



**Neurophotronics
Center**



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For Biomedical Imaging



fNIRS Data Analysis with Homer3

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Outline

- ◇ **Homer file formats**
- ◇ **Basic processing :**
 - ◇ Intensity to hemoglobin concentrations
 - ◇ Filtering
 - ◇ Block-averaging
- ◇ **More advanced processing :**
 - ◇ Other useful Homer functions
 - ◇ Exporting results
 - ◇ Plot probe
 - ◇ Group analysis

File formats

- Probe source-detector geometry : **.sd** files
- fNIRS experimental data : **.nirs** files
- fNIRS experimental data* : **.snirf** files **(new)**
- Data processing stream : **.cfg** files
- Processed data files : **groupResults.mat**

.SD file format

Describes the 2D source/detector geometry

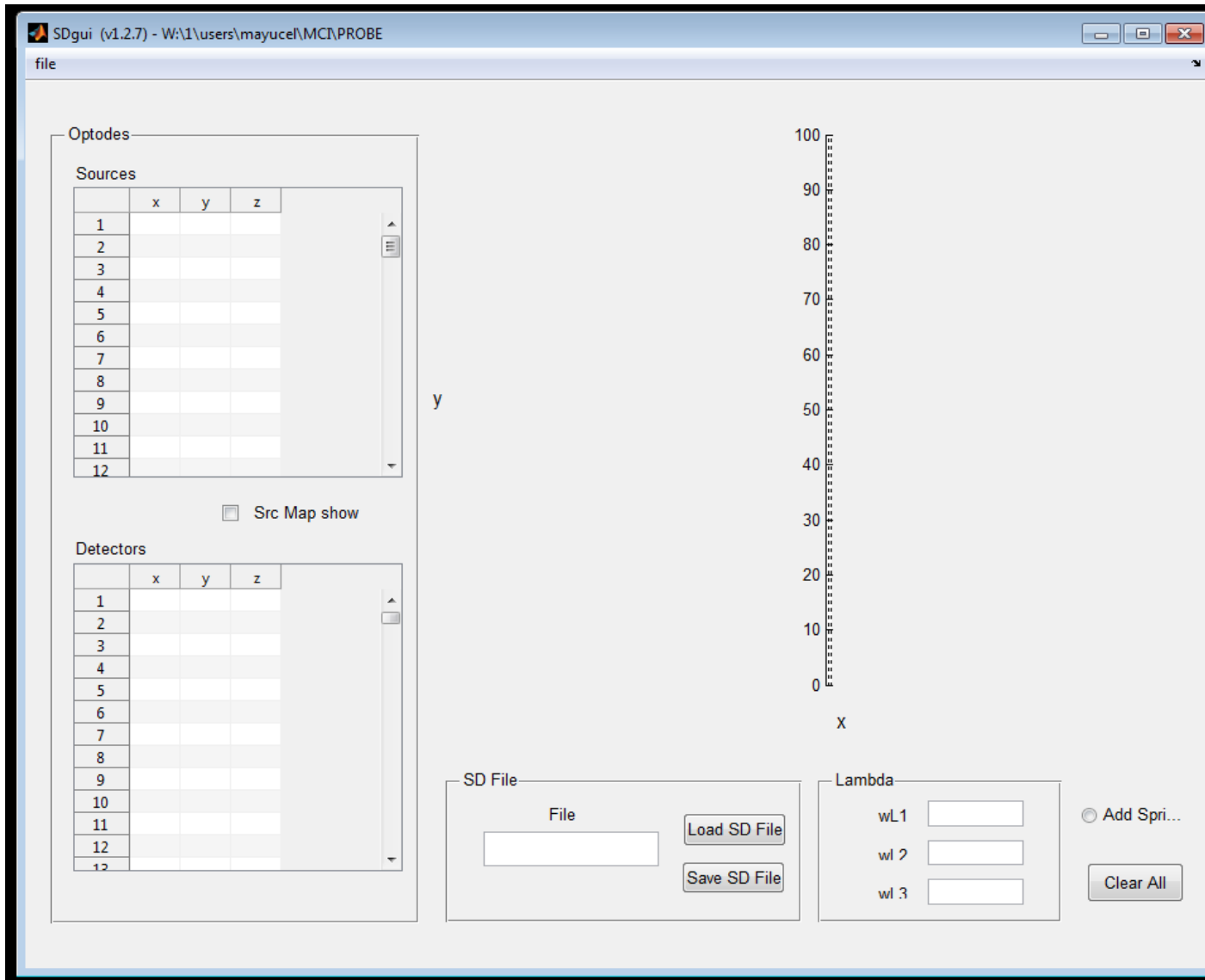
Matlab .sd file containing the structured variable **SD** with the following fields:

Field	Definition	Size	Example
Lambda	Wavelengths used for data acquisition	$1 \times n_{\text{Wavelengths}}$	[690 830]
nSrcs	Number of sources	1×1	1
nDets	Number of detectors	1×1	2
SrcPos	Array of source coordinates	$n_{\text{Srcs}} \times 3$	[0 0 0]
DetPos	Array of detector coordinates	$n_{\text{Dets}} \times 3$	[30 0 0; 0 30 0]
MeasList	List of measurement channels	$n_{\text{Channels}} \times 4$	[1 1 1 1; 1 2 1 1; 1 1 1 2; 1 2 1 2]
	<u>column 1</u> <u>column 2</u> <u>column 3</u> <u>column 4</u> source idx detector idx unused wavelength idx		

Note: The SD structure is also incorporated in the .nirs file format we will see in a few slides

.SD file format: the SDgui

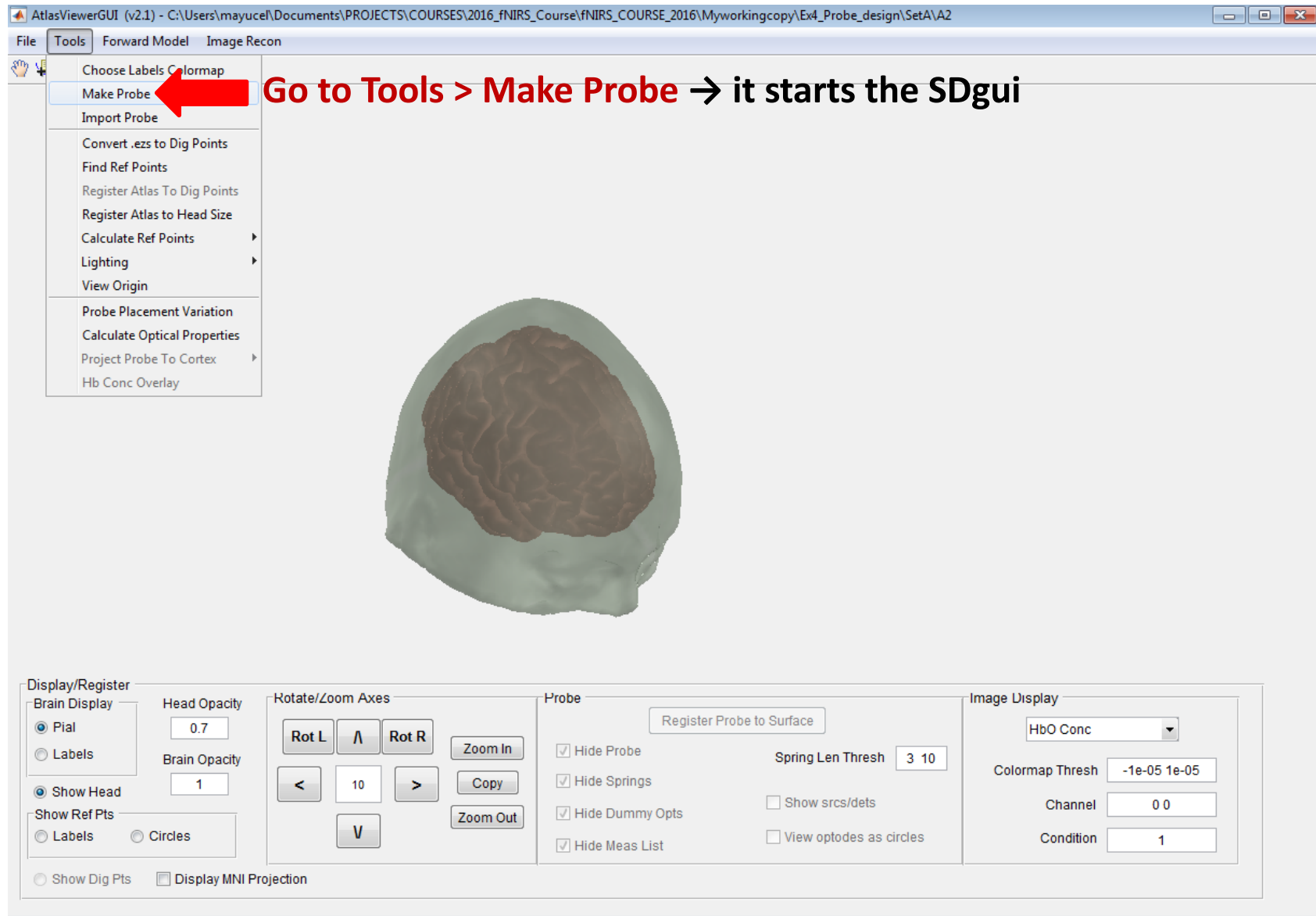
Enables you to create your own .sd files



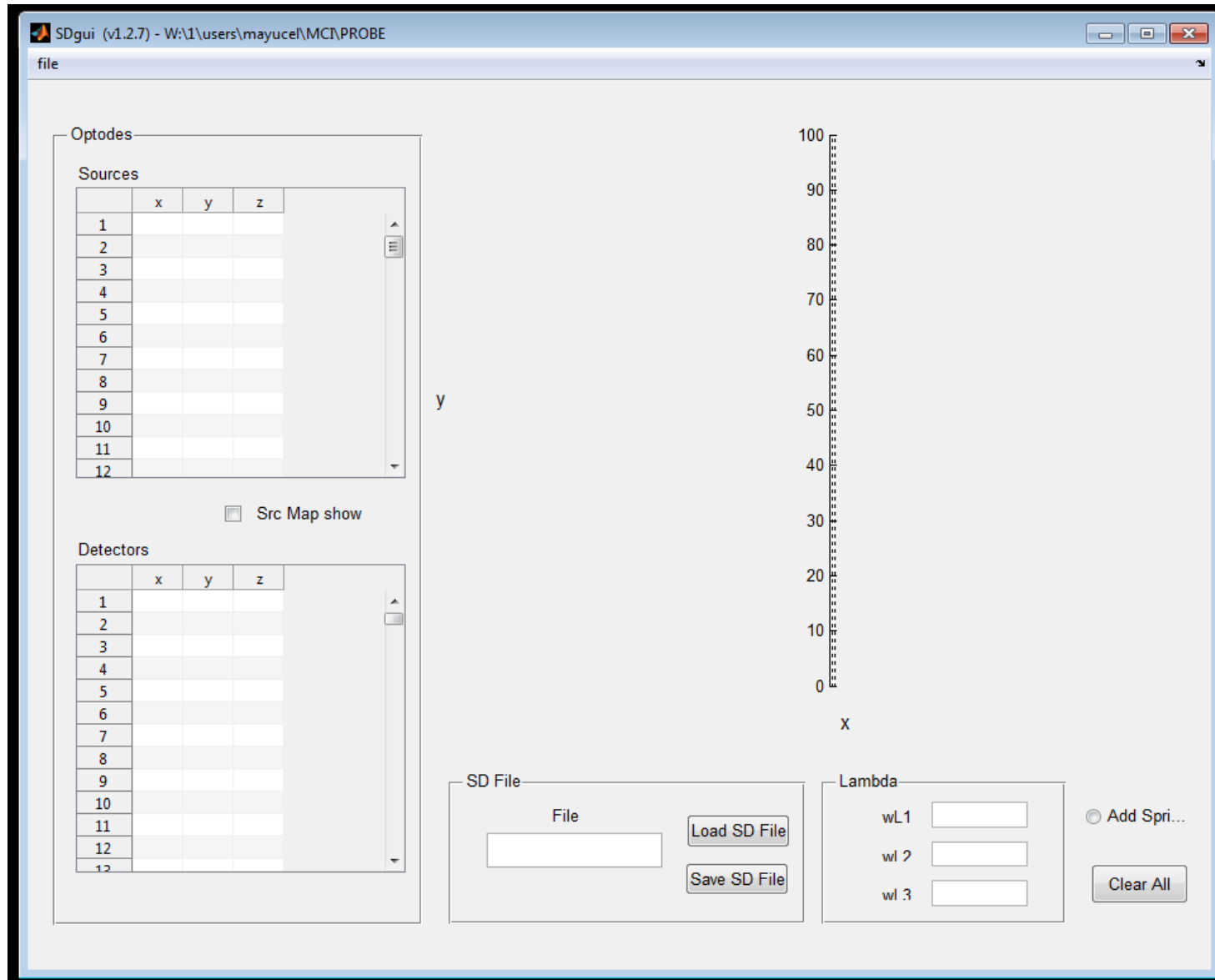
Sub-GUI of AtlasViewer

.SD file format: the SDgui

Start AtlasViewer



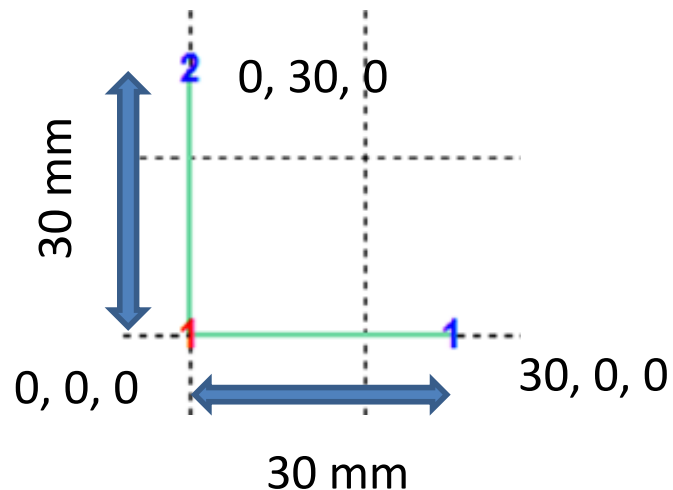
SDgui



How to start

1. Begin by naming the new probe using the text box at the bottom-center of the GUI
2. Enter the wavelengths of light that will be used in the experiment (690 830)

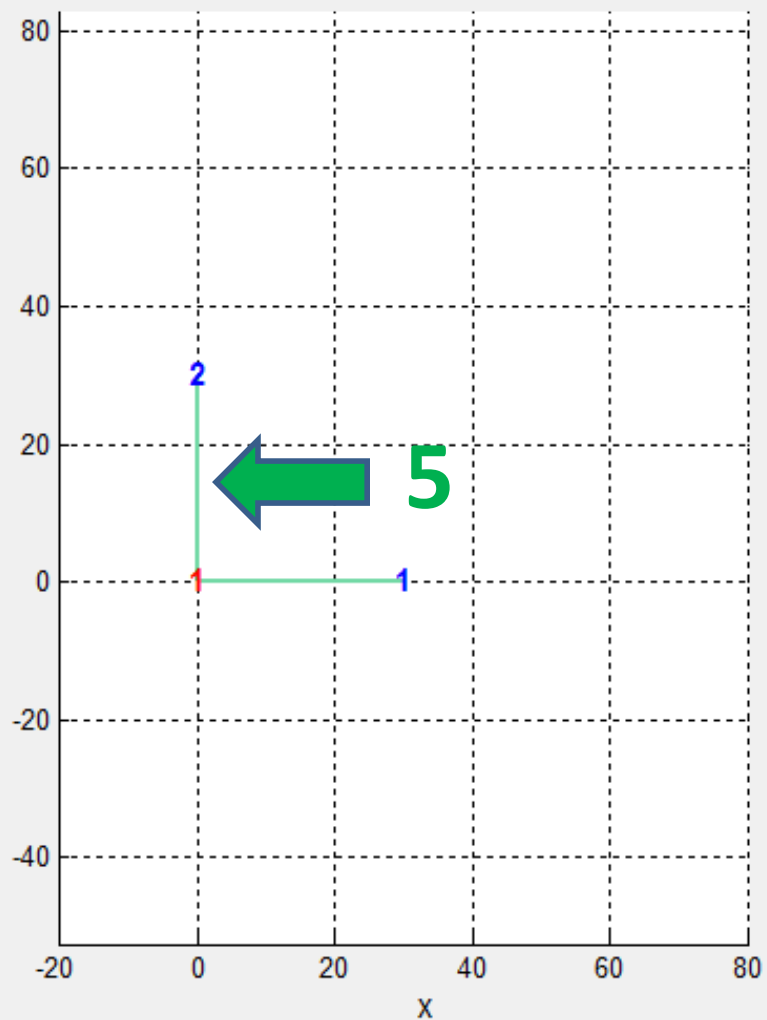
Hint: easier if you have your 2D design on a piece of paper with the distances eg:



Adding sources, detectors and channels

3. Place a source at $(0, 0, 0)$
4. Add detectors at $(30, 0, 0)$ and $(0, 30, 0)$
5. Connect measurement channels by clicking on optodes
 - to remove a channel do the same
 - you cannot connect two detectors or two sources

2D PROBE LAYOUT



Optodes

Sources

	x	y	z
1	0	0	0
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			

Src Map show

Detectors

	x	y	z
1	30	0	0
2	0	30	0
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
12			

SD File

File

test.SD

Load SD File

Save SD File

Lambda

wL1

690

wl 2

830

wl 3

Add Spri...

Clear All

.NIRS file format

Contains an fNIRS dataset

Matlab .nirs file containing the following variables:

Field	Definition	Size
SD	Probe geometry, same as .sd files	Structured variable
t	Array of data time points	$N_{\text{Time_points}} \times 1$
d	Array of raw intensity time course	$N_{\text{Time_points}} \times N_{\text{Channels}}$
s	Array of stimulus onsets. Different conditions are a way to separate stimuli into different groups	$N_{\text{Time_points}} \times N_{\text{Conditions}}$
aux	Array of auxiliary signals	$N_{\text{Time_points}} \times N_{\text{Aux channels}}$

Note 1: In addition to the above parameters, additional parameters can appear in the .nirs file as a result of processing the data set in HOMER3.

Note 2: Conversion scripts are available for some other data formats (Hitachi, NIRx, Shimadzu, ...), see <http://homer-fnirs.org/faq/>

.SNIRF file format

- many different fNIRS data file format
- difficult to use specific data analysis software and share data with collaborators
- **Common format: Shared Near InfraRed File Format**
<http://github.com/fNIRS/snirf>
- SNIRF provides numeric fNIRS data with time stamps and a so-called 'measurement list' for detailed measurement information (in **HDF5 format**)

github.com/fNIRS/snirf/blob/master/snirf_specification.md#snirf-data-format-summary

Finally, we have launched a SNIRF list server. The relevant addresses are here:

Mail list: snirf@fnirs.org

Help address: snirf-help@fnirs.org

Subscription address: snirf-subscribe@fnirs.org

Unsubscription address: snirf-unsubscribe@fnirs.org

Shared Near Infrared File Format V1.0 Specification

- Document Version: Draft 3
- License: This document is in the public domain.

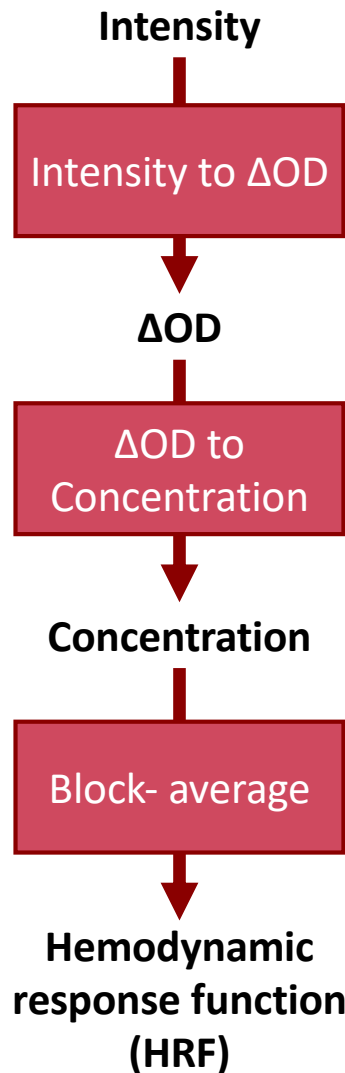
Table of Content

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 - data.measurementList.detectorIndex

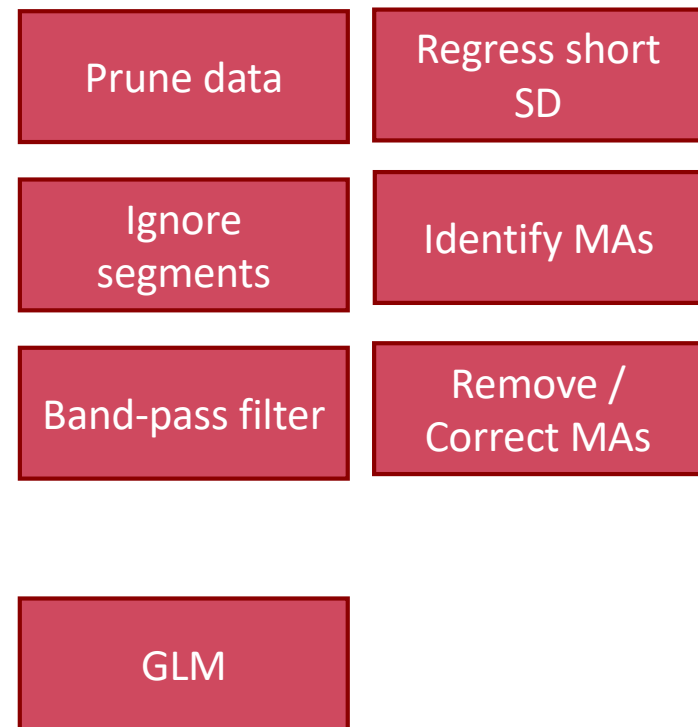
.CFG file format

A .cfg file describes the steps of data analysis, a sequence of **HOMER3 functions**

Simplest processing stream:



Multiple more advanced functions we can incorporate in the stream:



Note: In options, you can hover over each function to get help on the function and the parameters

.CFG file format: the Process Stream GUI

The Process Stream GUI enables you to create your own .cfg files

Start Homer3
Go to Tools > Edit Process Stream → it starts procStreamGUI

The screenshot displays the Homer3 (v1.14.1) application window. The 'Tools' menu is open, with 'Edit Processing Stream' selected. The main window features a large empty plot area with axes ranging from 0 to 1. Below the plot is a control panel with several sections: 'Current Processing Element' (empty list), 'Processing Level' (radio buttons for Group, Subj, Run), 'Plot Type Select' (radio buttons for Raw Data, OD, Conc; dropdown for HbO, HbR, HbT; checkboxes for HRF and Aux), 'Motion Artifacts' (checkboxes for Show Excluded Manual, Show Excluded Auto, Show Excluded by Chan, and Exclude Time), and 'Plot Window' (Pan Left/Right buttons, Fix X-range with value 0 400, and Fix Y-range with value -2 2). Buttons for 'Calculate', 'Edit Options', and 'Apply to all' are also visible.

.CFG file format

Add, remove, and move function usages in processing stream

The processing stream you're creating

User functions registry: The list of functions to choose from

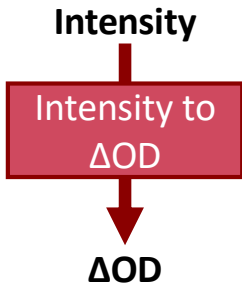
The screenshot shows the 'procStreamGUI' application window. It features a menu bar with 'File' and 'Edit Processing Stream'. The main interface is divided into several sections:

- Function names:** A table with columns 'Run', 'Subject', and 'Group'. It contains two sub-lists: 'Registry Functions' and 'Usage Options'. The 'Registry Functions' list includes items like 'hmrR_BandpassFilt', 'hmrR_BlockAvg', 'hmrR_GLM', etc. The 'Usage Options' list currently shows 'Bandpass_Filter'.
- Possible usages for function:** A set of control buttons: 'Add', 'Delete', 'Up', 'Down', 'Load', 'Save', and 'Exit'.
- Function usages:** A section titled 'Current Processing Stream' with a large empty list area for adding function usages.
- Help information:** A text area at the bottom showing the syntax and description for the selected 'Bandpass_Filter' function. The syntax is: `data2 = hmrR_BandpassFilt(data, hpf, lpf)`. The description states: 'Perform a bandpass filter on time course data.' The input parameters are: 'data' (SNIRF data type), 'hpf' (high pass filter frequency in Hz, typical 0 to 0.02), and 'lpf' (low pass filter frequency in Hz, typical 0.5 to 3).

Help information for the selected function or usage option

File Error Status:

.CFG file format



The screenshot shows the `procStreamGUI` window with the following components:

- Registry Functions:** A list of functions including `hmrR_BandpassFilter`, `hmrR_BlockAvg`, `hmrR_GLM`, `hmrR_Intensity2OD` (highlighted with a red arrow labeled '1'), `hmrR_MotionArtifact`, `hmrR_MotionArtifactByChannel`, `hmrR_MotionCorrectCbsi`, `hmrR_MotionCorrectPCA`, `hmrR_MotionCorrectPCArecurse`, `hmrR_MotionCorrectRLOESS`, `hmrR_MotionCorrectSpline`, `hmrR_MotionCorrectSplineSC`, `hmrR_MotionCorrectWavelet`, `hmrR_OD2Conc`, `hmrR_OD2Conc_new`, `hmrR_PCFilter`, `hmrR_PruneChannels`, and `hmrR_StimRejection`.
- Usage Options:** A list containing `Intensity_to_Delta_OD` (highlighted with a red arrow labeled '2').
- Buttons:** `Add`, `Delete`, `Up`, `Down`, `Load`, `Save`, `Exit`, and `Clear All`.
- Current Processing Stream:** A list containing `hmrR_Intensity2OD : Intensity_to_Delta_OD`.
- SYNTAX:**

```
dod = hmrR_Intensity2OD( intensity )
```
- UI NAME:**

```
Intensity_to_Delta_OD
```
- DESCRIPTION:**

```
Converts intensity data to optical density
```
- INPUT:**

```
intensity - SNIRF data type where the d matrix is intensity
```
- OUTPUT:**

```
dod - SNIRF data type where the d matrix is change in optical density
```
- USAGE OPTIONS:**

```
Intensity_to_Delta_OD: dod = hmrR_Intensity2OD(data)
```

.CFG file format

The screenshot displays the 'procStreamGUI' application window. It features a menu bar with 'File' and a toolbar with 'Run', 'Subject', and 'Group' buttons. The main interface is divided into three columns: 'Registry Functions', 'Usage Options', and 'Current Processing Stream'. The 'Registry Functions' column lists various functions like 'hmrR_BandpassFilt', 'hmrR_BlockAvg', etc. The 'Usage Options' column shows 'Bandpass_Filter'. The 'Current Processing Stream' column contains two entries: 'hmrR_Intensity2OD : Intensity to Delta_OD' and 'hmrR_BandpassFilt : Bandpass_Filter'. A red oval highlights this 'Current Processing Stream' column. Below the columns are buttons for 'Add', 'Delete', 'Up', 'Down', 'Load', and 'Exit'. A 'Clear All' button is also present, highlighted with a red oval. A text box in the center reads: 'Processing stream loaded from default config file. Start fresh with an empty processing stream by clearing all entries.' At the bottom, a 'SYNTAX:' section provides details for the 'hmrR_BandpassFilt' function, including its UI name, description, and input parameters.

Processing stream loaded from default config file. Start fresh with an empty processing stream by clearing all entries.

```
SYNTAX:
data2 = hmrR_BandpassFilt( data, hpf, lpf, 1)

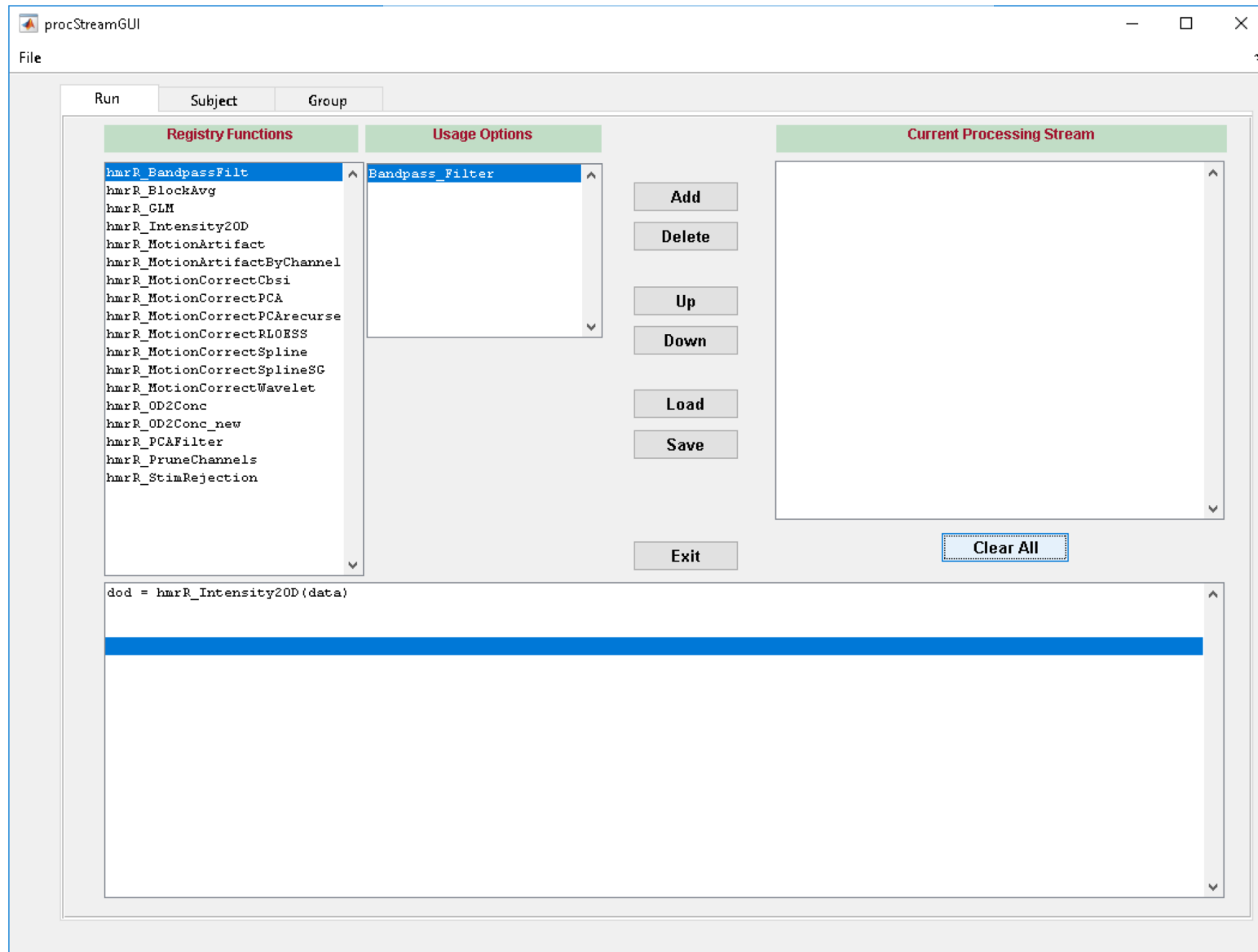
UI NAME:
Bandpass_Filter

DESCRIPTION:
Perform a bandpass filter on time course data.

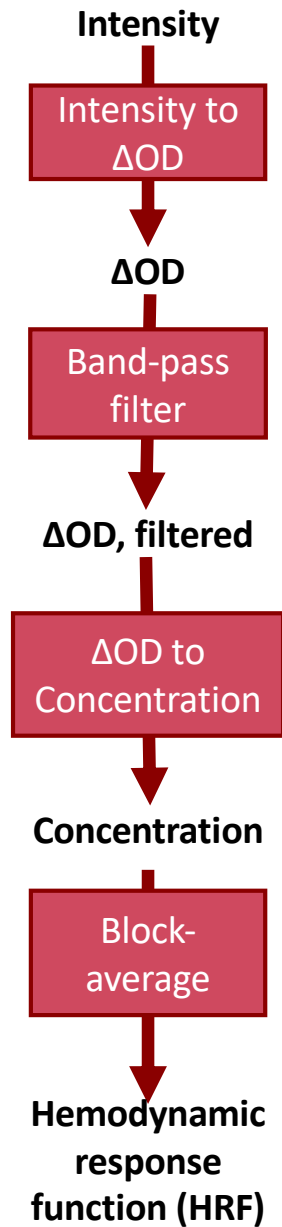
INPUT:
data - SNIRF data type containing data time course to filter, time
vector, and channels.
hpf - high pass filter frequency (Hz)
Typical value is 0 to 0.02.
lpf - low pass filter frequency (Hz)
Typical value is 0.5 to 3.
```

.CFG file format

Your GUI should look like this now,
with no entries in Current Processing
Stream window



.CFG file format



ProcStreamEditGUI: (1.14.2) - c:\j\ubb\workspaces\subjects\fmirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps

File

Run Subject Group

Registry Functions	Usage Options	Current Processing Stream
hmrR_BandpassFilt hmrR_BlockAvg hmrR_CLM hmrR_Intensity2OD hmrR_MotionArtifact hmrR_MotionArtifactByChannel hmrR_MotionCorrectCbsi hmrR_MotionCorrectPCA hmrR_MotionCorrectPCArecurse hmrR_MotionCorrectRLOESS hmrR_MotionCorrectSpline hmrR_MotionCorrectSplineSG hmrR_MotionCorrectWavelet hmrR_OD2Conc hmrR_OD2Conc_new hmrR_PCFilter hmrR_PruneChannels hmrR_StimRejection	Bandpass_Filter	hmrR_Intensity2OD : Intensity_to_Delta_OD hmrR_BandpassFilt : Bandpass_Filter hmrR_OD2Conc : Delta_OD_to_Conc hmrR_BlockAvg : Block_Average_on_Concentration

Add
Delete
Up
Down
Load
Save
Exit

SYNTAX:
data2 = hmrR_BandpassFilt(data, hpf, lpf)

UI NAME:
Bandpass_Filter

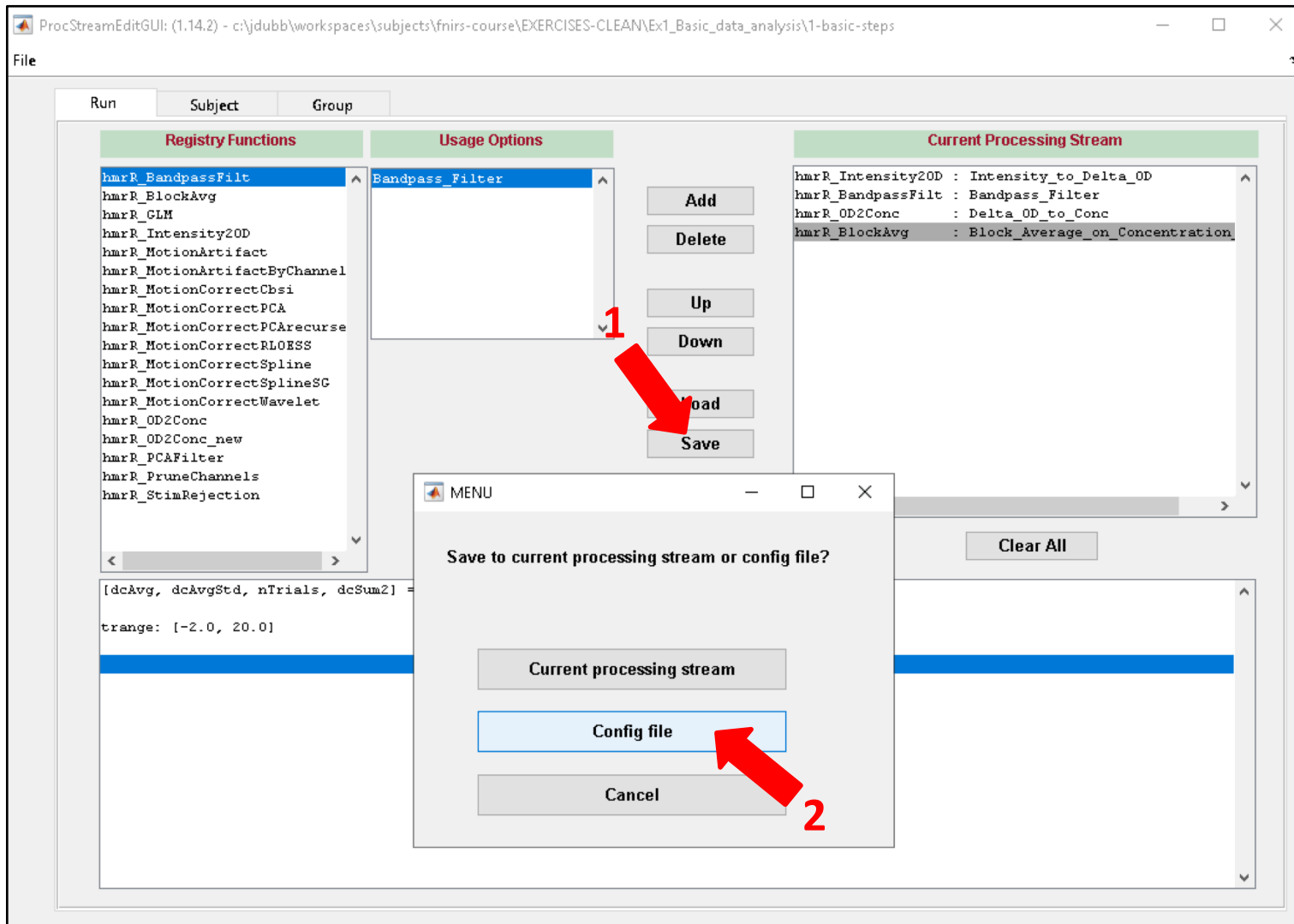
DESCRIPTION:
Perform a bandpass filter on time course data.

INPUT:
data - SNIRF data type containing data time course to filter, time vector, and channels.
hpf - high pass filter frequency (Hz)
Typical value is 0 to 0.02.
lpf - low pass filter frequency (Hz)
Typical value is 0.5 to 3.

Add:

- hmrIntensity2OD
- hmrBandpassFilt
- hmrOD2Conc
- hmrBlockAvg

.CFG file format



.CFG file format

**To load and change the processing stream file, open ProcStreamEditGUI:
Tools => Edit Processing Stream**

The screenshot shows the Homer3 (v1.14.1) software interface. The 'Tools' menu is open, and 'Edit Processing Stream' is highlighted with a red arrow. The main plot area shows a graph with a y-axis from 0 to 0.8 and an x-axis from 0 to 350. A smaller plot on the right shows a vertical line at x=1 and a horizontal line at y=1. The bottom panel contains several control sections: 'Current Processing Element' with a list containing 'simple_nirs_noStim_snirf'; 'Processing Level' with radio buttons for 'Group', 'Subj', and 'Run' (selected); 'Plot Type Select' with radio buttons for 'Raw Data', 'OD', and 'Conc', and a list box showing '690' and '830'; 'Motion Artifacts' with checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', 'Show Excluded by Chan', and 'Exclude Time'; and 'Plot Window' with 'Pan Left/Right' buttons and input fields for 'Fix X-range' (0.400) and 'Fix Y-range' (.2.2).

.CFG file format

The screenshot displays the Homer3 (v1.14.2) software interface. The main window shows a data plot with a green signal and an orange signal. A smaller window titled "ProcStreamEditGUI: (1.14.2)" is open, showing a list of registry functions and usage options. A red arrow points to the "Load" button in the "Current Processing Stream" section. The "Current Processing Element" section shows "simple_nirs_noStim.snirf". The "SYNTAX:" section contains the following code:

```
data2 = hmrR_BandpassFilt( data, hpf, lpf )
```

The "UI NAME:" section shows "Bandpass_Filter". The "DESCRIPTION:" section shows "Perform a bandpass filter on time course data." The "INPUT:" section shows the following parameters:

- data - SNIRF data type containing data time course to filter, time vector, and channels.
- hpf - high pass filter frequency (Hz). Typical value is 0 to 0.02.
- lpf - low pass filter frequency (Hz).

The "Current Processing Stream" section is empty. The "Clear All" button is visible. The "Exit" button is also visible. The "File" menu is open, showing "Run", "Subject", and "Group" options. The "Add", "Delete", "Up", "Down", "Load", "Save", and "Exit" buttons are visible. The "Load" button is highlighted with a red arrow. The "Current Processing Element" section shows "simple_nirs_noStim.snirf". The "1 files loaded successfully" and "0 files failed to load" status is shown at the bottom left. The "Current Processing Stream" section shows "1" and "2" in the right margin.

.CFG file format

The screenshot displays the ProcStreamEditGUI interface. A file selection dialog titled "Process Options Config File to Load From?" is open, showing the file "my_simple_processing.cfg" selected. A red arrow labeled "1" points to the file name in the dialog. Another red arrow labeled "2" points to the "Open" button in the dialog. The background shows a plot with a y-axis from 0 to 1 and a "Processing Stream" panel with a "bandpass_Filter" option. A status bar at the bottom left indicates "1 files loaded successfully" and "0 files failed to load".

Process Options Config File to Load From?

File name: my_simple_processing.cfg

File type: (*.cfg)

Open Cancel

1

2

Processing Stream

bandpass_Filter

1 files loaded successfully
0 files failed to load

```
INPUT:
data - SNIRF data type containing data time course to filter, time
vector, and channels.
hpf - high pass filter frequency (Hz)
Typical value is 0 to 0.02.
lpf - low pass filter frequency (Hz)
Typical value is 0.5 to 3.
```

.CFG file format

The screenshot displays the Homer3 (v1.14.1) software interface. The main window shows a plot with a y-axis from 0.7 to 1.0 and an x-axis from 200 to 350. A red arrow points to the 'Edit Options' button in the ProcStreamOptionsGUI dialog box, which is open over the plot. The dialog box contains the following parameters:

Function	Parameter	Value
hmrR_Intensity2OD		
hmrR_BandpassFilt	hpf	0.010
	lpf	0.500
hmrR_OD2Conc	ppf	1.0 1.0
hmrR_BlockAvg: Block_Average_on_Concentration_Data	trange	-2.0 20.0

Red text annotations provide instructions: '2 - This will open the ProcStreamEditGUI, where you can modify parameters of each function usage' (with an arrow pointing to the dialog box) and '1 - Click on 'Options'' (with an arrow pointing to the 'Edit Options' button).

The bottom panel of the interface includes a 'Current Processing Element' list with 'simple_nirs_noStim_snirf' selected, 'Processing Level' options (Group, Subj, Run), a 'Calculate' button, an 'Edit Options' button, a 'Plot Type Select' section with 'Raw Data' selected and a frequency range of 690-830, and a 'Motion Artifacts' section with checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan'. The 'Plot Window' section has 'Fix X-range' (0 400) and 'Fix Y-range' (-2 2) options.

Let's analyze some fNIRS data: HOMER3_UI

When opening Homer3, you need to select:

- **The dataset(s):** a folder containing at least one **.snirf** (or **.nirs**) file. If all you have are **.nirs** files, Homer3 will convert the files to the **.snirf** format.
- **The data processing stream:** a **.cfg** file. If you click 'Cancel', a default process stream will load.
- **Start Homer3**
- When prompted to select a **.nirs** folder, navigate to and select folder **/Exercises/Ex1_Basic_data_analysis/**
- When prompted to select a **.cfg** file, select **my_simple_processing.cfg** file we just created.

Note: If you're already in Homer3 and need to change the data directory or the .cfg file:

- Go to **File > Change Directory**, and select your nirs folder
- Go to **Tools > Edit Processing Stream** and click the Load button to select **.cfg** file

Homer3 MainGUI

The screenshot shows the Homer3 MainGUI interface with several key components highlighted and annotated:

- Data plot window:** A large empty plot area with a green border, intended for displaying data.
- Source / detector geometry window:** A smaller plot area with a red border, showing a coordinate system with axes labeled 1 and 2.
- Current Processing Element:** A panel with a dropdown menu showing 'simple_nirs_noStim.snirf' and radio buttons for 'Group', 'Subj', and 'Run'.
- Modify proc stream options and run proc stream:** A panel containing 'Calculate' and 'Edit Options' buttons, along with an 'Apply to all' checkbox.
- Motion artifacts/correction options and controls:** A panel with checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', 'Show Excluded by Chan', and 'Exclude Time'.
- Plot Type Select:** A panel with radio buttons for 'Raw Data', 'OD', and 'Conc', and dropdown menus for selecting parameters like '690', '830', '1', and 'aux1'.
- Plot Window:** A panel with 'Pan Left/Right' buttons, a 'Reset View' button, and checkboxes for 'Fix X-range' and 'Fix Y-range'.

Annotations and text overlays provide further context:

- Green text: "Data plot window" (over the main plot area).
- Red text: "Source / detector geometry window" (over the geometry plot).
- Purple text: "Select current processing element: run, subject or group. Current element's data will be calculated and displayed in the data plot window" (over the processing element panel).
- Blue text: "Modify proc stream options and run proc stream" (over the calculation panel).
- Pink text: "Motion artifacts/correction options and controls" (over the motion artifacts panel).
- Red text: "What data type to display" (over the plot type select panel).
- Red text: "Select which part of the data plot window to view" (over the plot window panel).

Displaying raw fNIRS data

The screenshot shows the Homer3 software interface. The main window displays a plot area with a y-axis from 0 to 1 and an x-axis from 0 to 350. A red arrow points to a vertical line at x=690 in the plot area, labeled with a '2' at the top and a '1' at the bottom. Another red arrow points to the 'Raw Data' radio button in the 'Plot Type Select' panel. The 'Current Processing Element' panel shows 'simple_nirs_noStim.snirf' selected. The 'Processing Level' panel has 'Run' selected. The 'Motion Artifacts' panel has 'Show Excluded Manual' checked. The 'Plot Window' panel has 'Pan Left/Right' buttons and 'Reset View' button. The status bar at the bottom left indicates '1 files loaded successfully' and '0 files failed to load'.

Click any optode in the source/detector geometry window to view raw data time series for its connected channels

1 files loaded successfully
0 files failed to load

Displaying raw fNIRS data



Displaying the raw fNIRS data

The screenshot displays the Homer3 software interface. The main window shows two plots: a large plot on the left with two data series (green and orange) over time (0-350), and a smaller plot on the right showing a vertical orange line at time 1 and a horizontal green line at time 1. The control panel at the bottom includes:

- Current Processing Element:** A list box containing 'simple_nirs_noStim_snirf'.
- Processing Level:** Radio buttons for 'Group', 'Subj', and 'Run' (selected).
- Plot Type Select:** Radio buttons for 'Raw Data' (selected), 'OD', and 'Conc'. A dropdown menu shows '690' and '830', with a red arrow pointing to '830' and the text 'Select wavelength to display'.
- Motion Artifacts:** Checkboxes for 'Show Excluded Manual' (checked), 'Show Excluded Auto', and 'Show Excluded by Chan'. There is also an 'Exclude Time' checkbox.
- Plot Window:** 'Pan Left/Right' buttons, 'Fix X-range', 'Fix Y-range', and a 'Reset View' button.

Buttons for 'Calculate', 'Edit Options', and 'Apply to all' are also visible.

Zooming in on data

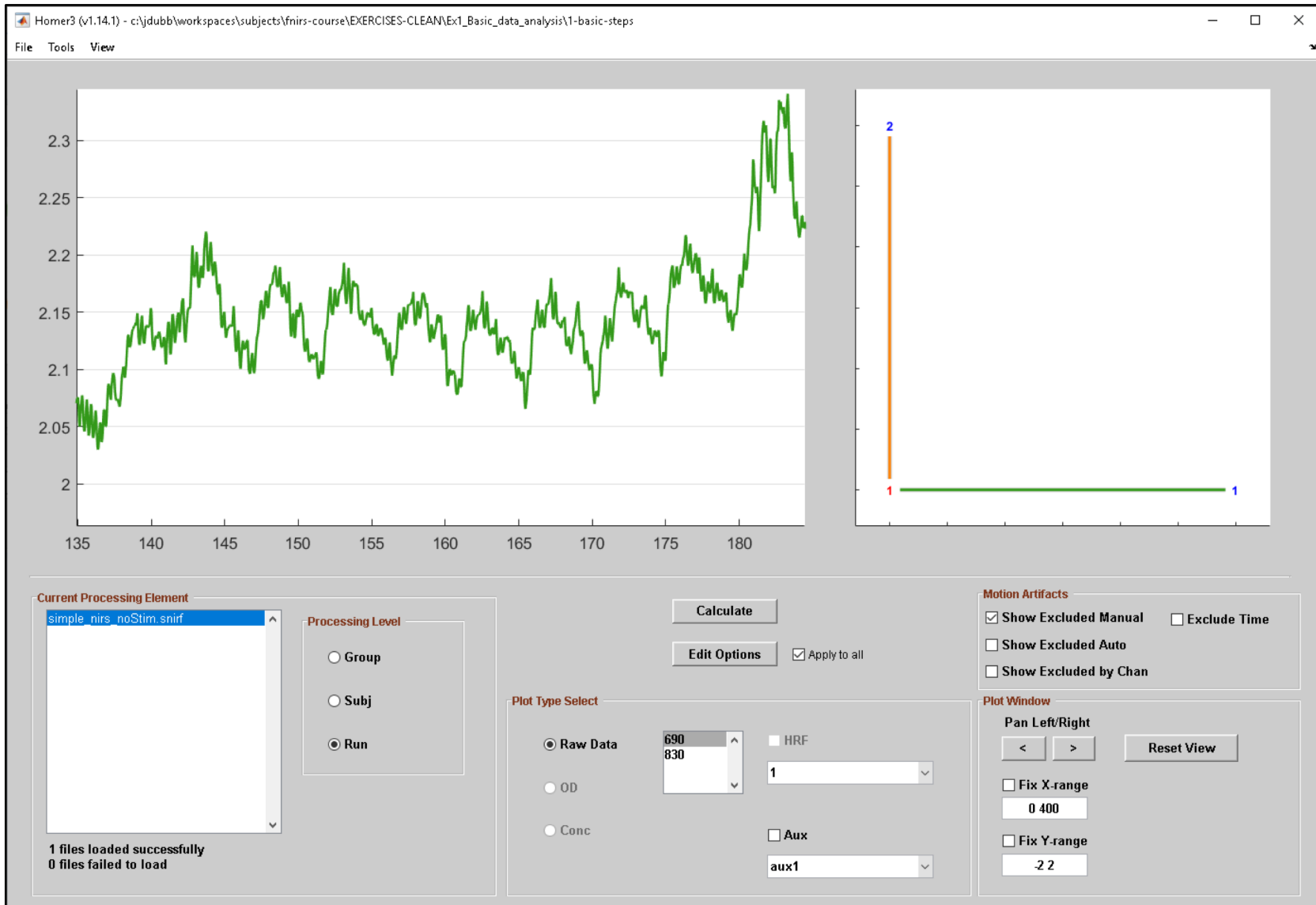
The screenshot displays the Homer3 software interface. The main window contains two data plots. The left plot shows two time-series signals: a green signal (top) and an orange signal (bottom). A red arrow points to a rectangular selection box on the green signal, with the text "Select data region to zoom in on by dragging mouse in the data plot window." The right plot shows a zoomed-in view of the selected region, with a vertical orange line labeled '2' and a horizontal green line labeled '1'.

Below the plots are several control panels:

- Current Processing Element:** A list box containing "simple_nirs_noStim.snirf".
- Processing Level:** Radio buttons for "Group", "Subj", and "Run" (selected).
- Plot Type Select:** Radio buttons for "Raw Data" (selected), "OD", and "Conc".
- Motion Artifacts:** Checkboxes for "Show Excluded Manual" (checked), "Show Excluded Auto", and "Show Excluded by Chan". The "Exclude Time" checkbox is unchecked, with a red arrow pointing to it and the text "Make sure 'Exclude Time' option is unchecked".
- Plot Window:** A "Reset View" button and checkboxes for "Fix X-range" (checked, value 0 400) and "Fix Y-range" (checked, value -2 2).

At the bottom left, a status bar indicates "1 files loaded successfully" and "0 files failed to load".

Zooming in



Modifying processing stream options

The screenshot displays the Homer3 software interface. The main window shows a plot of hmrR_Intensity2OD with a y-axis ranging from 2.0 to 2.3 and an x-axis from 135 to 150. A dialog box titled "ProcStreamOptionsGUI: (1.14.2)" is open, showing options for hmrR_BandpassFilt, hmrR_OD2Conc, and hmrR_BlockAvg. The hmrR_BandpassFilt section has hpf and lpf values set to 0.000. The hmrR_OD2Conc section has ppf values set to 6.0 6.0. The hmrR_BlockAvg section has a trange value of 2.0 20.0. A red arrow points to the "Edit Options" button in the main GUI, and another red arrow points to the hpf and lpf input fields in the dialog box. Red text annotations provide instructions: "1 - Open processing options by clicking Edit Options button in MainGUI" and "2 - Set hpf (high-pass filter) and lpf (low-pass filter) to 0, i.e. no filtering".

1 - Open processing options by clicking Edit Options button in MainGUI

2 - Set hpf (high-pass filter) and lpf (low-pass filter) to 0, i.e. no filtering

ProcStreamOptionsGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps

EXIT

hmrR_Intensity2OD

hmrR_BandpassFilt

hpf 0.000

lpf 0.000

hmrR_OD2Conc

ppf 6.0 6.0

hmrR_BlockAvg: Block_Average_on_Concentration_Data

trange 2.0 20.0

Apply to all

Plot Type Select

Raw Data

OD

Conc

HRF

1

Aux

aux1

Motion Artifacts

Show Excluded Manual Exclude Time

Show Excluded Auto

Show Excluded by Chan

Plot Window

Pan Left/Right

< >

Reset View

Fix X-range

0 400

Fix Y-range

-2 2

Current Processing Element

simple_nirs_noStim.snirf

1 files loaded successfully

0 files failed to load

Running the processing stream

The screenshot displays the ProcStreamOptions GUI with the following settings:

Parameter	Value
hmrR_Intensity20D	
hmrR_BandpassFilt	hpf: 0.000 lpf: 0.000
hmrR_OD2Conc	ppf: 6.0 6.0
hmrR_BlockAvg: Block_Average_on_Concentration_Data	trange: 2.0 20.0

The main plot shows two time-series signals: a green signal (Intensity) and an orange signal (Concentration). The x-axis represents time from 0 to 350, and the y-axis represents signal amplitude from 0.8 to 2.6. A secondary plot on the right shows a vertical line at time 0 with a value of 2, and a horizontal line at time 350 with a value of 1.

Processing Level: Group, Subj, Run

Plot Type Select: Raw Data, OD, Conc

Buttons: Calculate, Edit Options, Apply to all

Plot Window: Pan Left/Right, Fix X-range (0 400), Fix Y-range (-2 2)

1 files loaded successfully
0 files failed to load

hpf and lpf are set to 0

Click Calculate button to run proc stream

Intensity to ΔOD

The screenshot displays the Homer3 software interface. The main window shows a plot of Intensity (Y-axis, ranging from -0.2 to 0.25) versus Time (X-axis, ranging from 0 to 350). The plot contains two data series: an orange line and a green line, both showing high-frequency oscillations. A secondary plot on the right shows a single vertical orange line at time 0, with a green line at time 350, indicating a transition or event.

The control panel on the left includes the following settings:

- EXIT button
- hmrR_Intensity2OD
- hmrR_BandpassFilt: hpf = 0.000, lpf = 0.000
- hmrR_OD2Conc: ppf = 6.0 6.0
- hmrR_BlockAvg: Block Average on Concentration Data, trange = -2.0 20.0

The bottom control panel includes the following options:

- Current Processing Element: simple_nirs_noStim.snirf
- Processing Level: Group, Subj, Run
- Calculate button
- Edit Options button, Apply to all
- Plot Type Select: Raw Data, OD, Conc. A red arrow points to the OD option with the text "Select OD".
- Frequency range: 690 (selected), 830
- HRF: HRF, 1 (selected)
- Aux: aux1 (selected)
- Motion Artifacts: Show Excluded Manual, Exclude Time, Show Excluded Auto, Show Excluded by Chan
- Plot Window: Pan Left/Right, Fix X-range (0 400), Fix Y-range (-2 2), Reset View button

ΔOD to Hb concentrations

The screenshot displays a software interface for processing fNIRS data. The main window shows a time-series plot of HbO (orange) and HbR (green) concentrations over time (0 to 350 seconds). The left sidebar contains processing steps: hmrR_Intensity2OD, hmrR_BandpassFilt (with hpf and lpf set to 0.000), hmrR_OD2Conc (with ppf set to 6.0 6.0), and hmrR_BlockAvg: Block_Average_on_Concentration_Data (with trange set to -2.0 20.0). The bottom control panel includes 'Current Processing Element' (simple_nirs_noStim.snif), 'Processing Level' (Group, Subj, Run), 'Plot Type Select' (Raw Data, OD, Conc), 'Motion Artifacts' (Show Excluded Manual, Show Excluded Auto, Show Excluded by Chan), and 'Plot Window' (Pan Left/Right, Fix X-range, Fix Y-range). A red arrow points to the 'Conc' option in the 'Plot Type Select' section.

Select Conc

ΔOD to Hb concentrations

The screenshot displays the Homer3 software interface. The main window shows a plot of hemoglobin concentrations over time, with the x-axis ranging from 0 to 350 and the y-axis ranging from -1.5 to 2.5. The plot shows two data series: HbO (orange) and HbR (green). The HbO series starts at approximately 2.0 and fluctuates between 1.0 and 2.0, while the HbR series starts at approximately 0.0 and fluctuates between -1.0 and 1.0. A red arrow points to the 'Plot Type Select' dropdown menu, which is currently set to 'Conc'. The dropdown menu lists 'HbO', 'HbR', and 'HbT'. The 'Processing Level' is set to 'Run'. The 'Motion Artifacts' section is checked for 'Show Excluded Manual' and 'Exclude Time'. The 'Plot Window' section has 'Fix X-range' set to 0 400 and 'Fix Y-range' set to -2.2.

Current Processing Element: simple_nirs_noStim.snirf

Processing Level: Group Subj Run

Plot Type Select: Raw Data OD Conc

HbO
HbR
HbT

Calculate Edit Options Apply to all

Motion Artifacts: Show Excluded Manual Exclude Time Show Excluded Auto Show Excluded by Chan

Plot Window: Pan Left/Right: < > Reset View Fix X-range: 0 400 Fix Y-range: -2.2

Choose which hemoglobin specie(s) to display

Band-pass filtering

hpf 0.00
lpf 0.0

EXIT

hmrR_Intensity2OD

hmrR_BandpassFilt

hpf 0.000
lpf 0.000

hmrR_OD2Conc

ppf 6.0 6.0

hmrR_BlockAvg: Block_Average_on_Concentration_Data

trange -2.0 20.0

File Tools View

2

1

1

145 150 155 160 165 170 175 180 185

Current Processing Element

simple_nirs_noStim.snirf

Processing Level

Group

Subj

Run

Calculate

Edit Options Apply to all

Plot Type Select

Raw Data

OD

Conc

HbO

HbR

HbT

HRF

1

Aux

aux1

Motion Artifacts

Show Excluded Manual Exclude Time

Show Excluded Auto

Show Excluded by Chan

Plot Window

Pan Left/Right

< >

Reset View

Fix X-range

142 189

Fix Y-range

-2.2

1 files loaded successfully

0 files failed to load

Band-pass filtering

The screenshot displays the Homer3 software interface for band-pass filtering. On the left, a Windows desktop is visible with various application icons. The main window shows a plot of HbO (green), HbR (orange), and HbT (blue) concentration over time. The x-axis ranges from 145 to 185, and the y-axis ranges from -2 to 2. A secondary plot on the right shows a vertical line at x=142 and a horizontal line at y=-2.2.

The software interface includes a control panel with the following settings:

- hmrR_Intensity2OD**: EXIT
- hmrR_BandpassFilt**: hpf 0.000, lpf 0.500 (circled in red)
- hmrR_OD2Conc**: ppf 6.0 6.0
- hmrR_BlockAvg: Block_Average_on_Concentration_Data**: trange -2.0 20.0

The **Current Processing Element** is set to `simple_nirs_noStim.snirf`. The **Processing Level** is set to **Run**. The **Plot Type Select** is set to **Conc**. The **Plot Window** settings are: **Fix X-range** (checked) with values 142 189, and **Fix Y-range** (checked) with values -2 2. The **Motion Artifacts** settings are: **Show Excluded Manual** (checked), **Show Excluded Auto** (unchecked), and **Show Excluded by Chan** (unchecked).

Buttons for **Calculate**, **Edit Options**, and **Apply to all** are visible. The status bar indicates "1 files loaded successfully" and "0 files failed to load".

Band-pass filtering

EXIT

hmrR_Intensity2OD

hmrR_BandpassFilt

hpf	0.000
lpf	0.500

hmrR_OD2Conc

ppf	6.0 6.0
-----	---------

hmrR_BlockAvg: Block_Average_on_Concentration_Data

trange	-2.0 20.0
--------	-----------

1 files loaded successfully
0 files failed to load

Processing Level

- Group
- Subj
- Run

Calculate

Edit Options Apply to all

Plot Type Select

- Raw Data
- OD
- Conc

HbO
HbR
HbT

HRF

1

Aux

aux1

Motion Artifacts

- Show Excluded Manual Exclude Time
- Show Excluded Auto
- Show Excluded by Chan

Plot Window

Pan Left/Right

< >

Reset View

Fix X-range
142 189

Fix Y-range
-2 2

Reset data plot
view

Band-pass filtering

The screenshot displays a software interface for processing neuroimaging data. The main window shows a time-series plot of two signals (green and orange) with a high-pass filter (hpf) set to 0.010 and a low-pass filter (lpf) set to 0.500. The interface includes a parameter control panel on the left, a processing level selector (Run), and plot options on the right.

Parameter Control Panel:

- EXIT button
- hmrR_Intensity2OD
- hmrR_BandpassFilt: hpf 0.010, lpf 0.500 (circled in red)
- hmrR_OD2Conc: ppf 6.0 6.0
- hmrR_BlockAvg: Block_Average_on_Concentration_Data, trange 2.0 20.0

Processing Level:

- Group
- Subj
- Run

Plot Type Select:

- Raw Data
- OD
- Conc

Plot Options:

- Calculate button
- Edit Options button
- Apply to all checkbox
- HbO, HbR, HbT dropdown menu
- HRF dropdown menu (value: 1)
- Aux dropdown menu (value: aux1)

Motion Artifacts:

- Show Excluded Manual
- Exclude Time
- Show Excluded Auto
- Show Excluded by Chan

Plot Window:

- Pan Left/Right buttons
- Reset View button
- Fix X-range (value: 142 189)
- Fix Y-range (value: -2.2)

This dataset doesn't have stimulus onsets, so we will enter them manually

Open StimEditGUI under the Tools menu

nrR_Intensity2OD		
nrR_BandpassFilt	hpf	0.010
	lpf	0.500
nrR_OD2Conc	ppf	1.0 1.0
nrR_BlockAvg: Block_Average_on_Concentration_Data	trange	-2.0 20.0

Current Processing Element: simple_nirs_noStim_snirf

Processing Level: Group Subj Run

Plot Type Select: Raw Data OD Conc

HbO: HRF Aux

HbR: 1

HbT: aux1

Motion Artifacts: Show Excluded Manual Exclude Time Show Excluded Auto Show Excluded by Chan

Plot Window: Pan Left/Right: < > Reset View

Fix X-range: 0 400

Fix Y-range: -2 2

1 files loaded successfully
0 files failed to load

StimEditGUI

NOTE: Any edits to stims you make in StimEditGUI will automatically update the data plot window in MainGUI

simple_nirs_noStim.snirf :

EXIT Add / Edit Stims : 22

	Time	Duration	Value
1	21.9997	5	1

You can add one or multiple stimulus marks using this edit window

StimEditGUI

The screenshot shows the StimEditGUI application window. The title bar reads "StimEditGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps". The main window displays a plot area with a yellow highlight on the text "simple_nirs_noStim.snirf:". A dialog box titled "MENU" is open, showing "Add stim mark at t=22.0...". The dialog has three buttons: "1", "New condition", and "Cancel". A red arrow points from the text "2 - Select Condition 1" to the "1" button. Below the plot area, there is an "EXIT" button and an "Add / Edit Stims:" field containing the text "22:25:347". A red arrow points from the text "1 - Add stim marks time points every 25 seconds starting at t = 22s (Type: 22:25:347)" to this field. To the right of the main window, a table with columns "Time", "Duration", and "Value" is visible, with a dropdown menu showing "1" and a "Rename condition" button above it.

1

2 - Select Condition 1

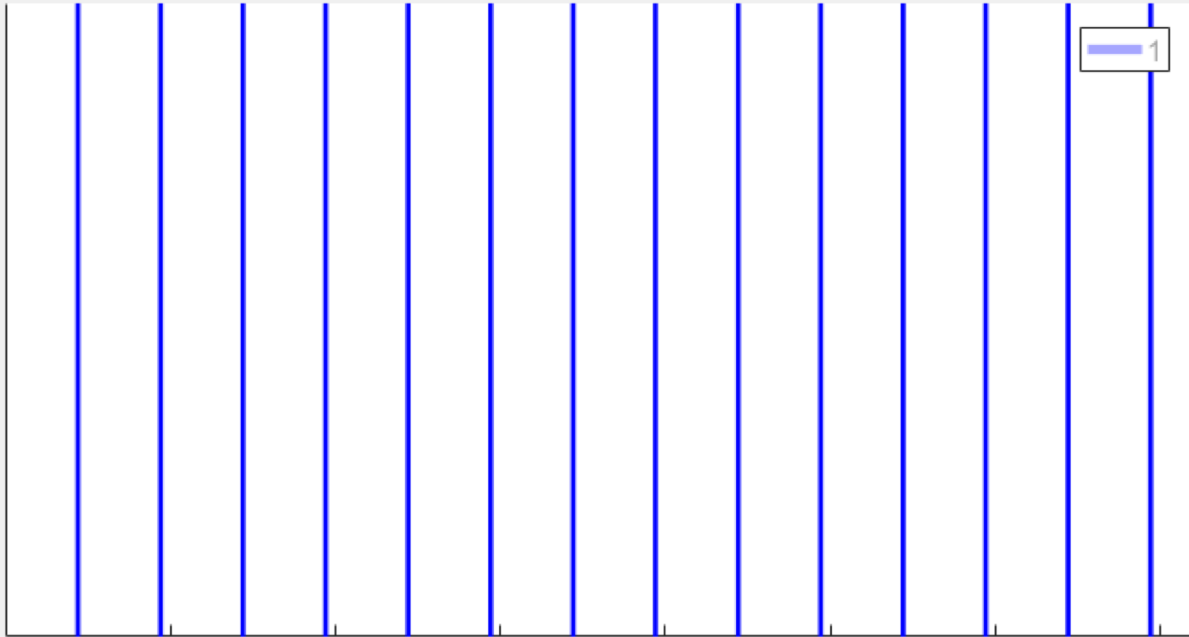
1 - Add stim marks time points every 25 seconds starting at t = 22s (Type: 22:25:347)

Time	Duration	Value
------	----------	-------

StimEditGUI

StimEditGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps

simple_nirs_noStim.snirf :



1

Rename condition

	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

EXIT

Add / Edit Stims : 22:25:347

StimEditGUI: Multiple conditions

The screenshot shows the StimEditGUI interface. At the top, the window title is "StimEditGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps". The main window displays a plot area with the text "You can create multiple conditions" in red. A dialog box titled "MENU" is open, showing "Add stim mark at t=22.0...". The dialog has three buttons: "1", "New condition", and "Cancel". A red arrow points to the "New condition" button. To the right of the dialog, a text box contains the text "either when you create the stim mark ...". The main window also features a table with columns "Time", "Duration", and "Value", and a "Rename condition" button. At the bottom, there is an "EXIT" button and a field labeled "Add / Edit Stims : 22:25:347".

You can create multiple conditions

either when you create the stim mark ...

Time	Duration	Value
------	----------	-------

EXIT Add / Edit Stims : 22:25:347

StimEditGUI: Multiple conditions

... or by modifying existing stim marks

The screenshot shows the StimEditGUI interface. The main window displays a timeline with vertical blue lines representing stimulus marks. A red arrow points to a dashed box around a mark at approximately 50 seconds. A red text box next to the arrow says "1 - To modify existing stim, drag mouse around it." The timeline has a scale from 0 to 350 seconds. Below the timeline is an "EXIT" button and a text field for "Add / Edit Stims : 22:25:347". On the right side, there is a dropdown menu set to "1" and a "Rename condition" button. Below these is a table with 14 rows of stimulus data.

	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

StimEditGUI: Multiple conditions

The screenshot displays the StimEditGUI interface. The main window shows a plot of stimulus marks with a black vertical line at t=47.0 and several blue vertical lines. A 'MENU' dialog box is open, titled 'Edit/Delete stim mark(s) at t=47.0-47.0 to...'. The dialog contains a list of conditions, with '1' selected. A red arrow points to the 'New condition' button in the dialog. To the right, a table lists the stimulus conditions.

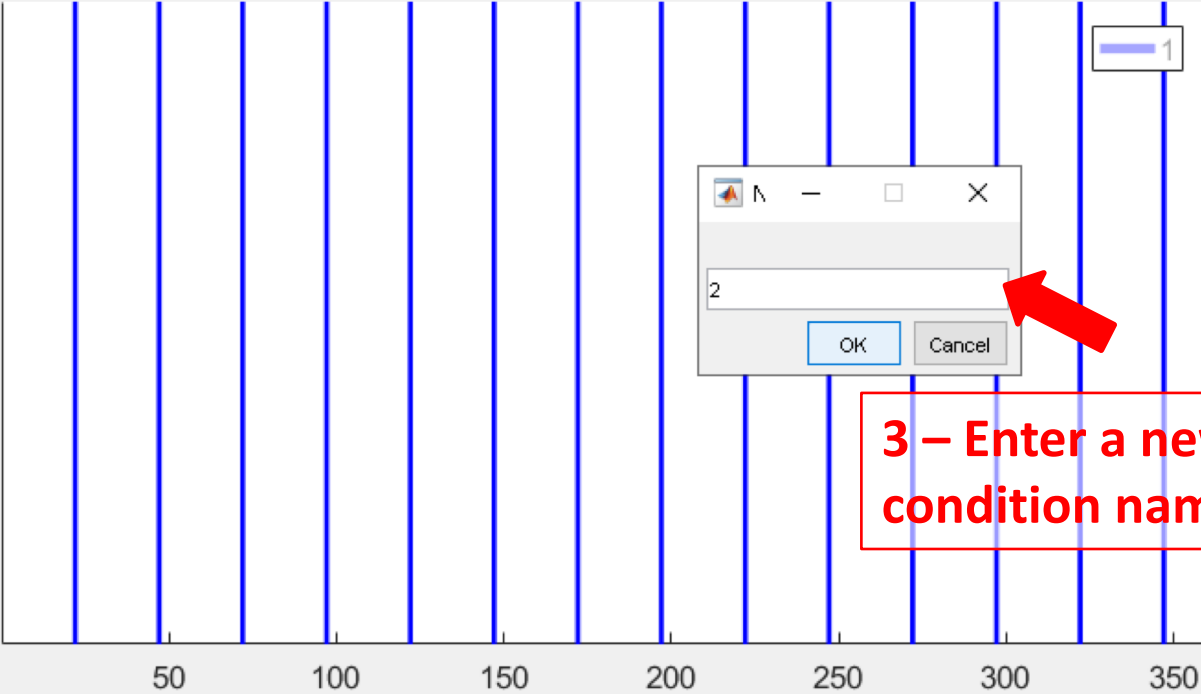
	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

2 – Select 'New condition'

StimEditGUI: Multiple conditions

StimEditGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps

simple_nirs_noStim.snirf :



1

Rename condition

	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

2

OK Cancel

3 - Enter a new condition name

50 100 150 200 250 300 350

EXIT Add / Edit Stims : 22:25:347

StimEditGUI: Multiple conditions

StimEditGUI: (1.14.2) - c:\jdubb\workspaces\subjects\fnirs-course\EXERCISES-CLEAN\Ex1_Basic_data_analysis\1-basic-steps



simple_nirs_noStim.snirf :



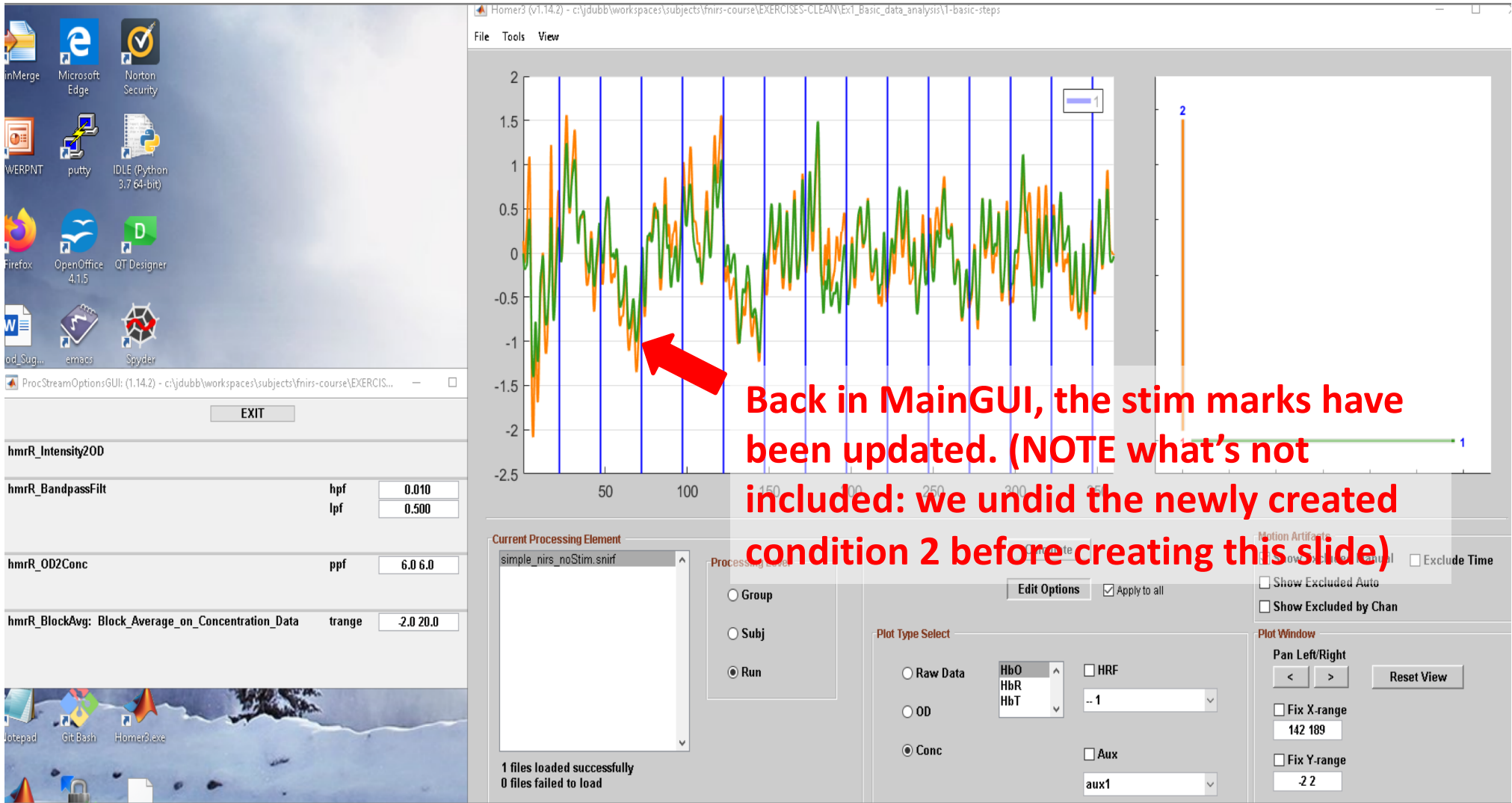
1

	Time	Duration	Value
1	21.9997	5	1
2	71.9996	5	1
3	97.0395	5	1
4	122.0394	5	1
5	147.0394	5	1
6	172.0393	5	1
7	196.9993	5	1
8	222.0392	5	1
9	247.0391	5	1
10	271.9991	5	1
11	297.0390	5	1
12	321.9990	5	1
13	346.9989	5	1

EXIT

Add / Edit Stims : 22:25:347

Stimulus onsets



Stimulus onsets: rejecting stim marks

To reject stim go back
to StimEditGUI

The screenshot shows the StimEditGUI interface. The main window displays a plot of stimulus onsets for a file named 'simple_nirs_noStim.snirf'. The x-axis represents time in seconds, ranging from 0 to 350 with major ticks every 50 units. The plot shows 14 vertical blue lines representing stimulus onsets. A red arrow points to the first onset at approximately 22 seconds, which is enclosed in a dashed rectangular box. A red text box next to the arrow says 'Drag mouse around the stim mark you wish to edit'. Below the plot, there is an 'EXIT' button and an 'Add / Edit Stims:' input field.

On the right side of the interface, there is a table showing the parameters for the selected stimulus (condition 1). The table has columns for 'Time', 'Duration', and 'Value'. The 'Time' column lists the onset times for each of the 14 stimuli, and the 'Duration' and 'Value' columns are constant at 5 and 1, respectively.

	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

Stimulus onsets: rejecting stim marks

The screenshot displays the Homer3 software interface. The main window shows a plot of stimulus onsets (blue vertical lines) and a time series plot (orange and green lines). A dialog box titled "MENU" is open, allowing the user to edit or delete a stimulus mark at $t=72.0-72.0$. The dialog box contains the following options:

- 1
- New condition
- Toggle active on/off (highlighted with a red arrow)
- Delete
- Cancel

The "Toggle active on/off" option is highlighted with a red arrow, indicating the user's intention to reject the stimulus mark.

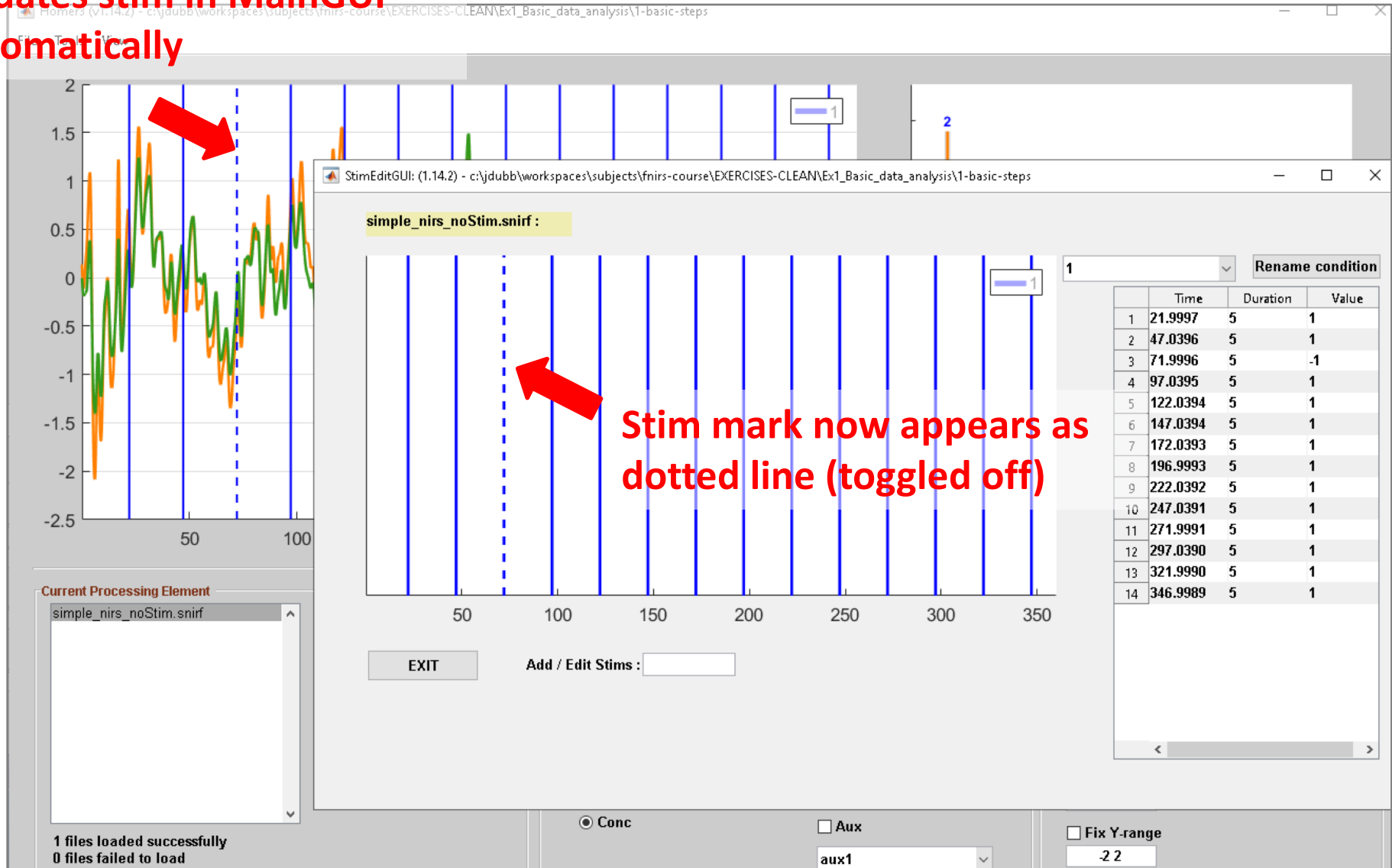
Below the dialog box, a table displays the stimulus marks:

	Time	Duration	Value
1	21.9997	5	1
2	47.0396	5	1
3	71.9996	5	1
4	97.0395	5	1
5	122.0394	5	1
6	147.0394	5	1
7	172.0393	5	1
8	196.9993	5	1
9	222.0392	5	1
10	247.0391	5	1
11	271.9991	5	1
12	297.0390	5	1
13	321.9990	5	1
14	346.9989	5	1

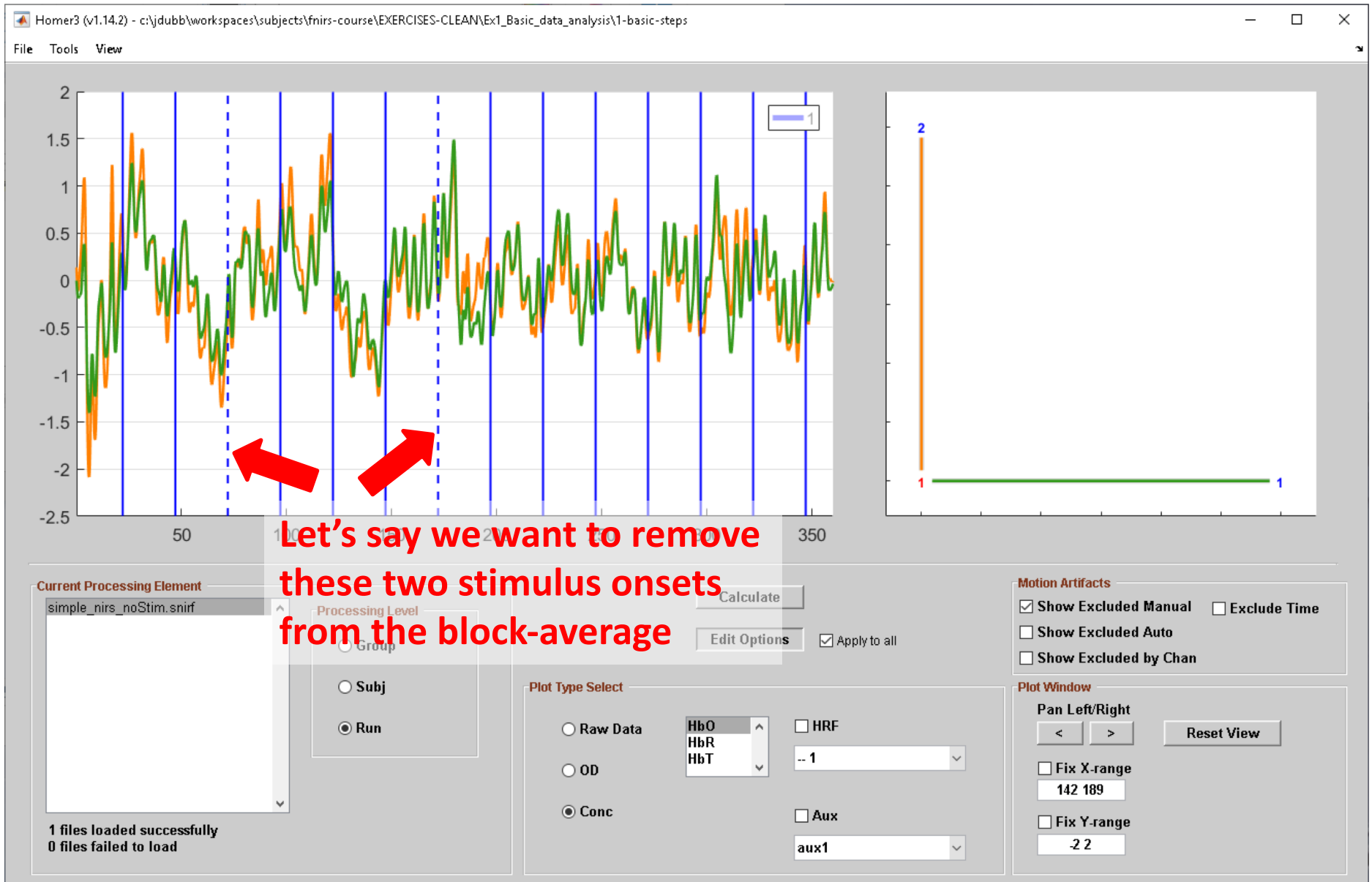
The "Current Processing Element" window shows the file "simple_nirs_noStim.snirf". The status bar indicates "1 files loaded successfully" and "0 files failed to load".

Stimulus onsets: rejecting stim marks

Updates stim in MainGUI
automatically



Stimulus onsets: rejecting stim marks



Calculating and displaying the HRF

The screenshot displays the Homer3 software interface. On the left is a Windows desktop with various application icons. The main window shows a graph with two curves (green and orange) plotted against time (0 to 20). Below the graph is a control panel with several sections:

- Current Processing Element:** A list containing 'simple_nirs_noStim.snif'.
- Processing Level:** Radio buttons for 'Group', 'Subj', and 'Run' (selected).
- Plot Type Select:** Radio buttons for 'Raw Data', 'OD', and 'Conc' (selected).
- Channel Selection:** A dropdown menu showing 'HbO', 'HbR', and 'HbT'.
- Buttons:** 'Calculate' and 'Edit Options'.
- Apply to all:** A checked checkbox.
- Plot Window:** A section with 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan' checkboxes. It also includes 'Pan Left/Right' buttons and a 'Reset View' button.

Annotations with red arrows and text are present:

- 1 – Select run:** Points to the 'Run' radio button in the Processing Level section.
- 2 – Calculate processing stream for current processing element:** Points to the 'Calculate' button.
- 2 – Show HRF:** Points to the 'HRF' checkbox in the Plot Window section.

At the bottom left of the control panel, it states: '1 files loaded successfully' and '0 files failed to load'.

Displaying the HRF

The screenshot displays the Homer3 software interface. The main window shows two plots: a large line graph on the left and a smaller bar chart on the right. The line graph plots HRF values (y-axis, -0.4 to 0.4) against time (x-axis, 0 to 20). It features four data series: a solid green line, a solid orange line, a dashed green line, and a dashed orange line. The solid lines show a positive peak around time 8, while the dashed lines show a negative peak at the same time. The bar chart on the right shows two vertical bars, one orange (labeled '2') and one green (labeled '1').

Below the plots is a control panel with the following sections:

- Current Processing Element:** A list box containing 'simple_nirs_noStim.snirf'.
- Processing Level:** Radio buttons for 'Group', 'Subj', and 'Run' (selected).
- Plot Type Select:** Radio buttons for 'Raw Data', 'Conc', and 'HRF' (selected). A dropdown menu is open, showing 'HbO', 'HbR', and 'HbT'. A red arrow points to the 'HbO' and 'HbR' options.
- Buttons:** 'Calculate', 'Edit Options', and 'Apply to all' (checked).
- Motion Artifacts:** Checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan'. 'Exclude Time' is also present.
- Plot Window:** 'Pan Left/Right' buttons, 'Reset View', and checkboxes for 'Fix X-range' (value 142 189) and 'Fix Y-range' (value -2.2).

On the left side of the interface, there is a parameter list:

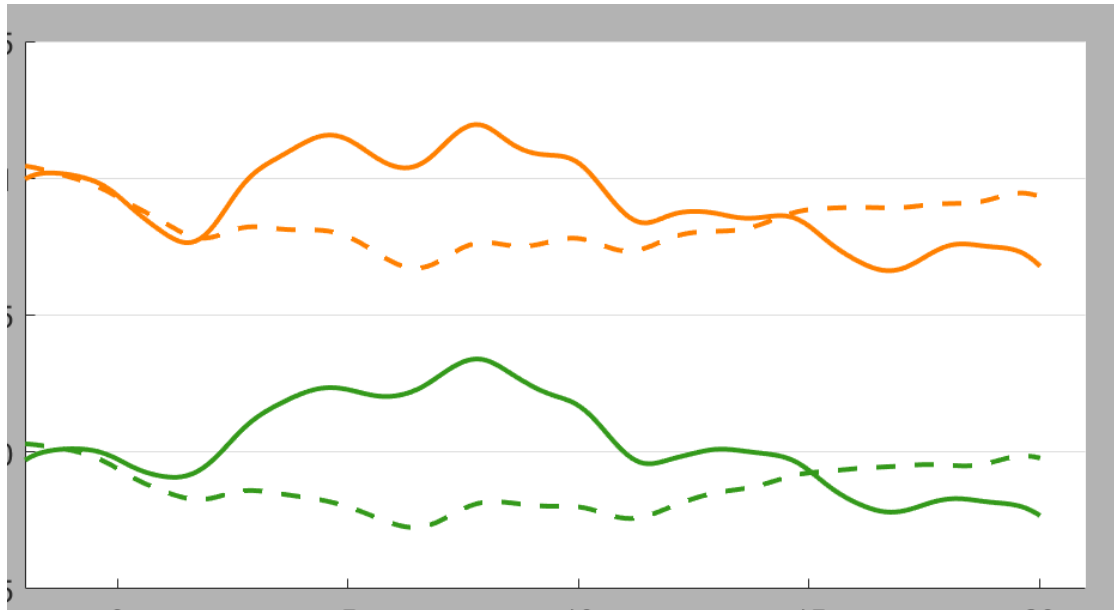
- EXIT
- mrR_Intensity2OD
- mrR_BandpassFilt: hpf 0.010, lpf 0.500
- mrR_OD2Conc: ppf 6.0 6.0
- mrR_BlockAvg: Block_Average_on_Concentration_Data, trange -2.0 20.0

At the bottom left, a status bar indicates '1 files loaded successfully' and '0 files failed to load'.

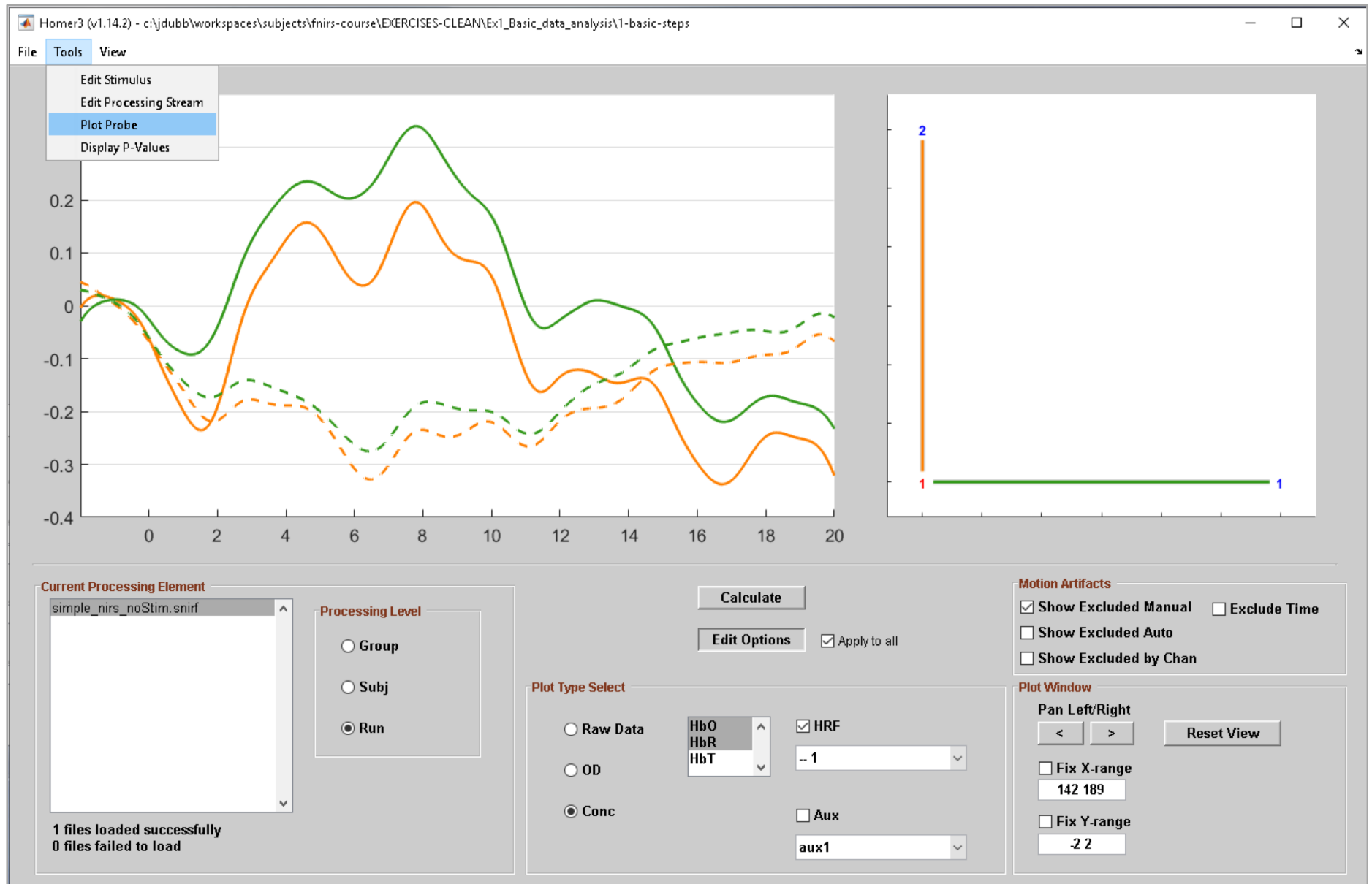
Display both HbO and HbR

Display options: waterfall

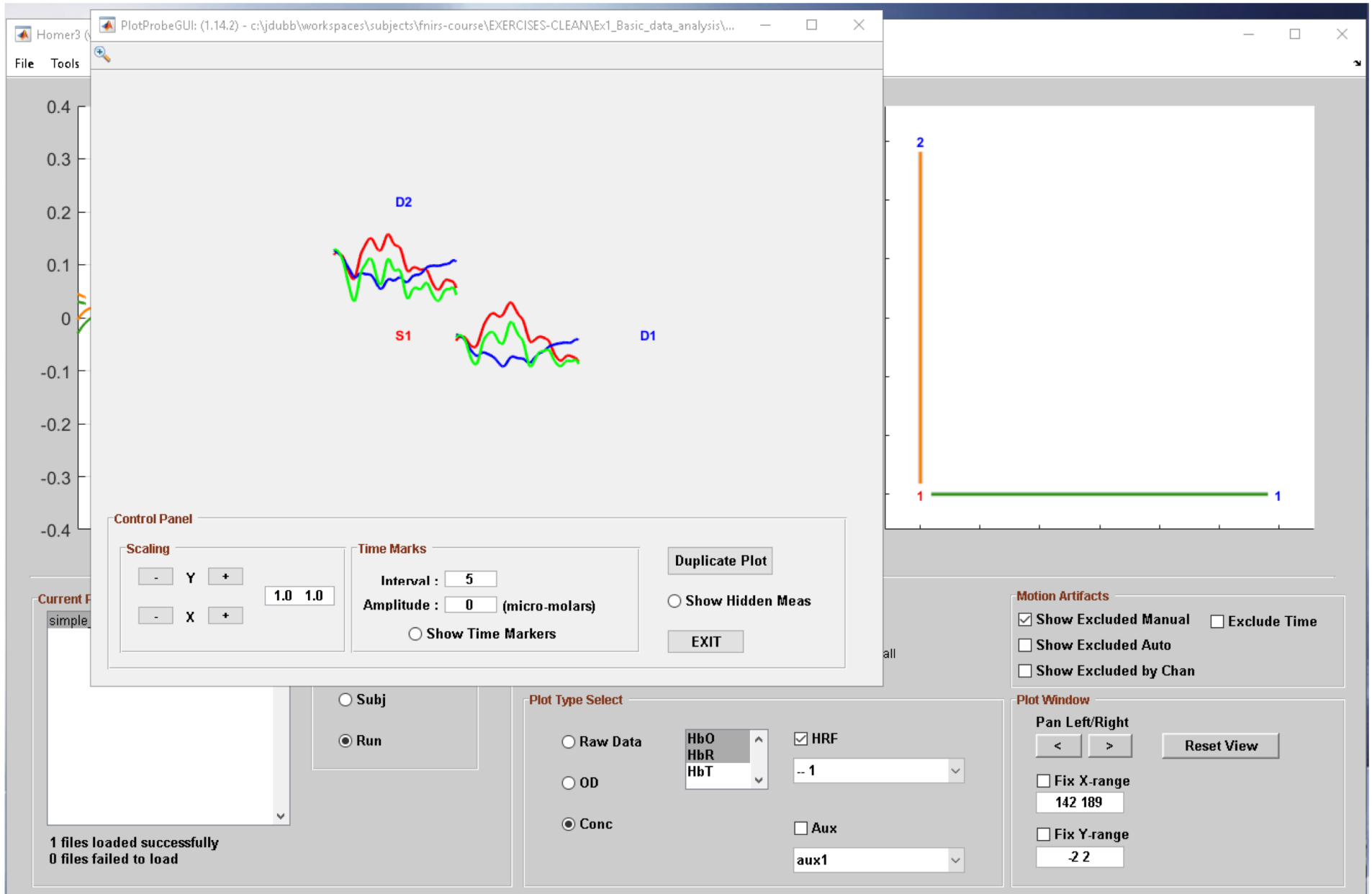
TO-DO, coming soon: Waterfall display of channels as shown below



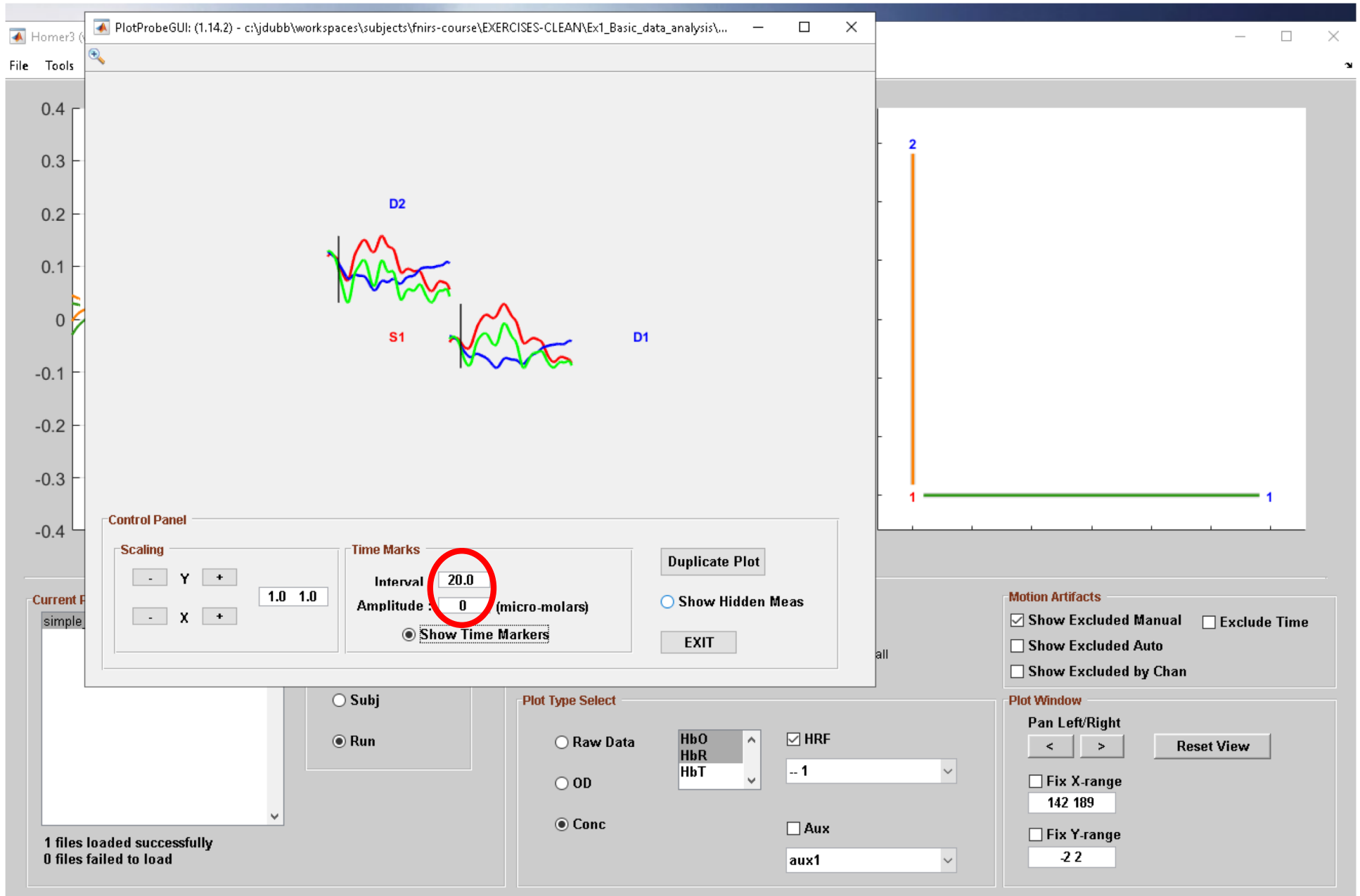
Visualize all HRFs: the Plot Probe feature



Visualize all HRFs: the Plot Probe feature



Visualize all HRFs: the Plot Probe feature

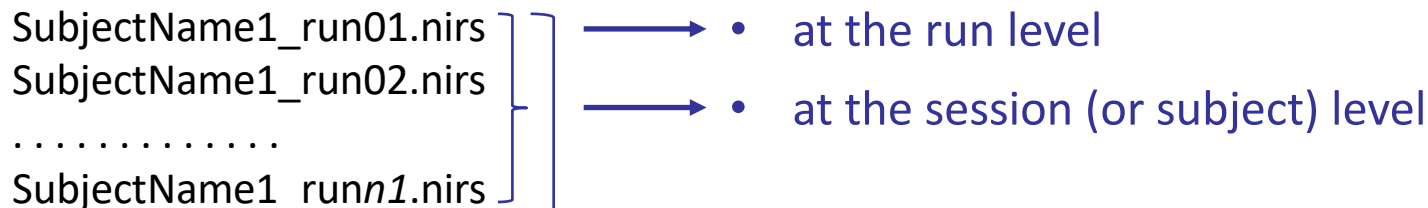


Group average: file names

Any directory that contains one or more files with the .nirs extension is considered by Homer3 to be a **group**, organized into sub-groups called **sessions** (or subjects).

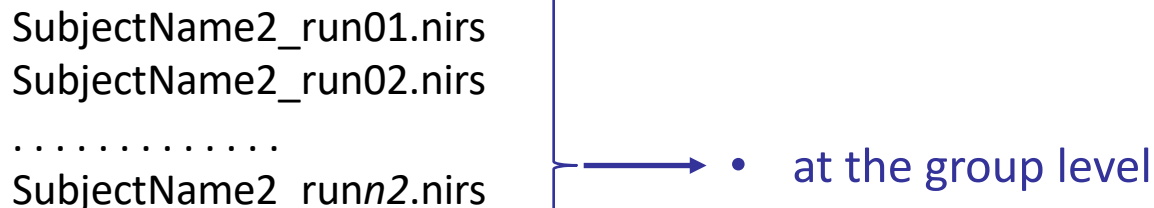
You can compute the HRF:

SubjectName1_run01.nirs
SubjectName1_run02.nirs
.....
SubjectName1_runn1.nirs



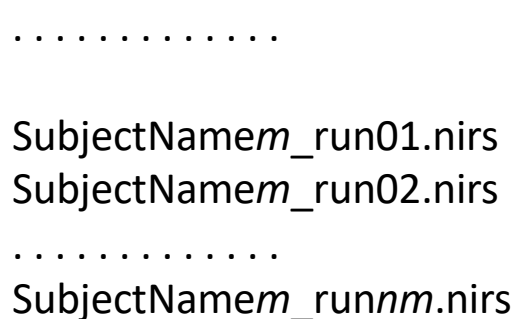
- at the run level
- at the session (or subject) level

SubjectName2_run01.nirs
SubjectName2_run02.nirs
.....
SubjectName2_runn2.nirs



- at the group level

.....
SubjectName m _run01.nirs
SubjectName m _run02.nirs
.....
SubjectName m _run m .nirs



Data processed in Homer3 is saved automatically to disk:

- Run data is saved in the corresponding **.nirs** file
- Subject and group processing results are saved to **groupResults.mat**

To go back to the state before any processing was done to the dataset, go to **File > Reset File**

Group average: example

File > Change directory to Exercises / Ex1_Basic_data_analysis / 2-group-averaging

The screenshot shows a software interface with a file explorer window and a plot window. The file explorer window is open to the 'Ex1_Basic_data_analysis' directory, with the '2-group-averaging' folder selected. A red arrow points to the '2-group-averaging' folder. Another red arrow points to the 'New Folder' button in the file explorer. The plot window shows a graph with a vertical axis labeled '2' and a horizontal axis labeled '1'. The plot area is mostly empty, with a few small markers. Below the plot window, there are several control panels: 'Plot Type Select' with radio buttons for 'Raw Data', 'OD', and 'Conc'; 'Motion Artifacts' with checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan'; and 'Plot Window' with 'Pan Left/Right' buttons and 'Fix X-range' and 'Fix Y-range' checkboxes.

Folder: Ex1_Basic_data_analysis

Plot Type Select

- Raw Data
- OD
- Conc

Motion Artifacts

- Show Excluded Manual
- Show Excluded Auto
- Show Excluded by Chan

Plot Window

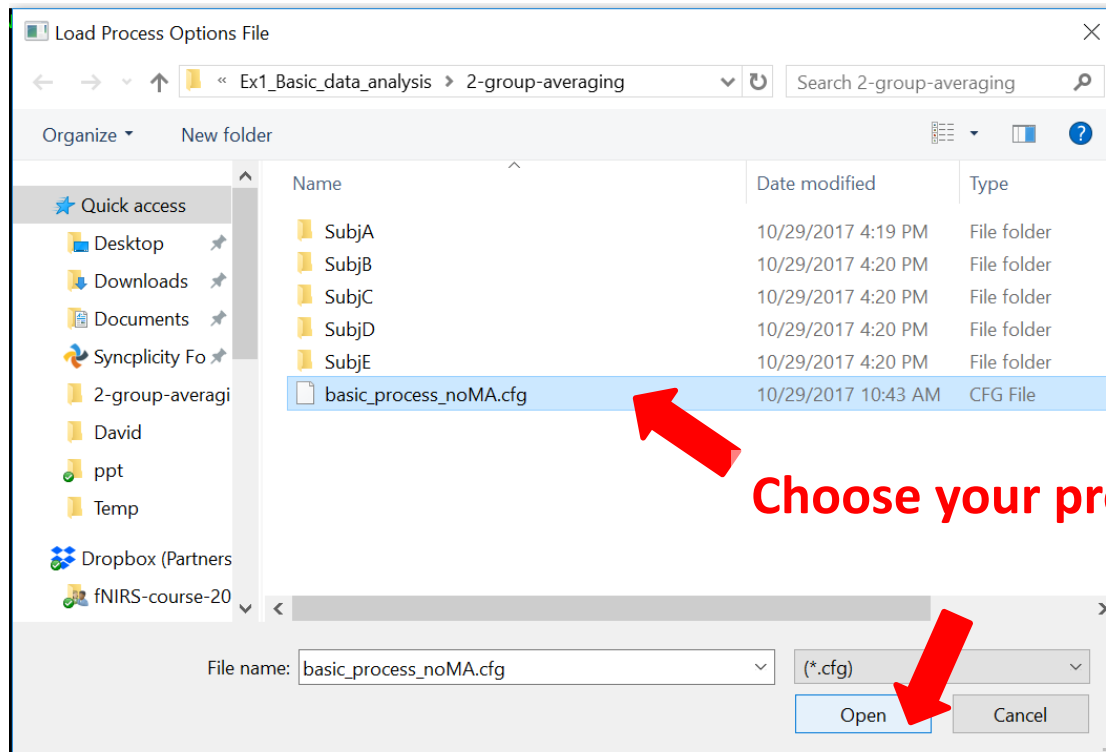
Pan Left/Right

Fix X-range: 0 400

Fix Y-range: -2 2

Group average: example

File > Load Process Options (*.cfg)



Choose your processing stream *.cfg

Group average: example

A screenshot of a Windows desktop environment. The taskbar shows icons for MATLAB R2017b, Visual Studio 2017, and a terminal window titled 'ProcStreamOptions:GUI: (1.14.2)'. The terminal window has an 'EXIT' button and displays parameters for 'hmrR_Intensity2OD', 'hmrR_BandpassFilter', 'hmrR_OD2Conc_new', and 'hmrR_BlockAvg: Block_Average_on_Concentration_Data'. The desktop background is dark blue with icons for various applications like Anaconda, MobaXterm, and Visual Studio 2019.

A screenshot of a software interface for group averaging. The main window displays a line plot of data over time (0 to 350) with a y-axis scale of $\times 10^4$. The plot shows four distinct data series: a blue line at the top, a magenta line in the middle, and a green line at the bottom. Vertical blue lines indicate time points. To the right is a network diagram with nodes numbered 1-31 and colored edges. Below the plots is a control panel with a 'Current Processing Element' list (circled in red), 'Processing Level' options (Group, Subj, Run), 'Calculate' and 'Edit Options' buttons, 'Plot Type Select' (Raw Data, OD, Conc), and 'Motion Artifacts' and 'Plot Window' settings.

Current Processing Element

- group-averaging
- SubjA
 - subjA_run01.snirf
 - subjA_run02.snirf
 - subjA_run03.snirf
- SubjB
 - subjB_run01.snirf
 - subjB_run02.snirf
- SubjC
 - subjC_run01.snirf
 - subjC_run02.snirf
- SubjD
 - subjD_run01.snirf
- SubjE
 - subjE_run01.snirf
 - subjE_run02.snirf

Processing Level

- Group
- Subj
- Run

Plot Type Select

- Raw Data
- OD
- Conc

Motion Artifacts

- Show Excluded Manual
- Show Excluded Auto
- Show Excluded by Chan

Plot Window

- Pan Left/Right: < > Reset View
- Fix X-range: 0 400
- Fix Y-range: -2 2

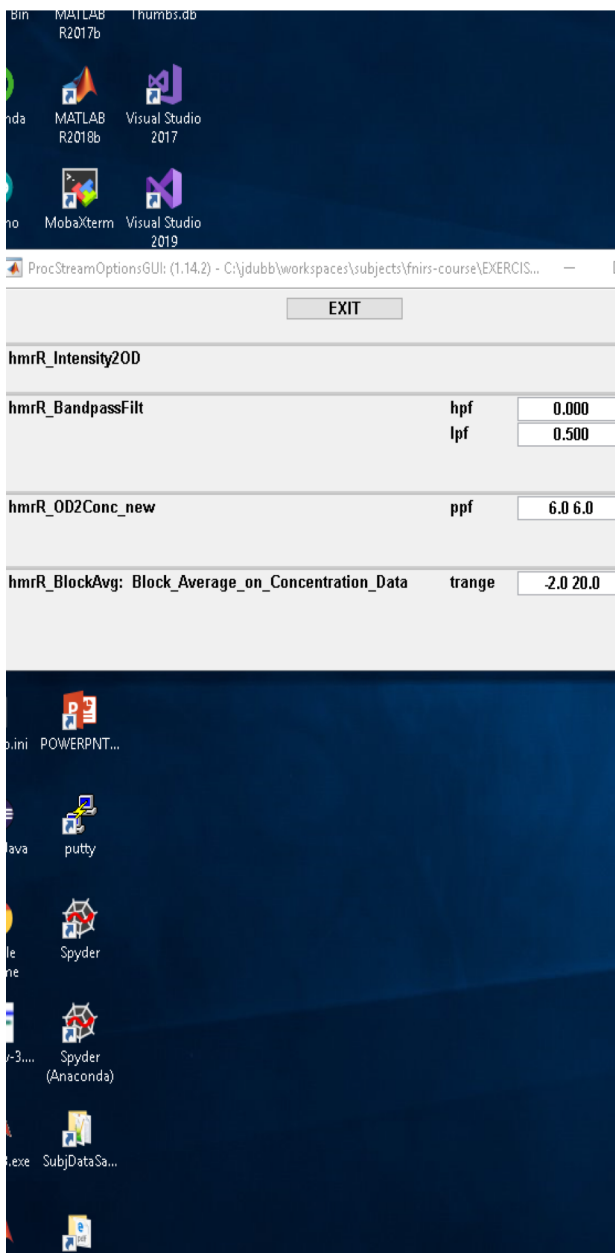
Folder structure

Group average: example

The screenshot displays a software interface for group averaging analysis. On the left, a control panel shows parameters for hmrR_Intensity2OD, hmrR_BandpassFilt (hpf: 0.000, lpf: 0.500), hmrR_OD2Conc_new (ppf: 6.0 6.0), and hmrR_BlockAvg: Block_Average_on_Concentration_Data (trange: -2.0 20.0). The main window shows a time-series plot of concentration data (y-axis: $\times 10^4$, x-axis: 0 to 350) with a group average line (blue) and individual subject data (orange, pink, green). A network graph on the right shows nodes (1-31) and edges. The bottom panel shows processing options for 'Run', 'Subj', and 'Group' levels, with 'Run' selected and circled in red. The 'Plot Type Select' section shows 'Raw Data' selected, and the 'Motion Artifacts' section shows 'Show Excluded Manual' checked.

You can run the analysis at the run level, session level, or group level

Run average: example



A screenshot of the Homer3 software interface. The main window displays a line graph with multiple colored lines (green, orange, blue, purple) representing different runs. The y-axis ranges from -0.2 to 0.5, and the x-axis ranges from 0 to 18. A smaller inset graph on the right shows a network-like structure with nodes and edges, labeled with numbers 1 through 31. Below the graph is a control panel with the following sections:

- Current Processing Element:** A list of files including '2-group-averaging', 'SubjA', 'subjA_run01.snirf', 'subjA_run02.snirf', 'subjA_run03.snirf', 'SubjB', 'subjB_run01.snirf', 'subjB_run02.snirf', 'SubjC', 'subjC_run01.snirf', 'subjC_run02.snirf', 'SubjD', 'subjD_run01.snirf', 'SubjE', 'subjE_run01.snirf', and 'subjE_run02.snirf'. A red arrow points to 'subjA_run01.snirf'.
- Processing Level:** Radio buttons for 'Group', 'Subj', and 'Run'. 'Run' is selected.
- Calculate:** A button to execute the processing.
- Edit Options:** A button with a checked 'Apply to all' checkbox.
- Plot Type Select:** Radio buttons for 'Raw Data', 'OD', and 'Conc'. 'Conc' is selected.
- HRF:** A checkbox labeled 'HRF' is checked. A red arrow points to it.
- Aux:** A dropdown menu showing 'aux1'.
- Motion Artifacts:** Checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan'. 'Show Excluded Manual' is checked.
- Plot Window:** A section with 'Pan Left/Right' buttons and a 'Reset View' button.

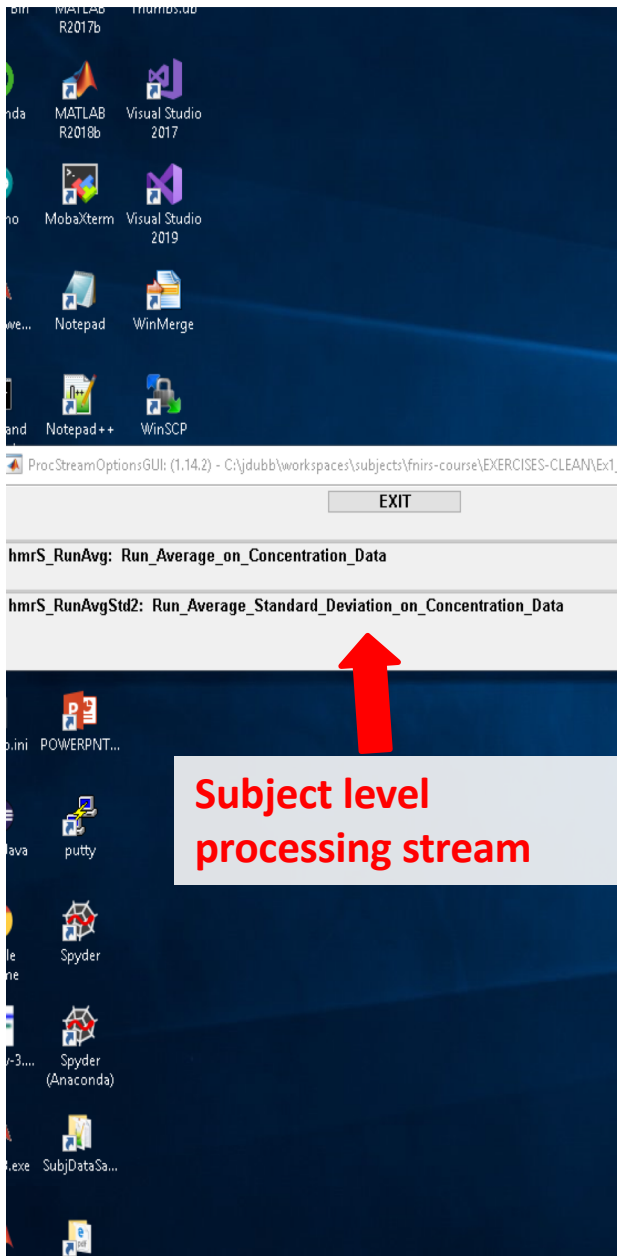
At the bottom of the control panel, it says '10 files loaded successfully' and '0 files failed to load'. A red arrow points to the 'Run' radio button.

2 – Run processing stream for current processing element: run 'SubjA_run01'

3 – Checkbox to show HRF

1 – Select run processing: 2 way to

Subject average: example



Subject level processing stream

A screenshot of the Homer3 software interface. The main window displays a line graph with multiple colored lines (solid and dashed) representing different subjects or runs. The x-axis ranges from 0 to 18, and the y-axis ranges from -1 to 0.5. To the right of the graph is a smaller plot showing a network of nodes and edges, with nodes labeled with numbers (1-12, 13-16, 17-28). Below the graph is a control panel with the following elements:

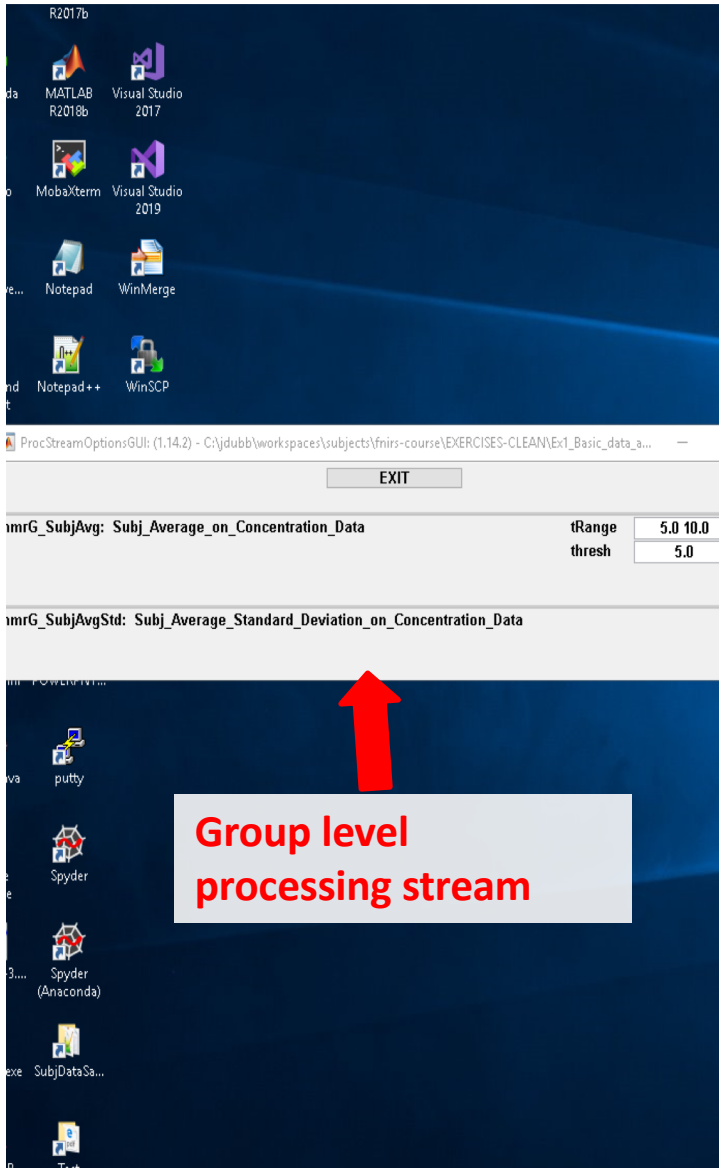
- Current Processing Element:** A dropdown menu showing 'z-group-averaging' and a list of subjects (SubjA, SubjB, SubjC, SubjD, SubjE) with their respective run files. A red arrow points to 'SubjA'.
- Processing Level:** Radio buttons for 'Group', 'Subj', and 'Run'. 'Subj' is selected, with a red arrow pointing to it.
- Calculate:** A button with a red arrow pointing to it.
- Edit Options:** A button with a red arrow pointing to it.
- Apply to all:** A checked checkbox.
- Plot Type Select:** Radio buttons for 'Raw Data' and 'HRF'. 'HRF' is selected.
- HRF:** A dropdown menu showing 'HbO', 'HbR', and 'HbT'. 'HbO' is selected.
- Aux:** A dropdown menu showing 'aux1'.
- Motion Artifacts:** Checkboxes for 'Show Excluded Manual', 'Show Excluded Auto', and 'Show Excluded by Chan'. 'Show Excluded Manual' is checked.
- Plot Window:** A section with 'Pan Left/Right' buttons and 'Reset View' button. There are also checkboxes for 'Fix X-range' and 'Fix Y-range'.

At the bottom left of the control panel, it says '10 files loaded successfully' and '0 files failed to load'. A red arrow points from the text '1 - Select subject processing. Two ways to do it.' to the 'Subj' radio button.

2 - Calculate processing stream for current processing element: subject 'SubjA'

1 - Select subject processing. Two ways to do it.

Group average: example



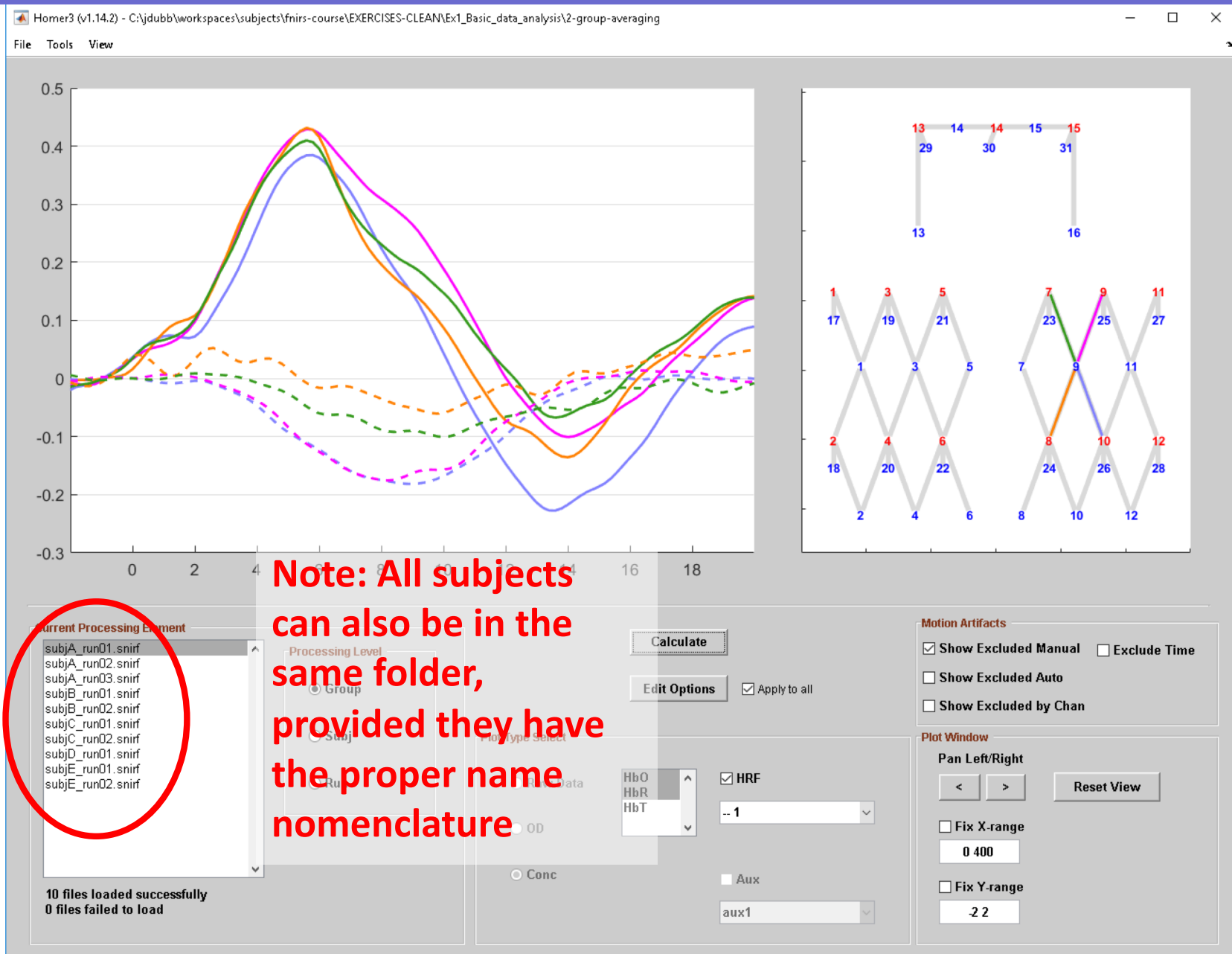
Group level processing stream

A screenshot of the Homer3 software interface. The main window displays a line graph with multiple colored lines (solid and dashed) representing different data series over time (0 to 18). The y-axis ranges from -0.3 to 0.5. To the right of the graph is a smaller plot showing a network of nodes and edges, with nodes numbered 1 through 31. Below the graph is a 'Current Processing Element' list showing a tree structure of processing elements, including '2-group-averaging', 'SubjA', 'SubjB', 'SubjC', 'SubjD', and 'SubjE'. The 'Group' radio button is selected under the 'Processing Level' section. A 'Calculate' button is visible. To the right of the interface are various control panels, including 'Motion Artifacts' and 'Plot Window'. Red arrows point from text boxes to the 'Group' radio button and the 'Calculate' button.

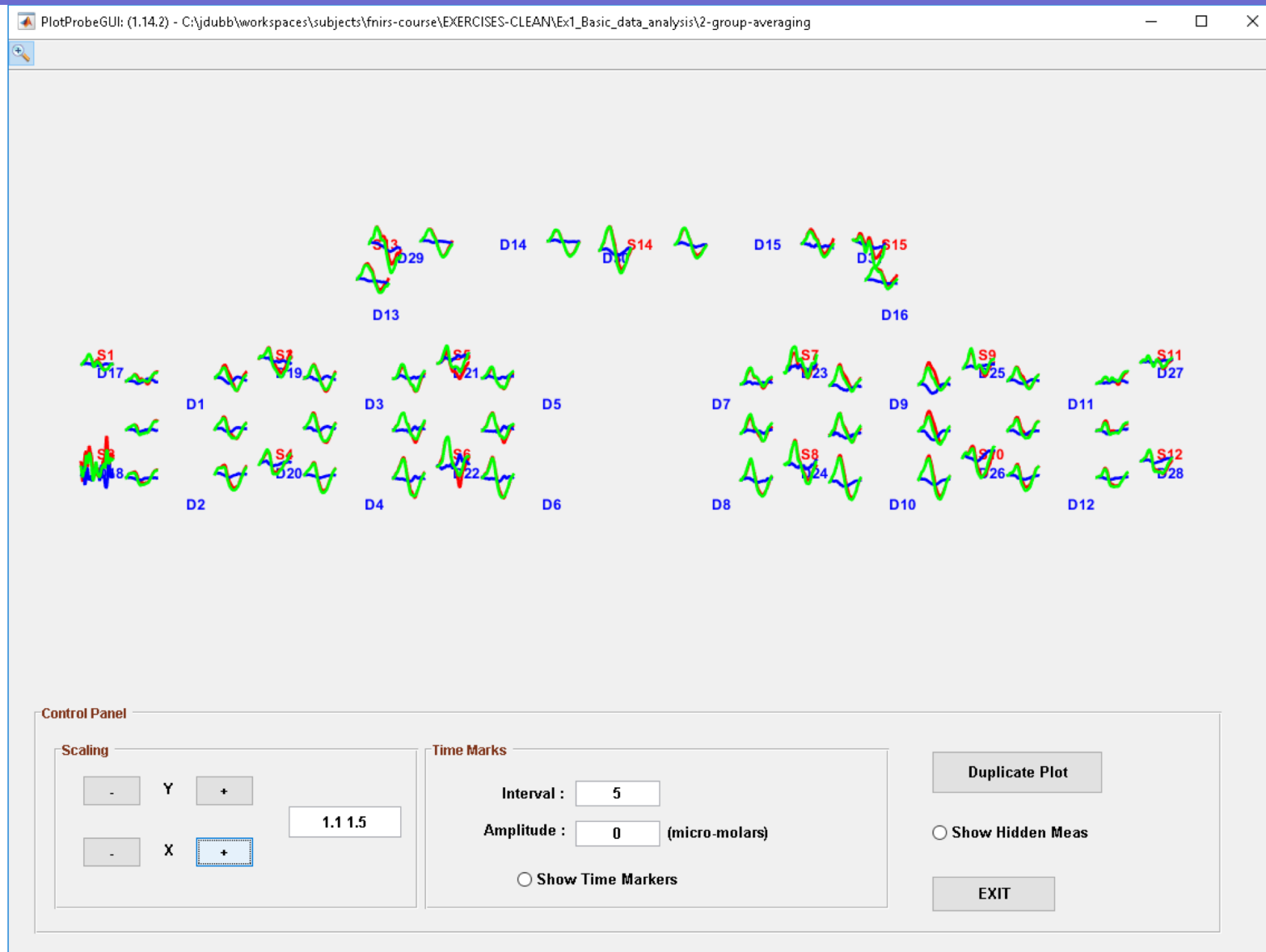
2 - Calculate processing stream for current processing element: group '2-group-averaging'

1 - Select Group processing. Two ways to do it.

Group average: example



Group average: example



We will get back to this dataset tomorrow and perform more advanced data analysis