be displayed (21 seconds in total). The three time periods are separated with a black vertical line. Be aware that the timing settings have to fit the recording time of your trials.

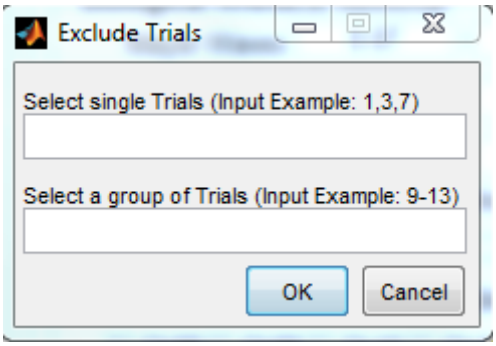


6.5 Artefacts



6.5.1 Exclude Trials

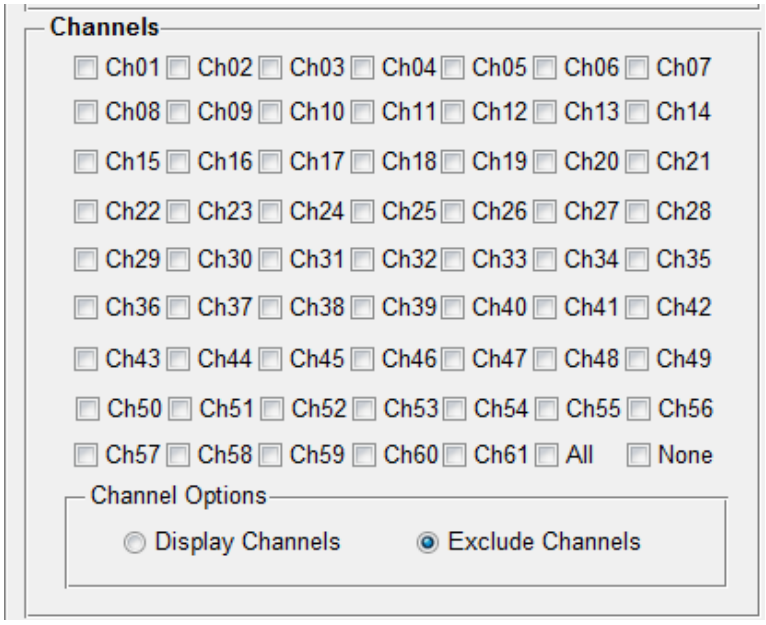
With this option you exclude trials which were recorded incorrectly or show obvious errors in their data. After clicking on the *Exclude Trials* checkbox, an input dialog box appears:



You can either select single trials or a group of trials you want to exclude. Make sure to fit the structure of the shown input examples.

6.5.2 Exclude Channels

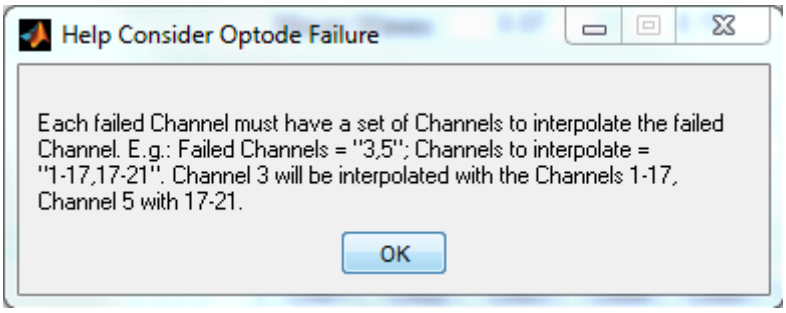
Using this option, you can exclude faulty channels, e.g. optodes where the impedance is too high or where you have an artefact-influenced signal. After clicking on the *Exclude Channels* checkbox, the radio button of the *Channel Options* panel switches to *Exclude Channels.*



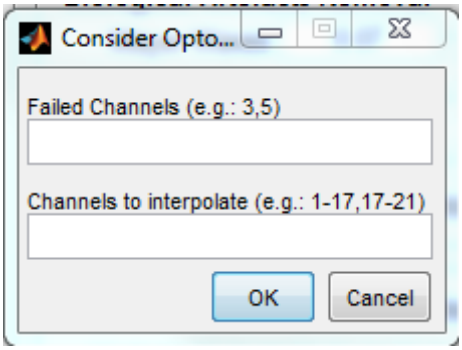
You can select the channels you want to exclude by clicking on the corresponding checkbox. By clicking on the checkbox *All*, all channels are selected; by clicking on *None*, you can undo your selection.

6.5.3 Consider Optode Failure

In contrast to the option *Exclude Channels*, the excluded channels will be interpolated with their surrounding channels. Therefore, you have to select the channel you want to exclude as well as the channels used for interpolation. After clicking on the *Consider Optode Failure* checkbox, a help window appears which explains how the channels will be interpolated.

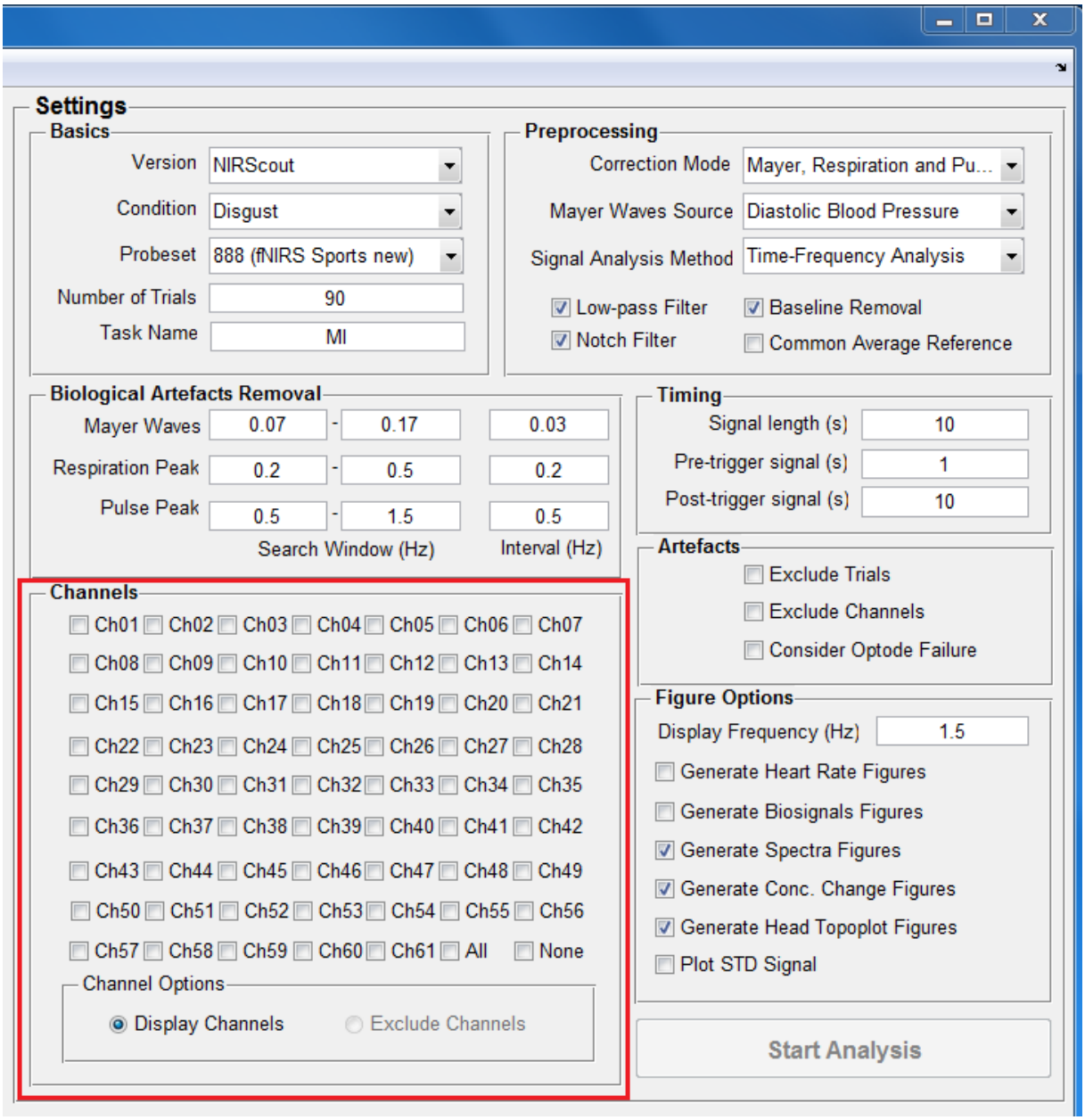


To make sure your input has the right structure, you can see again examples at the input dialog box:



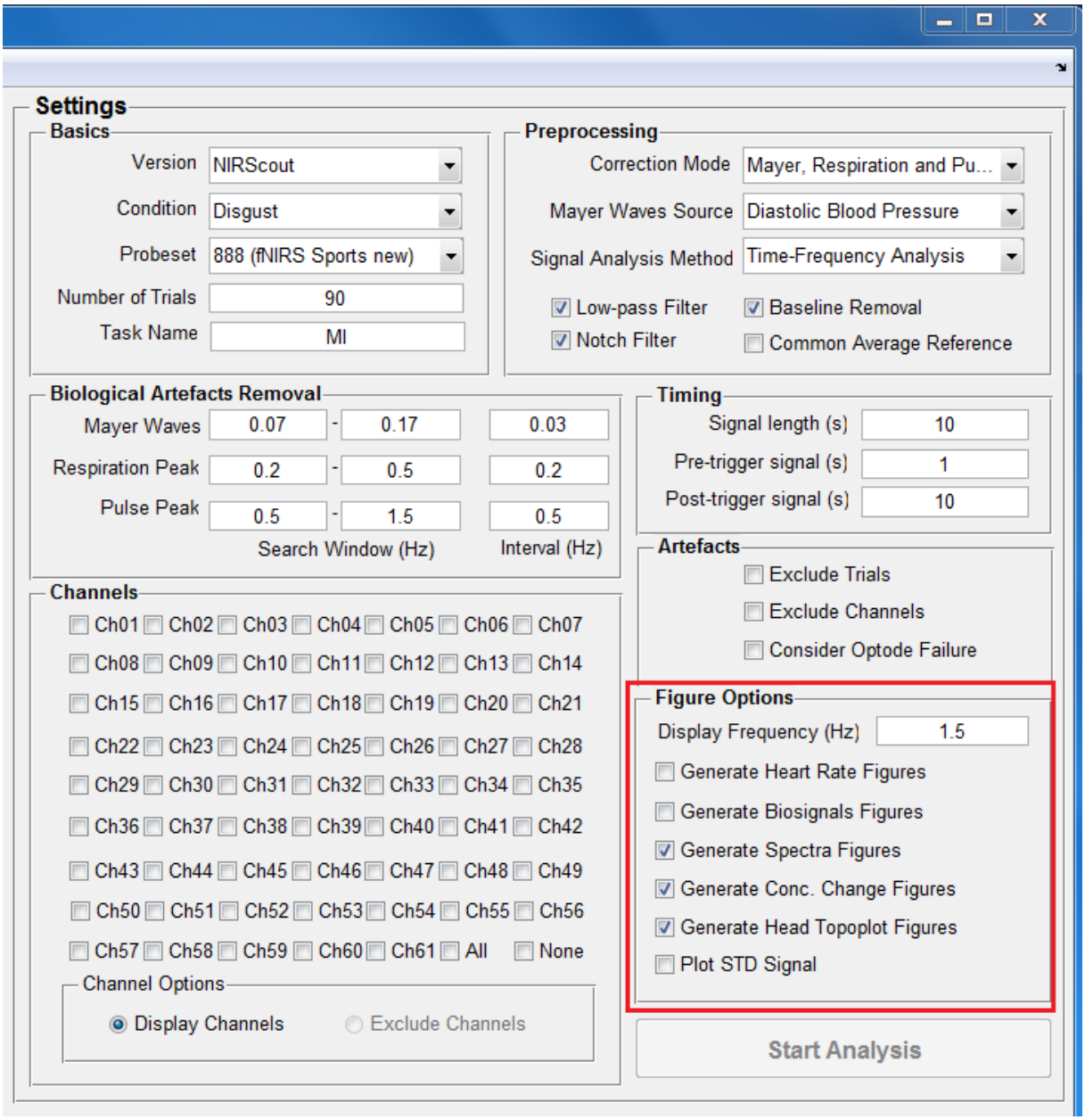
6.6 Channels

After an analysis, the concentration changes of oxy- and deoxyhaemoglobin over time, averaged over trials, for all channels are plotted into one figure. With this option, you can create concentration change figures for each channel individually by selecting the checkboxes for the corresponding channels. By clicking on the checkbox *All*, all channels are selected; by clicking on *None*, no channel is selected.



6.7 Figure Options

This chapter only describes which figures can be generated; a detailed explanation of the output figures can be found at chapter 10.



6.7.1 Display Frequency

With this option, you can determine the frequency range of your frequency spectrum figures of oxy- and deoxyhaemoglobin. An input of 1.5 for example means that the frequency spectrum is displayed from 0 to 1.5 Hz.

6.7.2 Generate Biosignals Figures

This option generates two figures:

1. The first figure (with the filename appendix *Physio_Signals*) contains for signals: blood pressure (mmHg), respiration peaks (a.u.), heart rate (bpm) and the electrocardiogram (ECG, a.u.).
2. The second figure (with the filename appendix *Physio_Signals_Mean*) shows the changes in the diastolic blood pressure (Δ mmHg), systolic blood pressure (Δ mmHg) and the heart rate (Δ bpm).

6.7.3 Generate Spectra Figures

Selecting this option generates 3 frequency spectrum figures:

1. The frequency spectrum of each channel without biological artefact correction (filename appendix *Spectra_Raw*)
2. The frequency spectrum of each channel with biological artefact correction (filename appendix *Spectra_Clean)*
3. Comparison of the frequency spectra with and without biological artefact correction, averaged over all channels (filename appendix *Spectra_Compared*)

6.7.4 Generate Conc. Change Figures

With this option you can generate figures of the concentration changes of oxy- and deoxyhaemoglobin over time, averaged over trials, for all channels. If you have selected channels individually (section 6.6), you also have to enable this option to create the single-channel figures.

6.7.5 Generate Head Topoplot Figures

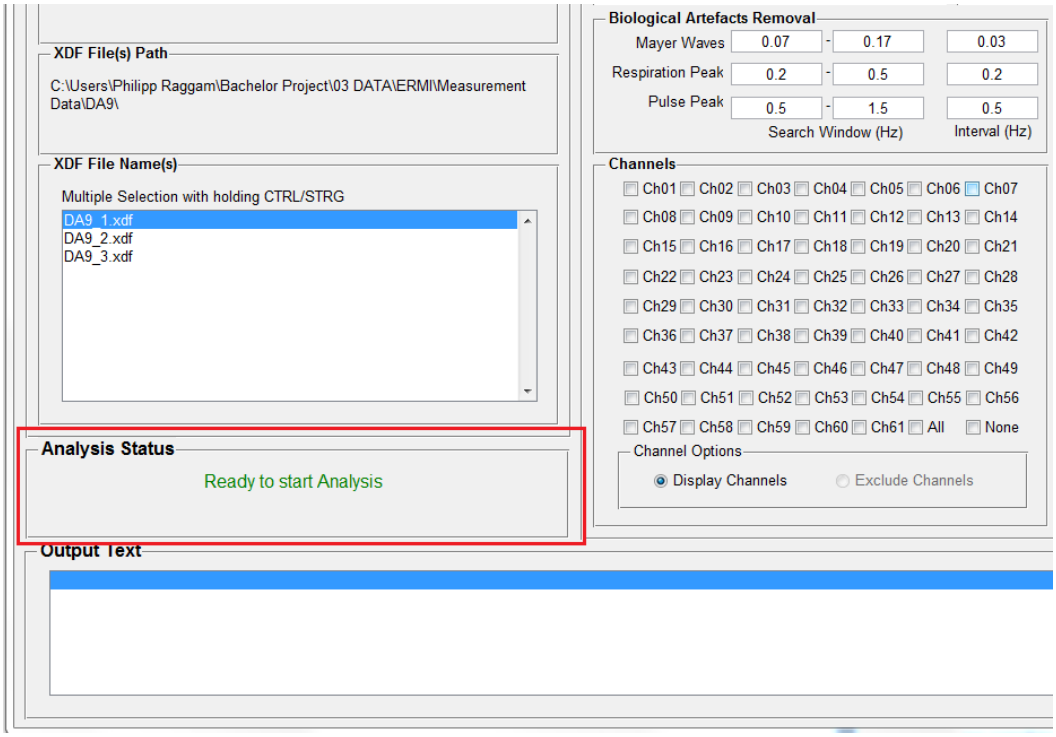
This option creates topoplot figures of the head: a coloured representation of the concentration changes of oxy- and deoxyhaemoglobin of all channels, divided into 4 time periods. The colour spectrum goes from red (positive concentration change) to blue (negative concentration change).

6.7.6 Plot STD Signal

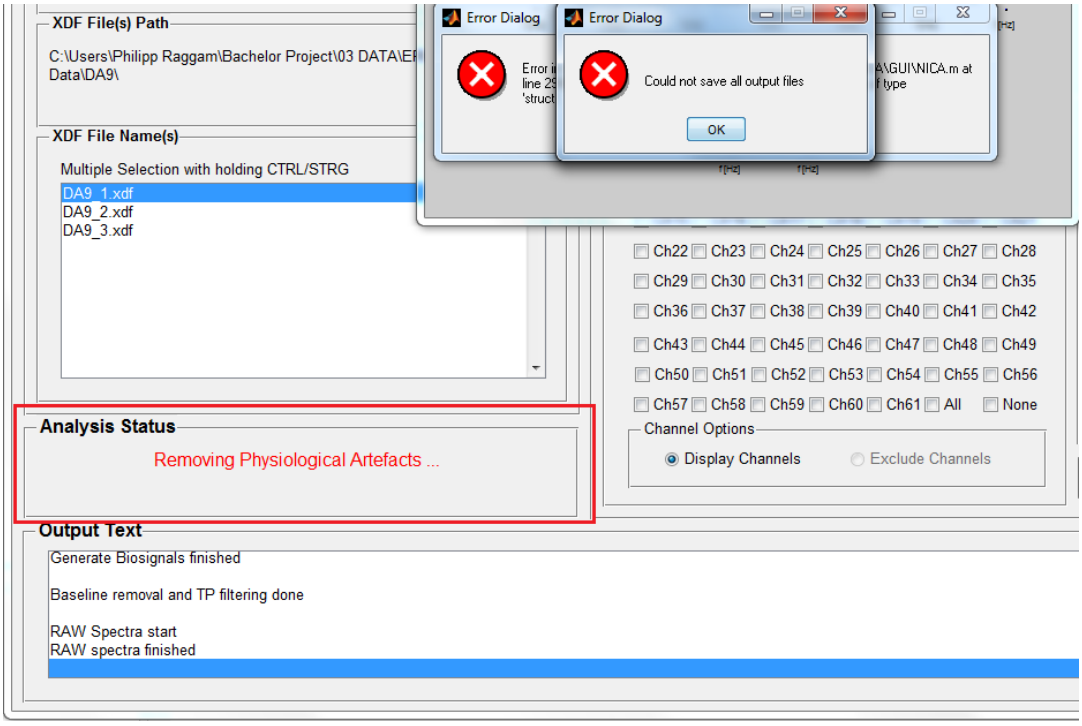
You can add the standard deviation plot to your concentration change figures.

7 Analysis Status

The analysis status gives you information about the current state of the analysis.

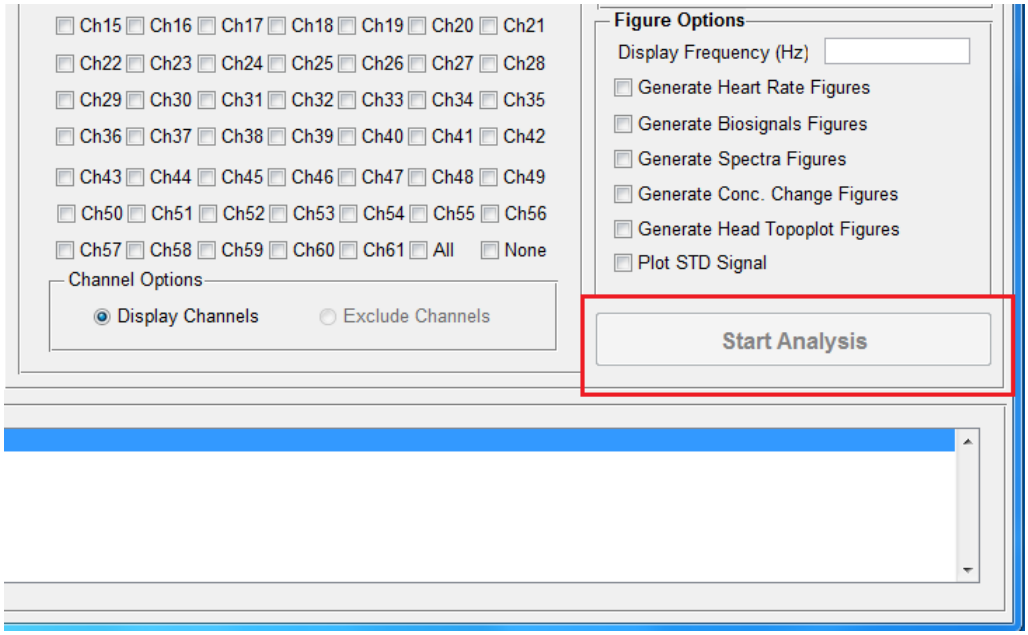


If everything is going well, the colour of the text is kept in green; if there is an error during the analysis, the text is displayed in red.

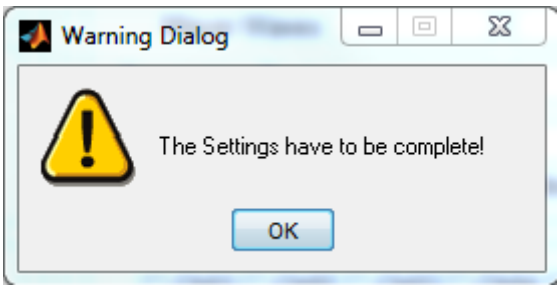


8 Start Analysis

The pushbutton *Start Analysis* is disabled until you have selected an analysis path and loaded the HDR- and XDF-files.

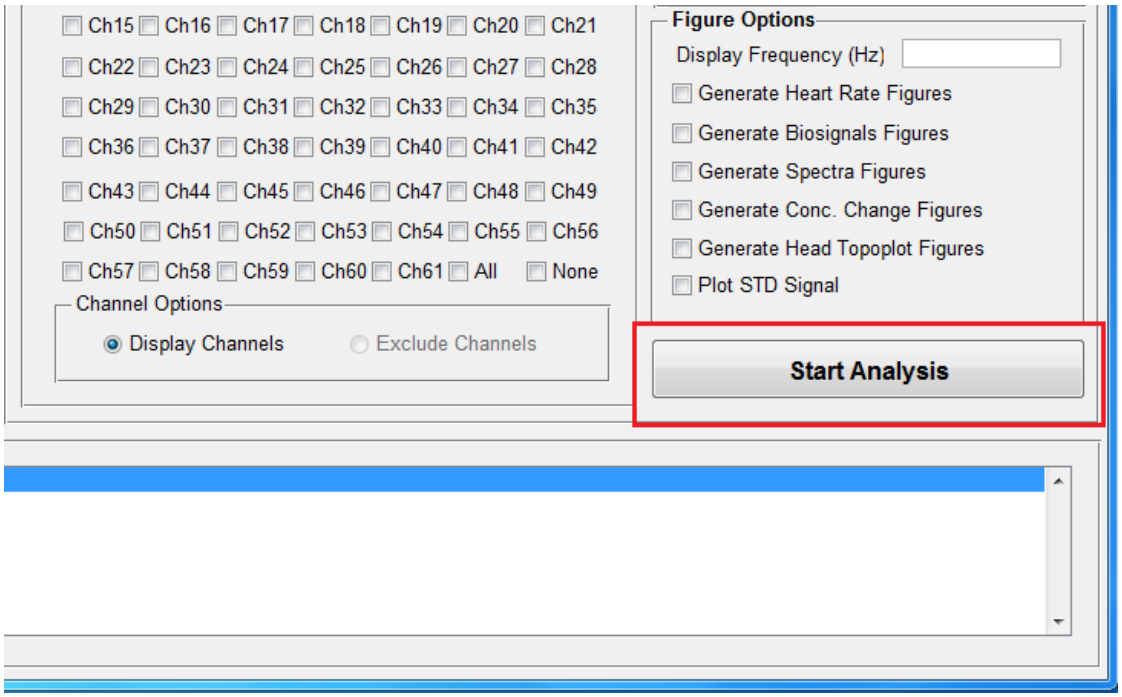


After selecting an analysis path and loading your measurement files, you have to enter your analysis settings. If your settings are incomplete, you will receive a warning:

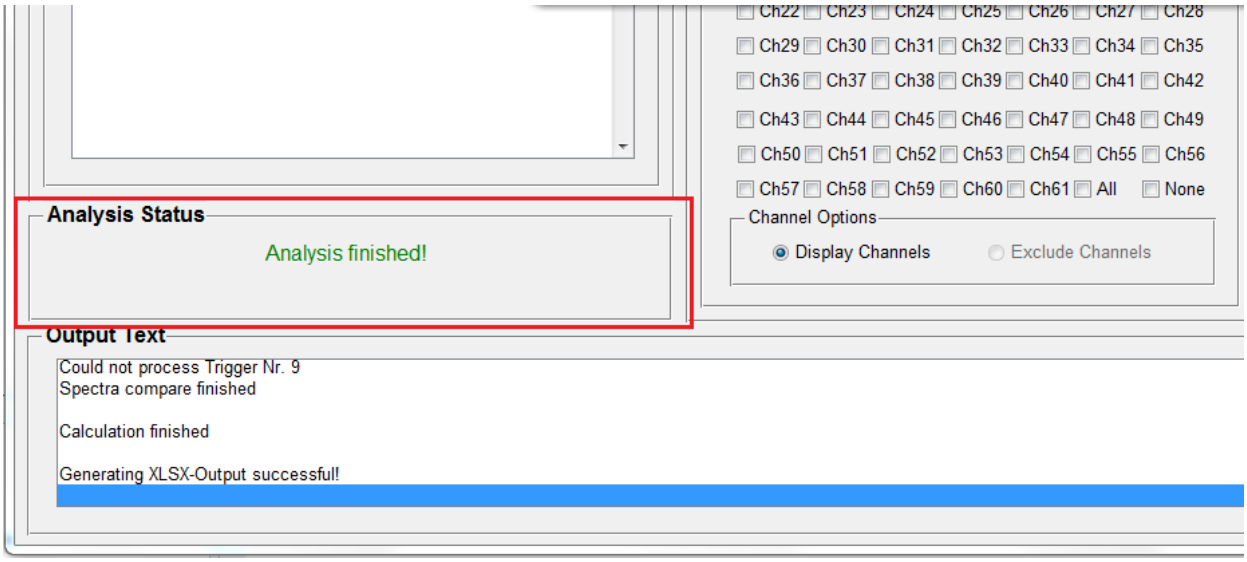


8.1 Single Analysis

If you have selected your analysis path, loaded your measurement files and all your settings are complete, you can start an analysis by clicking on the enabled pushbutton *Start Analysis.*



When the analysis has finished, you will hear a signal tone, and the analysis status displays the message *Analysis finished!*

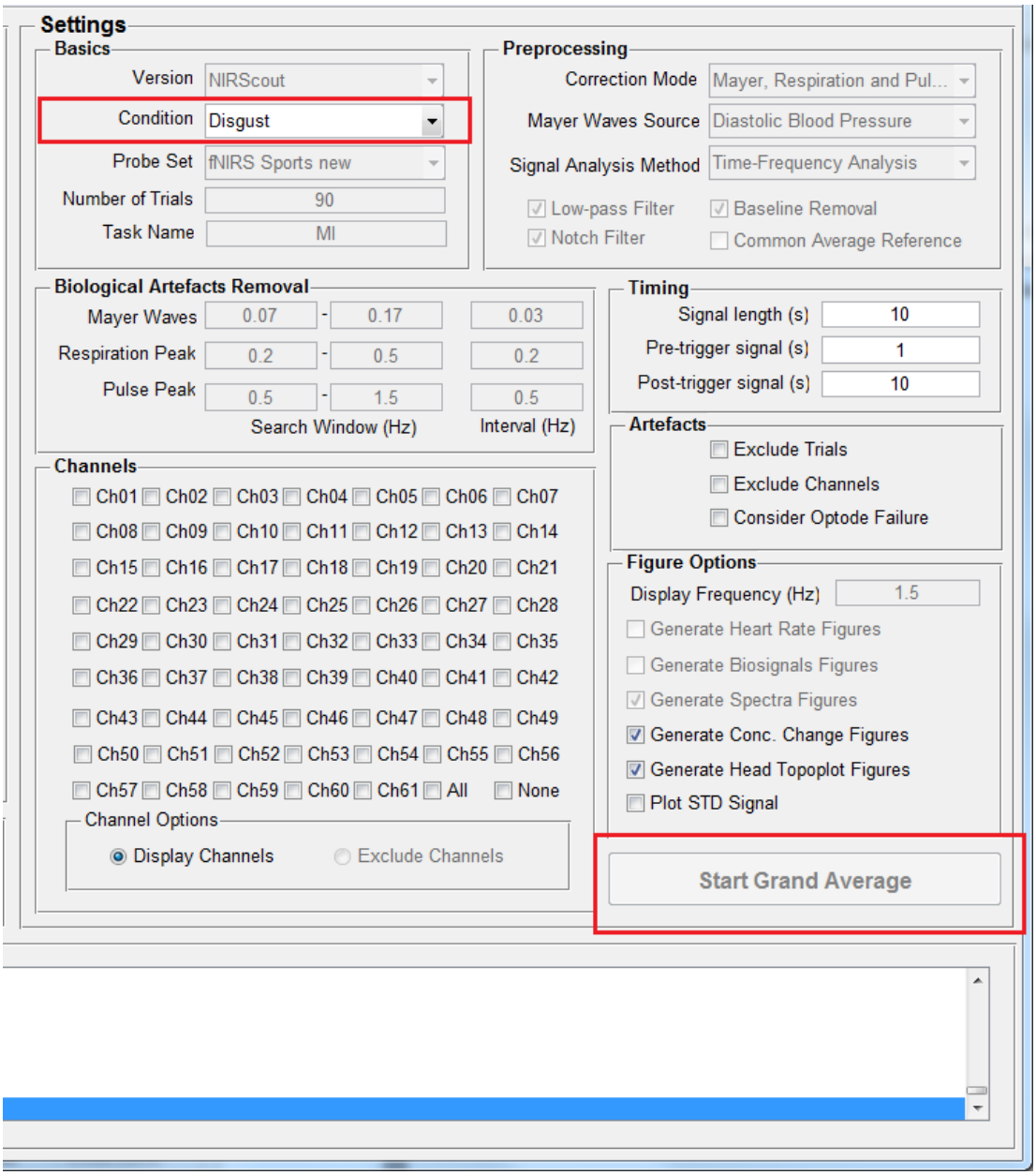


8.2 Grand Average

After you have finished all your single analyses, you can execute a grand average analysis of all your subjects. In order to do so, you have to choose the option *Grand Average/Start* at the menu bar (see chapter 4.4). After clicking on *Start*, the pushbutton *Start Analysis* changes its name to *Start Grand Average*. You have to select again an analysis path for the new output files. It is recommended to choose the same path as for your single analysis files.

You can also see that some setting options are disabled. This is simply because some settings can't be applied after a single analysis was done.

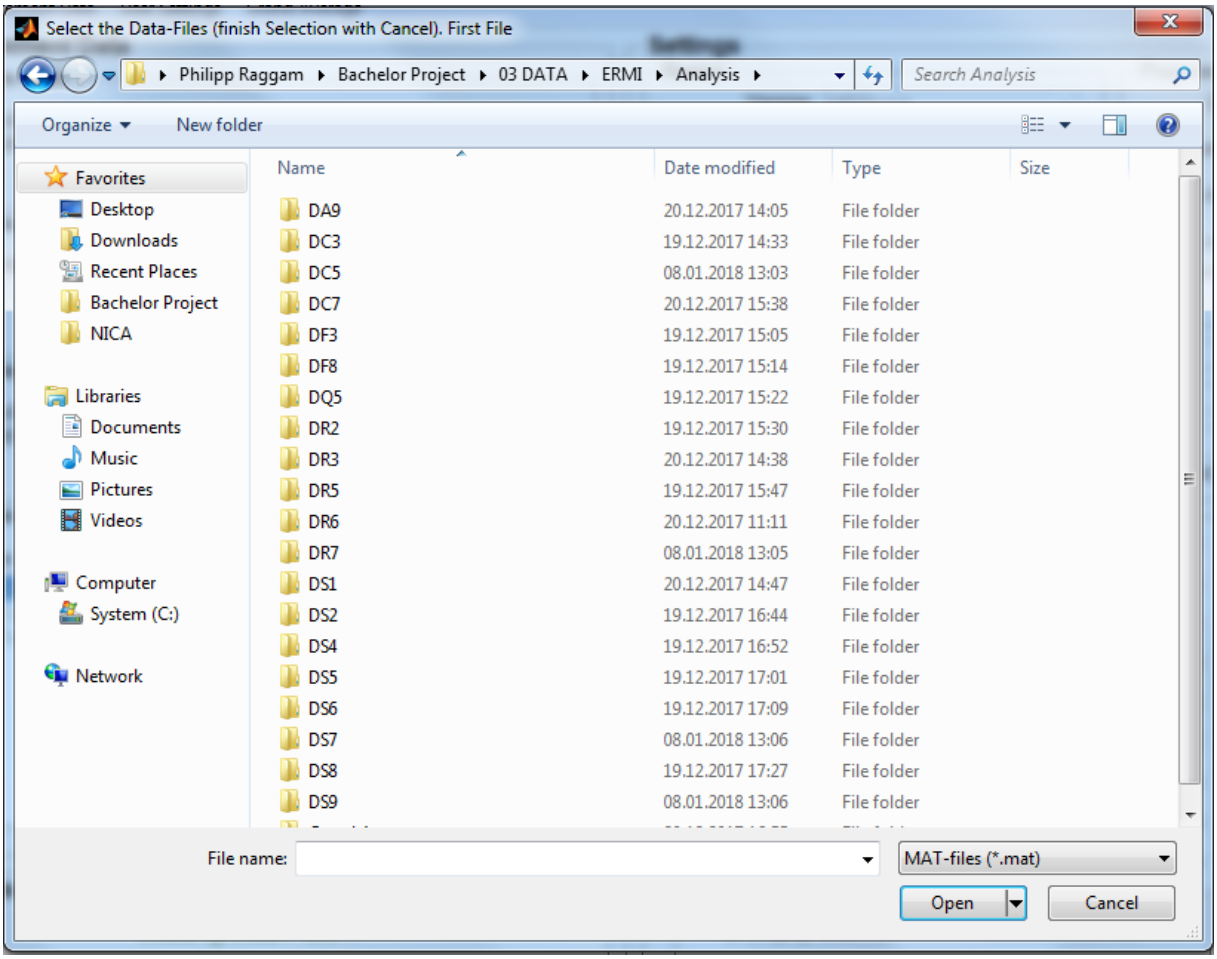
A very important option though is *Condition*. Your setting has to match with the conditions of the single analyses you want to average.



After you have selected your analysis path and finished your settings, the pushbutton *Start Grand Average* gets enabled and you can start your grand average analysis.

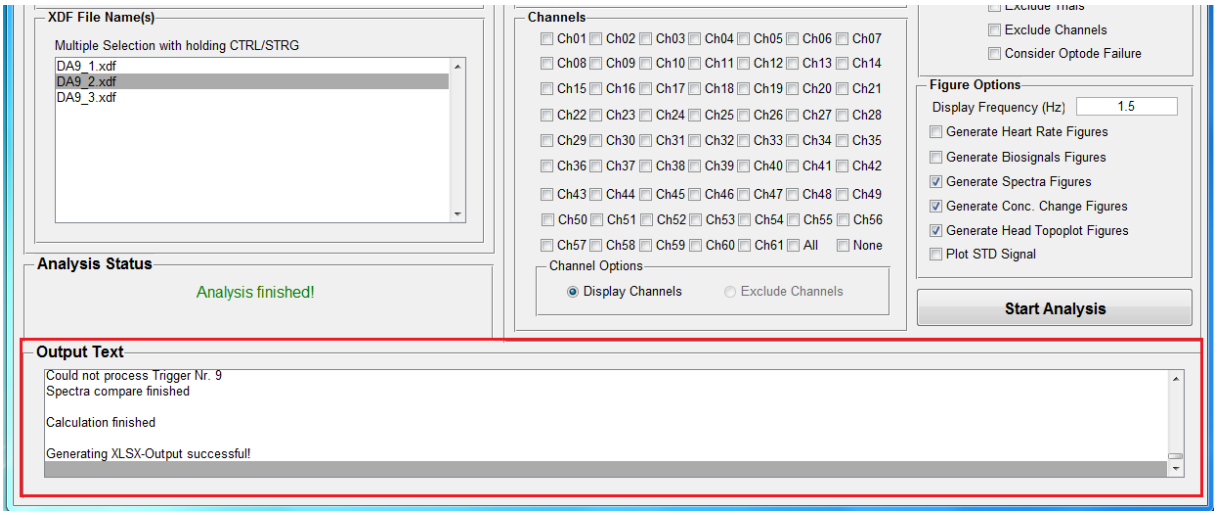
By clicking on the pushbutton *Start Grand Average* a file selection dialog box opens. You can now choose your files you want to have averaged. In order to do so, you have to select the MAT-file which was generated after the single analysis of your subject and saved accordingly to the condition. You can find a detailed description of the folder-structure at chapter 9.

After you have selected a MAT-file, the file selection dialog box opens again, and you can select your next file. This continues until you click on the *Cancel* button at the bottom right corner. The grand average analysis then starts automatically.



9 Output Text

The output text gives you a detailed explanation about the processes that are executed during an analysis. This can be especially useful, when an error occurs during an analysis. The output text is saved to a TXT-file (filename appendix *Text_Output*) in your analysis directory.



10 Output Files

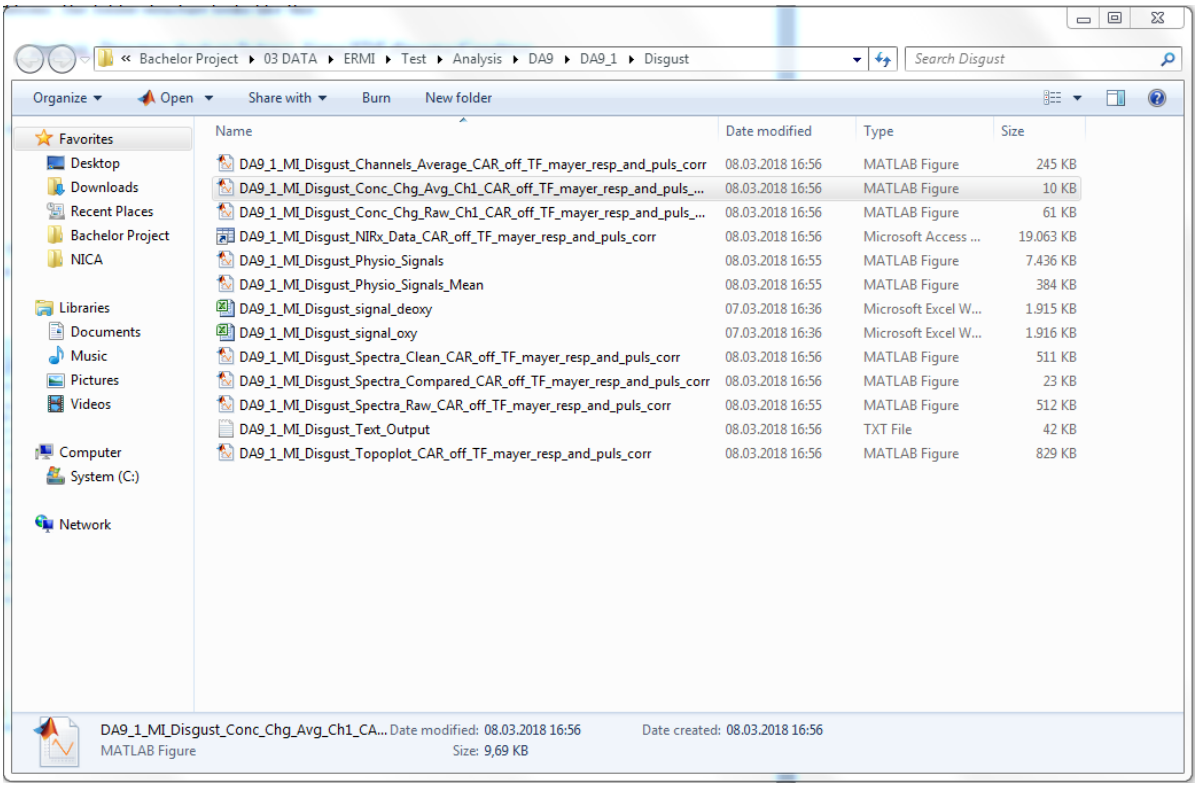
During an analysis, several output files are generated. The output files are saved to a directory, which is generated according to the name of your measurement data files and the conditions. The folder-structure looks like this:

Analysis_Directory/Analysis/Subject_Name/XDF-filename/Condition

The output files have the following structure:

XDF-filename_Task Name_Condition_Output Content_Preprocessing Settings

The output figures are saved as MAT-files, so you can still edit them afterwards (zoom in/out, use a data cursor, etc.)

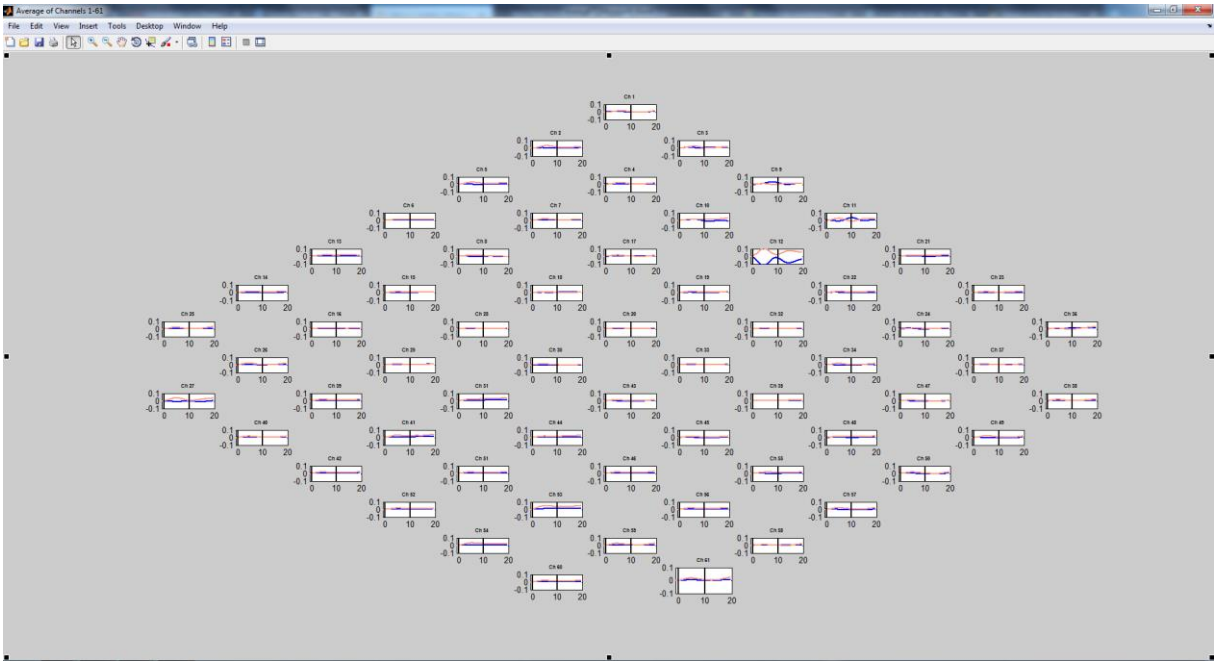


10.1 Data File

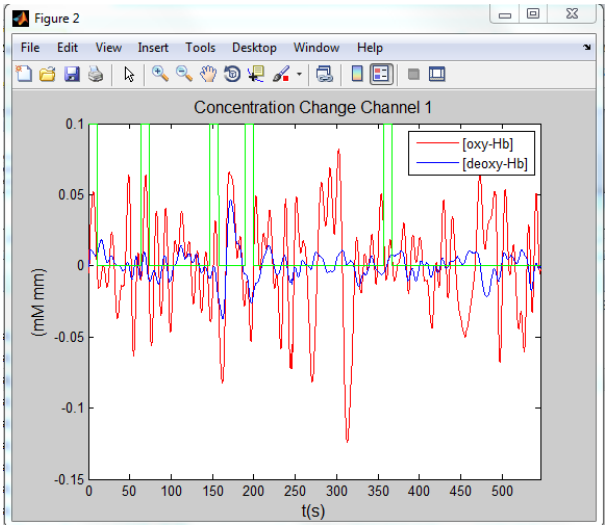
This file (appendix *NIRx_Data)* contains all the necessary information about your analysis (raw signals, oxy and deoxy signals, averaged signals, HDR-file information and user settings). Do not delete this file, because it is used for the grand average analysis.

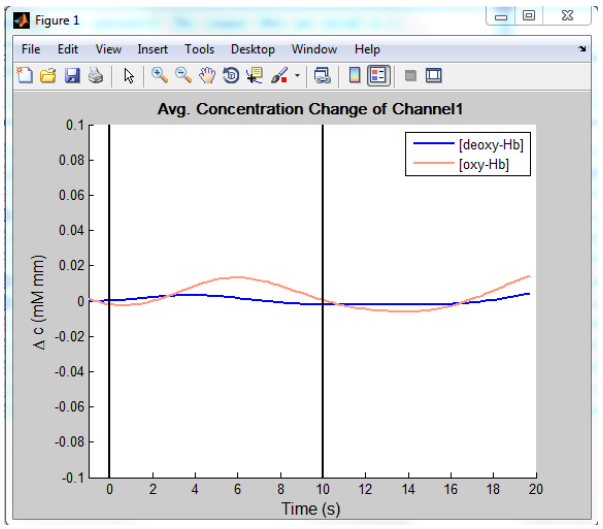
10.2 Concentration Change Figures

This figure (appendix *Channels_Average)* displays the concentration changes of oxy- and deoxyhaemoglobin averaged per trial of all channels individually. You can use the cursor to enlarge the figures individually.



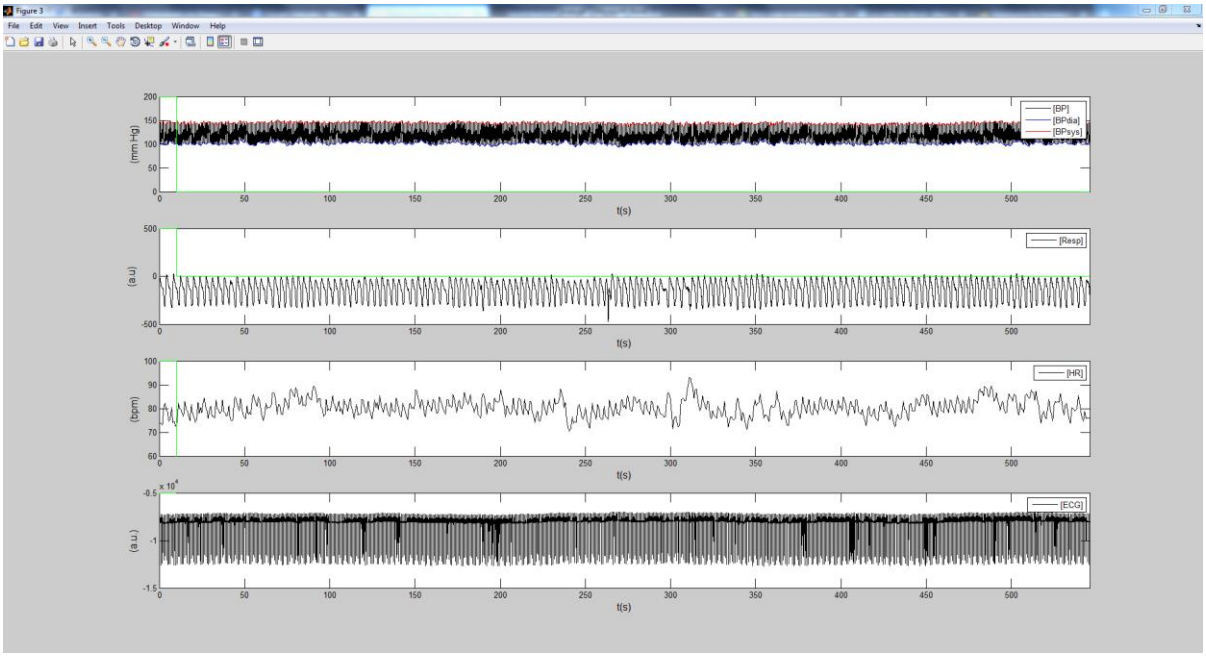
If you have selected a channel individually (*Settings/Channels*), two figures are generated to display the concentration changes of oxy- and deoxyhaemoglobin of the corresponding channel. The figure on the left shows the raw signal (appendix *Conc_Chg_Raw_Ch#*), including the triggers of the paradigm (in green). The figure on the right shows the averaged signal (appendix *Conc_Chg_Avg_Ch#*).



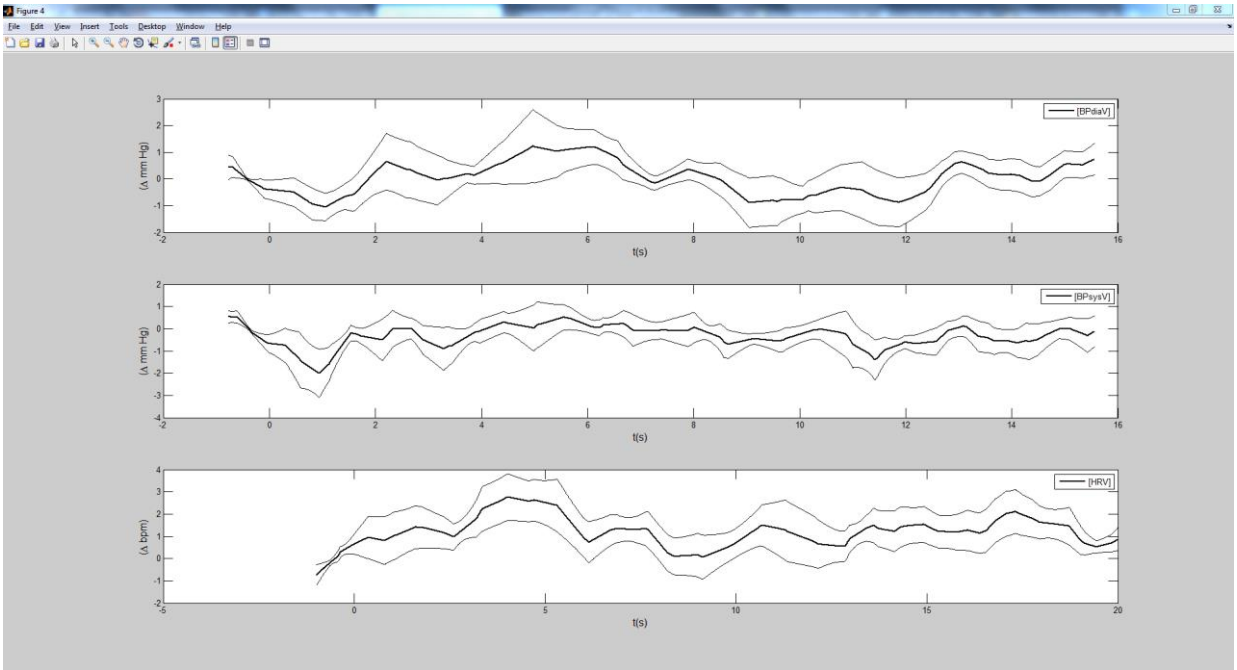


10.3 Biological Signals

The first figure (with the filename appendix *Physio_Signals*) contains for signals (from top to bottom): blood pressure (mmHg), respiration peaks (a.u.), heart rate (bpm) and the electrocardiogram (ECG, a.u.).

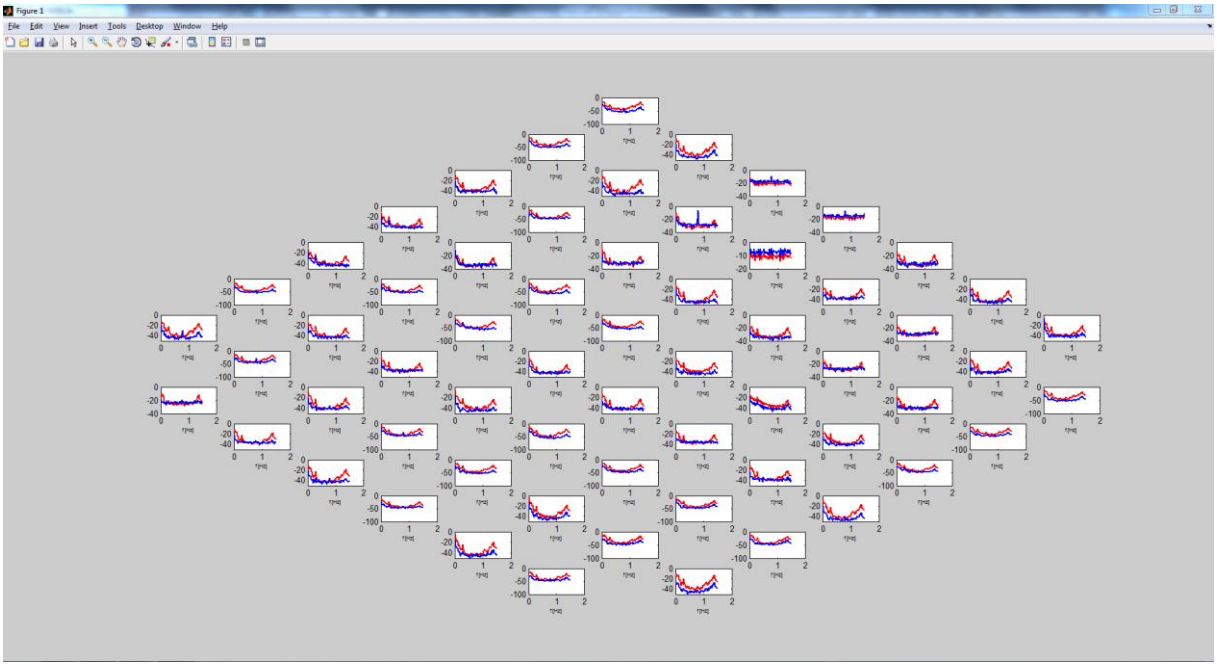


The second figure (with the filename appendix *Physio_Signals_Mean*) shows the changes in the diastolic blood pressure (Δ mmHg), systolic blood pressure (Δ mmHg) and the heart rate (Δ bpm).

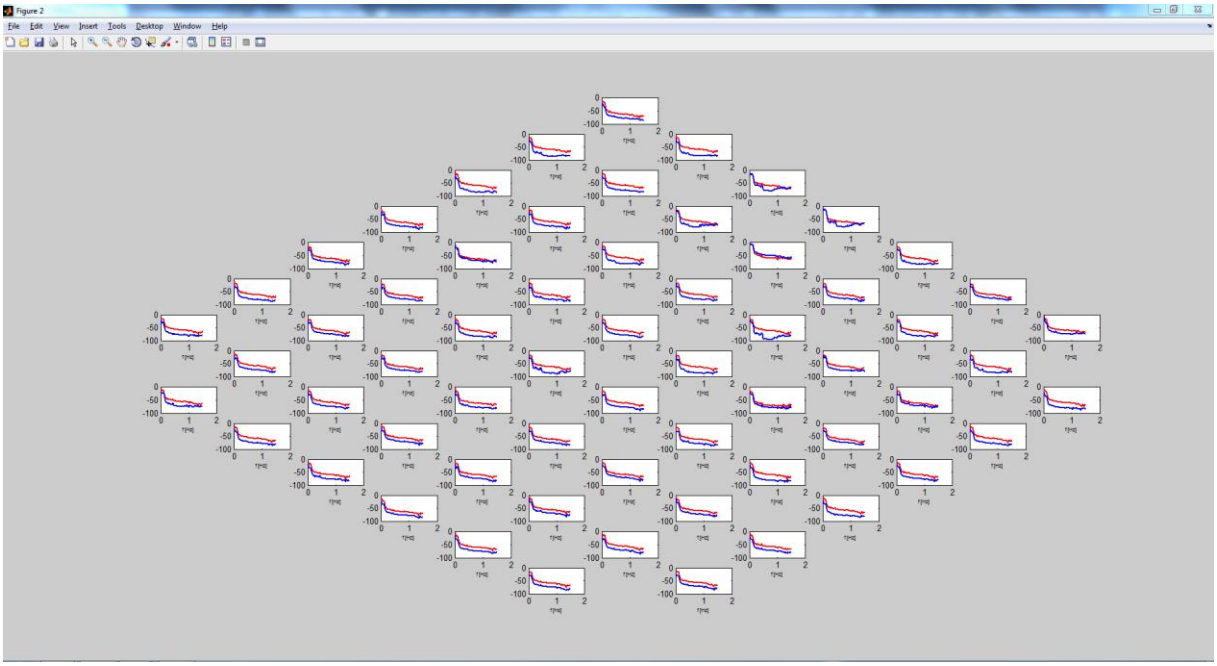


10.4 Spectrum Figures

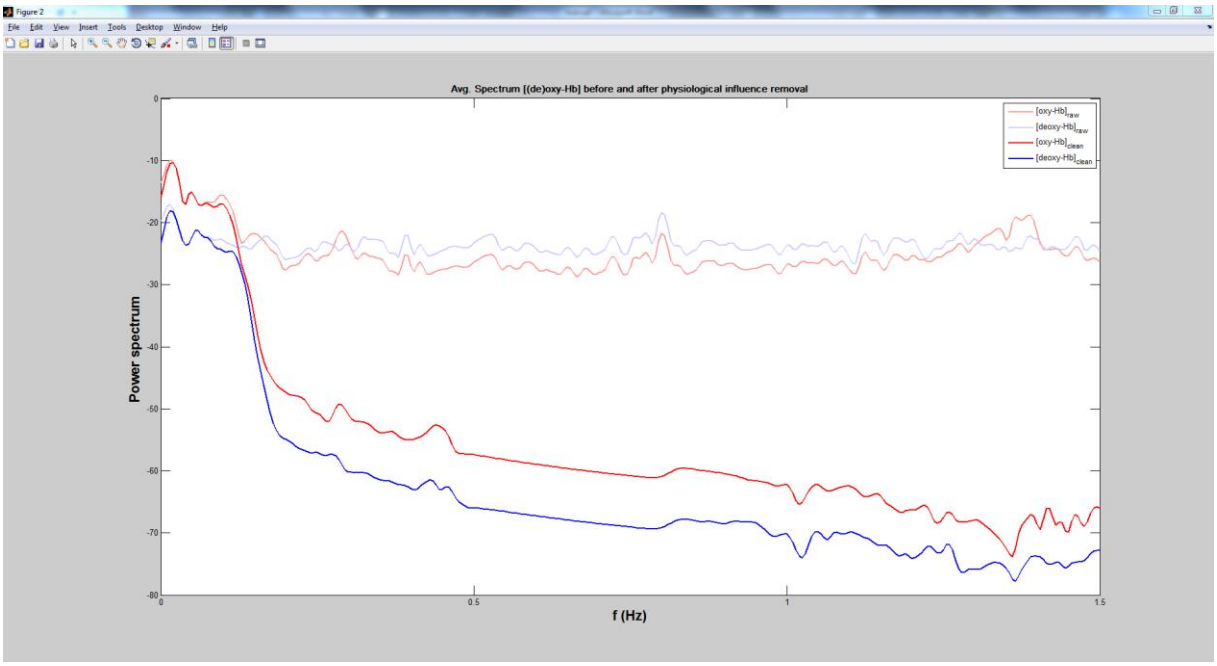
Frequency spectrum of each channel without biological artefact correction (filename appendix *Spectra_Raw*):



Frequency spectrum of each channel with biological artefact correction (filename appendix *Spectra_Clean):*

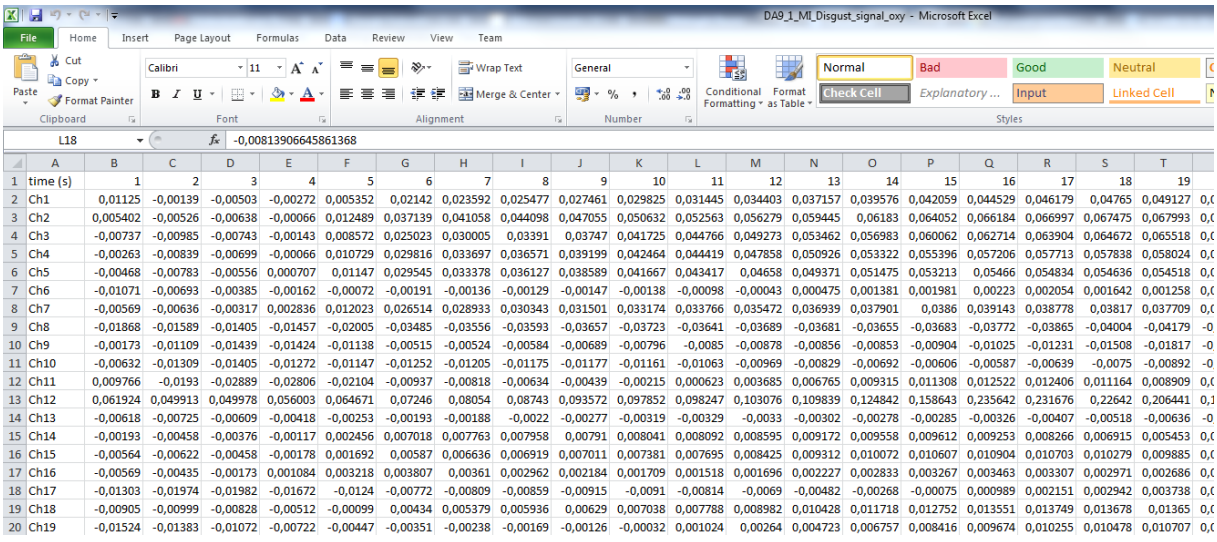


Comparison of the frequency spectra with and without biological artefact correction, averaged over all channels (filename appendix *Spectra_Compared*):



10.5 Excel Files

Two excel-files are generated (appendix *signal_oxy* and *signal_deoxy*), containing the value of the concentration change of oxy- and deoxyhaemoglobin of every time point of the recording of every channel. The structure of the Excel-sheet was created in order to fit the specifications of the analysis software *SPSS*.



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	time (s)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
2	Ch1	0,01125	-0,00139	-0,00503	-0,00272	0,005352	0,02142	0,023592	0,025477	0,027461	0,029825	0,031445	0,034403	0,037157	0,039576	0,042059	0,044529	0,046179	0,04765	0,049127
3	Ch2	0,005402	-0,00526	-0,00638	-0,00066	0,012489	0,037139	0,041058	0,044098	0,047055	0,050632	0,052563	0,056279	0,059445	0,06183	0,064052	0,066184	0,066997	0,067475	0,067993
4	Ch3	-0,00737	-0,00985	-0,00743	-0,00143	0,008572	0,025023	0,030005	0,03391	0,03747	0,041725	0,044766	0,049273	0,053462	0,056983	0,060062	0,062714	0,063904	0,064672	0,065518
5	Ch4	-0,00263	-0,00839	-0,00699	-0,00066	0,010729	0,029816	0,033697	0,036571	0,039199	0,042464	0,044419	0,047858	0,050926	0,053322	0,055396	0,057206	0,057713	0,057838	0,058024
6	Ch5	-0,00468	-0,00783	-0,00556	0,000707	0,01147	0,029545	0,033378	0,036127	0,038589	0,041667	0,043417	0,04658	0,049371	0,051475	0,053213	0,05466	0,054834	0,054636	0,054518
7	Ch6	-0,01071	-0,00693	-0,00385	-0,00162	-0,00072	-0,00191	-0,00136	-0,00129	-0,00147	-0,00138	-0,00098	-0,00043	0,000475	0,001381	0,001981	0,00223	0,002054	0,001642	0,001258
8	Ch7	-0,00569	-0,00636	-0,00317	0,002836	0,012023	0,026514	0,028933	0,030343	0,031501	0,033174	0,033766	0,035472	0,036939	0,037901	0,0386	0,039143	0,038778	0,03817	0,037709
9	Ch8	-0,01868	-0,01589	-0,01405	-0,01457	-0,02005	-0,03485	-0,03556	-0,03593	-0,03657	-0,03723	-0,03641	-0,03689	-0,03681	-0,03655	-0,03683	-0,03772	-0,03865	-0,04004	-0,04179
10	Ch9	-0,00173	-0,01109	-0,01439	-0,01424	-0,01138	-0,00515	-0,00524	-0,00584	-0,00689	-0,00796	-0,0085	-0,00878	-0,00856	-0,00853	-0,00904	-0,01025	-0,01231	-0,01508	-0,01817
11	Ch10	-0,00632	-0,01309	-0,01405	-0,01272	-0,01147	-0,01252	-0,01205	-0,01175	-0,01177	-0,01161	-0,01063	-0,00969	-0,00829	-0,00692	-0,00606	-0,00587	-0,00639	-0,0075	-0,00892
12	Ch11	0,009766	-0,0193	-0,02889	-0,02806	-0,02104	-0,00937	-0,00818	-0,00634	-0,00439	-0,00215	0,000623	0,003685	0,006765	0,009315	0,011308	0,012522	0,012406	0,011164	0,008909
13	Ch12	0,061924	0,049913	0,049978	0,056003	0,064671	0,07246	0,08054	0,08743	0,093572	0,097852	0,098247	0,103076	0,109839	0,124842	0,158643	0,235642	0,231676	0,22642	0,206441
14	Ch13	-0,00618	-0,00725	-0,00609	-0,00418	-0,00253	-0,00193	-0,00188	-0,0022	-0,00277	-0,00319	-0,00329	-0,0033	-0,00302	-0,00278	-0,00285	-0,00326	-0,00407	-0,00518	-0,00636
15	Ch14	-0,00193	-0,00458	-0,00376	-0,00117	0,002456	0,007018	0,007763	0,007958	0,00791	0,008041	0,008092	0,008595	0,009172	0,009558	0,009612	0,009253	0,008266	0,006915	0,005453
16	Ch15	-0,00564	-0,00622	-0,00458	-0,00178	0,001692	0,00587	0,006636	0,006919	0,007011	0,007381	0,007695	0,008425	0,009312	0,010072	0,010607	0,010904	0,010703	0,010279	0,009885
17	Ch16	-0,00569	-0,00435	-0,00173	0,001084	0,003218	0,003807	0,00361	0,002962	0,002184	0,001709	0,001518	0,001696	0,002227	0,002833	0,003267	0,003463	0,003307	0,002971	0,002686
18	Ch17	-0,01303	-0,01974	-0,01982	-0,01672	-0,0124	-0,00772	-0,00809	-0,00859	-0,00915	-0,0091	-0,00814	-0,0069	-0,00482	-0,00268	-0,00075	0,000989	0,002151	0,002942	0,003738
19	Ch18	-0,00905	-0,00999	-0,00828	-0,00512	-0,00099	0,00434	0,005379	0,005936	0,00629	0,007038	0,007788	0,008982	0,010428	0,011718	0,012752	0,013551	0,013749	0,013678	0,01365
20	Ch19	-0,01524	-0,01383	-0,01072	-0,00722	-0,00447	-0,00351	-0,00238	-0,00169	-0,00126	-0,00032	0,001024	0,00264	0,004723	0,006757	0,008416	0,009674	0,010255	0,010478	0,010707

10.6 Text File

The output text of an analysis is saved to a TXT-file (appendix *Text_Output*).

10.7 Head Topoplot

This figure contains topoplots of the head: a coloured representation of the concentration changes of oxy- and deoxyhaemoglobin of all channels, divided into 4 time periods. The colour spectrum goes from red (positive concentration change) to blue (negative concentration change).