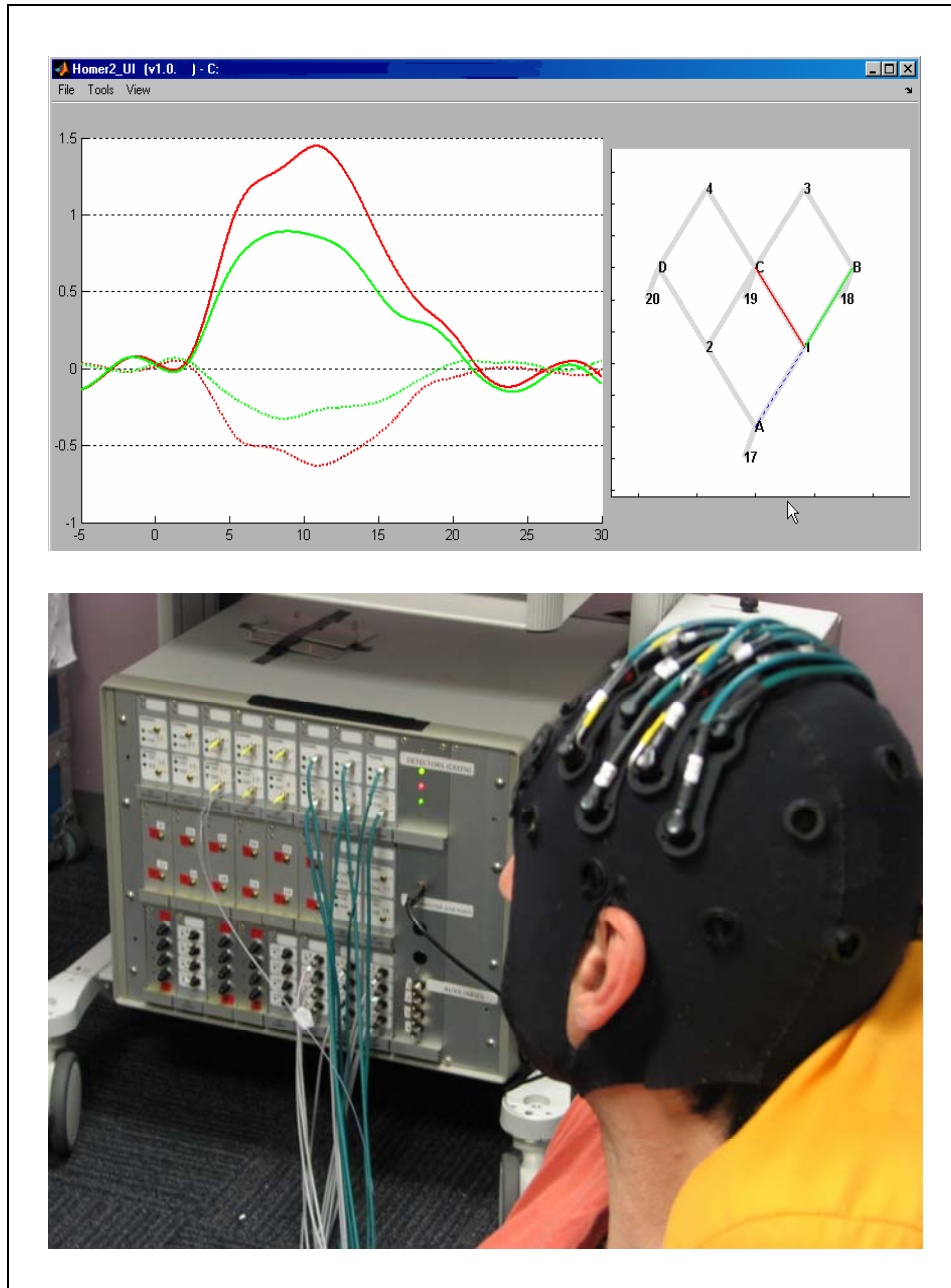


# HOMER2 Users's Guide

Nov 29, 2012



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## 1. Downloading HOMER2 source and documentation

<http://www.nmr.mgh.harvard.edu/Optics/resources/homer2/home2.htm>

There you will find separate downloads for the source, Homer2\_UI.zip or Homer2\_UI.7z (compressed HOMER2 source using the open source tool 7-Zip), and executable, Homer2\_UI.exe.

## 2. NIRS data format

The most basic unit of a HOMER2 data set is a matlab file in the NIRS format that is the result of data acquisition. An example of a device that generates files in this format is the continuous wave techen device called cw6.

The NIRS format has the following fields as a minimum requirement:

*t* - This variable is the data time points array. It contains the data acquisition times. The dimensions of this array are <number of time points> by 1.

*d* - This variable is the raw intensity time course. It is a 2D array where each element in row *i*, column *j* contains the raw intensity at time point *i*, in channel *j*. The dimensions of this array are <number of time points> by <number of measurement channels>

*SD* - This is a structured variable containing the source/detector geometry. It has the following fields:

*Lambda* - Wavelengths used for data acquisition; dimensions <number of wavelengths> by 1

*SrcPos* - Array of probe coordinates of the lasers; dimensions <number of lasers> by 3

*DetPos* - Array of probe coordinates of the detectors; dimensions <number of detectors> by 3

*nSrcs* - Number of lasers; scalar variable

*nDets* - Number of detectors; scalar variable

*MeasList* - List of source/detector/wavelength measurement channels. It's an array with dimensions, <number of channels> by 4. The meaning of the 4 columns are as follows:

- Column 1 index of the source from the *SD.SrcPos* list.
- Column 2 index of the detector from the *SD.DetPos* list.
- Column 3 is unused right now and contains all ones.
- Column 4 index of the wavelength from *SD.Lambda*.

*s* - This variable specifies the time points and condition of stimulus onsets. Conditions are a way to separate stimuli into different groups, where each group is averaged independently of stimuli belonging to other conditions. Initially the values in *s* are binary; 1 at time point *i* designating stimulus onset, 0 designating no stimulus at time point *i*. Note: Values of 1 can be modified during a Homer2\_UI session to be -1 or -2 depending on how they are disabled. The dimensions of *s* are <number of time points> by <number of conditions>.

*ml* - List of source-detector channels. This is a duplicate of the *SD.MeasList* above.

*aux* - auxiliary signal of same dimensions as *t*.

In addition to the above parameters, additional parameters can appear in the NIRS file as a result of processing the data set in Homer2\_UI (see section 6.6).

### 3. HOMER2 directory structure and data file organization

Any directory that contains one or more files with the .nirs extension is considered by Homer2\_UI to be a HOMER2 data set called a group. The group of .nirs files is also organized into sub-groups called subjects. Each .nirs file in the group is in the NIRS format described above and logically belongs to a subject. The name of each .nirs file determines to which subject it belongs. By organizing files in this way, it is possible to calculate and view the hemodynamic response to different stimuli averaged at the run level, at the subject level, and at the group level.

In order to have two or more .nirs files treated by Homer2\_UI as members of the same subject, the files have to be named using the following convention:

```
<subjectName1>_run01.nirs
<subjectName1>_run02.nirs
.....
<subjectName1>_run<n1>.nirs
<subjectName2>_run01.nirs
<subjectName2>_run02.nirs
.....
<subjectName2>_run<n2>.nirs
.....
<subjectNamem>_run01.nirs
<subjectNamem>_run02.nirs
.....
<subjectNamem>_run<nm>.nirs
```

This above shows the naming convention of the general group consisting of *m* subjects with each subject containing *n*<sub>1</sub>, *n*<sub>2</sub>, ..., *n*<sub>*m*</sub> runs respectively.

For example, the group

241-20101020\_run01.nirs  
241-20101020\_run02.nirs  
241-20101020\_run03.nirs  
242-20101021\_run01.nirs  
242-20101021\_run02.nirs  
242-20101021\_run03.nirs  
242-20101021\_run04.nirs  
265-20101213\_run01.nirs  
265-20101213\_run02.nirs  
269-20101229\_run01.nirs  
269-20101229\_run02.nirs

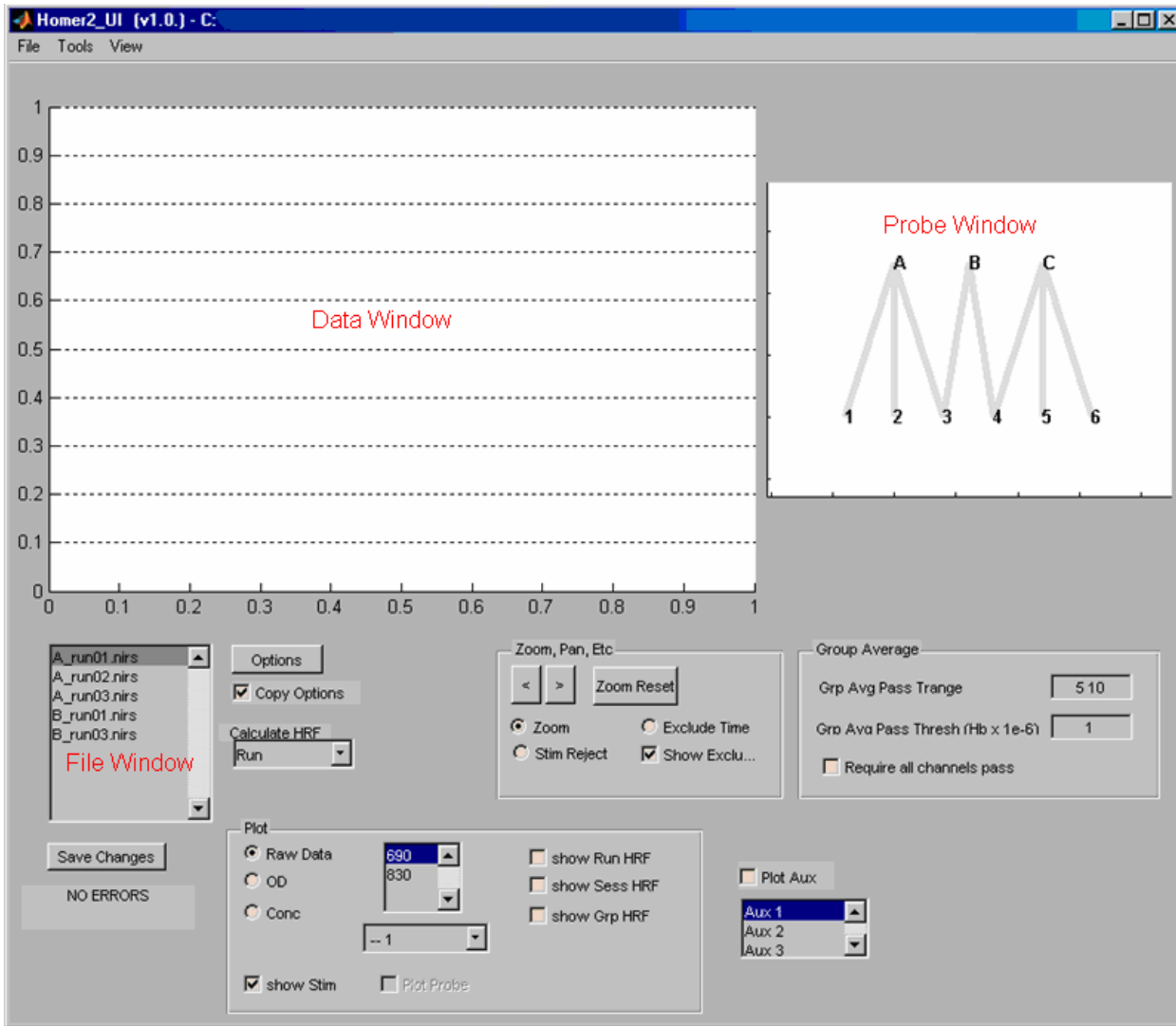
consists of the 4 subjects, 241-20101020, 242-20101021, 265-20101213 and 269-20101229, with 3, 4, 2 and 2 runs respectively, totaling 11 files.

NOTE: It is not necessary to name .nirs files according to the above convention if you don't care about associating multiple runs with each subject. If the .nirs file names do not contain run information in the naming format described above, then by default each file will be treated as the first and only run of a separate subject in the group.

## **4. GUI overview**

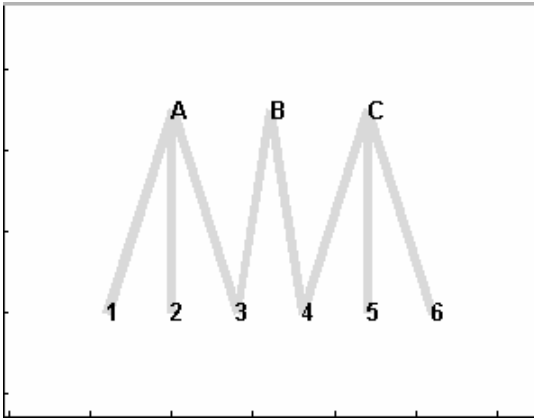
### **4.1 Running Homer2\_UI GUI**

The Main GUI is called *Homer2\_UI*. It contains the probe geometry window, data window, and the list of .nirs files comprising the HOMER2 data set. To run the GUI in matlab use the function *Homer2\_UI.m* with no arguments.

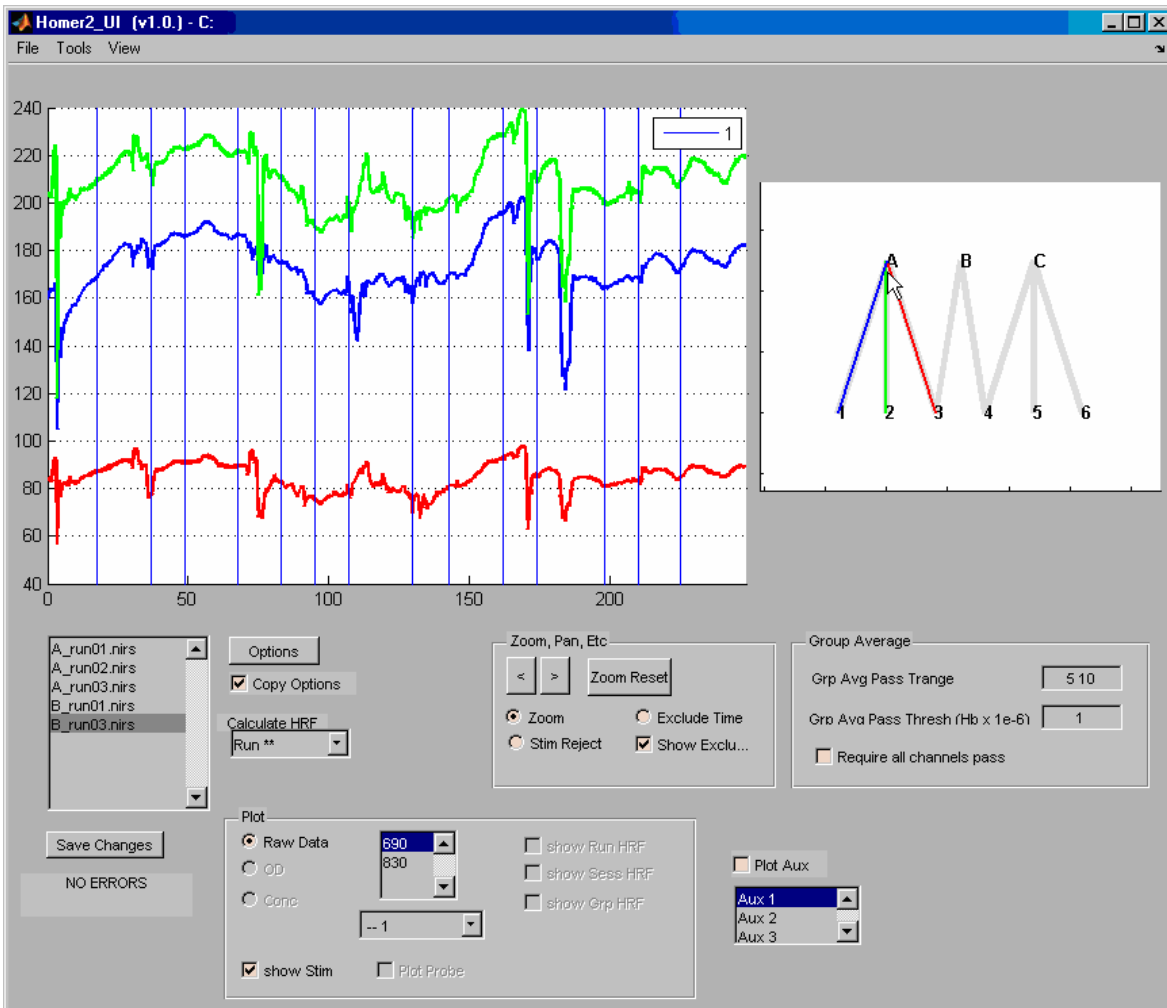


#### 4.1.1 Probe window

The *Probe Window* displays the probe geometry. Letters designate sources, and numbers designate detectors. Lines between them represent the source/detector measurement channels that are specified in the ml variable from the .nirs file.



To display one or more channels' data in the data window, click near a source or detector in the probe window. Clicking near a source will display data for all channels associated with that source. The same holds for clicking near a detector. Below is an example of *Homer2\_UI* GUI with the first 3 measurement channels selected, displaying their raw data:



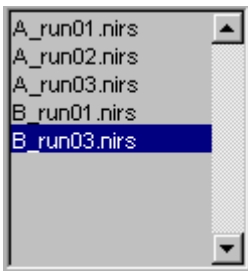


#### 4.1.1.1 Making channel data invisible

Typically, time courses for several channels are displayed simultaneously in the Data Window, since an optode usually has more than one channel associated with it. It is often useful to display only one time course at a time, especially if the time courses are close together and obscure each other. This can be done by un-displaying the channels one doesn't want to see. To un-display a channel's data **left-click the mouse** over channels in the Probe Window. This will un-display the data associated with that channel.

#### 4.1.2 File window

The *File Window* displays the list of files in the group data set of the current Homer2\_UI session. In this case the group contains 2 subjects called A and B with 3 and 2 runs (.nirs files) respectively. The data of subject B's second run is being displayed in this particular example.



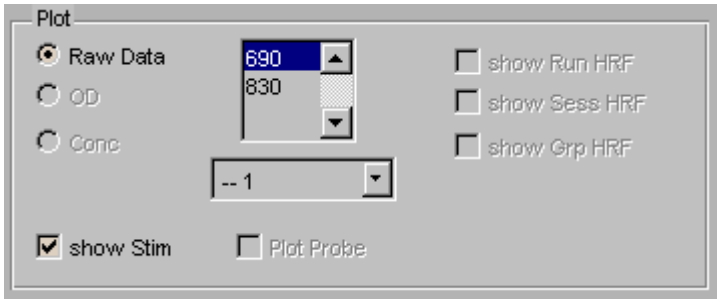
#### 4.1.3 Data Window and Plot Panel

The Data Window displays the data for the channels selected in the *Probe Window* for the file selected in the file window.

The specific data displayed in the *Data Window* is determined by the selections in the *Plot panel*. But generally speaking, it can be any of the following:

- a) raw data: for a selected wavelength
- b) optical density: for a selected wavelength
- c) hemoglobin concentration: HbO, HbR, HbT
- d) HRF for run, subject, or group: HbO, HbR, HbT

Depending on the data type selected, you can choose which wavelength or concentration to be displayed. It is possible to select more than one wavelength or channel to display by selecting the second choice with the right mouse button.



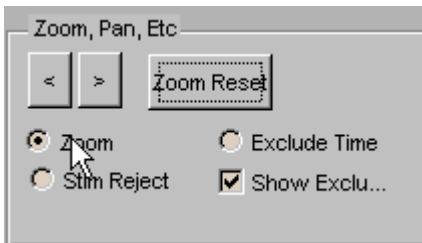
When a new data set is loaded (which has not yet been processed by HOMER2 ), the OD, Conc, HRF checkboxes and Plot Probe checkbox are disabled because those buttons are associated with data that is calculated from the raw signal. In this case the data displayed in the data window – after clicking on one of the channels in the probe window - is the raw signal by default.

#### 4.1.4 Processing options for group HRF: Group Average Panel

TBD

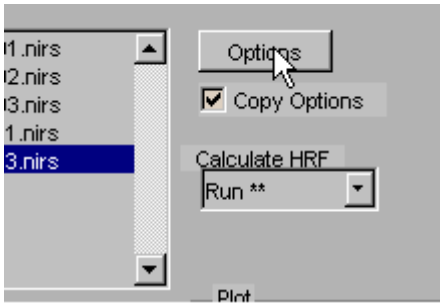
#### 4.1.5 Zoom, Pan, Etc. Panel

This panel allows the user to magnify and pan the data displayed in the *Data Window*. It also enables the user to manually exclude data time points which look to have motion artifacts and to toggle stimuli on or off. For more details, see section 6.1



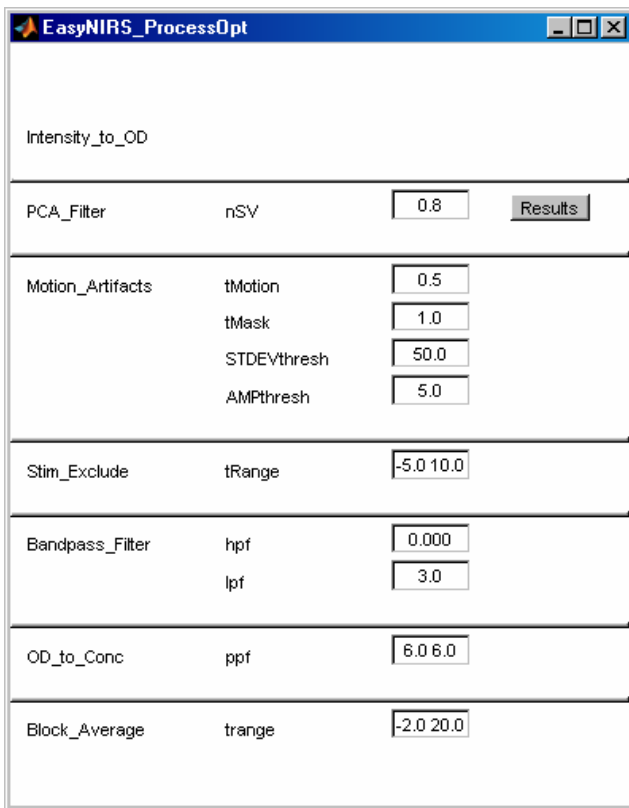
## 4.2 Processing stream options GUI

Clicking the *Options* button in Homer2\_UI GUI will bring up the *ProcessOpt* GUI.



The *ProcessOpt* GUI displays the configurable collection of functions (or processing stream) that processes the raw signal to calculate the evoked hemodynamic responses to presented stimuli. These functions typically include motion correction, calculate the optical density changes, band-pass filtering, calculate the hemoglobin concentration changes, and calculating the hemodynamic response function (HRF).

The exact calculation depends on the particular set of functions in the processing stream and the parameter settings – editable in the *ProcessOpt* GUI - associated with those functions.



The figure above shows a processing stream composed of 7 functions, beginning with a conversion from raw data to optical density and ending with a function that calculates the HRF from the hemoglobin concentration changes and given the stimulus marks that were not excluded by the stimulus rejection function (4<sup>th</sup> function from the top).

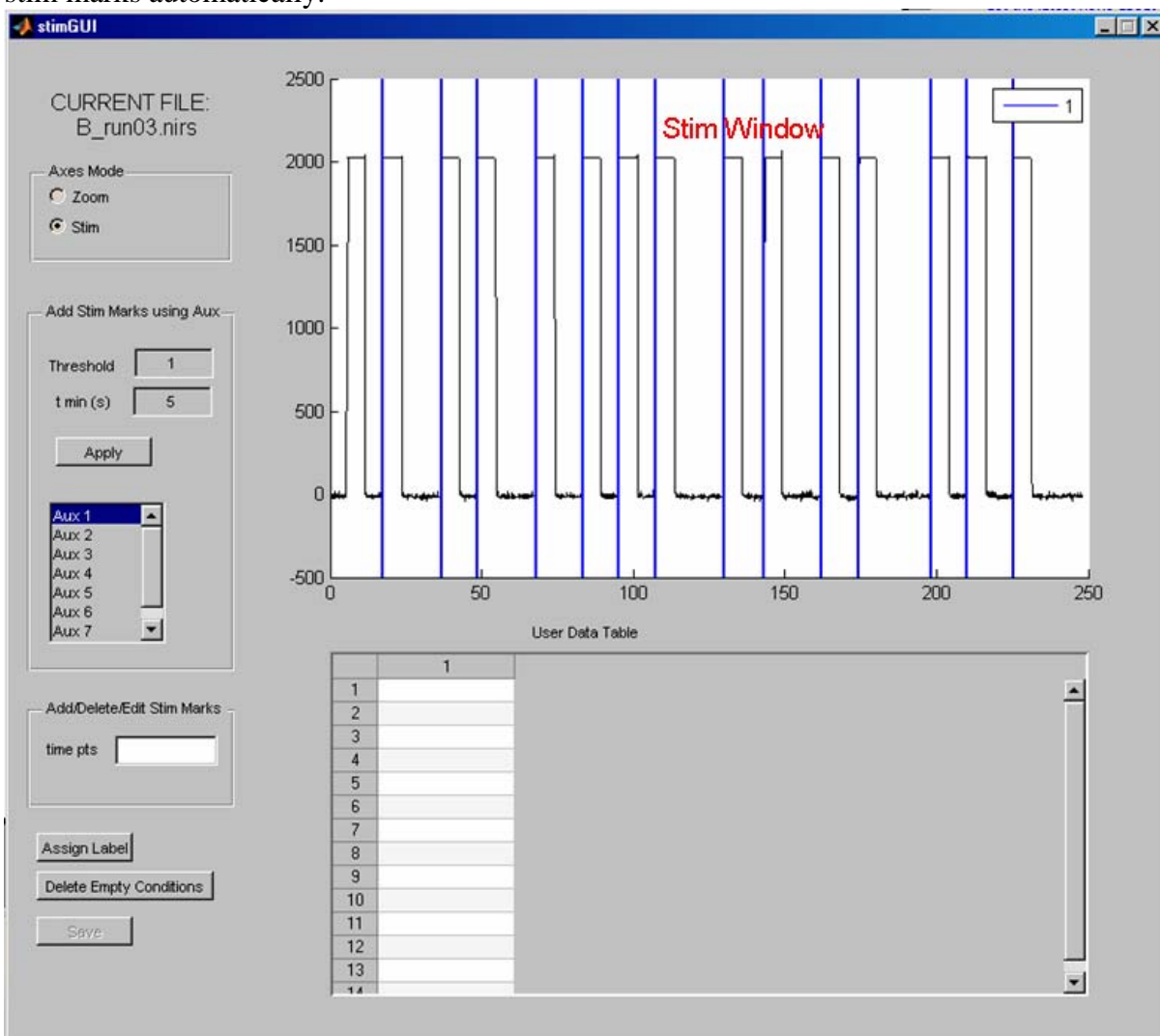
More information about the functions that can appear in the processing stream and their associated parameters can be found in the function reference section (see sections 7.2 and 8 below).

### 4.3 Stimuli GUI

The stimGUI allows the user to create, delete and modify the stimulus marks used to determine which time points are used to calculate the HRF.

To start stimGUI, select the stimGUI option from the Tools menu of Homer2\_UI.

Besides displaying the stimulus marks, the Stim Window also displays the specified auxiliary signal as a black line. The panel “Add StimMarks using Aux” allows the user to use a simultaneously recorded aux signal to set stim marks automatically.

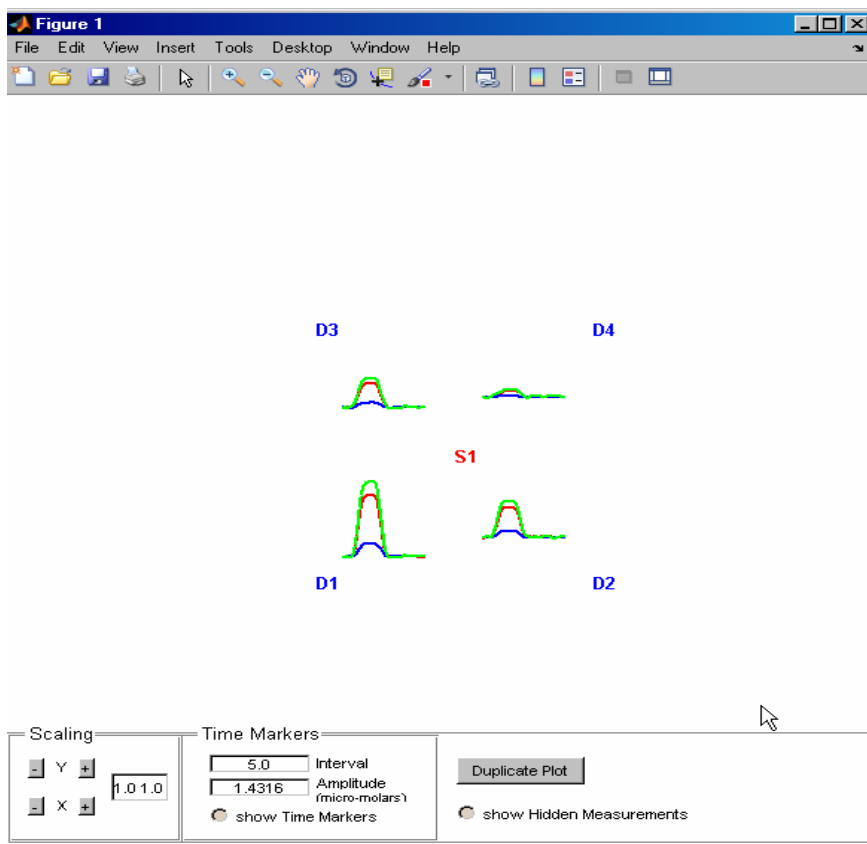


New stimulus marks can be added by mouse clicking in an area of the *Stim Window* that has no stimulus mark. Stimulus marks can be deleted or modified by selecting (dragging the mouse cursor) over existing stimulus marks in the *Stim Window*. Another way to do the same thing is to enter specific time points – if known - in the edit box of the “Add/Delete/Edit Stim Marks”. For details, see section 6.4.

Lastly, stimulus conditions can be further differentiated by utilizing the User Data Table. This table has a row of edit windows for each stimulus mark and a column for each user defined variable. The user can add more columns for each new variable. For details, see section 7.2.1. This table is useful, for example, to provide behavioral information related to each stimulus that can subsequently be used to select trials that meet specific criteria when estimating the HRF.

#### 4.4 Plot Probe GUI

The *plotProbe* GUI allows the user to view the HRF in probe space after data has been processed.



It has a controls panel at the bottom of the GUI which allows the user to

- scale the data
- view time markers starting with stimulus onset
- view amplitude by setting the size of the time markers and viewing them relative to the data.
- view pruned channel data which is ordinarily hidden

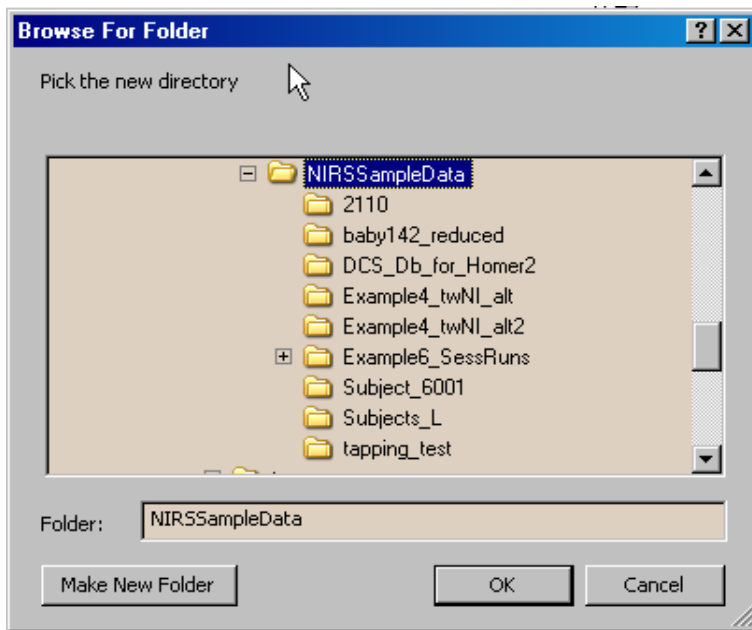
e) Duplicate current *plotProbe* GUI in separate figure.

For more details, see section 10.

## 5. Getting Started

### 5.1 Loading a data set into Homer2\_UI

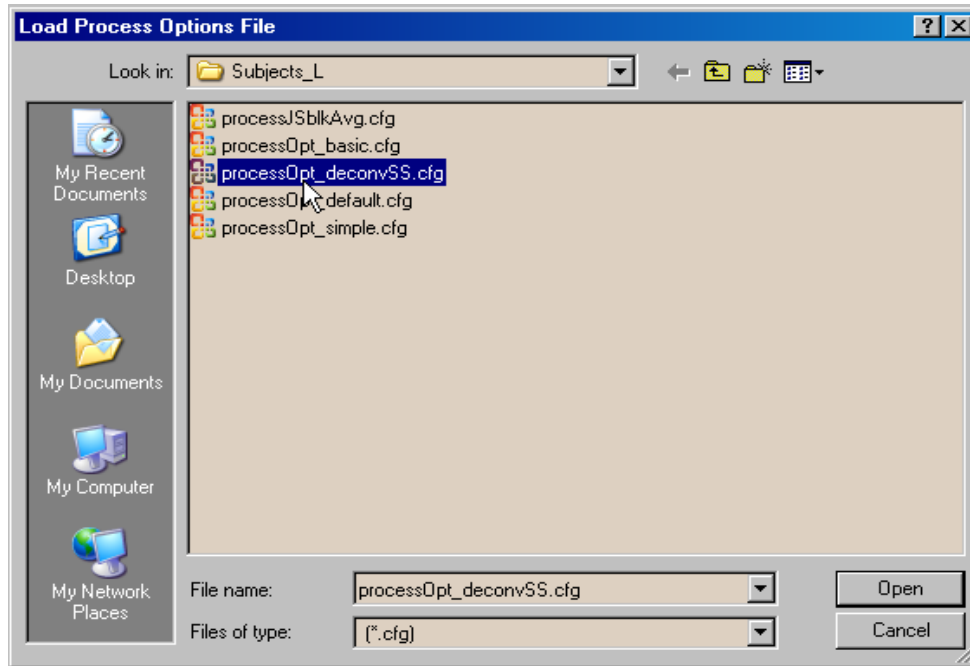
When Homer2\_UI first launches, it asks the user to select the folder containing the data set to be analyzed.



### 5.2 Choosing a processing stream configuration file

After choosing the folder containing the data set, the user is asked to choose a processing stream configuration file in the Load Process Options File window. If the data set has already been processed in Homer2\_UI, then the user is not asked to select the configuration file since it has been selected previously.

A processing stream configuration file specifies the set of functions that will be executed on the data, starting with the raw data and ending with a processing result such as HRF. Typically the end result will be the HRF, although it doesn't have to be.



If the user doesn't have a configuration file to load, a default one can be created by clicking the Cancel button in the Load Process Options File window.

Also the user can edit the current processing stream or create one from scratch by using the procStreamGUI which is accessed from the *Tools* menu in *Homer2\_UI* GUI. For details see Appendix A.

#### 5.4 Loading a new data set in an existing Homer2\_UI session

To load another data set in an existing Homer2\_UI session, go to the *File Menu* and choose *Change Directory*. Subsequent processing will be done on this data set and will have no impact on the previous data set. Furthermore, if this new data set has not yet been processed, then the user will be asked to select the processing stream configuration file. Otherwise, the processing stream configuration will be the same as when previously analyzed. The processing stream configuration for the new data set will not be impacted by the previous data set.

If the user wishes to utilize the same processing stream configuration for the new data set, then the user should export the configuration from the previous data set, and then load them into the new data set using the commands in the file menu.

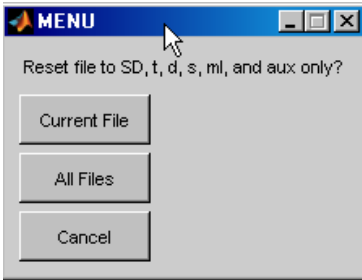
#### 5.5. Viewing data before processing

Click on one of the source-detector channels in the Probe Window to view the Raw Data.

#### 5.6 Undoing (resetting) changes to data set

Data that has been processed in Homer2\_UI is saved automatically to disk. Run data is saved in the corresponding .nirs, while subject and group processing results are save to groupResults.mat

To go back to the state before any processing was done to the data set, go to the File Menu and choose Reset File. The user will be given a choice whether to reset only the currently selected .nirs file or the whole data set.



The .nirs file(s) selected for reset will be returned to their original state. If All Files is selected, then groupResult.mat will be deleted in addition to all .nirs files being reset

This feature may be useful if the user wants to move .nirs files to a different data set and doesn't want the previous data to be displayed with the new data set. It is also useful for developers of HOMER2 to be able to return .nirs files to their original states.

## 6. Configuring data prior to processing

Before processing the raw data, the user can set many options which determine exactly which data is included or excluded in the processing, which will ultimately determine the processing result. The following two sections describe the major configurable options that can be set prior to processing.

### 6.1 Zooming , panning data displayed in Data Window

Use the Zoom, Pan, Etc panel in Homer2\_UI to zoom in and pan the magnified data, by clicking the Zoom radio button and then dragging the mouse over the data in the Data Window you want to magnify. To pan the zoomed data, click on the left or right arrow buttons in the Zoom, Pan, Etc panel. You can zoom out by right clicking the Data Window.

**To reset the data display** to the entire (original) time course, click on the **Zoom Reset button** in the Zoom, Pan, Etc panel.



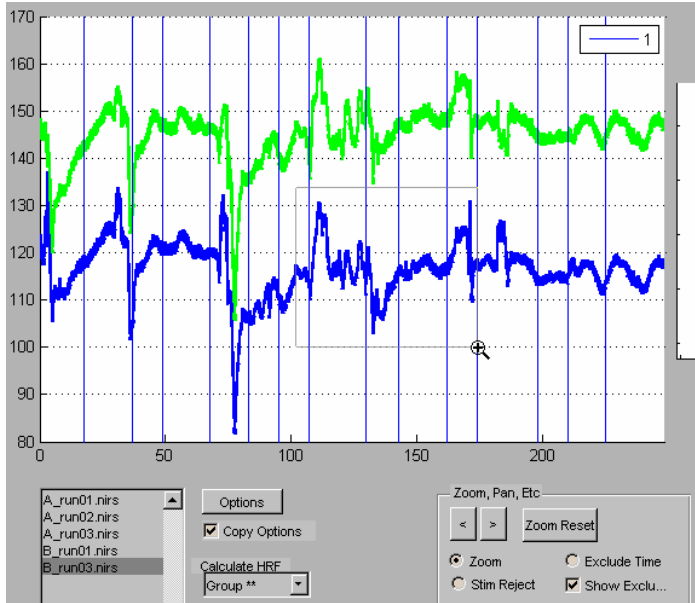
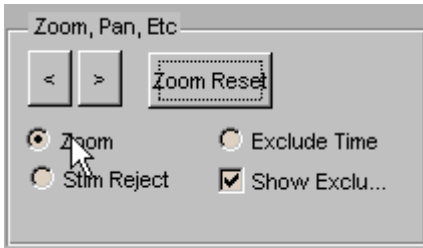
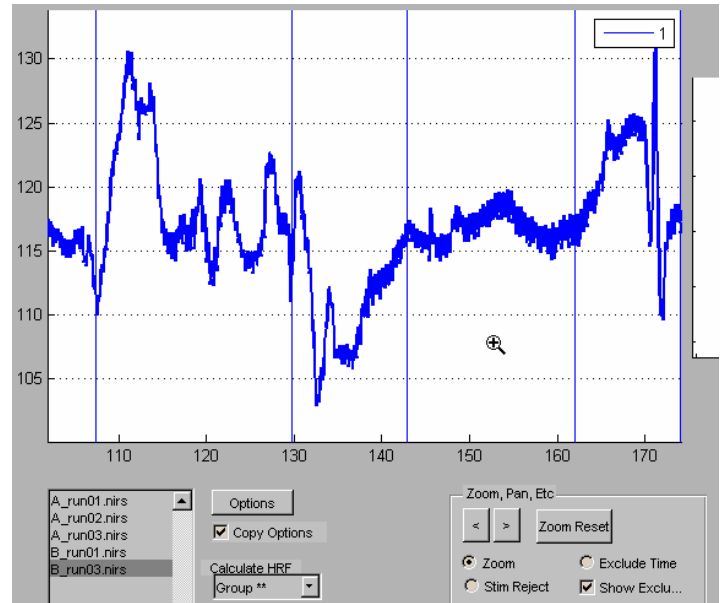


Figure 6.1: a) selecting section of data to be magnified



b) magnified section of data

To pan zoomed data click on the left or right arrow buttons in the Zoom, Pan, Etc panel.

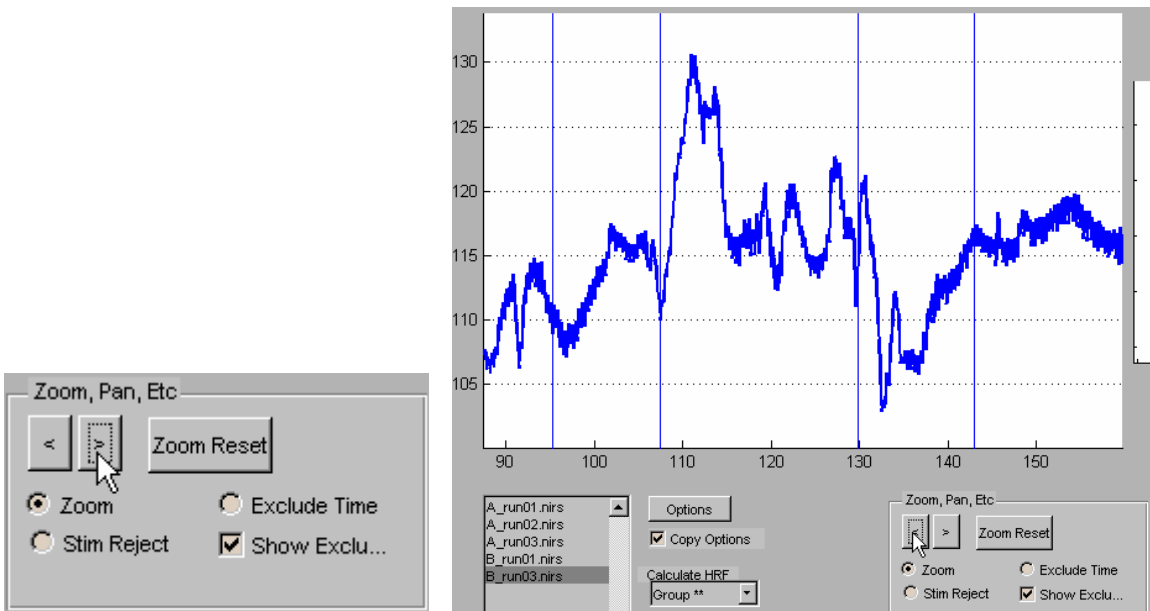


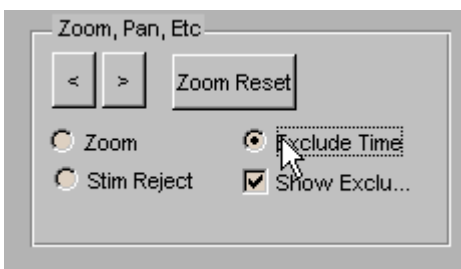
Figure 6.2: Panning data

## 6.2 Manually excluding data

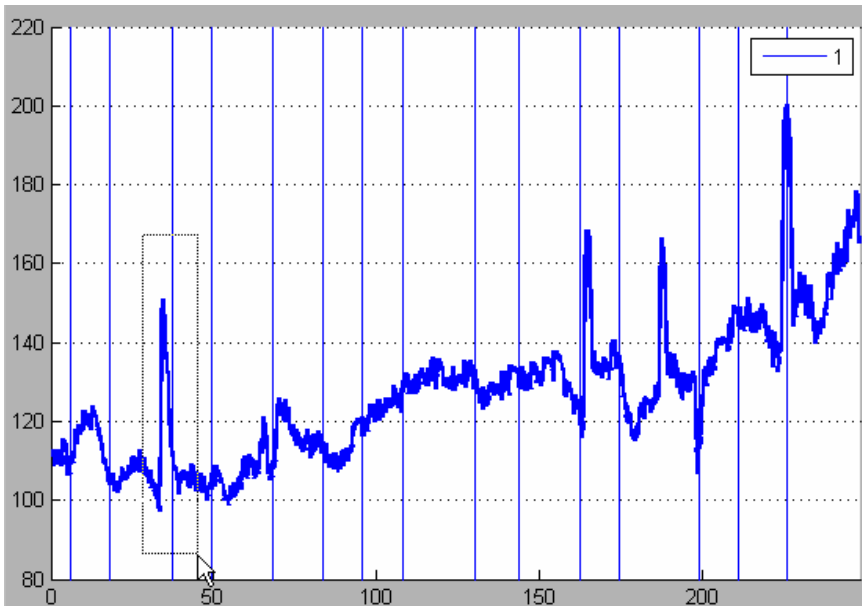
Excluding data manually means marking the time points where data is deemed to be invalid. While this by itself will not shorten the time course in the calculation of OD or Concentration, any stim marks contained within the marked time points will not be included in the HRF calculation.

Data can be determined to be invalid if the signal changes are due to a factor other than hemodynamic response to brain activity or physiology, such as motion of the subject. This can be done just by visually examining the raw signal in the data window.

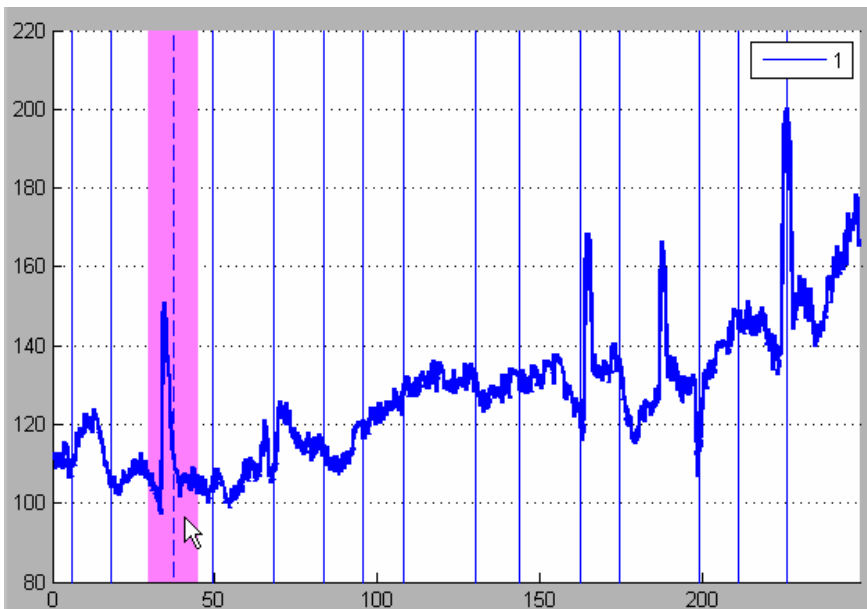
To manually exclude portions of data from being processed, first click the Exclude Time radio button in Zoom, Pan, Etc panel;



then drag the cursor in the data window across the time points that contain the unwanted data, as shown in the figure below.

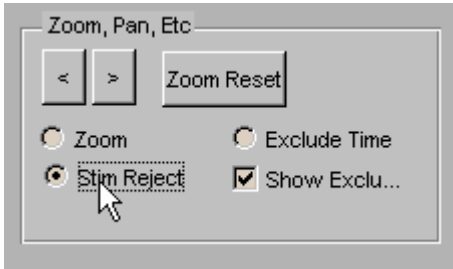


You should see a purple patch like the one shown below. Any stimulus marks within this temporal range will become dashed to indicate that this stimulus mark has been toggled off and will thus not be included in the HRF calculation. A purple patch can be deleted by simply mouse clicking on the purple patch and selecting the correct option in the pop-up window.

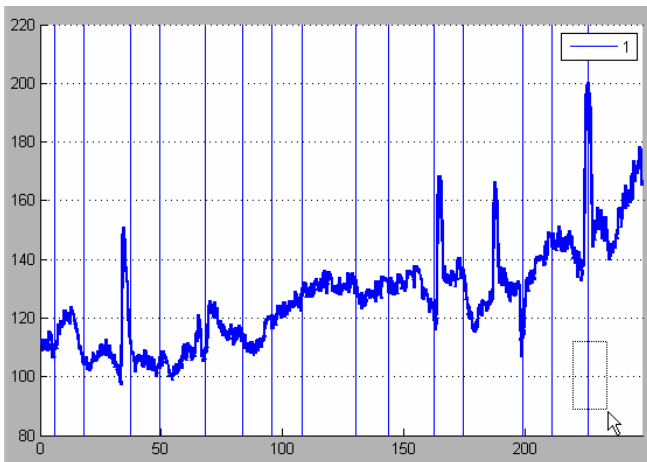


### 6.3 Excluding stimulus marks

In addition to excluding data, stimulus marks can be excluded or deleted directly. To exclude a stimulus mark, click the Stim Reject radio button in the Zoom, Pan, Etc panel of the main GUI



Then drag the mouse over the stimulus mark or marks that you want to exclude. The example below shows the last stim in the time course being excluded. This does not delete the stimulus mark but only makes it dashed to indicate that it has been manually removed.

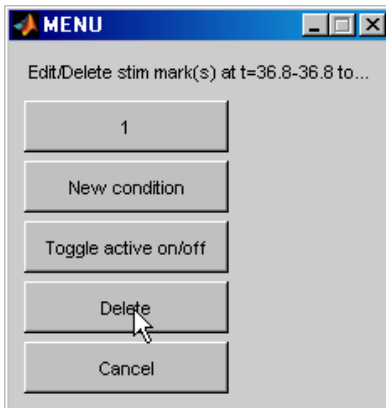
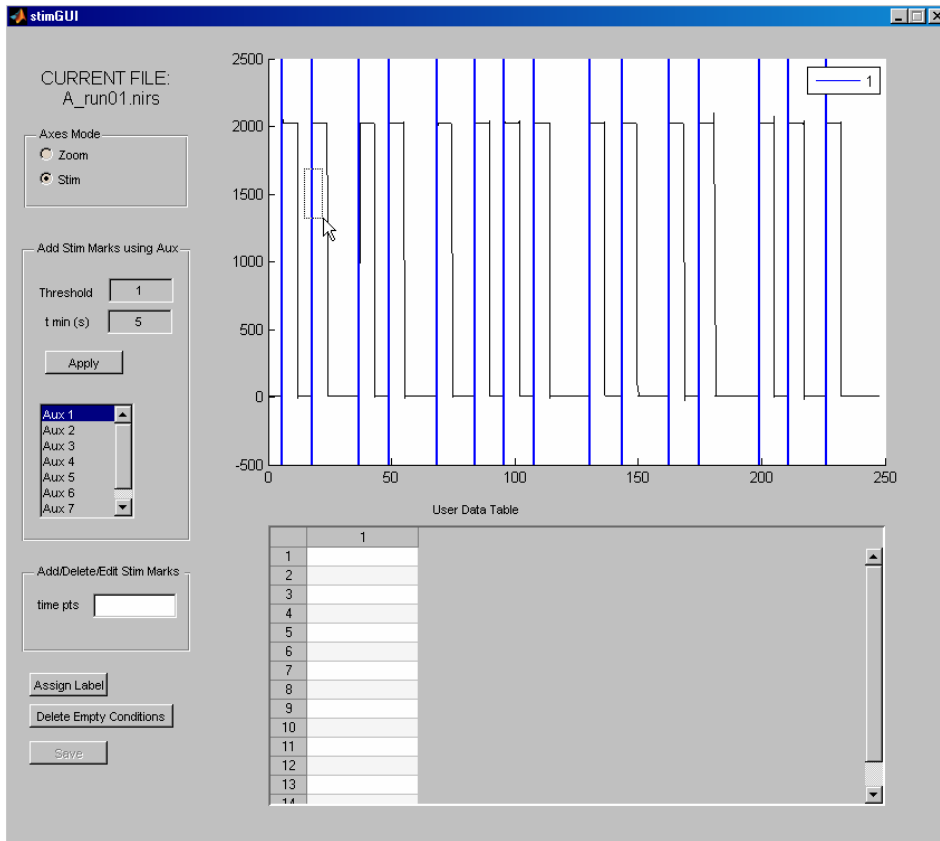


### 6.4 Adding, Deleting and Editing stim marks

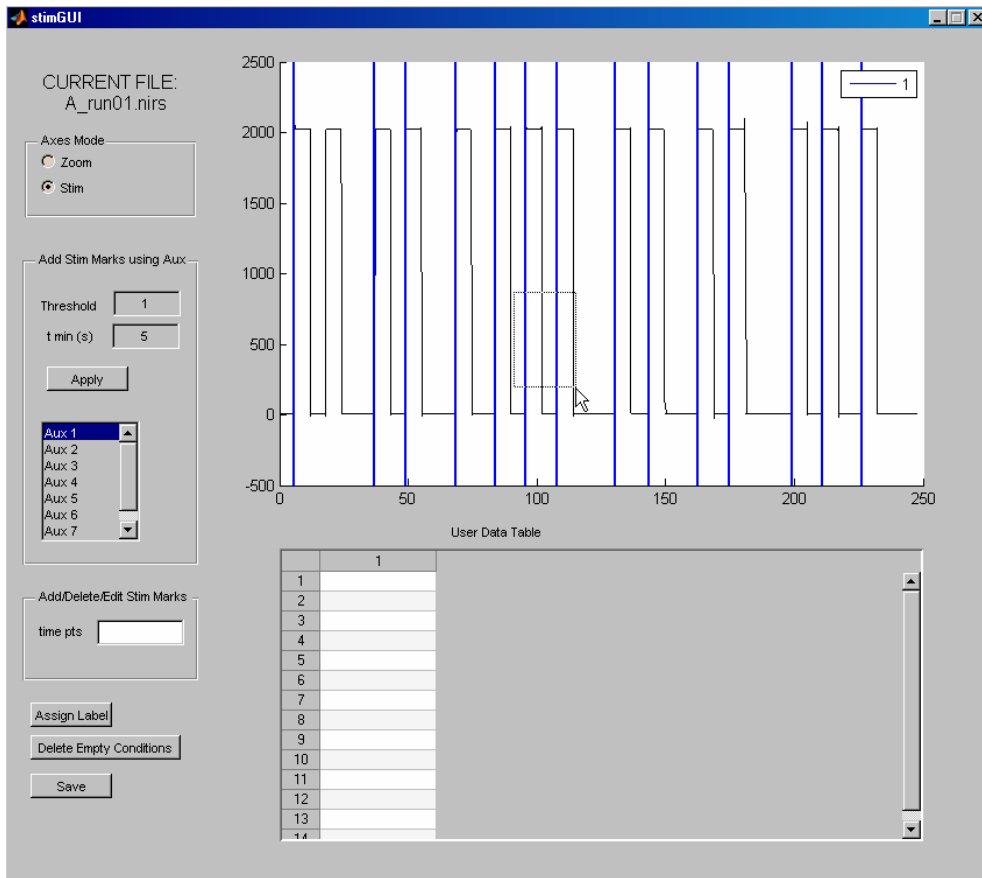
To permanently delete, add or modify a stimulus mark open the *stimGUI* from the Homer2\_UI *Tools Menu*.

#### 6.4.1 Deleting and modifying existing stimulus marks

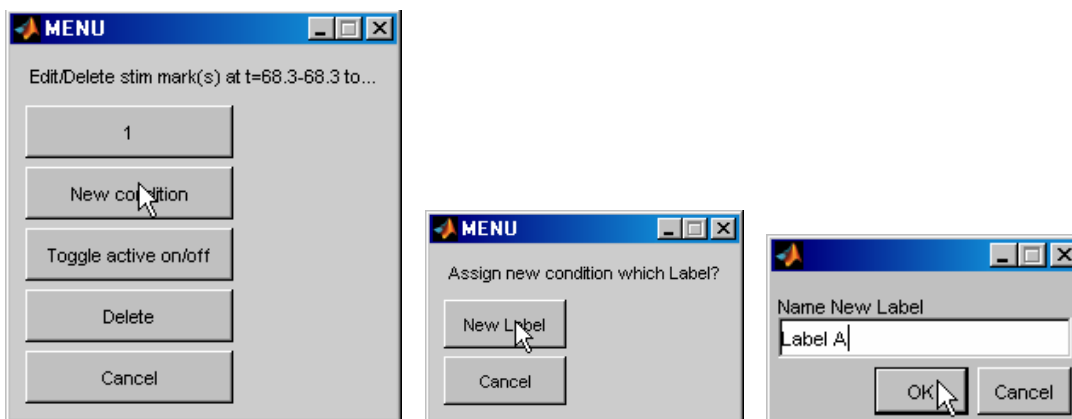
To delete a stimulus mark, select it by dragging the mouse over it in the *Stim Window* and click the Delete button in the pop-up window.



Groups of stimulus marks can be differentiated using different condition labels. These condition labels are subsequently used when calculating the HRF for the different stimulus conditions. The user can change the condition label of a stimulus mark from the *stimGUI* by dragging the mouse over the stimulus marks in the *Stim Window* and then creating a new condition or selecting an existing one.



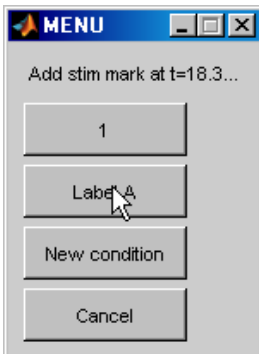
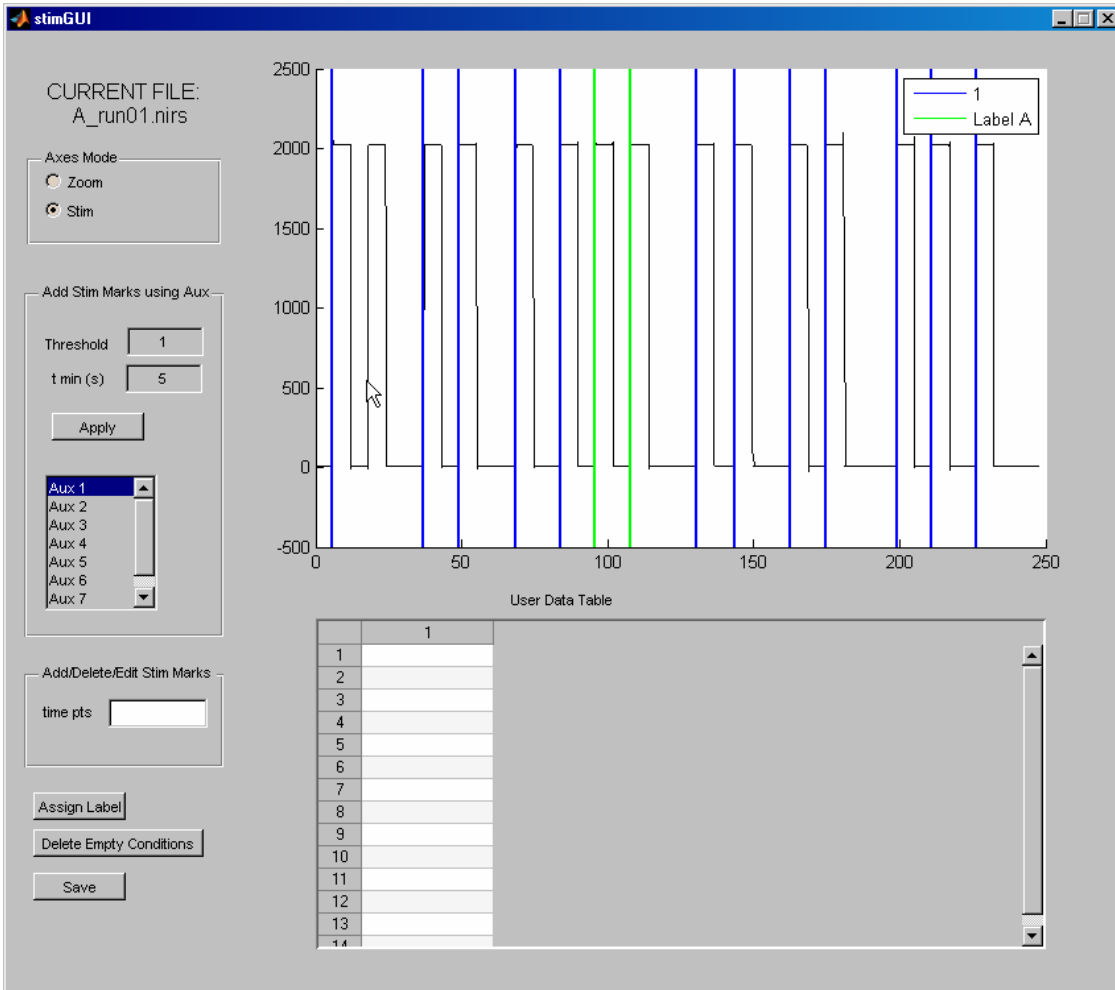
Since there's only one existing condition, you need to create a new condition label to differentiate the selected stimulus marks.



## 6.4.2 Adding new stimulus marks

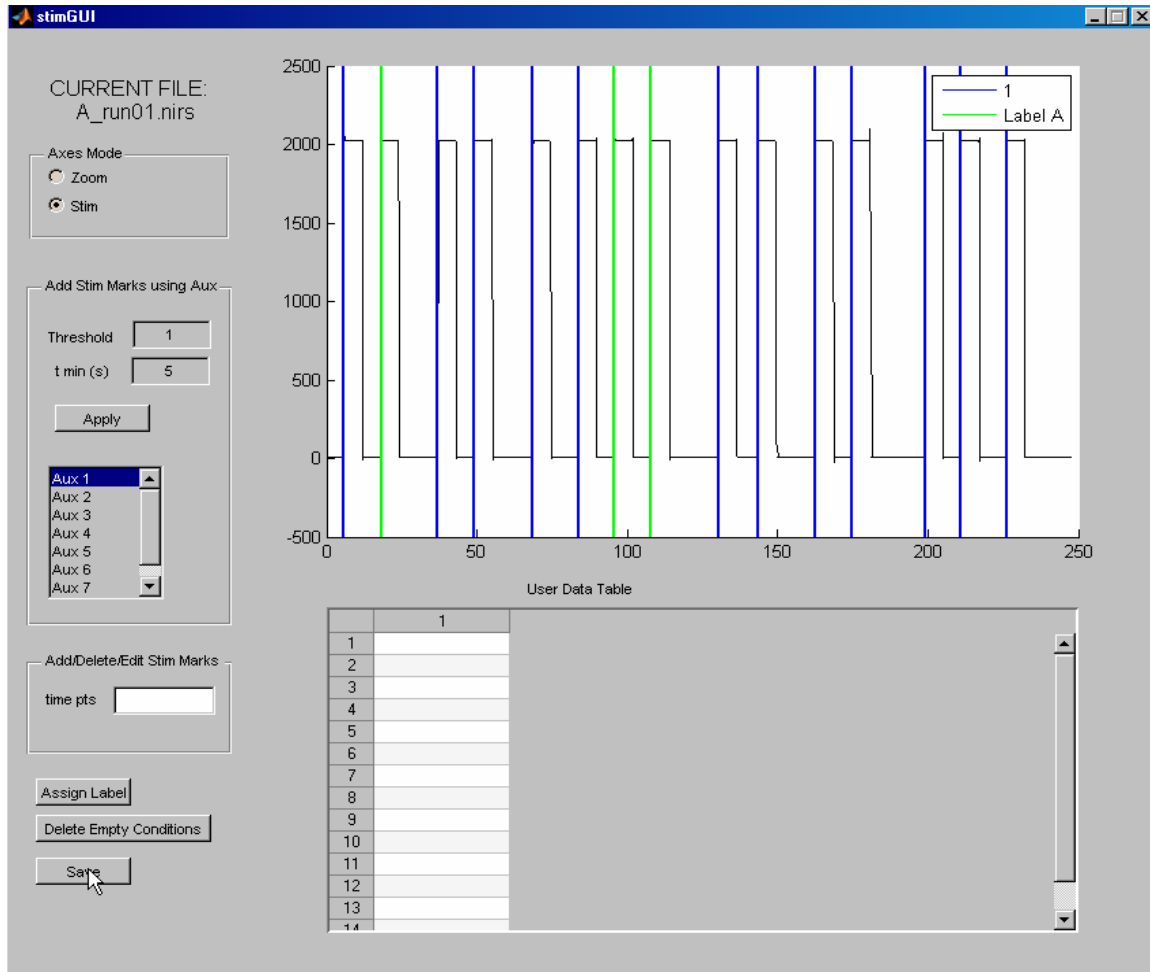
In the previous section, after deleting one stimulus mark and editing two, the *stimGUI* looks like the figure below:

We can add a new stimulus mark by clicking the mouse (without dragging) in the *Stim Window* at the time point where you want to place the new stimulus mark and where there's no existing stimulus mark.



### 6.4.3 Saving changes in the stimGUI

NOTE: If you exit *stimGUI* without saving the changes they will disappear. To have any changes take effect click on the Save button as shown below. The changes will then be saved in the .nirs file and appear in the main GUI.



### 6.4.4 User Data Table

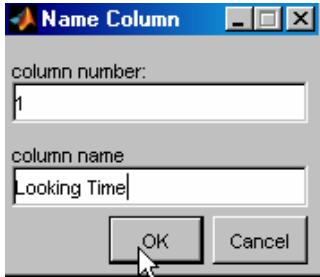
Stimulus marks belonging to the same condition can be further differentiated using the User Data Table. Any type of numerical information can be recorded in this data table and associated with each stimulus mark. This is particularly useful for recording any behavioral data associated with each individual stimulus. These data can be utilized in the processing stream to decide which stimuli trials are included in the estimation of the HRF and which stimuli trials are excluded.

The user data table has a row of edit windows for each stimulus mark and a column for each user variable. The user can add more columns for each new variable.

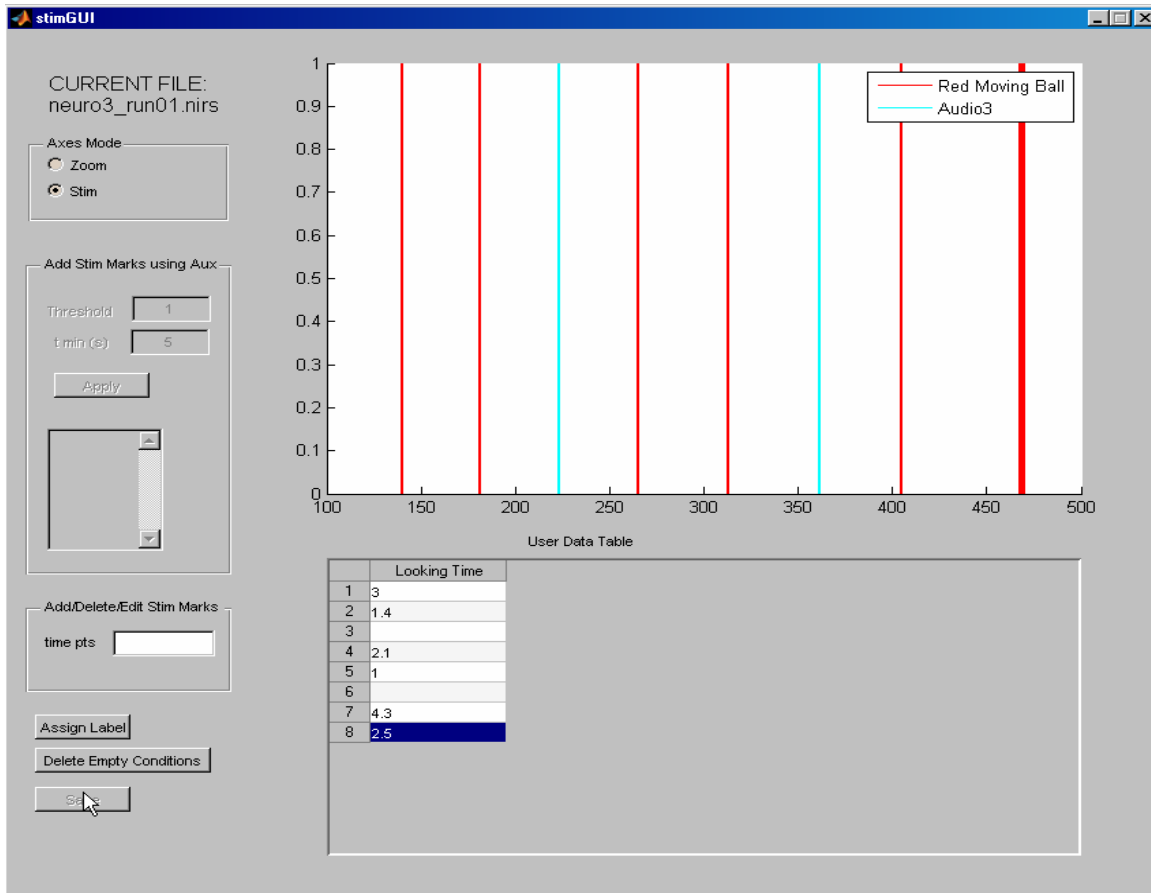


Here's an example of one such variable: baby subjects are given a visual stimuli which slowly moves across their field of vision for about 5 seconds. Once the data is acquired it might be desirable to estimate the HRF using only stimulus trials for which the infant actually looked at the object greater than a certain amount of time (e.g. 2 seconds). In this example there are 6 stimulus trials (see figure below) belonging to the visual condition and 2 stimulus trials belonging to another condition. The experimentally determined looking times for the visual condition (i.e. red stimulus marks) are 3, 1.4, 2.1, 1, 4.3, and 2.5 seconds respectively.

First name the column in the user table by left clicking over the column. A window comes up which allows a name to be entered:

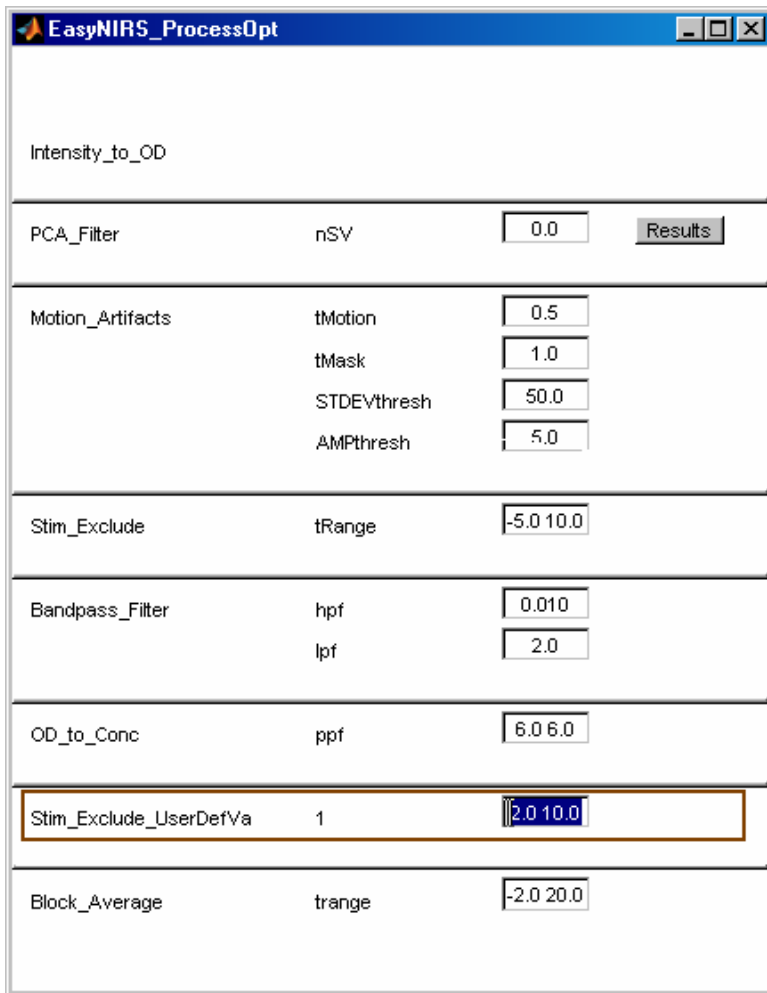


The user data table would then be used to enter the looking time of every stimulus mark. Note that in this case, data is not entered for trials for which the variable 'looking time' is not relevant.



Now to average only those stimulus trials with 'looking time' greater than 2 seconds,

- a) Bring up processing stream options from the Homer2\_UI.
- b) Find the function *Stim\_Exclude\_UserDefVars* and enter a range of 2 to 10.
- c) Recalculate the HRF for the run by choosing 'Run' from the Calculate HRF dropdown menu.

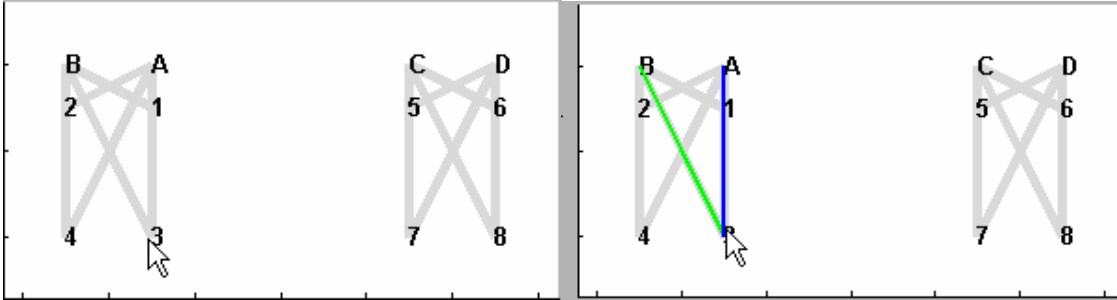


You will notice after the average is calculated that stimuli with looking time less than 2 seconds will be excluded from the HRF calculation and will become dot-dashed lines.

### 6.5 Manually pruning noisy or otherwise bad channels

To prune a channel means to exclude a channel's data from calculations for that run. If a channel is deemed bad - for instance, say in the example below channel A-3 is too noisy - it can be excluded by

- a) making the channel's data visible in the data display by clicking on a source or detector associated with that channel in the *Probe Window*.



b) then left clicking the mouse over that channel. It's background color will then change to pink and the foreground will become dashed.

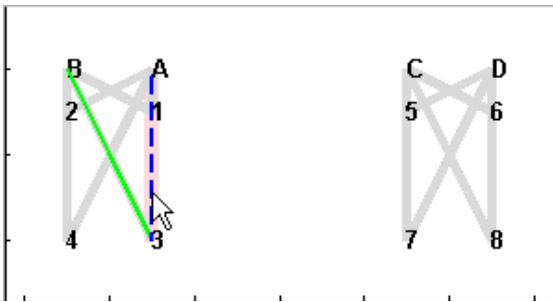


Figure 1

To undo the exclusion simply left click again on the channel.

## 6.6 Additional parameters saved to .nirs files

In addition to the initial parameters which define the .nirs data format - *SD*, *d*, *t*, *s*, *ml*, and *aux* - other parameters might be saved to the .nirs files as a result of manual configuration discussed in this section and the processing discussed in section 9.

Here we will just talk about the parameters that can be saved when manually configuring data.

As a result of manual configurations above, the following additional parameters will appear in a .nirs file:

tIncMan : Manual time exclusion

SD.MeasListAct : Manual channel pruning

CondNames : a list of condition names used for the stimulus marks

s0 : The s matrix is modified as a result of stimulus mark exclusion, deletion or addition of new stimulus marks. If the s matrix is changed in any way, the original s matrix is saved in s0.

- userdata : Contains the information entered into the user data table in the stimGUI.
- procInput : See section 9.1 for details
- procResult : See section 9.1 for details

## 7. Setting processing stream parameters

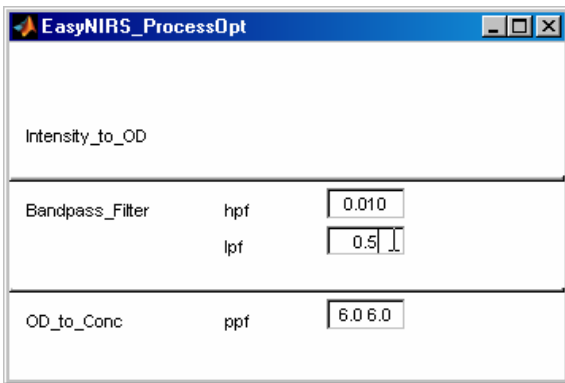
In addition to setting and editing stimulus marks, probe channels, and excluding or including raw data, the user can also edit the parameter options in the processing stream.

The *ProcessOpt* GUI (introduced in section 4.2) is the user interface to the processing stream. It is divided into rows by gray line dividers, each of which contains a processing stream function.

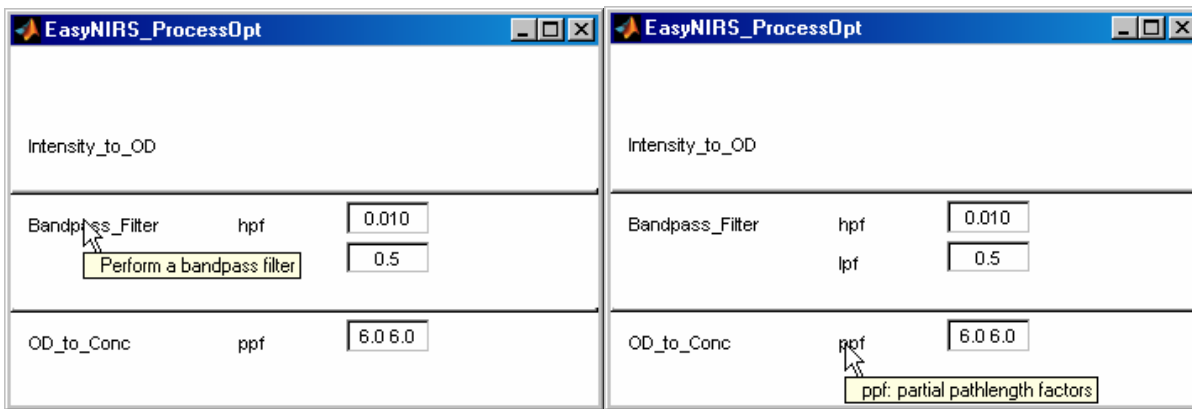
Each function contains 4 columns:

- column 1 – function name
- column 2 – parameters associated with the function
- column 3 – edit boxes where the parameter values can be set/modified
- column 4 – **results button (help)**

The example below shows a simple processing stream consisting of 3 functions: a) hmrIntensity2OD - converts raw data to optical density; b) hmrBandpassFilter - band-pass filters optical density; c) hmrOD2Conc converts optical density to hemoglobin concentration.



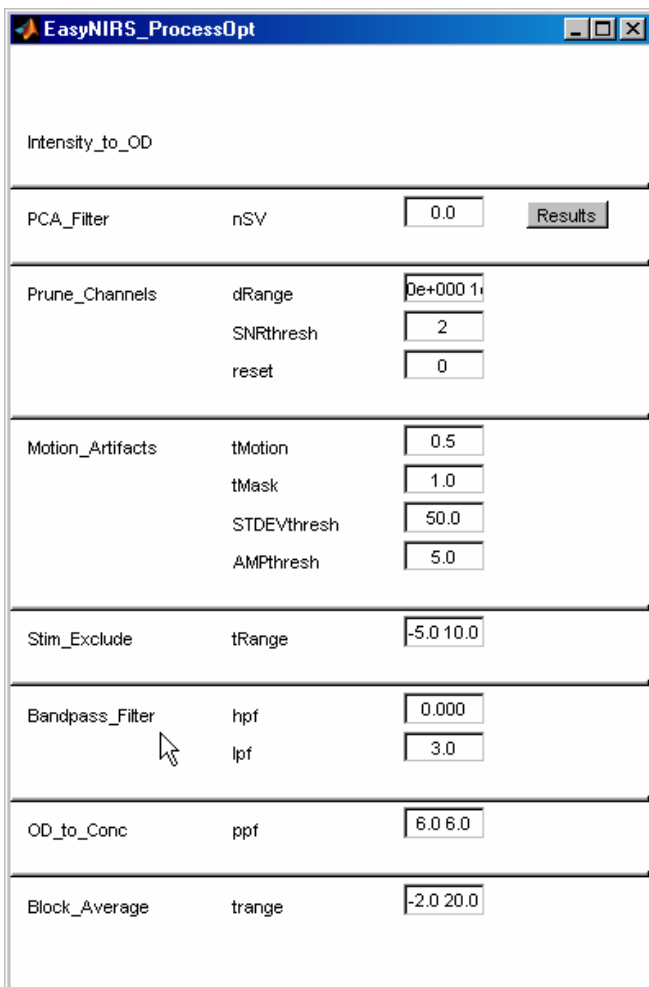
Passing the mouse slowly over the function or the parameter names will bring up a brief explanation from the help registry.



By adding one more function - hmrBlockAvg - to the processing stream (see section 9: Creating your own processing stream), one can obtain the hemodynamic response to the presented stimuli.

### 7.1 Some basic processing stream functions

Here is a ProcessOpt GUI with some of the basic processing stream functions followed by their descriptions:



#### **a) Conversion of Raw data to Optical Density**

hmrIntensity2OD.m:

TBD

#### **b) Filtering**

hmrBandpassFilt.m: Function band-pass filters noisy data or ....

#### **c) Identifying motion artifacts**

hmrMotionArtifact.m:

This function identifies motion artifacts in the raw data. Data time points that are determined to be a motion artifact are marked with a pink patch in the Data Window of Homer2\_UI..

Note: this function has to be used in conjunction with enStimRejection (or any user-defined stim rejection function) in order for the motion artifact identification to have an affect.

#### **d) Stim exclusion based on motion artifacts**

enStimRejection.m:

This function checks whether any stims are within rejection distance of any of the identified motion artifacts in the time course data.

#### **e) PCA filtering**

enPCAFilter.m:

TBD

#### **f) Automatic channel pruning**

enPruneChannels.m:

TBD

#### **g) Conversion of Optical Density to Hb concentration**

hmrOD2Conc.m:

TBD

#### **h) Calculating average stim response (HRF)**

hmrBlockAvg.m:

TBD

### **7.2 Meaning of Copy Options checkbox**

The *copyOptions* checkbox determines whether the processing stream parameter values apply only to the currently selected file when processing occurs or to all files in the group.

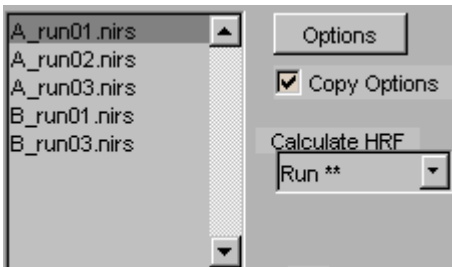
If the checkbox is checked then the current values will be copied to all files being processed. If the checkbox is unchecked, the editing will not affect any other file's parameter settings, and will therefore apply only to the selected file.

## 8. Processing data

To process the data, you must execute the processing stream. The user has the option of applying the processing stream to just the run selected in the *File Window*, all the runs belonging to the subject whose run is selected, or all the subjects in the group – that is, all the files in the *File Window*.

If the processing stream estimates the hemodynamic response to stimuli, then averaging over the stimuli will be performed on all the files for the subject for session calculations. Similarly for group calculations, averaging will first be performed for a subject, and then across subjects.

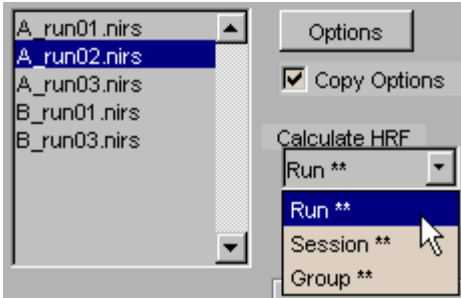
To process data, select one of the options in the dropdown menu *Calculate HRF*.



The double stars next to the *Calculate HRF* option means that for the selected file, either processing hasn't been done and therefore there's no processing result or the processing stream option values have been altered. The stars disappear if a processing result has been calculated for the current processing stream options.

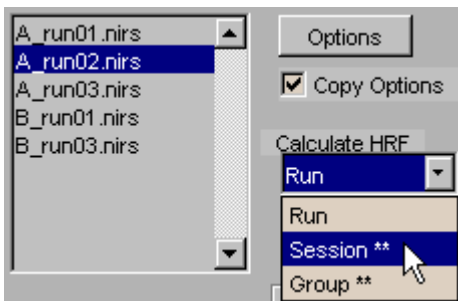
To process data for a single run, select the Run option from the *Calculate HRF* dropdown menu.





In this case, processing will be done only for the second run of subject A, that is A\_run02.nirs.

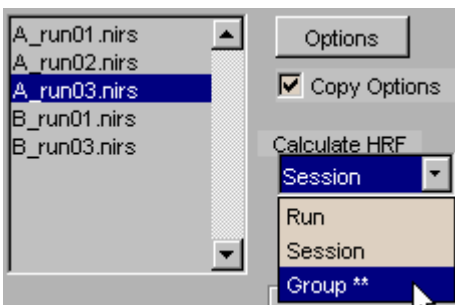
To process data for a single subject/session, select the Session option from the Calculate HRF dropdown menu.



In this case, processing will be done only for all 3 runs in subject A, that is,

A\_run01.nirs  
 A\_run02.nirs  
 A\_run03.nirs

To process data for the whole group, select the Group option from the Calculate HRF dropdown menu. Note: For a group calculation the selection in the File Window doesn't matter since all the files are members of the current group.



In this case, processing will be done for all the files in this group, that is

A\_run01.nirs

A\_run02.nirs  
A\_run03.nirs  
B\_run01.nirs  
B\_run03.nirs

## 8.1 Additional data processing variables saved to .nirs files

The following additional parameters will be saved in the .nirs files as a result of data processing:

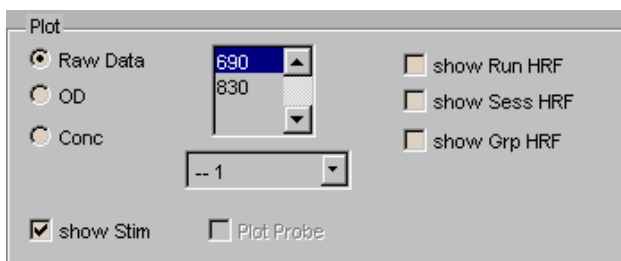
- procInput : This variable contains the processing stream functions, their parameters and values used to process data.
- procResult : Contains the results of processing including optical density, concentration, optical density and concentration averages, and any other variables that are the result of executing the processing stream

## 9. Viewing Processed and Unprocessed Data

The combination of button setting in the plot panel determines what data is displayed in the *Data Window*.

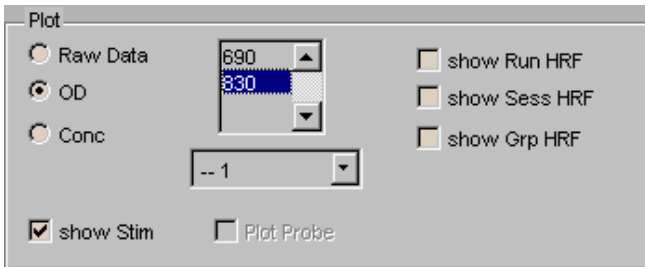
### 9.1 Raw Data

Raw data is displayed by clicking the *Raw Data* radio button and selecting one or both of the wavelengths in the center listbox. In the example below, raw data is displayed at 690nm.



### 9.2 Optical Density

Optical density is displayed by clicking the *OD* radio button and selecting one or both of the wavelengths in the center listbox. In the example below, optical density is displayed at 830nm.



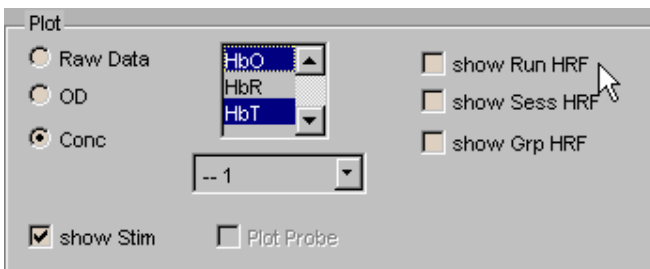
To view time courses for both wavelengths, right-click on one and then the other wavelength in the listbox while holding down the shift key.

### 9.3 Hemoglobin Concentration

Hemoglobin concentration is displayed by

- clicking the Conc radio button
- selecting one, two or three of the Hb types from the listbox in the center. To view time courses for more than one Hb type, right-click on the listbox selections while holding down the shift key.

In the example below, HbO and HbT concentrations are displayed.

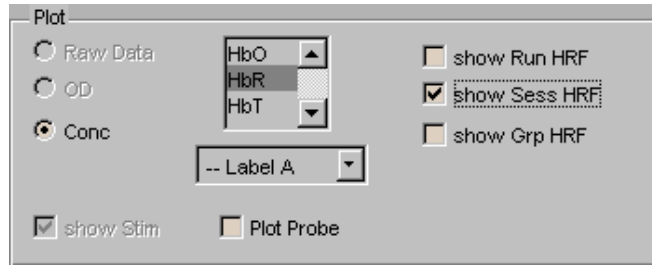
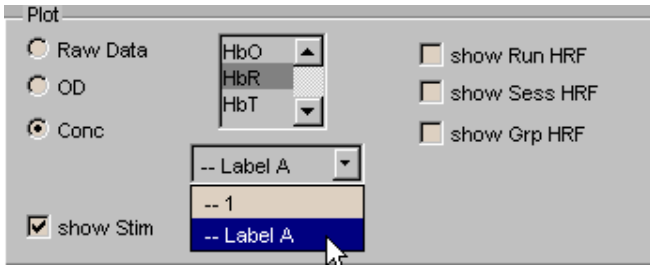


### 9.4 Hemodynamic response function (HRF)

The HRF is displayed by selecting

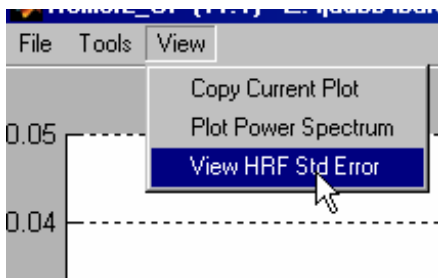
- Conc radio button (OD can be selected as well if the HRF was also calculated for OD in the processing stream),
- one, two or three of the **Hb types** from the listbox in the center,
- one of the **conditions** in the dropdown menu,
- check one of 3 show\* HRF checkboxes on the right.

In the example below, the subject HRF is displayed for Deoxy-Hemoglobin, for condition Label A.



### 9.4.1 Viewing HRF standard error

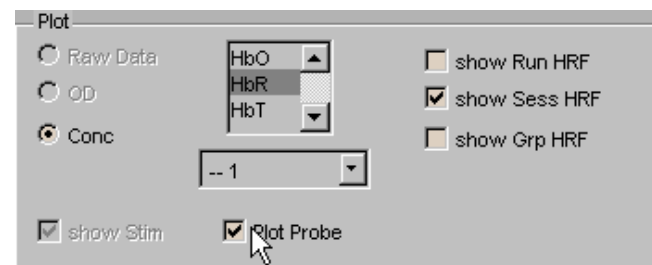
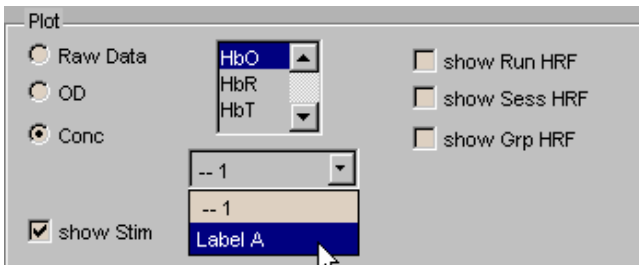
To view the standard error for HRF in the *Display Window*, click on the *View HRF Std Error* in the *View* menu



### 9.5 Displaying HRF for the whole probe: Plot Probe

To display HRF for the whole probe

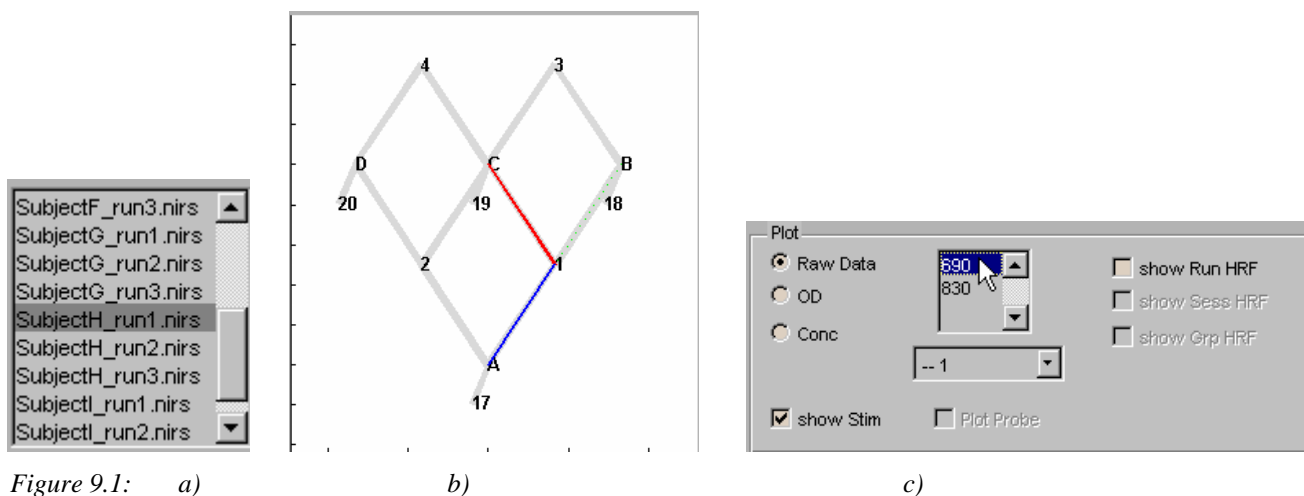
- select the *Conc* radio button
- select the stim condition from the dropdown menu,
- select one, two or three of the Hb types from the listbox in the center,
- click one of the 3 *show \*HRF* checkboxes on the right,
- check the *Plot Probe* checkbox.



Here's what the Plot Probe window looks like:

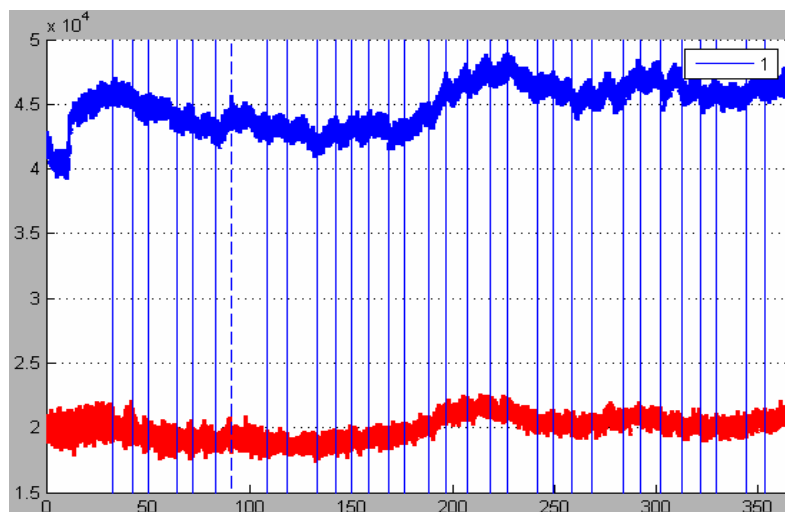
## 9.6 Example: stepping through all data types

In the example below, the raw data at 690nm is displayed for channels D-3 and D-6 of file SubjectH\_run1.nirs



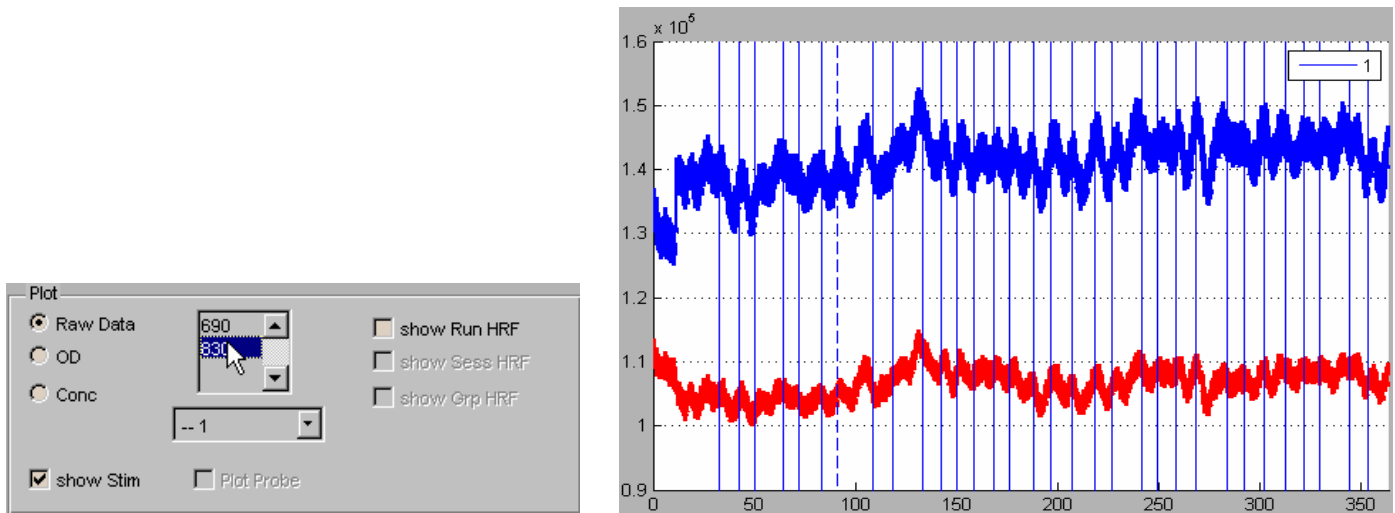
The data displayed in the *Data Window* is determined by the selections shown above in the Figure 9.1: a) *File Window*, b) *Probe Window*, and c) *Plot Panel*. In this case the displayed data is raw data at 690nm, for channels C-4 and C-6 for run B\_run01.nirs.

The resulting data display for the above selections:



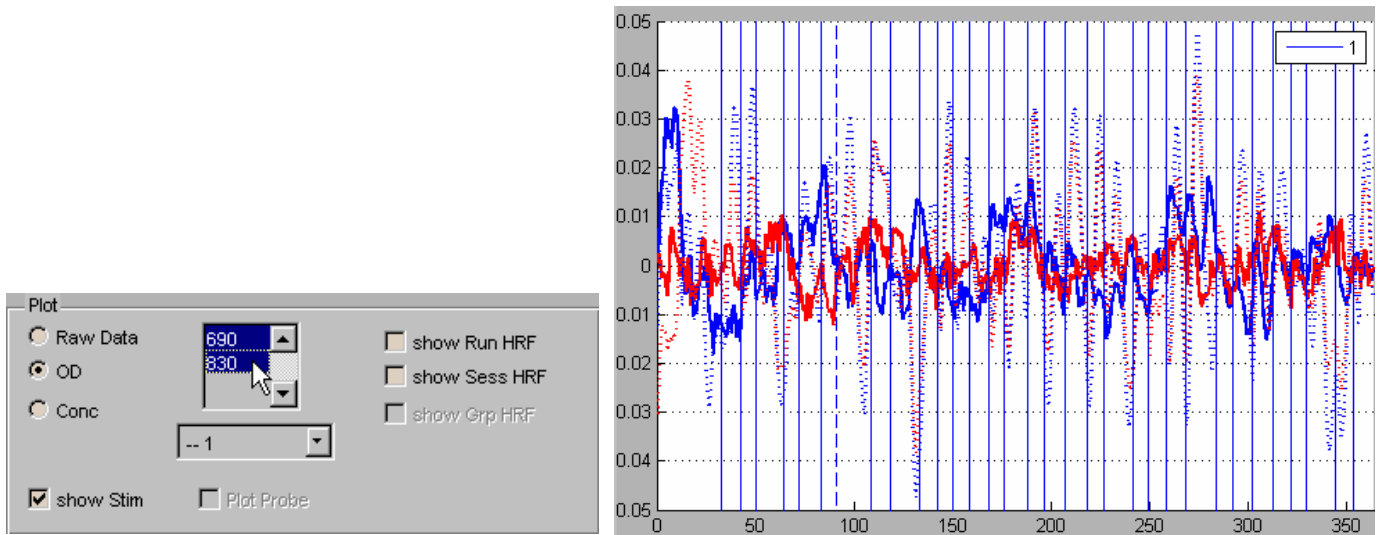
Keeping the File and Probe Window selections constant, we change only the Plot panel selections to display the other data types:

Viewing raw data at either wavelength:



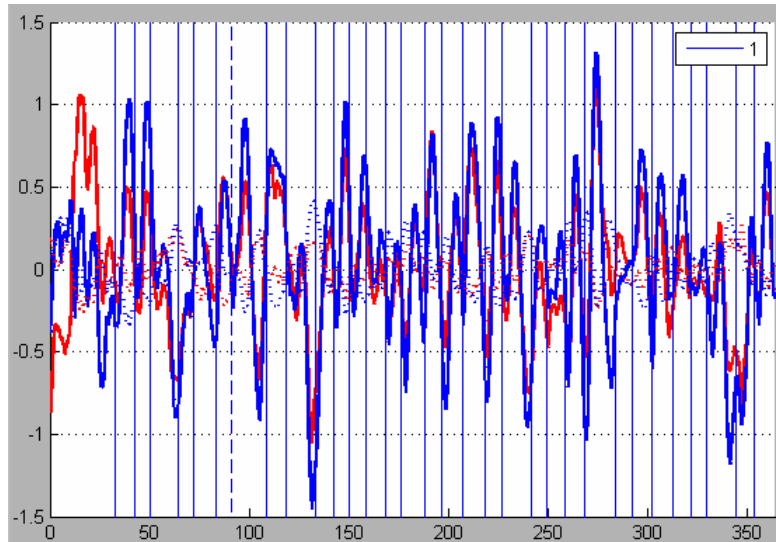
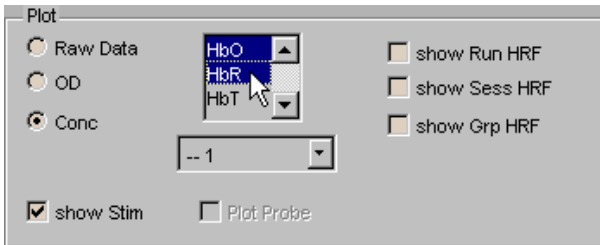
*Raw data at 830nm time course*

Viewing optical density both wavelengths:



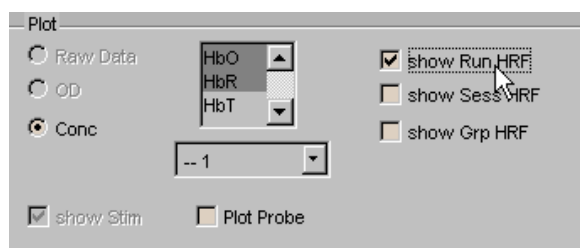
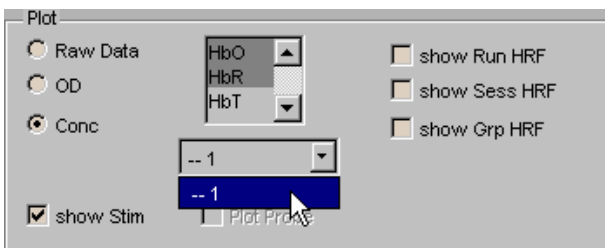
*Optical Density displayed simultaneously at 690 and 830 nm*

Viewing HbO, HbR simultaneously:



*Oxy and De-oxy hemoglobin concentrations. displayed simultaneously*

Viewing HbO and HbR HRF for condition 1 in Figure 9.2, we see the level of HbO sharply rises after stimulus onset and then fall toward the end of the HRF time course. Within the same time period the level of HbR falls not as sharply and then rises toward the end of the time period. This type of response pattern is indicative of activation.



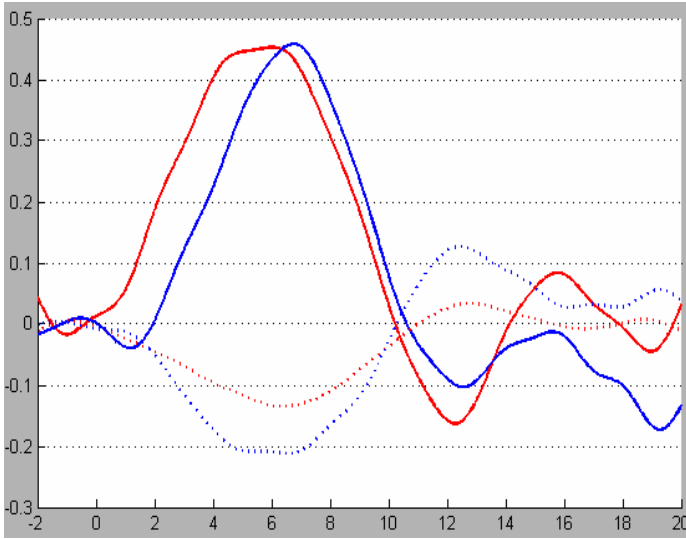
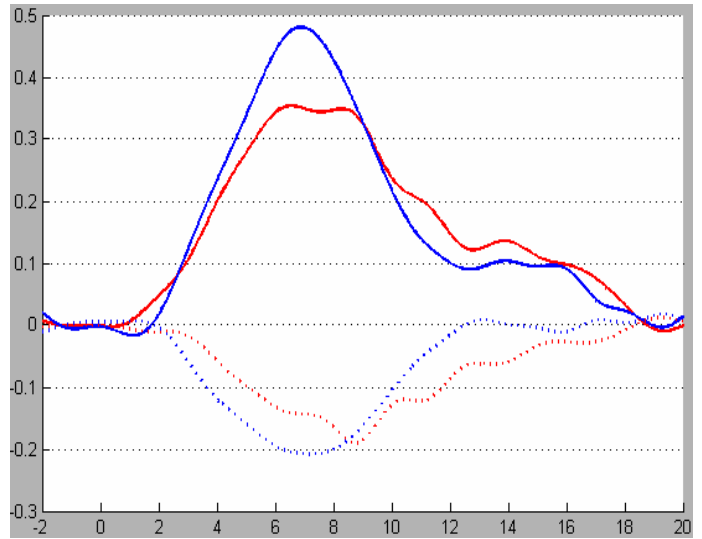


Figure 9.2: a) Run HRF for channels A1 and C1



b) Group HRF for channels A1 and C1

To view the HRF for the whole probe, check the *Plot Probe* checkbox in the *Plot Panel*. Figure 9.2 below shows the group HRF for the whole probe.

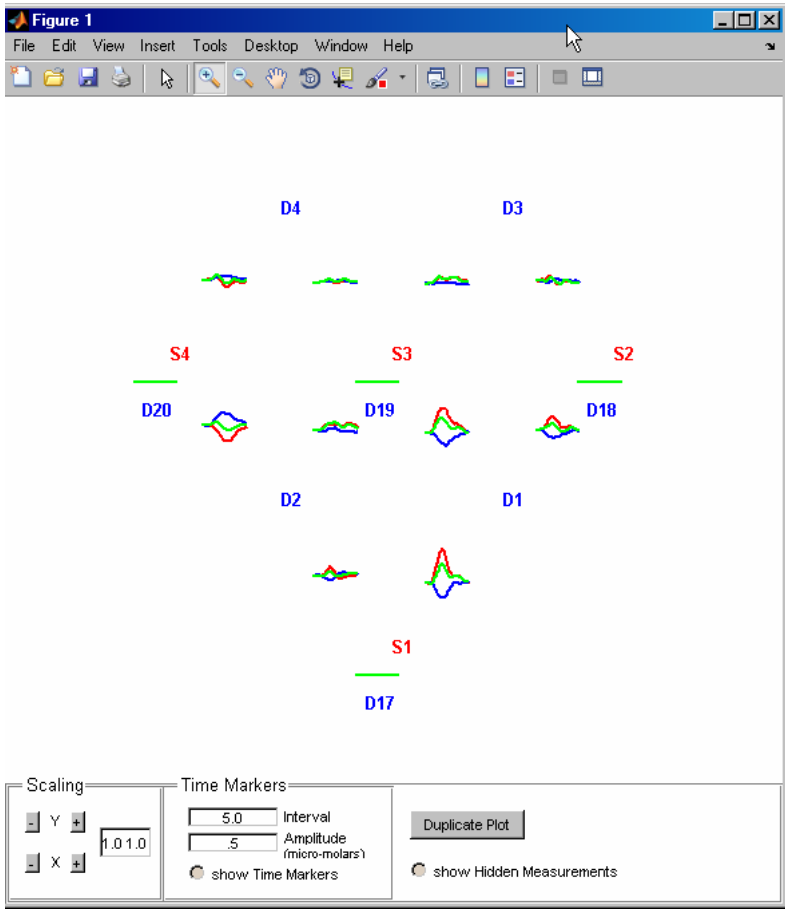


Figure 9.2



## 10. Plot Probe

The *plotProbe* GUI displays the HRF in probe space for the selected file, condition and HRF type. The control panel has several features allowing the user to determine how the data is displayed.

### 10.1 Scaling data

TBD

### 10.2 Viewing time markers and amplitude

TBD

### 10.3 Viewing amplitude

TBD

### 10.4 Viewing pruned channel data

TBD

## 11. Determining and localizing activation

To determine if a block average shows a hemodynamic response to brain activation, we look for a particular pattern – the more similar to this pattern the stronger the brain activation.

A typical pattern that is indicative of brain activation for a particular channel is the following: HbO concentration gradually rises after stimulus onset and then gradually falls to pre-stimulus levels, while HbR concentration does the opposite; gradually falls after stimulus onset and then gradually rises back to pre-stimulus level.

In addition, usually the duration of the response for HbO and HbR is very similar. A typical example is Figure 49 from section 10.6, reproduced below

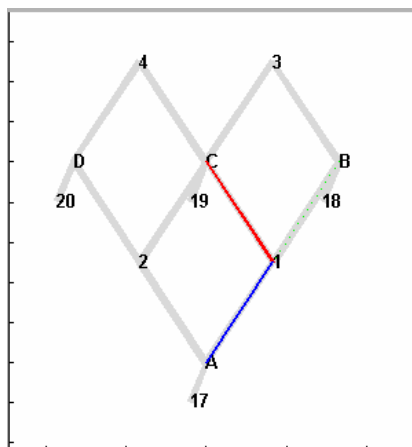
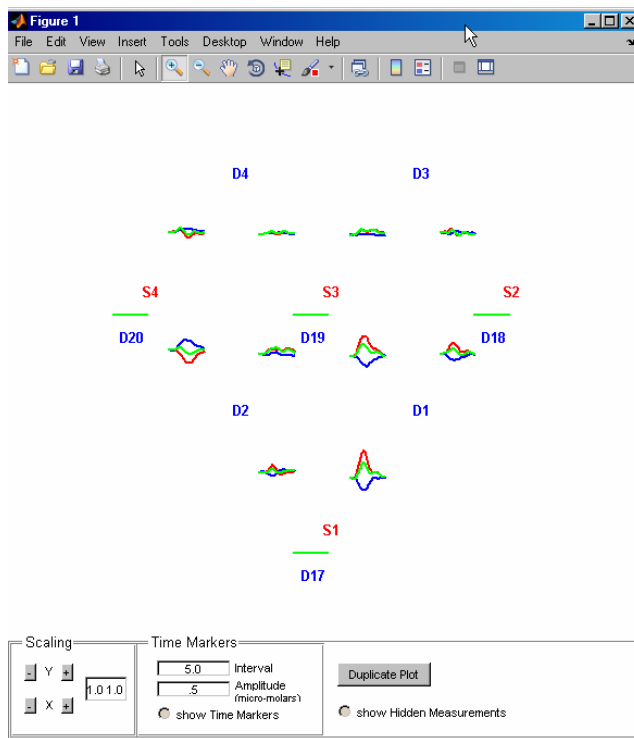


Figure 11.1: a) probe geometry



b) plotProbe display of HRF in the probe space

This *plotProbe GUI* in Figure 11.1 shows the strongest activation in channels S3-D1 , S1-D1 and to a lesser extent. S2-D1. In the *Probe Window* (Figure 50a) these channels correspond to C1, A1, and B1 respectively. The data for the rest of the channels either don't exhibit the pattern or are much weaker responses.

## 12. Examples

This section shows several fully worked out examples on sample data sets. The data sets can be downloaded from the HOMER2 web page (there an option of 2 different fomats)

<http://www.nmr.mgh.harvard.edu/optics/resources/homer2/SampleData.zip>

<http://www.nmr.mgh.harvard.edu/optics/resources/homer2/SampleData.7z>

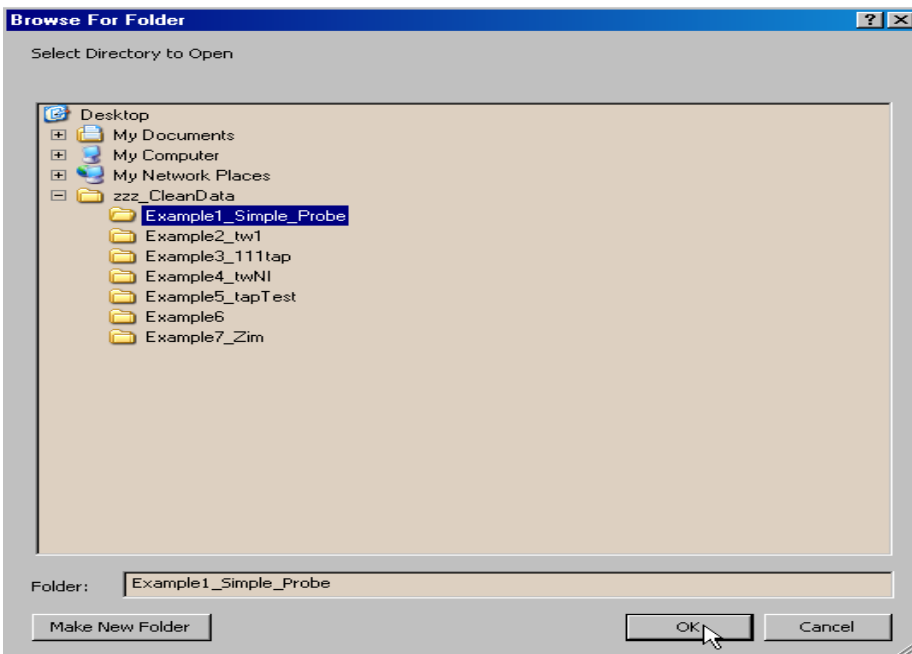
The following examples assume Homer2\_UI and SampleData was downloaded to the Desktop. But should work the same from any directory. To start, click on the Homer2\_UI icon on the desktop



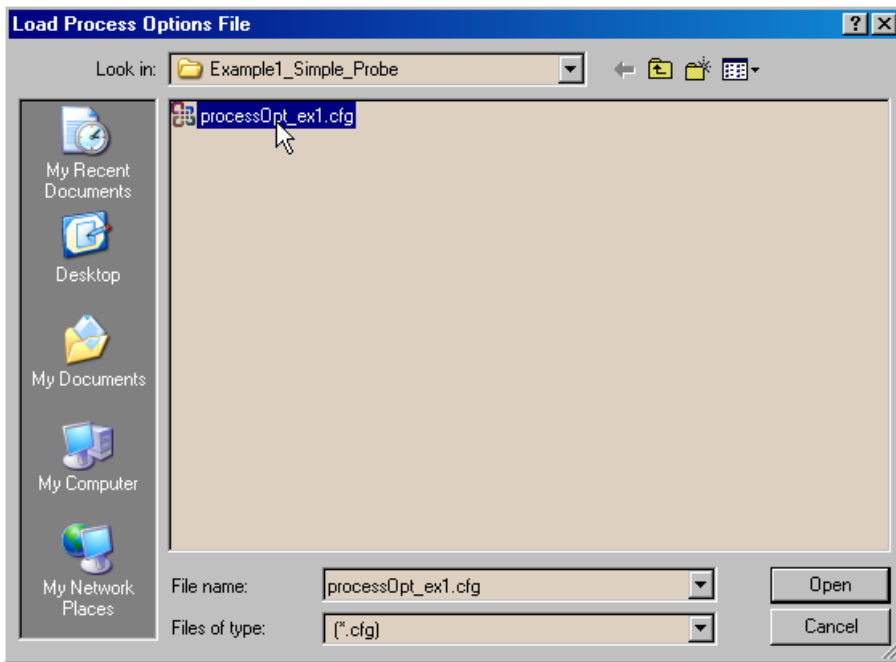
## 12.1 Simple Probe

This example illustrates how to obtain average response from a single run with a simple 4 channel probe and 3 trials and to filter out noise from the average response

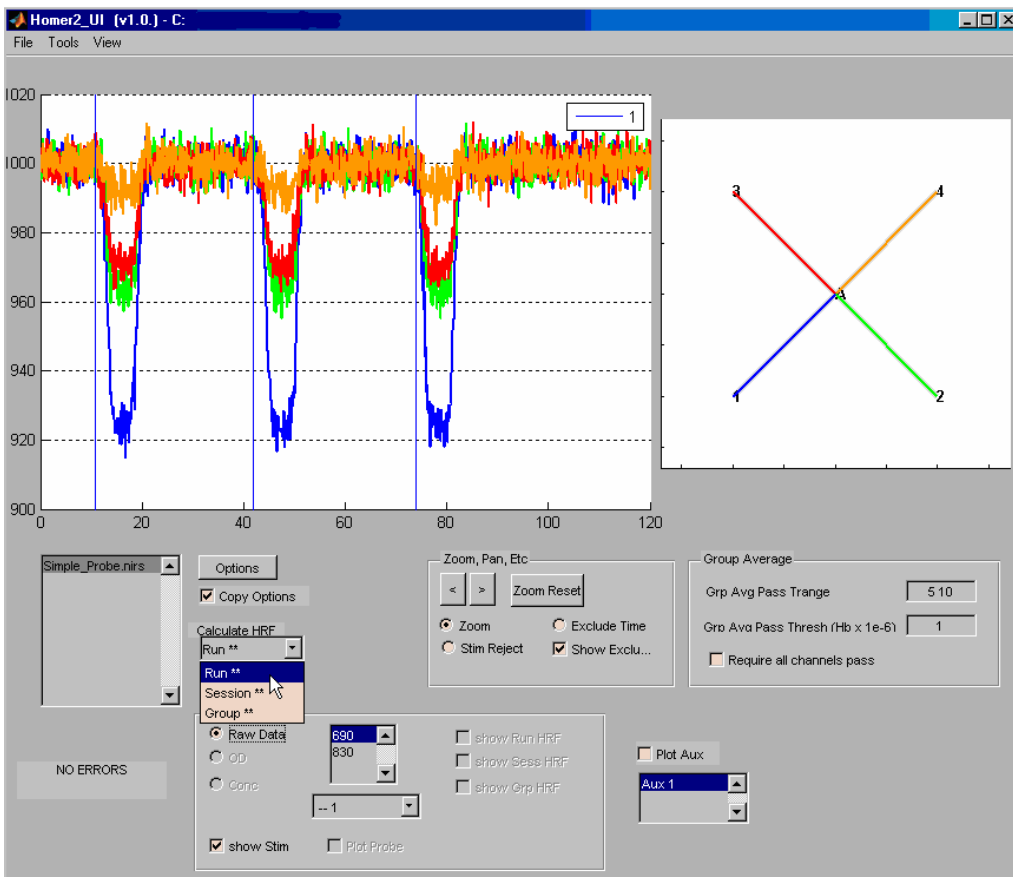
1. After clicking on the Homer2\_UI icon, you'll be asked to select one of the sample data set directories. Click on Example1\_Simple\_Probe.



2. Choose the config file processOpt\_ex1.cfg



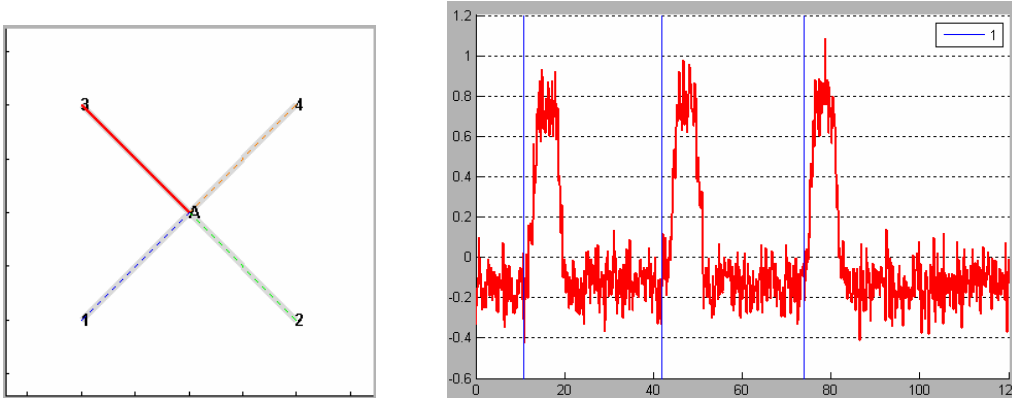
3. To process the data choose Run from the Calculate HRF dropdown menu.



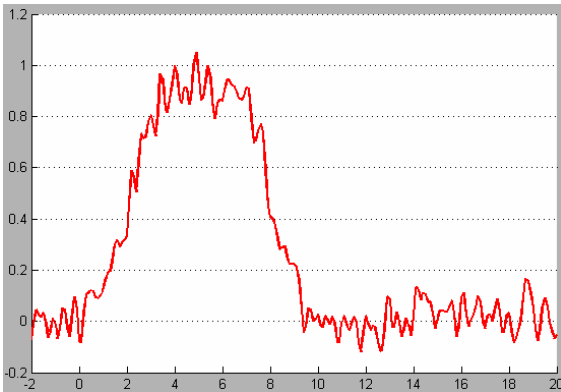
4. View Concentration for only one channel (A3) by

- a) right clicking over channels A1,A2 and A4 and
- b) clicking on the Conc radio button.

You should now see a probe and data window that looks like this:

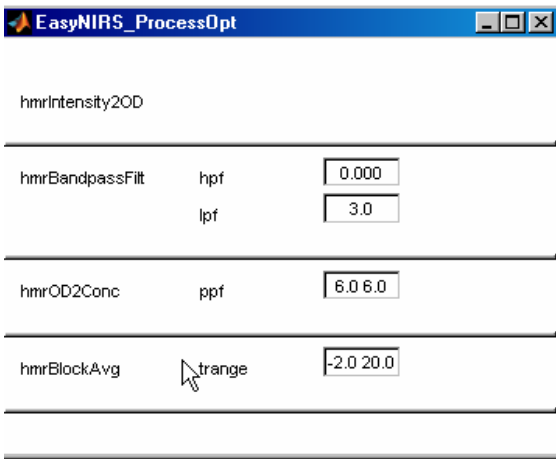


5. View HRF by clicking on the show Run HRF checkbox in the Plot Panel



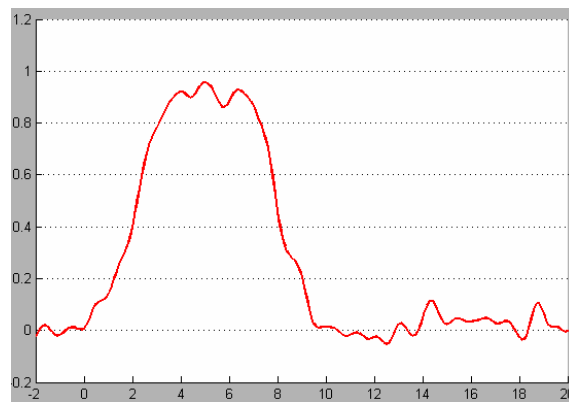
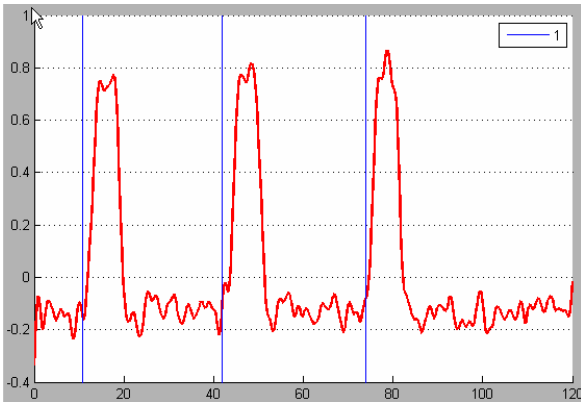
6. Click the Options in Homer2\_UI to look at the processing stream that was used to calculate the above Hb concentration and HRF results.

It shows that the HRF time range that was averaged using the function `hmrBlockAvg` is 2 seconds before and 20 seconds after stimulus onset. Also it shows that the Hb concentration and HRF data above are noisy because the frequency of the noise is higher than 3Hz.



7. To get rid of the noise lower the value of the low-pass filter parameter (lpf) for the bandpass filter function (hmrBandpassFilt) in the processing stream. To do this

- click the Options button in Homer2\_UI
- find hmrBandpassFilt function and its user parameters, hpf and lpf. Since the frequency of the noise is smaller than 3hz, try lowering the lpf to 1 or .5 hz.
- Select Run from Calculate HRF dropdown menu to recalculate the HRF with the new lpf setting  
You should see a smoother signal for Hb Concentration and HRF



## 12.2 Single subject finger tapping data,

TBD

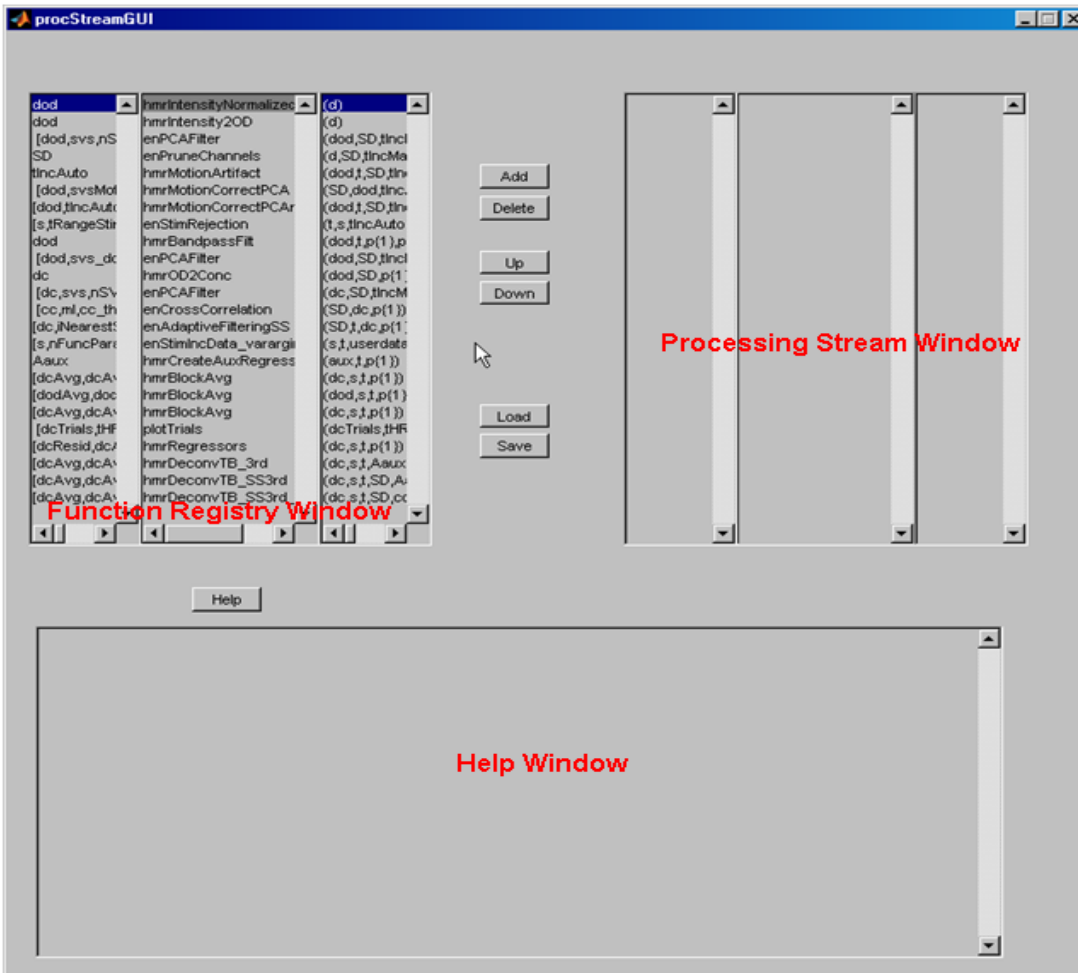
## 12.3 Multi-subject, multi-run finger tapping data

TBD

## Appendix A: Creating your own processing stream (for advanced users)

If a user is familiar with the processing stream functions, and have specific data processing needs that vary from the basic default configuration, a custom processing stream can be built from the complete list of functions listed in the Process Stream GUI.

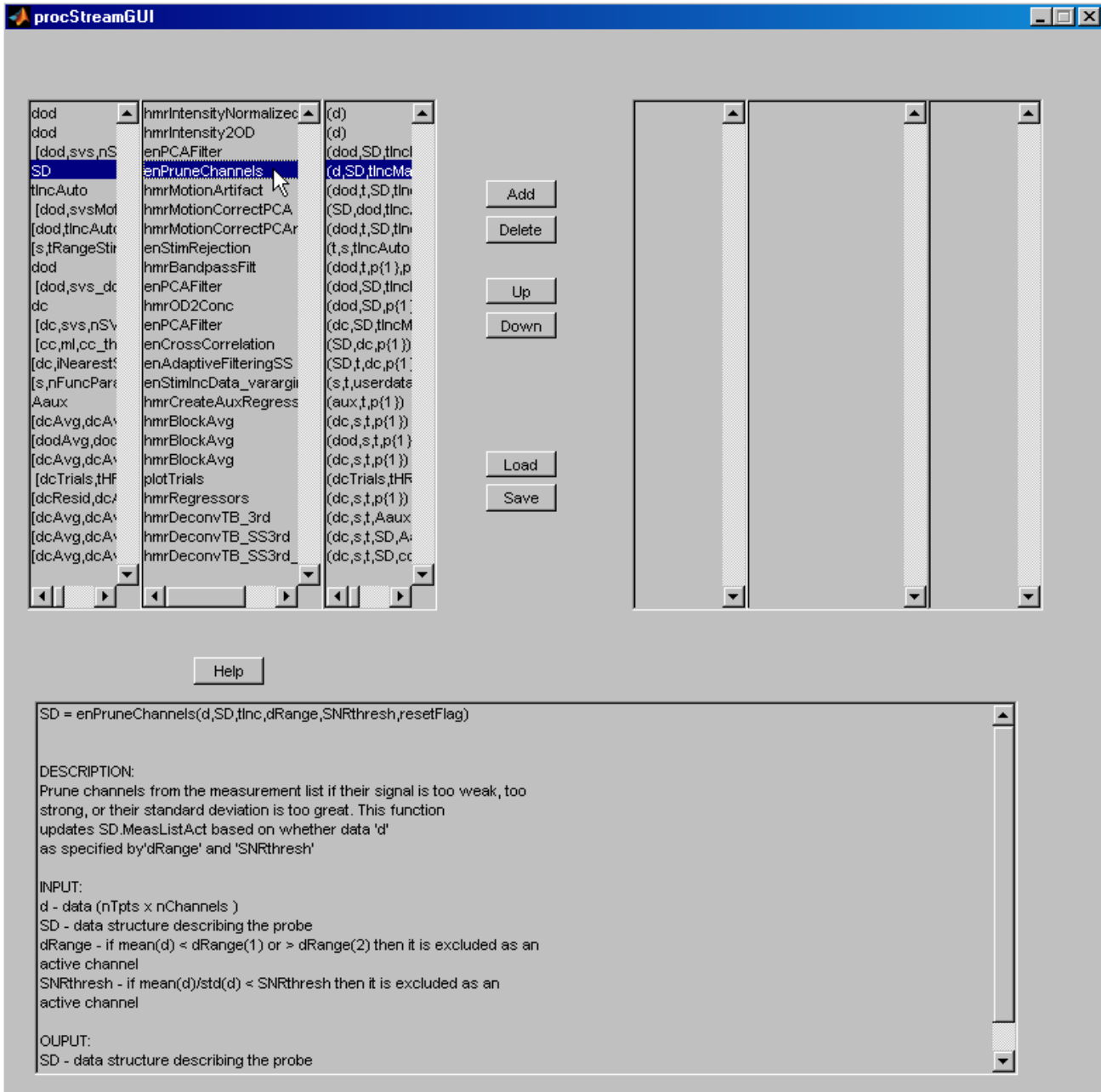
To start the Process Stream GUI, go into the Tools Menu and select Process Stream GUI.



The GUI has 3 sections as seen above: File Registry Window, Processing Stream Window, and Help Window. The Function Registry and Processing Stream windows each have 3 columns:

- left column - contains the function's output parameters,
- middle column - contains the function name,
- right column - contains the input arguments.

You can familiarize yourself with the available functions by browsing the list in the Function Registry Window on the upper left section and reading the function description in the Help window.



## A.1 Building a processing stream

Here's an example of building a very simple 3-function processing stream which

- a) converts raw data to optical density;
- b) converts the filtered optical density to Hb concentration;
- c) and finally calculates the average response

The 3 functions from the Function Registry Window we would choose for this processing are



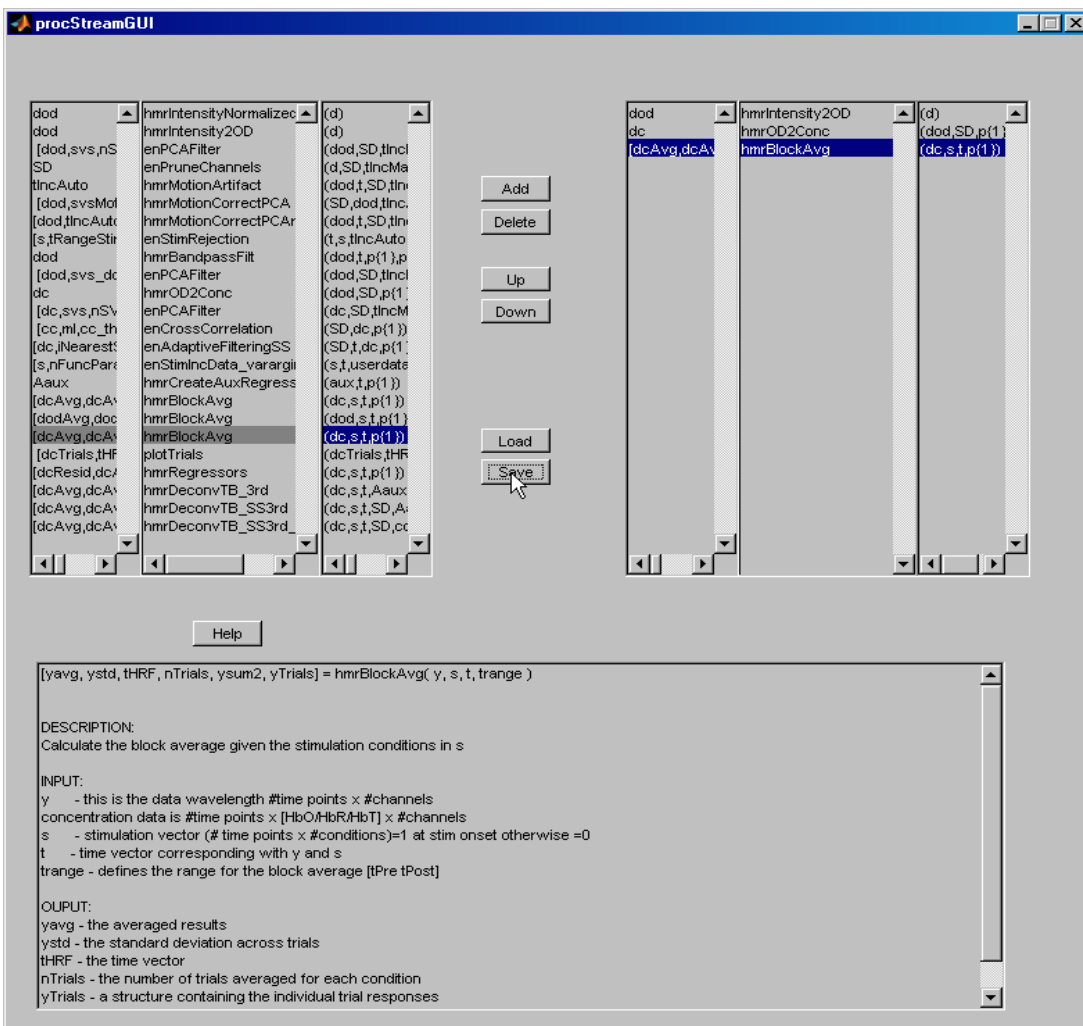
- a) hmrIntensity2OD
- b) hmrOD2Conc
- c) hmrBlockAvg

Note that a function can have multiple versions - the one you use will depend on the type of data you are processing. In this example, there are 3 versions of hmrBlockAvg in the File Registry.

To build this processing stream select each of the 3 functions above from the File Registry and click the **Add** button.

The order can be changed by selecting a function in the Processing Stream Window and clicking the Up or Down button to move the function one space up or down in the processing stream list.

When you have the desired configuration, click the Save button to save this stream to a config file.



## **A.2 Loading and editing a processing stream**

To load a processing stream into the Process Stream GUI, click the Load button and choose a processing stream config file. It will appear in the Processing Stream Window on the right. Now you can add, delete or move functions in the loaded processing stream. When done, click the Save button to save the new configuration to a file.