

fNIRS Analysis Environment

User's Manual



Software and documentation developed by the Optical Tomography Group (<u>http://OTG.downstate.edu</u>) of SUNY Downstate Medical Center (450 Clarkson Ave., Brooklyn, NY, 11203; <u>http://www.downstate.edu</u>)

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Getting Started

Introduction

NAVI (Near-infrared Analysis, Visualization and Imaging) is a versatile software environment developed to support the study of time-varying near infrared measurements of tissue using the **DYNOT** and **NIRScout** imaging systems. NAVI is composed of modules for assessing instrument performance, editing detector data, constructing images from multi-channel data, extracting dynamic features from detector or image data, and visualizing detector and image data. These modules, which are linked to an automated file manager and a project-specific metadata ledger, provide you with abilities that are both convenient and powerful.

NAVI uses the **MATLAB** run-time component and is distributed as a stand-alone program for Windows[®].

This chapter provides information about installing NAVI, its main components, preparing data and initializing projects.

Installation

Contents in the Product CD/External hard disk

The **NIRXpackage** on the product-release hard disk comprises three folders:

• *NIRX_NAVI:* NAVI is a versatile software environment developed to support the study of time-varying near infrared measurements of tissue using the **DYNOT** and **NIRScout** imaging systems. This folder contains four subfolders:

src_navi_2010_p: a p-file version (i.e., executable but not editable) of NAVI
navi_models: contains four pre-calculated FEM brain models
navi_demodata: contains two DYNOT data sets for demonstration purposes
navi_manual: explains how to install and use NAVI

 NIRX_BrainModelGenerator: Brain Model Generator is a MATLAB-based interactive FEM model generation tool. It allows users to independently generate FEM brain models appropriate for novel experimental source/detector geometries. This folder contains two subfolders:

src_modelgenerator_p: a p-file version of the model generator code *modelgenerator_manual*: explains how to install and use the generator

• *NIRX_Brain_Library*: This folder contains a pre-calculated MR-based FEM brain model library. The model generator code creates new models by operating on constituents of the library.

System Requirements

- 1.4 GHz Intel Pentium IV processor (or equivalent), or faster;
- Windows 2000, XP, Vista, or 7;
- 2 GB RAM, or more;
- 1024×768, 16-bit display (32-bit recommended);
- 100 Gbyte available disk space, or more

Installation

The current release of NAVI, V2.1, is run under MATLAB 7.x with the necessary toolboxes.

To install the p-file version of NAVI on your computer, please take the following steps:

- 1. Place the installation CD in your computer, and navigate to the CD's *src_navi_2010_p* directory.
- 2. Create a workspace for NAVI on one of your computer's hard drives (for example, *C:\NIRXpackage\NIRX_NAVI*), and copy the entire src_navi_2010_p folder to that location.
- 3. Add the newly created folder to the MATLAB Search Path, as follows:
 - Launch MATLAB by double-clicking the MATLAB icon on your desktop.
 - Select and click on Set Path... in the File menu, or enter "pathtool" at the MATLAB prompt. This will open the Set Path GUI, which is used to view and modify the MATLAB search path.
 - Click on Add with Subfolders in the Set Path window. This will open the Browse For Folder window. In Browse For Folder, navigate to the src_navi_2010_p directory on your

computer's hard drive. Select/highlight the src_navi_2010_p folder and click on **OK**.

- Click on **Save** on the Set Path window, then on **Close**, and then quit MATLAB.
- 4. Create an icon to conveniently launch NAVI. The simplest way to do this is to make a copy of the MATLAB startup icon (found on the desktop) and rename it to "NAVI." The default folder for use of MATLAB is the "work" directory. To change the default setting, right-click on the new icon, select **Properties** from the resulting pop-up menu, select the **Shortcut** tab in the resulting NAVI Properties pop-up window, and change the contents of the **Start in:** line to the NAVI workspace folder (for example, *C:\NAVI2b1\work* in the figure shown here), and click on **OK**.



Once NAVI is installed, double-clicking on the NAVI icon on your computer's desktop will automatically launch the home screen shown below. Alternatively, you can just enter "navi" at the MATLAB command prompt.



Main Components

File Manager and Electronic Ledger

When processing experimental data, the NAVI computing environment automatically generates a hierarchical file structure for each project while simultaneously recording all processing steps in an electronic ledger.

NAVI treats each DYNOT- or NIRScout-based experimental data set as a separate specific project. Loading raw data into NAVI immediately initializes the electronic ledger (also called the dataInfo file), which records information regarding details of data collection and FEM model selection. Once initialized, the dataInfo file keeps track of all facets of NAVI-based data processing associated with the project. Meanwhile, the automated file manager creates a hierarchical tree structure for the project and uses the information extracted from the dataInfo file to control file input and output. In combination, these abilities provide a single portal to access all files associated with any project.

Image Generator

The Image Generator portal contains the Detector Preprocessing, Image Reconstruction and Data Export modules.

- **Detector Preprocessing:** This module provides functions for editing, frequency-filtering, and normalizing the multi-wavelength raw data time series, and it also computes the corresponding hemoglobin-concentration time series. [See Chapter 3.]
- Image Reconstruction: This module employs a linear reconstruction method (truncated SVD) to compute the wavelength-dependent absorption coefficients, from which estimates of the time-varying molar concentrations of oxygenated (oxy-), deoxygenated (deoxy-) and total hemoglobin (Hb), and the Hb oxygen saturation (HbO₂Sat), are derived. [See Chapter 4.]
- **Data Export:** This module provides functions for exporting NAVI-based data or images in different data formats, so that you can view and analyze them using other software applications. [See Chapter 5.]

Data Viewer

The Data Viewer portal comprises three modules: Detector Time Series Viewer, Hemodynamic Image Viewer, and Data Processing Info Viewer. [See Chapter 6.]

- **Detector Time Series Viewer:** This allows you to view channel-specific time series (*i.e.*, Source-Detector pairs), and to edit data (*e.g.*, exclude specific channels that have poor signal-to-noise ratios or excessive artifact levels) and save the changes. Changes are stored in wavelength-dependent and hemoglobin-concentration detector-data files created by NAVI, so that the original imager-generated data files are not overwritten.
- Hemodynamic Image Viewer: This allows you to view 3D images, either as a stack of 2D sections (you may choose the axial, coronal or sagittal orientation, and switch from one to another

at will), as 3D volume-rendered objects, or as an overlay onto an MR image. Also available are options for animation of a selected 2D section of a 3D image time series, for changing the resolution of the image display grid, and for adjusting the display scale.

• **Data Processing Info Viewer:** This module lets the user examine the information included in the project-specific dataInfo file.

Data Analyzer

The **Data Analyzer** portal contains four modules that are used for generation of block-averaged data and for feature extraction.

Data Generation: This module provides for the generation, viewing and saving of user-defined block-averaged data (*i.e.*, averages over time intervals that correspond to repetitions of experimental condition). [See Chapter 7.]

Multivariate Analysis: This module (a user-selected option in the **Feature Extraction** module) employs functions to extract information by means of either data-driven or model-based analyses such as Principal Component Analysis (PCA), Molgedey-Schuster Analysis (MSA), Independent Component Analysis (ICA), or the General Linear Model (GLM). [See Chapter 8, and note also that more advanced GLM capabilities are incorporated in the naviSPM utility described in Chapter 11.]

Spectral Analysis: This module (a user-selected option in the **Feature Extraction** module) employs functions to extract power spectra and related information, using Power Spectral Density, Cross-Spectral Density, Coherence, and Cross-Correlation methods. [See chapter 8.]

Event Analysis: This module (a user-selected option in the **Feature Extraction** module) employs functions to extract event-related features such as Slope (*i.e.*, numerical differentiation), Time-Delay, and Area under Curve (*i.e.*, numerical integration). [See Chapter 8.]

Utilities

The **Utilities** portal contains (among other things as described in Chapters 10 and 11) the **FEM Model Generator**, which is as a toolbox that provides greater flexibility in designing and testing novel illumination-detection arrangements, including simultaneous multi-site measurements, without the overhead associated with generating new FEM models. [See Chapter 9.]

Data Preparation

Prior to using NAVI for a new project, some simple preliminary steps should be taken. This section guides you through the setup of your DYNOT- or NIRScout-based experimental data files and shows you how to select the proper FEM model from the NAVI-based model library before you start to process the experimental data with NAVI.

Experimental Data Setup

Any measurement using a **NIRx** imager system produces the following data files:

- *filename.wl1* [*i.e.*, detector readings for wavelength 1 (760 nm)]
- *filename.wl2* [*i.e.*, detector reading for wavelength 2 (830nm)]
- *filename.set* [gain settings table]
- *filename.evt* [event records]
- *filename_config.txt* [information regarding experimental configuration]

Generally, *filename* is defined by the imaging system before the measurement starts, and it employs a syntax that uniquely identifies the experiment and the date on which the data were collected. The user is permitted to modify the imager-default value of *filename*; note, however, that a *filename* containing a space, or any other special character besides one or more underscores, will not be accepted by NAVI or other companion software such as **GiD**.

Normally, *filename.wl1* and *filename.wl2* are the detector data files for the 760 and 830 nm measurement wavelengths, respectively; *filename.set* contains the gain settings assigned to all measurement by the imaging system, based on the detected signal strengths; the optional *filename.evt* file (*i.e.*, NAVI will execute properly if this file is empty or absent, but the other four files are essential) contains user-recorded information associated with the measurement protocol (*e.g.*, starting and/or ending times for different experimental conditions); and *filename_config.txt* contains information regarding the experimental configuration used for data collection (*e.g.*, number of laser diodes, numbers of sources and detectors, data sampling rate).

Prior to processing an experimental data using NAVI, please do the following:

Step 1: If a NAVI workspace for the data doesn't already exist, create one on your local hard drive or on a networked drive. For example, you can create a folder called *work* as your NAVI's workspace, as a subfolder of NAVI2p1.



Step 2: Create a folder inside the NAVI workspace for a new project. For example, you can create a folder called *left_motor_cortex* as a subfolder of *work* for your new project.



Step 3: Specify a experimental data set, copy all files generated by the imager and paste them into the project folder. For example, copy all files in the *data**left_motor_cortex* folder from the NAVI product CD, and paste them into your computer's *NAVI2p1**work**left_motor_cortex* folder.

🖃 🚞 NAVI2p1	📕 keith .set	10 KB	SET File
🛅 doc	keith.evt	1 KB	EVT File
🗉 🚞 models	keith.wl1	6,379 KB	WL1 File
🗉 🚞 psrc	keith.wl2	6,379 KB	WL2 File
🖃 🧰 work	keith_config.txt	1 KB	Text Document
🖃 🚞 left_motor_cortex			

FEM Model Setup

NAVI reconstructs an image time series from the normalized multiple-wavelength experimental data group, using a fast and stable reconstruction algorithm. This is accomplished by using an FEM model that incorporates information about the source-detector arrangement and the external geometry of the tissue structure being studied.

Provided on the CD is a basic FEM model library for users engaged in brain research. Currently available in this library are four models that consider an experimental source-detector geometry having more measurement channels than NIRx imaging systems presently can accommodate. This allows you to employ any number of source-detector arrangements for an experiment and to use the FEM toolbox to generate the corresponding model. The four models can be found in the *models/brains* folder of the NAVI product CD:

i) frontal_cortex (comprises a 5×10 optode configuration, enabling use of up to 50 sources and 50 detectors)



ii) occipital_cortex (comprises a 5×10 optode configuration, enabling use of up to 50 sources and 50 detectors)



iii) left_motor_cortex (comprises a 9×7 optode configuration, enabling use of up to 63 sources and 63 detectors)



iv) right_motor_cortex (comprises a 9×7 optode configuration, enabling use of up to 63 sources and 63 detectors)



Each model in the model library contains an assortment of files, which contain information regarding the FEM mesh node coordinates, the computed operators for image reconstruction, the surface coordinates of sources and detectors, surface renderings of the FEM mesh and tissue geometry, MRI brain image templates and the modelInfo file used for generating new FEM models that correspond to user-specified

source-detector arrangements. (It is not a cause for concern if there are different numbers of files in different model folders.)

It is important to select the FEM model that matches the experimental condition for data collection. If the correct model is not directly available (*e.g.*, the user may decide to use fewer source and/or detector fibers than the allowable maximum), then a new FEM model must be generated. This can be accomplished using the FEM Model Generator module in the Utilities portal, if the experimental source-detector configuration fits within the boundaries of one of the basic models provided. Otherwise, you will need to inform NIRx of the intended fiber arrangement, so that their software engineers can create a new FEM mesh for your application.

You may find it convenient to copy the entire FEM model library to your NAVI workspace. The following steps will be helpful for establishing a FEM model that corresponds to a particular experimental setup. For the example given below we use data contained in the NAVI product CD. This considers a setup containing 25 Sources and 25 Detectors used to record activation of the left motor cortex during a finger tapping experiment.

Step 1: If the brain library folder is not already present on you computer's hard drive, then copy it from the product CD into the NAVI workspace.

Step 2: Find the model that corresponds to your basic experimental setup (*i.e.*, occipital, frontal, motor). In this example select the Left_Motor_Cortex_ 9×7 model. As shown above, this model contains a rectangular array of 63 optodes. Because this is a larger number than was actually used in the experiment, the model cannot be directly used in processing the experimental data. To proceed, it is necessary to first use the FEM Model Generator to create a new model that corresponds to the given experimental setup. Once generated, it is automatically placed in the directory of the selected basic model. See Chapter 9 for a detailed description on use of the FEM Model Generator.

🖃 🚞 NAVI2.0	Left_Motor_s25d25		File Folder
🛅 doc	🔤 box14_sdcoords_9x7_new	2 KB	File
🖃 🚞 models	🗩 coords	292 KB	FEM File
🖃 🧰 Brains	🗩 det	105 KB	FEM File
🚞 Frontal_Cortex	EMModel	7 KB	JPG File
🖃 🚞 Left_Motor_Cortex_9x7	國 head_box14_D4T32_gid.msh	946 KB	MSH File
🗀 Left_Motor_s25d25	🛅 head_box14_D4T32_gid_modelInfo	208 KB	MATLAB MAT-file
🚞 Occipital_Cortex	Manad_box021	7 KB	JPG File
🚞 Right_Motor_Cortex_9x7	🔤 mri_nir×01	16,385 KB	DAT File
	sd_coords	5 KB	FEM File
		253,916 KB	FEM File

Project Initialization

Project initialization is the first step in processing a new project in NAVI. This step creates a unique dataInfo file and records information regarding details of data collection and FEM model selected for this project.

To initiate a project, use the Load function in the Image Generator portal by taking the follow steps.

Step 1: Launch NAVI, as described above in the section on Installation.

Step 2: Select the "From File System" option from the pull-down menu next to the Load button.

Load	From File System
dataInfo File (NAVI-	From File System
Imager Type:	

Note: NAVI has been developed with the goal of providing access to experimental data in two ways. One is "From File System" and the other is "From Database." The second option currently is under construction and will be available at a later date.

Step 3: Select an imager type from the **Imager Type**: pull-down menu to match the type of measuring head used during data collection.

Load	From File Conten	
LUQU	From File System	<u> </u>
dataInfo File (NAV	/I-Created)	-
Imager Type:	None (Please Choose One)	-
	None (Please Choose One)	
	Brain Imager	
	Breast Imager	
	Small Animal Imager	
	Limb Imager	
	Infant Imager	
	Phantom Imager	
	Large Animal Imager	
	MultiSite	

Step 4: Select the "Configure File (Experimental)" option from the pull-down menu below the Load button.

	Load	From File System 💌]	
d	dataInfo File (NAVI-Created)			
d	dataInfo File (NAVI-Created)			
C	Configure File (Experimental)			
-[B	Batch Processing Setting File			

Step 5: Click on the Load button to start the process of project initialization:

Load	From File System	-
Configure File (Experimental)		
Imager Type:	Brain Imager	•

In the first pop-up window that opens, select a file whose name ends in "*_config*" and having the file extension "*.txt*" from the specified project folder, and click on **Open** to load it:

Pick an Exp	erimental Config File				?	X
Look in: 🔀	left_motor_cortex	•	¢	£	💣 🎟 •	
keith_conf	ìg.txt					
				_		
File name:	keith_config.txt				Open	
Files of type:	*_config.bd		•	•	Cancel	

In the second pop-up window that opens, specify a file having the file extension ".*FEM*" from the folder with the selected FEM model, and click on Open to load it:

Input Model	File		? 🗙
Look in: 🔎	Left_Motor_s25d25	• 🗢 🗈 (* 💷 •
Coords.FE	м		
sd_coords	FEM		
▶]w.FEM			
File name:	coords.FEM		Open
Files of type:	Model Files (*.FEM)	•	Cancel

During the project initialization, a progress bar appears to show how generation of the dataInfo file is proceeding.



Following this process, NAVI creates a dataInfo file in MATLAB binary format (having the "*.mat*" file extension) and a folder called *Detectors* that contains binary wavelength-dependent raw data files within the project folder (*i.e.*, exact copies of the content of the imager-generated .wl1 and .wl2 files, but in a different file format). The syntax for the newly generated dataInfo file is:

filename_dataInfo.mat

For the example considered here, you would find a file called *keith_dataInfo.mat* and a folder called Detectors with the binary files *keithb.wl1* and *keithb.wl2* in the project folder.



As noted previously, the dataInfo file (the electronic ledger) is unique for a specific project and plays a key role in applications of NAVI. After the project initialization, the dataInfo file immediately becomes the only file you need to load during subsequent NAVI sessions for the project. Additionally, as data processing proceeds, the dataInfo file is continually updated to maintain a record of every analysis operation that has been performed.

File Management



Introduction

Processing of data sets generated by the **DYNOT** and **NIRScout** imagers with **NAVI** often generates a large number of files comprising multiple data types. To organize these, NAVI provides a file manager module, which employs a hierarchical data structure linked to a project-specific electronic ledger to organize, access, and save the multiple large-scale data types in a convenient and efficient manner.

Hierarchical Data Organization

Starting from the NAVI's work directory (workspace) on your computer, the file manager creates a hierarchical data structure for each project, as shown below. A project is a set of files with a fixed set of file branches, whose fine structure depends on the analysis steps invoked. The root workspace is collection of all projects.



Electronic Ledger

Each project has its own unique electronic ledger (the dataInfo file), which contains information regarding the recorded processing steps. The electronic ledger keeps track of all facets of data generation, including instrument scanning parameters, FEM mesh details, and selected parameters used for data filtering, editing, feature extraction, *etc.* In short, all of the particulars needed to uniquely define the operations used for all steps of data processing are stored automatically in an organized and easily accessible format. In future versions of NAVI we plan to embed elements of the electronic ledger to provide for a searchable metadata database.

Data Types

Listed below are the data types involved in file input and/or output for applications of NAVI modules:

- Raw detector data
- FEM model
- Preprocessing detector data
- Image data
- Extracted feature data
- Metadata

The raw detector data (see Chapter 1) includes the files for wavelength-dependent detector data, gain settings, event file and source-detector configuration generated by **NIRx** imaging systems. They are the input for the **Detector Preprocessing** module (see Chapter 3).

The FEM model contains the files for the pre-generated inverse operators, the coordinates of FEM mesh nodes, and source-detector locations as well, as the grid level library produced by NAVI. These are required input files for the **Image Reconstruction** (Chapter 4) and the **Hemodynamic Image Viewer** (Chapter 6) modules, as well as other modules built in the **Data Analyzer** portal when the "image" data type is selected (Chapter 8).

Output of the Detector Preprocessing module includes frequency-filtered and normalized wavelength-dependent detector data files. They can be used as input for the **Data Export** (Chapter 5) and **Detector Time Series Viewer** (Chapter 6) modules, as well as for modules built in the Data Analyzer portal, and the normalized detector data are required input for the Image Reconstruction module.

Output of the Image Reconstruction module includes files containing values of the position- and time-dependent multi-wavelength absorption coefficients, and files containing the position- and time-dependent concentrations of oxygenated and deoxygenated hemoglobin. They can be used input for the Data Export module, Hemodynamic Image Viewer module, and modules built in the Data Analyzer portal.

Extracted feature data are the output for all modules built in the Data Analyzer portal and can be input for all modules contained in the Data Viewer portal.

File Input

File input in NAVI is straightforward. All that is required is that you load the project-specific dataInfo file within a selected portal, as shown below. All of the background linkages needed for data processing are invisible to the user and are performed automatically.

		_
Load	From File System	_
dataInfo File (N/	AVI-Created)	-
Imager Type:	None (Please Choose One)	•



File Output

Depending on the process you select, NAVI will produce one of four types of result files, each directed to a process-specific location in the hierarchical data structure.

- Results produced by detector preprocessing
- Results produced by image reconstruction
- Results produced by data analysis
- Results produced by file format conversion

Results produced by detector preprocessing

Successful application of the Detector Preprocessing module produces a filtered detector dataset, filtered-normalized detector dataset, and an update to the electronic ledger. These files are saved in MATLAB format and are stored in the NAVI file structure using names defined by the predefined file syntax.

After Detector Preprocessing, you can find a subfolder named Detectors in the working project folder. Inside the Detectors subfolder are two output files with the following filename syntax:

f_[raw data file name without extension].NAV [for filtered data]

n_f_[raw data file name without extension].NAV [for normalized data]

Results produced by image reconstruction

Successful application of Image Reconstruction produces the wavelength-dependent absorption coefficient image time series, the oxygenated and deoxygenated hemoglobin image time series, and an update to the electronic ledger. NAVI automatically saves these files in MATLAB format and similarly places them into the file structure tree of the working project using file names defined by the predefined file syntax.

The following files are generated by this procedure and stored in a subdirectory called Images, which NAVI creates (if it does not already exist) in the working project folder:

i_n_f_[raw data file name prefix]_wl1.NAV [wavelength-based]

i_n_f_[raw data file name prefix]_wl2.NAV [wavelength-based]

i_n_f_[raw data file name prefix]_hboxy.NAV [oxygenated hemoglobin]

i_n_f_[raw data file name prefix]_hbred.NAV [deoxygenated hemoglobin]

Results produced by data analysis

For any function belonging to the Data Analyzer portal, selection of the Save option while specifying values for user-controlled parameters will have the result that all processing information associated with the selected functions will be recorded in the project's dataInfo file, while the results generated by the analysis will be saved in MATLAB binary-format files, with file names matching the predefined file syntax.

Repeated use of a selected operation will produce a series of files identified in accordance with the name of the selected function, and numbered sequentially. For instance:

project1\AnalysisResults\PCA\

- Results1.mat
- Results2.mat
- Results3.mat

Results produced by data export

NAVI provides a Data Export module that allows you to export NAVI-based detector and image data, in several different formats. The available formats make it possible for you to edit, view and analyze the exported data with other software packages, such as AFNI, SPM, or GiD. Please see Chapter 5: Data Export to learn more about use of that module.



Detector Preprocessing

Introduction

The **Detector Preprocessing** module in the **Image Generator** portal performs important data conditioning operations that precede image reconstruction.

Detector Preprocessing	Detector Preprocesssing			
GUI, as it appears prior to clicking on Set	Run	Set Parameters		
Parameters	Filter Data	Low Pass 👤		

The Detector Preprocessing GUI is composed of the following components:

- A pull-down menu for specifying the type of frequency filter
- The **Set Parameters** button
- The **Run** button
- The **Filter Data** checkbox
- The **Normalize Data** checkbox

This module includes the following operations:

- Optional frequency filtering. This serves to exclude frequency components that are present in the raw data but that lie outside a user-defined frequency band of interest.
- Identification of useable channels. This operation excludes measurement channels that are excessively noisy, have DC offsets that are too low, or have an excessive tendency to drift, by comparing the temporal variance during a user-specified baseline period (*i.e.*, a time interval in which data values should be relatively constant) to the temporal mean value.
- Normalization of the filtered-data time series. This compensates for signal variations attributable to differences among channels' gain settings and for features in the detector time series that arise from nonphysiological causes, such as fluctuations in the power delivered by the NIR lasers.
- Saving of the results.

Setting Parameters

Take the following steps to complete parameter setting for detector preprocessing.

First, specify a frequency filtering type from the pull-down menu, as shown in the accompanying figures. For example, select "Band Pass" filtering for the specified data.

Detect	or Preprocesssing		Detector Preprocessing	
Run	Set Parameters		Run	Set Parameters
🗖 Filter Data	Low Pass 💌	-	🗖 Filter Data	Band Pass 💌
🗖 Normalize Da	Low Pass High Pass Band Pass		🗖 Normalize Da	ata
	No Filtering			

Next, click on the Set Parameters button to open a new GUI, which contains four panels that show you the default values of control parameters and allows you to modify them. The four panels are labeled **Frequency Filtering**, **Coefficient of variation (CV)**, **Detrend the Raw Data before Normalization?**, and **Normalization**. Shown here is the default GUI associated with the Band Pass filtering option.

Set Parameters for Detector Preprocessing					
Set Parameters for Detector Preprocessing					
Frequency Filtering					
Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15					
Width of Roll Off: [15 15] % High Cutoff Frequency (Hz): 0.5					
Coefficient of Variation (CV)					
Baseline Specification: CV Threshold:					
[1 628] frames 🗸 25 %					
Reset View CV Histogram					
Detrend the Raw Data before Normalization?					
No O Yes					
Normalization					
Baseline Specification: Normalized To:					
[1 628] frames 🗸 None 🖌					
Reset					
Save & Exit Exit without Saving					

Frequency Filtering

- Sampling Rate (Hz): This parameter is the number of tomographic data sets collected per second. For a given NIRx imaging system, the sampling rate is a constant unless the user increases or decreases the number of source locations for the measurement protocol. NAVI gets the default value for the sampling rate from the _config.txt file produced by the imaging system during the data collection.
- *Cutoff Frequency (Hz)*: These parameters specify the frequency range that is retained (or *passed*) for all subsequent stages of data processing and analysis. The number of user-supplied cutoff frequencies, and their meaning, depends on the type of filter selected.
 - If you select a low-pass filter, frequencies higher than the (single) specified cutoff will be removed (or *stopped*) from the data. Low-pass filters commonly are used as data smoothers. The default value for the cutoff frequency is 0.15 Hz.
 - If you select a high-pass filter, frequencies lower than the (single) specified cutoff will be removed from the data. High-pass filters are useful for (among other purposes) detrending data time series that show tendency to slowly drift over time. The default value for the cutoff frequency is 0.5 Hz.
 - If you select a band-pass filter, you will need to specify two cutoff frequencies (default values are 0.15 Hz and 0.5 Hz). NAVI will retain all frequencies that lie within the range (or *passband*) defined by the lower and upper cutoffs, and will remove frequencies that are either smaller than the low cutoff or greater than the high cutoff.
- *Width of Roll off:* The figure below illustrates "ideal" low-pass, high-pass and band-pass filter response functions; note that they are step-functions, and the percentage of signal that is passes is either 0 or 100, switching instantly from one to the other at the cutoff frequencies. However, it turns out that frequency-response functions of this type are *not* ideal in terms of



the behavior of the filtered data in the vicinity of rapid transitions in the measured signal. An illustration of the phenomenology that can result is shown in the following figure, where the blue curve is a simulation of data obtained from an experiment wherein the subject performed



a task that induced a hemodynamic response, starting at about the 44th second and ending at about the 82nd second. The red curve shows the result obtained when a low-pass filter having a filter-response function like that depicted above is applied. The slowly decaying large-amplitude oscillations that straddle the transitions between low and high signal levels are an artifact known as "ringing." An effective method for reducing the magnitude of the artifact is to use a filter whose frequency response function, as for the green curve in the figure shown



here, changes gradually from passing 100% of the signal to passing 0%. The gradual transition is called "roll off," and the "width of roll off" is the distance along the frequency axis over which the percent of signal passed changes from 0% to 100% (in the illustrated example, the width is 0.075 Hz). Comparing the red (Width of roll off = 0) and green (Width of roll off = 50%) curves in the following figure shows that the oscillations decay substantially faster when a gradually changing frequency response function is used.



In the NAVI Frequency Filtering panel, you will specify a width for the transition in the frequency response function. The unit for this parameter is percentage of the cutoff frequency, with a default value of 15%. If you have selected a filter of the Band Pass type, you will need to specify *two* roll-off widths (they do not have to be equal to each other), the first for the low-frequency cutoff and the second for the high–frequency cutoff.

The following figures show the default setting values of *Cutoff Frequency* and *Width of Roll off* for the different available filter types.

	Frequency Filtering			
Low Pass Filter	Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15			
	Width of Roll Off: 15 %			
	Frequency Filtering			
High Pass Filter	Sampling Rate (Hz): 2.15			
	Width of Roll Off: 15 % High Cutoff Frequency (Hz): 0.5			
Band Dass Filter	Frequency Filtering			
Band Pass Filter	Frequency Filtering Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15			
Band Pass Filter	Frequency Filtering Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15 Width of Roll Off: [15 15] % High Cutoff Frequency (Hz): 0.5			
Band Pass Filter	Frequency Filtering Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15 Width of Roll Off: [15 15] % High Cutoff Frequency (Hz): 0.5			
Band Pass Filter	Frequency Filtering Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15 Width of Roll Off: [15 15] % High Cutoff Frequency (Hz): 0.5 Frequency Filtering			
Band Pass Filter No Filter	Frequency Filtering Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.15 Width of Roll Off: [15 15] % High Cutoff Frequency (Hz): 0.5 Frequency Filtering Sampling Rate (Hz): 2.15			

Coefficient of Variation (CV)

For any data time series, one can compute a mean value and a standard deviation. The CV is defined as the ratio of the standard deviation to the mean, multiplied by 100 in order to express the result in percentage-point units. If the time interval used for the CV computation is one in which the subject is at rest, not performing any tasks and with no stimulus applied, then we would expect that the data recorded in any given measurement channel would have a nearly constant value, *i.e.*, that the CV should be a small number. If a large CV is obtained in practice, this could indicate that there was a problem with the data from that channel (*e.g.*, a low signal-to-noise ratio, or an uncorrected slow drift in the detector), and the user may wish to exclude that channel from subsequent image reconstruction and feature extraction computations. NAVI offers the user the option of automatically excluding all channels with CV values exceeding a user-specified threshold value.

Baseline Specification: For each set of measurement data you will be asked to designate a "baseline" time interval for the CV computation. The specified baseline may be as brief as a few consecutive measurement frames, or it may include the entire time range for the specified data set (this is NAVI's default value). However, the premise that each channel's CV should be close to zero is true only for the intervals in which the data are not expected to vary over an appreciable range. Thus the small-CV assumption is invalid for intervals in which a subject is performing a task or is responding to a stimulus. The user should always take care to select a suitable time interval for the CV baseline.

Use the pull-down menu to select either seconds or (measurement) frames as the time unit in which you wish to specify the CV baseline. Next, enter the starting and ending times of your preferred CV baseline in the text field next to the pull-down menu. You may press the **Reset** button to cancel any values entered in the previous two fields and restore the defaults. The following figures illustrate the use of these three components.



CV Threshold: This parameter is used to exclude data channels that are excessively noisy. The value entered serves as the upper limit for acceptable computed CV values. Data from channels that have CVs higher than the threshold (or less than zero) are excluded from subsequent processing. For help in selecting a proper threshold, clicking on the **View CV Histogram** button to open a new window that will show you histograms of the CVs for both measurement wavelengths. This will allow you to

estimate the number of channels that will be excluded, for any particular choice of the CV Threshold parameter.

Detrend Raw Data before Normalization

The **Detrend the Raw Data Before Normalization?** panel gives you the option of applying an additional detrending operation, based on the use of interpolating polynomials as described below, to the raw data sets before the final normalization steps are carried out. The default selection is "No". If you do want to apply the polynomial detrending, then click the "Yes" radio button to bring up the dialog window shown in the following figure. As illustrated here, there are three text fields in which you will specify values of parameters that NAVI uses to calculate the polynomials that approximate the long-term trends for each channel.

📣 Set Parameters for Detrend Function	<u>- 🗆 ×</u>
Specify a Degree Number 10	
Specify a Time Segment Number: 1	
Specify Time Segments (frames) [1:54]	
OK Cancel	

Enter a single number (positive integer) in the *Specify a Degree Number* field; this parameter is the degree of the polynomial (*i.e.*, exponent of the highest-order term) used to fit the raw data time series. A second positive integer is entered in the *Specify a Time Segment Number* field; this is the number of distinct sub-intervals of contiguous measurement frames that the interpolating polynomial will attempt to fit (typically the user will fit the polynomial to the time intervals in which the subject was at rest, and will skip over intervening time intervals that correspond to performance of a task or application of a stimulus). In the *Specify Time Segments* field, enter the starting and ending times for each of the sub-intervals that the interpolating polynomials will attempt to fit. (The time unit is frames in the example shown here, but the unit will be seconds if you specify seconds as the time unit for the CV and normalization computations in the parent GUI.) Click the "OK" button on the dialog window to finalize your selection of detrending parameters.

A GUI to assist users in the selection of detrending parameter values, previewing the results obtained for a proposed set of user-specified parameters, is still under construction at this time.

Normalization

Usually it is not meaningful to quantitatively compare the raw data values from different measurement channels, for a number of reasons: the signals recorded in different channels are amplified with different gain factors, and the absolute signal level is a function of several variable optical coupling efficiency factors (*e.g.*, coupling at the interfaces between laser and source optical fiber, source and detector optical fibers and the subject's skin, and between detector optical fiber and photodiode). As an alternative to carrying out laborious calibration steps, the raw data values are converted to dimensionless *relative* detector readings, by computing the ratio of the each measurement frame's raw data to the average value of the raw data within a user-specified reference time interval.

In addition to the preceding considerations, when processing optical time series data it is important to: 1) somehow keep track of power fluctuations in the light source, in order to avoid artifacts that can result from misattributing these variations in measured signal levels to biological phenomena; 2) not allow signal fluctuations of <u>uninteresting</u> biological origin (*e.g.*, global variations in blood pressure, changes in superficial circulation) to overwhelm the (typically deeper and more localized) fluctuations of interest. In order to minimize the impact of these factors, NAVI implements normalization operations that involve comparing each channel to others in its vicinity.

Baseline Specification: This aspect of the Normalization panel refers to the within-channel referencing described at the bottom of p. 7. For each set of measurement data you are asked to designate a "baseline" time interval, which can be any contiguous set of measurement frames that you wish to use as the reference for comparison to other measurement sub-intervals. Most commonly, the user selects a time interval in which the subject is at rest, not performing any tasks and with no stimulus applied, as the baseline. However, the specified baseline may be as brief as a few consecutive measurement frames, or it may include the entire time range for the specified data set (this is NAVI's default value). Also, typically the same values are used here as in the CV module, but this is not obligatory.

Use the pull-down menu to select either seconds or (measurement) frames as the time unit in which you wish to specify the normalization baseline. Next, enter the starting and ending times of your preferred normalization baseline in the text field next to the pull-down menu. You may press the **Reset** button to cancel any values entered in the previous two fields and restore the defaults.

Normalized To: This aspect of the Normalization panel refers to the between-channel referencing described at the top of p. 8. Use the pull-down menu to specify the type of the reference channels used for detector data normalization. There are five options available in the pull-down menu shown in the following.



- **Optical References:** If you are using a DYNOT system that provides a distinct optical reference time series (*i.e.*, a direct measurement of the time-varying laser output, made in synchrony with the DYNOT experiment) for each source location, you can choose this option.
- **One Optical Reference:** If you are using a DYNOT system that provides a single optical reference time series, rather than a separate one for each source location, you can choose the option.
- Co-located S/D channel: In many DYNOT systems, for each source location there is a co-located detector channel. Normally, most of the light detected by the co-located channels does not penetrate to tissue deeper than the skin. Thus these channels contain little relevant physiological information regarding deep tissue processes. However, they
do contain useful information about the temporal variations in light levels that are either of nonbiological origin or are caused by uninteresting biological events.

- *Regression*: For each channel, it is reasonable to expect that the measurement contains a contribution from the common superficial/global signal. You can choose the option to remove it by use of regression. The option provides you with three ways to derive the superficial regressor: 1) from all co-located measurements, and only from these; 2) from all first-nearest-channel measurements, and only from these [this is an appropriate option for users of NIRScout imagers]; 3) both (1) and (2).
- *None:* Select this option if you do not want to perform a between-channel normalization step. It means that there is not any reference channel used for detector data normalization. This option is the default setting for data normalization.

The following figure shows the final parameter settings that have been used in the processing of data sets illustrated in this manual.

Set Parameters for Detector Preprocessing	×		
Set Parameters for Detector Preprocessing			
Frequency Filtering			
Sampling Rate (Hz): 2.15 Low Cutoff Frequency (Hz): 0.02			
Width of Roll Off: [1515] % High Cutoff Frequency (Hz): 0.3			
Coefficient of Variation (CV)			
Baseline Specification: CV Threshold:			
[0 25] seconds 🔽 25 %			
Reset View CV Histogram			
Detrend the Raw Data before Normalization?			
© No C Yes			
Normalization			
Baseline Specification: Normalized To:			
[0 25] seconds Co-Located S/D Channel			
Reset			
Save & Exit Exit without Saving			

When you choose the regression option in the pull-down menu, two radio buttons appear below the pull-down window, as shown in the following figure:



You can click on one or both of the radio buttons, in order to specify which of the three methods, described on p. 9, that you want to use for generating the regressor. If you choose a method that involves use of the 'Nearest channels' measurements, clicking the **Save & Exit** button will bring up a new GUI titled 'Set Nearest Detectors'. The GUI, as in the example shown in the figure below, allows you to graphically specify the nearest detectors for each source.



The GUI contains the following components:

• The **Set** button

- The **Clear** button
- The **Save & Close** button
- The Close button
- A figure depicting the FEM model that was selected when the dataInfo file was initialized
- A graphics panel that displays the arrangement of all detectors and of <u>one</u> source
- A text field that indicates <u>which</u> source is currently depicted along with all of the detectors
- A slider for selecting the source that you wish to display along with all of the detectors
- A pull-down menu for specifying the view orientation of the detector array

The following figure shows an example of how to specify the detectors that are nearest a given source. In this example the user is indicating which detectors are nearest to Source 6 (filled pink circle), and he has already specified three of them (filled blue circles). To specify the fourth one, click on the **Set** button, move the crosshairs until they are centered on the position of Detector 8, then press the primary mouse button to select it as another nearest neighbor of Source 6. You will need to press the **Set** button each time that you want to select another detector. If you subsequently decide that an incorrect detector was selected, you can delete your most recent choice by clicking on the **Clear** button. (Repeatedly clicking on Clear deletes the detectors in the order opposite to that in which they were assigned.) When you are finished specifying the nearest neighbors of the current source, move the slider position to either proceed to another source or to review the selections you have already made.



If you have previously selected the nearest-neighbor channels for the FEM model that you are using, clicking the **Save & Exit** button (in the parent GUI) will bring up the GUI shown here, which asks if you wish to either repeat the selection process or review your previous nearest-detector settings.

✓ ResetView01	
Nearest detector set Do you want to re-set or v	tings have been done. iew the nearest detectors?
O Yes	⊙ No
0	к

Exit without Saving

Pressing the **Exit without Saving** button in the Set parameters for Detector Preprocessing GUI closes that GUI without any of the parameter settings you made taking effect. Thus there is no impact on the working data set.

Save and Exit

After all preprocessing parameters are set, click on the **Save and Exit** button to:

- **U** Close the **Set Parameters** GUI
- Save the newly specified parameters into a temporal file located in the NAVI working folder.
- Enable the **Run** button with the *Filter Data* and *Normalize Data* checkboxes checked.

	Detector Preprocessing		
GUI for Detector Preprocessing after parameters setting	Run	Set Parameters	
	🔽 Filter Data	Band Pass 🔹	
	🔽 Normalize Data		

Starting Detector Preprocessing

Click the **Run** button to start the following operations:

- Frequency-filter the wavelength-dependent raw data sets.
- Perform CV calculation on all data time series, and label the channels with CVs exceeding the specified threshold (or negative CVs) to exclude them from subsequent processing steps.
- Normalize the filtered wavelength-dependent detector data.
- Update the dataInfo file with all pertinent information related to the detector preprocessing, and save both the filtered and filtered-and-normalized data.

During the detector preprocessing, progress bars appear to show how calculations are proceeding.

🛃 Progress Bar	🛃 Progress Bar
Preprocessing > Filtering	Normalizing

Result Output

Successful application of **Detector Preprocessing** produces a filtered detector dataset and a filtered-and-normalized detector dataset in its corresponding *Detectors* folder, as well as an update of the electronic ledger (dataInfo file) in its corresponding project folder.

The following tree structure shows the files and folders created or modified by the preprocessing computations, for the data set used in this user's guide.

🖃 🚞 NAVI2p1	Detectors		File Folder
🚞 doc	🗩 keith .set	10 KB	SET File
🗉 🧰 models	keith.evt	1 KB	EVT File
🗉 🚞 psrc	keith.wl1	6,379 KB	WL1 File
🖃 🧰 work	keith.wl2	6,379 KB	WL2 File
🗉 🧰 left_motor_cortex	keith_config.txt	1 KB	Text Document
🚞 Detectors	🔊 keith_dataInfo	79 KB	Microsoft Office Acc



Introduction

Image Reconstruction

The **Image Reconstruction** module of the **Image Generator** portal performs what is perhaps the most central role in NAVI: reconstructing image time series from the normalized data produced by the preprocessing utility (see Detector Preprocessing, Chapter 3). The image-reconstruction module uses linear perturbation-based algorithms to estimate the spatial distributions of wavelength-dependent absorption and scattering coefficients. It also employs the pre-stored FEM model library to accelerate its performance. Subsequently, a second linear transformation converts the wavelength-based absorption-coefficient images into time series of hemodynamic images (*i.e.*, oxy-Hb, deoxy-Hb, tissue blood volume, HbO₂ saturation). Using the Image Reconstruction module, you can reconstruct thousands of images in only a few minutes.



The GUI for **Image Reconstruction** has the following components:

- The **Set Parameters** button
- The **Run** button
- The Reconstruct Image checkbox

Setting Parameters

Setting parameters is the first step you need to take in order to perform Image Reconstruction.

Click the **Set Parameters** button in the Image Reconstruction module to open a new window that will allow you to either accept or change the default settings.

setReconstruction	
Set Parameters for Ima	ge Reconstruction
Options for TSVD	Time Range Specification
98 % Cumulative Singular Values 💽	[1 628] frames 💌
View SV Spectrum	Reset
Save & Exit	Exit without Saving

Options for TSVD

Truncated singular value decomposition (TSVD) is the numerical algorithm that NAVI uses to compute images of absorption and diffusion coefficients. A complete (*i.e.*, <u>not</u> truncated) SVD computation would make use of all the information in the normalized detector data and in the FEM model. The result, however, would be uninterpretable images dominated by the random fluctuations, or noise, that inevitably is present in measurement data. It turns out that the effect of noise can be greatly diminished by truncating, which means leaving out those components of the model that are responsible for attempting to recover fine details (*i.e.*, high spatial resolution) of the image.

The user-specified truncation parameter is a cutoff value that determines how many singular values will be retained. The three components are a text field in which you enter a value for the truncation parameter, a pull-down menu used to select the units for the truncation parameter, and a **View SV Spectrum** button:



Currently, there is no simple, automatable procedure for choosing the optimal value of the truncation parameter for a given experimental data set. Setting the truncation parameter too high produces images that are noise-dominated, while setting it too low results in loss of spatial resolution or possibly even more severe distortions (*e.g.*, all hemodynamic information may be forced into superficial regions of the image). Pressing the **View SV Spectrum** button launches a tool that can assist you in selecting an appropriate value for the truncation parameter.

Click on the **View SV Spectrum** to opens a pop-up window displaying a pair of graphs, as shown here:



The top subfigure is a line graph representation of all the singular values for the imagereconstruction weight matrix, in order of decreasing magnitude (notice that they range over many orders of magnitude, necessitating use a logarithmic y-axis scale). The lower subfigure is a plot of the cumulative percentage of the singular values. The graphs convey the same information in two different ways: if the *n*th singular value is x_n , then the corresponding cumulative percentage is $y_n = 100 \sum_{i=1}^n x_i / \sum_{i=1}^N x_i$. The horizontal red line in the lower plot shows the numerical value currently entered in the 'Options for TSVD' text field, which is the default 98% for the example shown. The vertical red line, which passes through the intersection of the horizontal red line and the blue cumulative percentage curve, shows the number of SVs that corresponds to the specified cumulative percentage. In this example, you thus learn that 60 SVs must remain [out of a maximum of 625 (25 sources × 25 detectors)] to reach the 98% mark. Note that the total number of data channels, the number that survive the CV threshold computation described in Chap. 3, the number of weight matrix nodes, and the number of SVs retained are clearly indicated in the pop-up window (yellow circles in preceding figure).

After you have decided how many singular values to retain for the image reconstruction computations, enter the selected number in the 'Options for TSVD' text field. You may specify either the specific number of singular values you want to retain or the corresponding cumulative percentage of summed singular values, by selecting the appropriate option from the 'Options for TSVD' pull-down menu.

Through extensive empirical testing, we have found the quality of reconstructed images usually is good when the value selected for '% Cumulative Singular Values' is 98 (the default setting). However, the number that works best for a particular experimental data set may be lower than this if the data time series have high noise levels, or higher if only a few SVs are needed to achieve 98%.

Time Range Specification

This allows you to specify the time interval for which you want to generate reconstructed images. Its default value is the entire range of the user-specified data set, in units of measurement frames. Similar to the panel used to specify baseline time intervals for detector preprocessing (Chap. 3), 'Time Range Specification' allows you to specify the time interval of interest in units of either frames or seconds, by selecting an option from the pull-down menu.

Press the **Reset** button to restore the default time range setting.

Note that, owing to the speed of the image reconstruction computation, usually there is little to be gained from selecting only a sub-interval of the entire time range for image reconstruction. However, the option of doing so is available.

Time Range Specification			
[1 628]	frames 💌	
Reset			

Exit without Saving

Pressing the **Exit without Saving** button in the Set Parameters for Image Reconstruction GUI closes that GUI without any of the parameter settings you made taking effect. Thus there is no impact on the working data set.

Save and Exit

After all image reconstruction parameters are set, click on the Save & Exit button to:

- **U** Close the **Set Parameters** GUI.
- Save the newly specified parameters into a file located in the NAVI working folder.
- Enable the **Run** button, with the 'Reconstruct Image' checkbox checked.

GUI for Image	Image	e Reconstruction	
Reconstruction , after parameters are	Run	Set Parameters	
set.	Reconstruct Image		

Starting Image Reconstruction

Click the **Run** button to start the following sequence of operations:

- Compute the wavelength-dependent optical coefficient images.
- Calculate the hemodynamic images.
- **O** Save results.

During the process, progress bars appear to show how calculations are proceeding.



Result Output

Successful application of Image Reconstruction produces two wavelength-dependent optical absorption coefficient image time series and two hemodynamic image time series (oxyHb and deoxyHb) in the corresponding *Images* folder, as well as an update to the electronic ledger (dataInfo file) in its corresponding project folder.

🚞 Images

The following tree structure shows the files and folders created or modified by the Image Reconstruction computations, for the experimental data set used in this user's guide.

🖃 🚞 NAVI2p1	Detectors		File Folder
🚞 doc	🚞 Images		File Folder
🗉 🧰 models	🗩 keith .set	10 KB	SET File
🗉 🚞 psrc	keith.evt	1 KB	EVT File
🖃 🧰 work	🖉 keith.wl 1	6,379 KB	WL1 File
🖃 🧰 left_motor_cortex	🖬 keith.wl2	6,379 KB	WL2 File
C Detectors	keith_config.txt	1 KB	Text Document
🚞 Images	📕 keith_dataInfo	252 KB	Microsoft Office Acc



Appendix 1 – Image Reconstruction Strategy

Perturbation Equation

When you use a DYNOT or NIRScout imager to perform an fNIRS measurement, you record data from a number of distinct "channels," (tens to hundreds, in almost all cases), where a channel is defined by specifying a particular pairing of source and detector optodes, as illustrated in Figure A1.1.



Clearly there are many factors that determine the light intensity recorded by a channel. These include the:

- distance between the source and detector optodes constituting a channel;
- location of the optodes on the scalp or other external tissue surface (*e.g.*, Channel A and Channel B in Fig. A1.1 can record different light intensities at the same time, even though they have the same inter-optode distance);
- relevant optical coupling efficiencies (*e.g.*, of all the light that is emitted by the source optode, what percentage actually penetrates into the tissue?);
- brightness of the light source;
- position-dependent absorption and scattering coefficients of the tissue.

Note that the final item listed is the one that you are trying to learn about by performing the fNIRS measurement. As for the others: if the measuring head is properly positioned on the tissue structure of interest, then the first three will not vary to any significant degree during the course of the measurement; and NAVI provides tools (see Normalization section in Chap. 3: Detector Preprocessing) to compensate for fluctuations in the source light intensity.

We can summarize the preceding enumeration of factors that influence the detected light intensity as follows:

$$\boldsymbol{R}_{c}(t) = f \left[\boldsymbol{S}_{c}(t), \mathbf{r}_{so}, \mathbf{r}_{do}, \{ \boldsymbol{\varepsilon}_{1}, \boldsymbol{\varepsilon}_{2}, \ldots \}, \boldsymbol{\mu}_{a}(\mathbf{r}, t), \boldsymbol{\mu}_{s}(\mathbf{r}, t) \right],$$
(1)

where:

- $R_c(t)$ = time-varying recorded light intensity,
- $S_c(t)$ = time-varying light-source strength,
- \mathbf{r}_{so} = location of the source optode,
- \mathbf{r}_{do} = location of the detector optode,
- ε_1 , etc. = optical coupling efficiencies,
- $\mu_a(\mathbf{r},t)$ = position- and time-dependent tissue absorption coefficient,
- $\mu_s(\mathbf{r},t)$ = position- and time-dependent tissue scattering coefficient.

(The inter-optode distance r_{sd} does not need to appear explicitly in Eq. (1), because $r_{sd} = ||\mathbf{r}_{so} - \mathbf{r}_{do}||$.) Eq. (1) tells us that there is *some* mathematical function f[...]—whose functional form we are not yet specifying—that deterministically relates the information inside the brackets on the right-hand side to the time-varying detected light signal on the left-hand side. The goal of image reconstruction is to compute the values $\mu_a(\mathbf{r},t)$ and/or $\mu_s(\mathbf{r},t)$ from the measured values of $R_c(t)$.

All right then, what is the functional form of the mysterious f[...]? The answer is that in the great majority of cases, we just don't know (and neither does anyone else). There are some very special cases—one example is if the object being imaged is a perfect sphere, and the μ_a and μ_s coefficients are spatially uniform—for which it is possible to determine the mathematical form of f[...]. However, the biological imaging studies that you will be involved in are not included in this category; for these real-world cases, the mathematical form of f[...] cannot be determined. Fortunately, there is a highly successful data analysis strategy that we can bring to bear for solving these image-reconstruction problems.

Our initial step is to recognize that, over the entire range of light-source strengths that you will ever consider using, $R_c(t)$ is *absolutely linear* with respect to $S_c(t)$. This means that if the source becomes, say, 20% brighter, then the detected light signal will also increase by precisely 20%. And if the source grows, say, 10% dimmer, the detected light signal will decrease by precisely 10%. A consequence of this linear relation is that we can simplify Eq. (1), changing it to

$$R_{c}(t) = S_{c}(t) \cdot g \left[\mathbf{r}_{so}, \mathbf{r}_{do}, \{\varepsilon_{1}, \varepsilon_{2}, \ldots\}, \mu_{a}(\mathbf{r}, t), \mu_{s}(\mathbf{r}, t) \right],$$
(2)

where $S_c(t) \cdot g[...] = f[...]$. A rearrangement of Eq. (2) gives us

$$\frac{R_{c}(t)}{S_{c}(t)} = g\left[\mathbf{r}_{so}, \mathbf{r}_{do}, \left\{\varepsilon_{1}, \varepsilon_{2}, \ldots\right\}, \mu_{a}(\mathbf{r}, t), \mu_{s}(\mathbf{r}, t)\right], \\
\equiv R_{c}'(t),$$
(3)

where $R'_{c}(t)$ is the detected light signal *normalized to* the light source strength.

To continue, we recognize that each of the time-varying quantities in Eq. (3) can be expressed as the sum of two quantities: a time-invariant average value plus a time-dependent fluctuation about that average. Mathematically, this means that we can transform Eq. (3) to

$$\overline{R'_{c}} + \Delta R'_{c}(t) = g \left[\mathbf{r}_{so}, \mathbf{r}_{do}, \{\varepsilon_{1}, \varepsilon_{2}, \ldots\}, \overline{\mu_{a}(\mathbf{r})} + \Delta \mu_{a}(\mathbf{r}, t), \overline{\mu_{s}(\mathbf{r})} + \Delta \mu_{s}(\mathbf{r}, t) \right],$$
(4)

where ' \bar{x} ' stands for the time-averaged value of *x* and ' $\Delta x(t)$ ' is the symbol for the temporal fluctuations of *x*. Now, even though we don't know the precise functional form of g[...], there are some facts that can be asserted incontrovertibly, based on our knowledge of light propagation physics and the composition of biological tissue. One such fact is that we can expect that $\Delta R'_c(t)$ will be a smooth, continuous function of $\Delta \mu_a(\mathbf{r},t)$ and $\Delta \mu_s(\mathbf{r},t)$, as illustrated by the left-hand plot in

Figure A1.2, and will not exhibit the kinds of phenomena seen in the right-hand plot. An important practical consequence is that, even if we don't know the functional form of g[...], we *do* know that it can be written as a converging infinite series:¹



Figure A1.2. In fNIRS tissue measurements, the magnitude of the detected light signal in a smooth continuous function of the absorption coefficient (varying the scattering coefficient would produce a qualitatively similar result), as indicated in the left-hand sketch. Abrupt changes in either the signal value or in its rate of change, as shown in the right-side sketch, are not consistent with the known physics of interactions between biological tissue and NIR light.

$$\overline{R'_{c}} + \Delta R'_{c}(t) = g \left[\mathbf{r}_{so}, \mathbf{r}_{do}, \{\varepsilon_{1}, \varepsilon_{2}, \ldots\}, \overline{\mu_{a}(\mathbf{r})}, \overline{\mu_{s}(\mathbf{r})} \right] + \int \left[\frac{\partial \overline{R'_{c}}}{\partial \overline{\mu_{a}(\mathbf{r})}} \cdot \Delta \mu_{a}(\mathbf{r}, t) + \frac{\partial \overline{R'_{c}}}{\partial \overline{\mu_{s}(\mathbf{r})}} \cdot \Delta \mu_{s}(\mathbf{r}, t) \right] d\mathbf{r} \\
+ \iint \left[\frac{\partial^{2} \overline{R'_{c}}}{\partial \overline{\mu_{a}(\mathbf{r})}^{2}} \cdot \Delta \mu_{a}(\mathbf{r}, t)^{2} + \frac{\partial^{2} \overline{R'_{c}}}{\partial \overline{\mu_{s}(\mathbf{r})}^{2}} \cdot \Delta \mu_{s}(\mathbf{r}, t)^{2} + \frac{\partial^{2} \overline{R'_{c}}}{\partial \overline{\mu_{a}(\mathbf{r})} \partial \overline{\mu_{s}(\mathbf{r})}} \cdot \Delta \mu_{a}(\mathbf{r}, t) \cdot \Delta \mu_{s}(\mathbf{r}, t) \right] d\mathbf{r}^{2} \quad (5) \\
+ HOT,$$

and the acronym *HOT* stands for "higher-order terms." The crucial insight that allows us to proceed beyond Eq. (5) is that in the biological imaging context, the magnitude of the absorptioncoefficient fluctuations will substantially smaller than the temporal mean value, and likewise for the scattering coefficient. The mathematical expressions for the preceding assertions, which certainly are correct on the time scale of an fNIRS measurement session (*i.e.*, from ten minutes to an hour), are $|\Delta \mu_a(\mathbf{r}, t)| \ll \overline{\mu_a(\mathbf{r})}$ and $|\Delta \mu_s(\mathbf{r}, t)| \ll \overline{\mu_s(\mathbf{r})}$. As a consequence of the inequalities, we can safely neglect all of the terms after the first line in Eq (5); in other words, we can write:

$$\overline{R_c'} + \Delta R_c'(t) = g \left[\mathbf{r}_{so}, \mathbf{r}_{do}, \{\varepsilon_1, \varepsilon_2, \ldots\}, \overline{\mu_a(\mathbf{r})}, \overline{\mu_s(\mathbf{r})} \right] + \int \left[\frac{\partial \overline{R_c'}}{\partial \overline{\mu_a(\mathbf{r})}} \cdot \Delta \mu_a(\mathbf{r}, t) + \frac{\partial \overline{R_c'}}{\partial \overline{\mu_s(\mathbf{r})}} \cdot \Delta \mu_s(\mathbf{r}, t) \right] d\mathbf{r}.$$
(6)

Now there is a one-to-one correspondence between the terms on the left-hand and right-hand sides of Eq. (6), and we can see that it is only the second term on each side that contains a dependence on time. Put another way, only the second term contains information about hemodynamics, which is what we're interested in. Thus we simplify the equation even more, to:

¹ Another practical consequence—the subject for another chapter but worth mentioning here—is that if you do see discontinuities in your measurement data, your first assumption should be that you have poor skin-optode contact.

$$\Delta R_{c}'(t) = \int \left[\frac{\partial \overline{R_{c}'}}{\partial \mu_{a}(\mathbf{r})} \cdot \Delta \mu_{a}(\mathbf{r}, t) + \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} \cdot \Delta \mu_{s}(\mathbf{r}, t) \right] d\mathbf{r}$$

$$= \int \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{a}(\mathbf{r})}} \cdot \Delta \mu_{a}(\mathbf{r}, t) d\mathbf{r} + \int \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} \cdot \Delta \mu_{s}(\mathbf{r}, t) d\mathbf{r},$$
(7)

Up to this point, we have only been taking account of how $\mu_d(\mathbf{r},t)$ and $\mu_s(\mathbf{r},t)$ vary over time. The next step in our derivation involves making a biologically reasonable assumption about how these coefficients vary across *space*. In particular, we will assume that two points that are separated by only a small distance cannot have hugely different $\Delta \mu_a$ values or hugely different $\Delta \mu_s$ values. In that case, any point in the tissue that we're examining can be regarded as the center of a small volume (or "voxel," which is an abbreviation of "volume element"²) that has approximately $\max(\Delta\mu_a) - \min(\Delta\mu_a) \ll \langle \Delta\mu_a \rangle,$ values: constant $\Delta \mu_a$ and $\Delta \mu_s$ and $\max(\Delta \mu_s) - \min(\Delta \mu_s) \ll \langle \Delta \mu_s \rangle$, where $\langle x \rangle$ ' stands for the volume-averaged value of x. Since the magnitudes of the fluctuations about the average values are too small to interest us, we will simply assert that value of $\Delta \mu_a$ really is constant throughout the voxel, and likewise for $\Delta \mu_s$.

The preceding approximation allows us to further simplify the equation relating the measurements to the optical coefficients, because instead of having to somehow figure out the values of $\Delta \mu_a$ and $\Delta \mu_s$ at an infinite number of points, now we only need to compute them for a finite number of the small volumes. Eq. (7) changes to:

$$\Delta R_{c}'(t) = \Delta \mu_{a}(V_{1}) \cdot \int_{V_{1}} \frac{\partial \overline{R_{c}'}}{\partial \mu_{a}(\mathbf{r})} d\mathbf{r} + \Delta \mu_{a}(V_{2}) \cdot \int_{V_{2}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{a}(\mathbf{r})}} d\mathbf{r} + \dots + \Delta \mu_{a}(V_{N}) \cdot \int_{V_{N}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{a}(\mathbf{r})}} d\mathbf{r} + \Delta \mu_{s}(V_{1}) \cdot \int_{V_{1}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r} + \Delta \mu_{s}(V_{2}) \cdot \int_{V_{2}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r} + \dots + \Delta \mu_{s}(V_{N}) \cdot \int_{V_{N}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r},$$
(8)

where *N* is the number of voxels; $\Delta \mu_a(V_i)$ means "the constant value of $\Delta \mu_a$ in the *i*th voxel" (and likewise for $\Delta \mu_s$); and \int_{V_i} means "perform this integration over the volume of the *i*th voxel."

At first glance, it might not be apparent that Eq. (8) is simpler than Eq. (7). The reason why it is, is that the $\Delta \mu_a$ and $\Delta \mu_s$ terms are no longer inside the integrals. What this means in practice is that the quantities $\int_{V_1} \frac{\partial \overline{R'_c}}{\partial \overline{\mu_a(\mathbf{r})}} d\mathbf{r}$, $\int_{V_1} \frac{\partial \overline{R'_c}}{\partial \overline{\mu_s(\mathbf{r})}} d\mathbf{r}$, etc., can all be pre-computed (using methods described in papers available at <u>http://otg.downstate.edu/publications.htm</u>), at our convenience and independently of any specific set of measurement data, and read in whenever they are needed. Note also that, while an expression such as $\int_{V_1} \frac{\partial \overline{R'_c}}{\partial \overline{\mu_a(\mathbf{r})}} d\mathbf{r}$ may look complicated, it is just one number when all is said and done (because it is a definite integral carried out over the

just one number when all is said and done (because it is a definite integral carried out over the volume of a specific voxel). Therefore we will also simplify the *appearance* of the integrals in Eq. (8), by defining a new set of symbols for them:

² Yes, we know that there is no 'x' anywhere in "volume element." The person who coined the word was going for a 3-D analogue for the word "pixel."

$$w_{1,c}^{a} \equiv \int_{V_{1}} \frac{\partial \overline{R_{c}'}}{\partial \mu_{a}(\mathbf{r})} d\mathbf{r}, \quad w_{2,c}^{a} \equiv \int_{V_{2}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{a}(\mathbf{r})}} d\mathbf{r}, \quad \dots, \quad w_{N,c}^{a} \equiv \int_{V_{N}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{a}(\mathbf{r})}} d\mathbf{r};$$

$$w_{1,c}^{s} \equiv \int_{V_{1}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r}, \quad w_{2,c}^{s} \equiv \int_{V_{2}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r}, \quad \dots, \quad w_{N,c}^{s} \equiv \int_{V_{N}} \frac{\partial \overline{R_{c}'}}{\partial \overline{\mu_{s}(\mathbf{r})}} d\mathbf{r}.$$
(9)

The numbers defined in Eq. (9) are called *weights*: $w_{1,c}^a$ is the absorption weight in the first voxel, $w_{2,c}^s$ is the scattering weight in the second voxel, etc., and the ",c" in the subscript reminds us that these weights are defined for the specific measurement channel that we are considering. Substitution of the Eq. (9) expressions into Eq. (8) leads to:

$$\Delta R_{c}'(t) = \Delta \mu_{a}(V_{1}, t) \cdot w_{1,c}^{a} + \Delta \mu_{a}(V_{2}, t) \cdot w_{2,c}^{a} + \dots + \Delta \mu_{a}(V_{N}, t) \cdot w_{N,c}^{a} + \Delta \mu_{s}(V_{1}, t) \cdot w_{1,c}^{s} + \Delta \mu_{s}(V_{2}, t) \cdot w_{2,c}^{s} + \dots + \Delta \mu_{s}(V_{N}, t) \cdot w_{N,c}^{s},$$
(10)

and readers with knowledge of linear algebra may recognize that each row in Eq. (10) is a simple dot product of two vectors:

$$\Delta \mathbf{R}_{c}^{\prime}(t) = \begin{bmatrix} w_{1,c}^{a} & w_{2,c}^{a} & \dots & w_{N,c}^{a} \end{bmatrix} \begin{bmatrix} \Delta \mu_{a}(V_{1},t) \\ \Delta \mu_{a}(V_{2},t) \\ \vdots \\ \Delta \mu_{a}(V_{N},t) \end{bmatrix} + \begin{bmatrix} w_{1,c}^{s} & w_{2,c}^{s} & \dots & w_{N,c}^{s} \end{bmatrix} \begin{bmatrix} \Delta \mu_{s}(V_{1},t) \\ \Delta \mu_{s}(V_{2},t) \\ \vdots \\ \Delta \mu_{s}(V_{N},t) \end{bmatrix}, \quad (11)$$

which can be written in a more compact way by defining a symbol for each vector:

$$\mathbf{w}_{c}^{a} \equiv \begin{bmatrix} w_{1,c}^{a} \\ w_{2,c}^{a} \\ \vdots \\ w_{N,c}^{a} \end{bmatrix}, \quad \mathbf{w}_{c}^{s} \equiv \begin{bmatrix} w_{1,c}^{s} \\ w_{2,c}^{s} \\ \vdots \\ w_{N,c}^{s} \end{bmatrix}, \quad \Delta \boldsymbol{\mu}_{a}(t) \equiv \begin{bmatrix} \Delta \boldsymbol{\mu}_{a}(V_{1},t) \\ \Delta \boldsymbol{\mu}_{a}(V_{2},t) \\ \vdots \\ \Delta \boldsymbol{\mu}_{a}(V_{N},t) \end{bmatrix}, \quad \Delta \boldsymbol{\mu}_{s}(t) \equiv \begin{bmatrix} \Delta \boldsymbol{\mu}_{s}(V_{1},t) \\ \Delta \boldsymbol{\mu}_{s}(V_{2},t) \\ \vdots \\ \Delta \boldsymbol{\mu}_{s}(V_{N},t) \end{bmatrix},$$

$$\Rightarrow \qquad (12)$$

$$\Delta R_{c}^{\prime}(t) = \left(\mathbf{w}_{c}^{a}\right)^{\mathrm{T}} \left(\Delta \boldsymbol{\mu}_{a}(t)\right) + \left(\mathbf{w}_{c}^{s}\right)^{\mathrm{T}} \left(\Delta \boldsymbol{\mu}_{s}(t)\right).$$

(The superscript 'T' denotes the transpose operation: $\begin{bmatrix} x \\ y \end{bmatrix}^{T} = \begin{bmatrix} x & y \end{bmatrix}$). It is straightforward to combine the terms on the right-hand side of Eq. (12) into a single dot product:

$$\Delta R_c'(t) = \begin{bmatrix} \mathbf{w}_c^a \\ \mathbf{w}_c^s \end{bmatrix}^{\mathrm{T}} \begin{bmatrix} \Delta \boldsymbol{\mu}_a(t) \\ \Delta \boldsymbol{\mu}_s(t) \end{bmatrix},$$
(13)

which is the *one-channel perturbation equation*.

Please take note of the following facts about Eq. (13):

• The right-hand side is the product of two factors, and the first one contains all of the dependence on the locations of the source and detector optodes while the second one contains all of the information about the time-varying absorption and scattering coefficients of the tissue.

- While we derived the equation by considering the measurement data $R_c(t)$ collected by *some* particular channel, at no point did we specify *which* channel we were considering. This means that the final result we obtained is completely general: we will get an equation having the form of Eq. (13) for *every* channel in a multichannel measurement.
- The only difference between the equations for the multiple channels will be that each one will have different specific numerical values in its $\begin{bmatrix} \mathbf{w}_c^a \\ \mathbf{w}_c^s \end{bmatrix}$ vector. Since all of the measurements are collected simultaneously, $\begin{bmatrix} \Delta \boldsymbol{\mu}_a(t) \\ \Delta \boldsymbol{\mu}_s(t) \end{bmatrix}$ necessarily is the same for all channels.

In order to ensure that our image reconstruction computation will find a single $\begin{bmatrix} \Delta \mu_a(t) \\ \Delta \mu_s(t) \end{bmatrix}$

that is consistent with measurements from all channels simultaneously, we combine all the onechannel perturbation equations into a single system of algebraic equations. Using the symbol M to denote the total number of channels that were present during the measurement, the algebraic system is:

$$\begin{bmatrix} \Delta R_{1}'(t) \\ \Delta R_{2}'(t) \\ \vdots \\ \Delta R_{M}'(t) \end{bmatrix} = \begin{bmatrix} \begin{bmatrix} \mathbf{w}_{1}^{a} \\ \mathbf{w}_{1}^{s} \end{bmatrix}^{\mathrm{T}} \\ \begin{bmatrix} \mathbf{w}_{2}^{a} \\ \mathbf{w}_{2}^{s} \end{bmatrix}^{\mathrm{T}} \\ \vdots \\ \begin{bmatrix} \mathbf{w}_{M}^{a} \\ \mathbf{w}_{M}^{s} \end{bmatrix}^{\mathrm{T}} \end{bmatrix} \begin{bmatrix} \Delta \boldsymbol{\mu}_{a}(t) \\ \Delta \boldsymbol{\mu}_{s}(t) \end{bmatrix}, \quad (14)$$

where we have replaced the generic subscript 'c' with specific numerical values that range from 1 to M. Thus the first row in Eq. (14) contains information pertaining to the measurement channel #1 (e.g., Channel A in Fig. A1.1), the second row contains information pertaining to the measurement channel #2 (e.g., Channel B in Fig. A1.1), and so on down the line. Next, just as we did for Eqs. (8) and (11), we streamline the appearance of Eq. (14) by defining new symbols for some of the terms:

$$\Delta \mathbf{R}'(t) \equiv \begin{bmatrix} \Delta R_1'(t) \\ \Delta R_2'(t) \\ \vdots \\ \Delta R_M'(t) \end{bmatrix}, \quad \mathbf{W} \equiv \begin{bmatrix} \begin{bmatrix} \mathbf{w}_1^a \\ \mathbf{w}_1^s \end{bmatrix}^T \\ \begin{bmatrix} \mathbf{w}_2^a \\ \mathbf{w}_2^s \end{bmatrix}^T \\ \vdots \\ \begin{bmatrix} \mathbf{w}_M^a \\ \mathbf{w}_M^s \end{bmatrix}^T \end{bmatrix}, \quad \Delta \boldsymbol{\mu}(t) \equiv \begin{bmatrix} \Delta \boldsymbol{\mu}_a(t) \\ \Delta \boldsymbol{\mu}_s(t) \end{bmatrix}, \quad (15)$$

and substituting the Eq. (15) into Eq. (14) gives us

(16)

$$\Delta \mathbf{R}'(t) = \mathbf{W} \Delta \boldsymbol{\mu}(t),$$

which is the *multi-channel perturbation equation*. The process of reconstructing images involves using a numerical analysis algorithm to solve Eq. (16) for $\Delta \mu(t)$, when W (pre-computed) and $\Delta \mathbf{R'}(t)$ (measured) are given as input. Additional information about the specific methods that NAVI uses is given in the next section of this Appendix.

Normalized Difference Method

A close examination of Eq. (9) reveals a reason why you might expect that the perturbationequation approach derived in the preceding section would be difficult to apply in practice: computation of the correct weights requires accurate knowledge of $\overline{\mu_a(\mathbf{r})}$ and $\overline{\mu_s(\mathbf{r})}$, the positiondependent, time-averaged absorption and scattering coefficients. However, in functional medical imaging studies there really is no good (or noninvasive, or economically feasible) way to obtain accurate knowledge of $\overline{\mu_a(\mathbf{r})}$ and $\overline{\mu_s(\mathbf{r})}$. What has tended to happen instead is that people doing fNIRS imaging research take the best "initial guess" that they can think of for the time-averaged coefficient values (these are also often referred to as "reference" values); here we will use the symbols $A(\mathbf{r})$ and $S(\mathbf{r})$ refer to the initial guesses for the absorption and scattering coefficients, respectively. The next step is to compute the weights that correspond to those initial guesses:

$$\tilde{w}_{i,j}^{a} \equiv \int_{V_{i}} \frac{\partial \overline{R_{j}^{\prime}}}{\partial A(\mathbf{r})} d\mathbf{r}, \quad \tilde{w}_{i,j}^{s} \equiv \int_{V_{i}} \frac{\partial \overline{R_{j}^{\prime}}}{\partial S(\mathbf{r})} d\mathbf{r}, \quad (17)$$

where the voxel index *i* ranges from 1 to *N*, the channel index *j* ranges from 1 to *M*, and we are using the '~' symbol to indicate that the quantities defined in Eq. (17) are not really the true weights for the tissue that you took the measurements from. The initial-guess-based weights are used, in place of the unknown correct ones, in Eq. (16), and finally a numerical algorithm is used to solve the resulting equation, $\Delta \mathbf{R}'(t) = \tilde{\mathbf{W}} \Delta \tilde{\boldsymbol{\mu}}(t)$, for $\Delta \tilde{\boldsymbol{\mu}}(t)$.

The fatal flaw in the preceding approach is that the argument that took us from Eq. (5) to Eq. (6)—and, by extension, to all subsequent equations in the first section of this Appendix—is no longer valid once we replace $\overline{\mu_a(\mathbf{r})}$ and $\overline{\mu_s(\mathbf{r})}$ with $A(\mathbf{r})$ and $S(\mathbf{r})$. There is no reason to expect that $|\Delta \mu_a(\mathbf{r},t)| \ll A(\mathbf{r})$ or that $|\Delta \mu_s(\mathbf{r},t)| \ll S(\mathbf{r})$, and in fact all experience indicates that those inequalities are *not* satisfied. And so, while we surely are free to substitute $A(\mathbf{r})$ and $S(\mathbf{r})$ for $\overline{\mu_a(\mathbf{r})}$ and $\overline{\mu_s(\mathbf{r})}$ in Eq. (5), the second-derivative and higher-order terms will no longer be negligible. As a consequence, while we can go through the motions of computing $\Delta \tilde{\mu}(t)$ as described in the preceding paragraph, we have no reason to expect that $\Delta \tilde{\mu}(t)$ will be a good approximation to the true $\Delta \mu(t)$.

Okay then, what can we do to get out of this predicament? The critical insight here is that it isn't enough to substitute $\tilde{\mathbf{W}}$ for \mathbf{W} in the multi-channel perturbation equation: to be consistent, we *also* have to replace the $\overline{R'_c}$ term that we haven't thought about since Eq. (6). You will recall $\overline{R'_c}$ (measured) is the normalized light signal detected for tissue having optical coefficient values of $\overline{\mu_a(\mathbf{r})}$ and $\overline{\mu_s(\mathbf{r})}$ (unknown and unknowable). What we need instead is $\tilde{R'_c}$, which is the normalized light signal detected for tissue of $A(\mathbf{r})$ and $S(\mathbf{r})$. Fortunately, the

same computational techniques that are used to produce $\tilde{\mathbf{W}}$ can be used to generate \tilde{R}'_c values for all of the measurement channels. Then we gather the \tilde{R}'_c values for all channels into a vector, which we will call $\tilde{\mathbf{R}}'$, taking care to arrange the channels in the same order in $\tilde{\mathbf{R}}'$ that they have in $\Delta \mathbf{R}'(t)$.

Now we need to appropriately combine the computed $\tilde{\mathbf{R}}'$ and $\tilde{\mathbf{W}}$ with the measured $\Delta \mathbf{R}'(t)$ in order to produce a mathematically consistent analogue for Eq. (16). This is accomplished via the following process, which we call the *normalized difference method*:

- For each channel, compute the ratio $\Delta R'_c(t)/\overline{R'_c}$. Recall that the numerator $\Delta R'_c(t)$ is the difference between time-varying and time-averaged detected light signals: $\Delta R'_c(t) = R'_c(t) \overline{R'_c}$. Thus the dimensionless ratio $\Delta R'_c(t)/\overline{R'_c}$ is a *normalized difference*.
- For each channel, multiply $\Delta R'_c(t)/\overline{R'_c}$ (derived from measurement data) and the corresponding $\tilde{R'_c}$ value (computed, based on the initial guesses $A(\mathbf{r})$ and $S(\mathbf{r})$): $\Delta \tilde{R'_c}(t) = \tilde{R'_c} \cdot \left[\Delta R'_c(t)/\overline{R'_c} \right]$, or, equivalently, $\Delta \tilde{R'_c}(t) = \Delta R'_c(t) \cdot \left(\tilde{R'_c}/\overline{R'_c} \right)$. Note that this amounts to adjusting the measured $\Delta R'_c(t)$ by some channel-dependent multiplicative constant.
- The single-channel perturbation equation for normalized differences, analogous to Eq. (13), is:

$$\Delta \tilde{R}_{c}'(t) = \begin{bmatrix} \tilde{\mathbf{w}}_{c}^{a} \\ \tilde{\mathbf{w}}_{c}^{s} \end{bmatrix}^{\mathrm{T}} \begin{bmatrix} \Delta \tilde{\boldsymbol{\mu}}_{a}(t) \\ \Delta \tilde{\boldsymbol{\mu}}_{s}(t) \end{bmatrix}.$$
(18)

The way to interpret the terms $\Delta \tilde{\boldsymbol{\mu}}_{a}(t)$ and $\Delta \tilde{\boldsymbol{\mu}}_{s}(t)$ is that these are the amounts by which we would need to change the absorption and scattering coefficients, with respect to the initial guesses $A(\mathbf{r})$ and $S(\mathbf{r})$, in order to see a change in detected light signal equal to $\Delta \tilde{R}'_{c}(t)$. Put another way, if $\{A(\mathbf{r}), S(\mathbf{r})\}$ inside the tissue gives us \tilde{R}'_{c} in the measurement channel, then $\{A(\mathbf{r}) + \Delta \tilde{\boldsymbol{\mu}}_{a}(t), S(\mathbf{r}) + \Delta \tilde{\boldsymbol{\mu}}_{s}(t)\}$ will give us $\tilde{R}'_{c} + \Delta \tilde{R}'_{c}(t)$.

• After generating an equation having the form of Eq. (18) for all the individual, combine them all into the multi-channel perturbation equation for normalized differences, analogous to Eq. (16):

$$\Delta \tilde{\mathbf{R}}'(t) = \tilde{\mathbf{W}} \Delta \tilde{\boldsymbol{\mu}}(t), \tag{19}$$

and solve the resulting system for $\Delta \tilde{\mu}(t)$. In contrast with the approach considered at the beginning of this section, Eq. (19) does not suffer from any mismatch between the tissue properties corresponding to the weights and to the time-averaged detector signals. Consequently, the conditions that must be satisfied in order to use Eq. (6) in place of Eq. (5) are not violated. It follows that when Eq. (19) is used, we can expect that $\Delta \tilde{\mu}(t)$ will be a good approximation to the true $\Delta \mu(t)$. (See <u>http://otg.downstate.edu/Publication/PeiAO01.pdf</u> for computational examples illustrating the robustness of the normalized difference method to substantial discrepancies between $\{\overline{\mu_a(\mathbf{r})}, \overline{\mu_s(\mathbf{r})}\}$ and $\{A(\mathbf{r}), S(\mathbf{r})\}$, and see <u>http://otg.downstate.edu/Publication/SchmitzRSI02.pdf</u> for a demonstration of its successful application to laboratory data.)

5

Data Export

Introduction

NAVI provides a **Data Export** module that allows users to export NAVI-based detector and image data in a number of file formats. The available formats make it possible for you to edit, view and analyze the exported data with other, commonly available software packages, such as **AFNI**, **SPM**, or **GiD**.



This module contains two pull-down menus. One of them allows you to select the data that will be converted, while the other specifies the conversion format.



The types of data that may be exported, and the valid file formats for each type, are as follows:

- Hboxy Images reconstructed images of oxygenated hemoglobin; to all three file formats
- Hbdeoxy Images reconstructed images of deoxygenated hemoglobin; to all three file formats
- Hbtot Images computed images of total hemoglobin; to all three file formats
- HbO₂Sat computed images of hemoglobin oxygen saturation; to all three file formats
- Filtered Detectors frequency-filtered detector data; to ASCII (plain text) format only
- Normalized Detectors normalized detector data; to ASCII (plain text) format only

Currently available data formats are:

- Analyze: used by AFNI, Analyze, and other image processing applications
- **GiD:** a product of the International Center for Numerical Methods in Engineering, which, among other things, provides 3D volume-rendering capabilities that are not part of NAVI
- **ASCII:** can be viewed most text editor (*e.g.*, WordPad) or spreadsheet (*e.g.*, Microsoft Excel) applications

Exporting Data

Take the following steps to complete a specified data export.

- 1. Specify the data you want to export.
- 2. Specify a format from the pull-down menu. For example, select 'Analyze Format'.
- 3. Click the **Export** button to start processing. Should an invalid data format be selected, the following warning message will appear:



If all user specifications are valid, a new pop-up window will appear, that will allow you to specify the starting and ending measurement frames for the time interval that you want to export:

🐓 Specify Time Range for Converting Images 🛛 🛛 🚺
Starting Time Point:
Ending Time Point: 628
OK Cancel

After you finalize your selections by clicking the **OK** button, a progress bar will appear:

🛃 Progress Bar	
5% images converted	

Please be patient while waiting for the conversion and exporting operations to complete, as this process can involve lengthy computations.

After the data conversion and export process has completed a new pop-up window will open, providing information about the location of the output files.



Results Output

Depending on the format and dataset selected, NAVI's automated file manager will save the exported data files into a subfolder named 'Analyze', 'GiD', or 'ASCII'.

Analyze Format

Selection of this format creates a subfolder named 'Analyze', which will contain two files for each time frame in the specified image data set. These new files will have a NAVI-defined file name syntax, a number that identifies the image time frame, and the extensions '.hdr' (header file) and '.img' (image data). For example:

i_n_ f_ + [raw data file name without extension] +# (time frame).hdr

 $i_n _f + [raw data file name without extension] +#(time frame).img$

The following figure shows the example output of Hboxy image files exported into Analyze format:

🖃 🚞 NAVI2p1	i_n_f_keith_Hboxy_000001.hdr	1 KB	HDR File
🚞 doc	i_n_f_keith_Hboxy_000001.img	250 KB	IMG File
🗉 🧰 models	i_n_f_keith_Hboxy_000002.hdr	1 KB	HDR File
🗉 🧰 psrc	i_n_f_keith_Hboxy_000002.img	250 KB	IMG File
🖃 🧰 work	🔤 i_n_f_keith_Hboxy_000003.hdr	1 KB	HDR File
🖃 🚞 left_motor_cortex	i_n_f_keith_Hboxy_000003.img	250 KB	IMG File
Detectors	i_n_f_keith_Hboxy_000004.hdr	1 KB	HDR File
🖃 🚞 Images	i_n_f_keith_Hboxy_000004.img	250 KB	IMG File
🧰 Analyze	i_n_f_keith_Hboxy_000005.hdr	1 KB	HDR File
- ~	i_n_f_keith_Hboxy_000005.img	250 KB	IMG File
	🖾 i_n_f_keith_Hboxy_000006.hdr	1 KB	HDR File
	🖾 i_n_f_keith_Hboxy_000006.img	250 KB	IMG File
	🖾 i_n_f_keith_Hboxy_000007.hdr	1 KB	HDR File
	i_n_f_keith_Hboxy_000007.img	250 KB	IMG File
	🖾 i_n_f_keith_Hboxy_000008.hdr	1 KB	HDR File
	i_n_f_keith_Hboxy_000008.img	250 KB	IMG File
	🖾 i_n_f_keith_Hboxy_000009.hdr	1 KB	HDR File
	i_n_f_keith_Hboxy_000009.img	250 KB	IMG File
	i_n_f_keith_Hboxy_000010.hdr	1 KB	HDR File
	i_n_f_keith_Hboxy_000010.img	250 KB	IMG File

GiD Format

Selection of this format creates a subfolder named 'GiD', which will contain a new file for each time frame in the specified image data set. These new files will have a NAVI-defined file name syntax, a number that identifies the image time frame, and the extension '.flavia.res'. For example:

i_n_ f_+[raw data file name without extension]+#(time frame).flavia.res

It deserves emphasis that to view images in GiD format, a GiD-based FEM mesh folder must be present in the same folder as the exported image files. You can not view the images without their GiD-based FEM mesh even if you can covert them into the files with GiD format. Note that the FEM models in the current brain library do not contain corresponding GiD meshes. Therefore computed images cannot be immediately viewed using the GiD package.

ASCII Format

Selection of this format creates a subfolder named 'ASCII', which will contain a single file in the case of image data, or multiple files in the case of detector data, that has the same file name as the specified data set. These files can be opened and viewed with any standard text-editing (for example, WordPad, Notepad, or Word[®]) or spreadsheet (for example, Excel[®], PSI-Plot, ProStat) application.

6

Data Viewing

Introduction

NAVI provides three viewing modules in its **Data Viewer** portal:

- Detector Time Series Viewer
- Hemodynamic Image Viewer
- Data Processing Info Viewer

You can use these three modules to view, respectively, detector-channel time series, hemodynamic images, and recorded information pertaining to the measurement and to all data processing operations that have been performed so far.



Loading a project-specific dataInfo file will enable those modules for which the corresponding computations have been completed. For example, if you have performed data preprocessing (Chap. 3) but not yet image reconstruction (Chap. 4), then the **Detector Time Series Viewer** and **Data Processing Info Viewer** buttons will be enabled, but **Hemodynamic Image Viewer** will remain "grayed out," as it is in the preceding figure. If image reconstruction has been performed, then after the dataInfo file is loaded the Data Viewer portal will appear as illustrated in the next figure:



As indicated above, if image reconstruction has not yet been completed, the portal will appear as follows after the dataInfo file has been loaded:



The following sections will show you how to use these three modules to view the different NAVIbased data sets and data processing information.

Detector Time Series Viewer

Pressing the **Detector Time Series Viewer** button brings up a new GUI, which allows you to display, edit and export the detector-channel time series. From the pull-down menu highlighted in the following figure, select 'with wavelength dependence data' (the default) to view raw, frequency-filtered, or filtered-and-normalized detector-channel data. Alternatively, select 'with hemoglobin states data' to view time series of one or more hemodynamic variables.



The functionalities provided by the module are:

- Display of time series for an individual detector channel, and its power spectral density (PSD) vs. frequency.
- Simultaneous display of multiple time series for a single channel, and their PSDs; this allows comparisons of different experimental variables (*e.g.*, normalized detector-channel time series at two measurement wavelengths, three states of hemoglobin [Hb]).
- Stacked display of time series for all detector channels, for a single specified variable.
- Colored contour-surface display of time series for all detector channels, for a single specified variable.

In addition, the module offers control functions that allow you to easily:

- Switch to a different display variable (*e.g.*, from raw detector data to normalized detector-data time series, or from deoxy-Hb concentration to HbO₂ saturation);
- Select which specific channel to display;
- Specify the time interval for the currently displayed variable as well as for its PSD estimate;
- Change the scales on all plots (*i.e.*, zoom in/out);
- Reset the plots to their default display settings; save a user-specified time series for later use as, for example, a model function in GLM calculations (see Chapter 8, Feature Extraction).

There are small differences between the GUIs designed for viewing the 'wavelength dependence' and 'hemoglobin states' data categories. As the GUIs contain nearly the same functionalities, we present a detailed description of the wavelength-dependent detector data GUI, and refer to the hemoglobin-state data GUI only to point out the differences between the two.



GUI used for viewing wavelength-dependent detector data.

Selecting a Specific Source and Detector

The components of the **Measurement Geometry** field (upper right corner of the GUI depicted on p. 4) allow you to select a specific channel (*i.e.*, a specific source-detector combination) in order to view its time-dependent signal response.



Source selection

There are two ways to select a source:

- 1. Directly type the source number in the 'Source No:' text field;
- 2. Use the "<<" and ">>" buttons to scroll through the sources. The selected source is identified as a numbered square highlighted in red.

Detector selection

You can select a detector by clicking on one of the numbered squares that diagrams the locations of all optical fibers used for the measurement. The selected detector is highlighted in green.

Alternatively, you can scroll through all the channels' time series in rapid succession, by using the scroll bar found near the bottom of the Measurement Geometry field.

Selecting a Specific Detector Data Set

Wavelength Dependence Data

The components of the **Detector View Option** field (right side of the GUI depicted on p. 4) allow you to select a specific wavelength-dependent data type for viewing.

Detector data type: Use the pull-down menu at the top of the **Detector View Options** field to select raw, frequency-filtered or filtered-and-normalized data for viewing.



Number of viewed wavelength data sets: Use the 'Single Wavelength' and 'Multiple Wavelength' radio buttons in order to view the time series for either a single measurement wavelength or for both wavelengths simultaneously. If you choose the Single Wavelength option, then use the pull-down menu next to the radio button to select a wavelength (see p. 7). If you choose the Multiple Wavelength option, each wavelength's data will be plotted in a different color.



Wavelength specification: As mentioned above (p. 6), if you choose the single-wavelength view, you also need to specify which wavelength to view, from the pull-down menu next to the Single Wavelength radio button.





<u>Hemoglobin States Data</u>

The components in the Detector View Option field (right side of the GUI depicted below) allow you to select a specific hemoglobin-state-dependent data for viewing.

Number of viewed hemoglobin data sets: Use the 'Single Hb State' and 'Multiple Hb States' radio buttons in order to view the time series for either a single hemodynamic variable or for Hboxy, Hbdeoxy and Hbtot simultaneously (the HbO₂Sat variable is not included in the multiple states display; to view HbO₂Sat time series, it is necessary to use the single-state option). If you choose the Single Hb State option, then use the pull-down menu next to the radio button to select a hemodynamic variable. In the Multiple Hb States option, each variable will be plotted in a different color.



Hb state specification: As mentioned above, if you choose the single-state view, you also need to specify which hemodynamic variable to view, using the pull-down menu next to the Single Hb State radio button.





Changing the Time Interval

The detector-data viewer provides two methods for specify a time interval to display.

Specify by Graphics

This choice allows you to graphically specify a time interval by clicking on the 'Specify by Graphics' button. This will enable a set of crosshairs, as illustrated below, that you can move by using the mouse. A time segment is indicated by twice clicking the primary mouse button, the first time to indicate the beginning of the time interval, and the second time to indicate the end of the time interval.



An updated plot of the data time series is produced, as in the following figure. The precise start and end measurement frames for the selected time window are displayed in the 'Time Range (frame)' text field found below the upper plot.



Specify by Typing

You can type the starting and ending time frames directly into the 'Time Range (frame)' text field. Pressing the Enter key will update the display. An example of the use of this method is shown here:


<u>Reset</u>

Press the 'Reset' button in order to restore the starting and ending time frames to their default values (*i.e.*, 1 and the last measurement time frame of the specified data set, respectively), as shown in the following figure:



Rescaling the Amplitude

You can rescale the vertical axes, for both upper and lower sub-figures, by using their respective 'Scale Y-Axis' buttons. By default, each data channel's time series is scaled to its own minimum and maximum values. In contrast, using a Scale Y-Axis button will apply a user-defined scale range to all the channel-based time series plots in the specified data set.



The following is an example of use of the scaling function for upper panel, while use of the scaling function for lower panel is similar.

Step 1: Click the Scale Y-Axis button to open a pop-up window as shown below:

Specify Scales for Upper Figure	
Minimum Value of Amplitude (default is min(the entir -0.0016055	data set)):
Maximum Value of Amplitude (default is max(the ent 0.0010444	e data set)):
	OK Cancel

Step 2: Enter the desired minimum and maximum values for the display range of the vertical axis. For example:

Specify Scales for Upper Figure		×
Minimum Value of Amplitude (default is min(the entir	e data set)):	
-1e-4		
Maximum Value of Amplitude (default is max(the ent	tire data set)):	
1e-4		
	ок	Cancel

Step 3: Click the **OK** button to close the pop-up window. You will see an updated plot, with the new vertical scale limits, in the rescaled sub-figure:

JataView by Hemoglobin States	
File Edit View Insert Tools Window Help Others	
x 10 ⁻⁴ Individual Time Series for the Specified Hemoglobin State(s)	Measurement Geometry
Hboxy	Source No: << 1 >>
	D21 D22 D23 D24 D25 D16 D17 D18 D15 D20 D11 D14 D15 D15 D15
Amp	D6 D7 D8 D3 D10
.1	D1 D2 D3 D4 D5
100 200 300 400 500 600	
Scale Y-Axis Time Range (frame) 1 628 Specify by Graphics Reset	Exclude Undesired Channel
v 10 ⁻¹⁰ The Corresponding PSD Frequency Series	Detector View Options
	Single Hb State Hboxy Multiple Hb States
	Other Views
4	View Group TS Map All TS Corresponding to Upper Figure Data
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1 Frequency (Hz)	Save Time Series in Upper Figure 💌
Scale Y-Axis Scale X-Axis Reset	

Note: You can reset the minimum and maximum values of the vertical-scale range to their default values by typing "auto" in the corresponding text fields, as shown below. In addition, the default vertical scale will automatically be restored if you toggle between the 'Single

Wavelength' and 'Multiple Wavelength' options, or between 'Single Hb State' and 'Multiple Hb States', or if you select a different single wavelength or a different single Hb state.

Specify Scales for Upper Figure		
Minimum Value of Amplitude (default is min(the entir auto	re data set)):	
Maximum Value of Amplitude (default is max(the entire data set)): auto		
	ок	Cancel

Excluding Bad Channels

Sometimes, even after performing detector preprocessing, an experimental data set may still contain data channels that you regard as suspect and would like to exclude from subsequent image reconstruction and feature extraction computations. The detector data GUIs have an 'Exclude Undesired Channel' utility that allows to manually exclude these channels.

Mea	asurement Geor	netry
Sour	e No: << 1	>>
D21	D22 D23	24 D25
D16	D17 D18 D	D20
D11	D12 D13 D	14 D15
D6	D7 D8 D	9 D10
D1	D2 D3 D	4 D5
	x-y viewing 💌	
•		F
Exc	lude Undesired Ch	annel

Clicking on the **Exclude Undesired Channel** button opens a pop-up window that asks you to confirm the decision. Change the "no" default setting to "yes" and click the 'OK' button to start the process.

A Channel Exclution Option	
Do you really want to exclude the channel from the e [yes/no]	xperimental data sets?
20	OK Cancel

After excluding a channel, you will see a redrawn plot of the specified time series, with the message "Bad Channel Detected" overlaid on it. Simultaneously, the dataInfo file will be automatically updated with information related to the exclusion. As an example, the following figure shows the channel with Source 1 and Detector 24 excluded and identified as a bad channel.



Note: The manual exclusion process can not be reversed. Therefore you must be very careful, when using the manual exclusion operation, not to inadvertently exclude a good channel. Note also that the same "Bad Channel Detected" message shown above also appears when you view time series for channels that were excluded by NAVI based on the CV threshold computation.

Other Views

The components in the **Other Views** field (lower right corner of the GUIs depicted on pp. 4 and 8) allow you to view a specified detector data set in a number of different display formats.

Other Views	🗶 Corresponding to Upper Figure Data 💽
	Corresponding to Upper Figure Data
View Group TS Map All TS	Corresponging to Lower Figure Data
Corresponding to Upper Figure Data	
Save Time Series in Upper Figure	in Upper Figure in Upper Figure in Lower Figure

View Group TS

This choice (*i.e.*, view groups of time series) allows you to display a selected number of detector-data time series simultaneously in a stacked format, over any desired interval of time frames. Several controls are provided to allow adjustment of the number of time series displayed and the vertical and horizontal axis scales. An example of application of the **View Group TS** function is shown in the following figure:



<u>Map All TS</u>

This choice allows you to display the specified data set as a contour surface, with time plotted along the x-axis and detector channel along the y-axis. You can change the color scale of the map by using the "Scale Y-Axis" buttons in the upper and lower panels of the parent GUI. An example of application of the **Map All TS** function is shown in the following figure:



Saving a Selected Time Series

This uility allows you to save one or more specific time series, displayed in either the upper or lower sub-figures, into ASCII files with user-defined filenames. This functionality can be useful if you discover an interesting temporal behavior that you want to use subsequently in additional processing steps (*e.g.*, correlation analysis or GLM [see Chap. 8]).

Hemodynamic Image Viewer

The **Hemodynamic Image Viewer** module provides GUIs (a parent and many children) with functionalities for viewing individual Hb-state images and for displaying, editing and exporting selected Hb-state image-pixel time series.

Data Viewer
Load dataInfo From File System 💌
Detector Time Series Viewer with wavelength dependence data
Hemodynamic Image Viewer
Data Processing Info Viewer

The functions for viewing Hb-state images include:

- Display a 2D tiling of an individual 3D hemodynamic image, with a choice of axial, sagittal or coronal views.
- Simultaneous display of mutually orthogonal 2D sections of an individual 3D hemodynamic image.
- Animation of a specified 2D section of an individual 3D hemodynamic image.
- Overlay of 2D sections of a 3D hemodynamic image onto a corresponding MR anatomical image.

In addition, the control functions for viewing Hb-state images allow you to:

- Switch to a different display variable (*i.e.*, a different Hb state);
- Specify the display time interval for single-pixel time series;
- Change the scales on all plots (*i.e.*, zoom in/out);
- Switch to a different view direction (*i.e.*, axial, sagittal or coronal view)
- Change the grid level for display

Click the **Hemodynamic Image Viewer** button to open the parent GUI with its default settings:

- Time (frame): 1
- *Hb State: Hboxy*
- View Direction: Axial View (top to bottom)
- Grid Dimensions: 40×40×40



Selecting a time frame

Select a time frame for image viewing by:

- 1. Entering a number in the 'Time (frame)' field, or
- 2. Using the scroll bar to scroll through the time frames.

For example, typing the number 222 in the 'Time (frame)' text field causes the (default) 1^{st} image in the time series to be replaced with the 222^{nd} image, as shown in the updated GUI below.

	Display Options:	
•	Time (frame):	
	Hb State: Hboxy Axial View (Top to Bottom)	
	Orthogonal View	
	Change Display Grid	
	Rescale Image	
	Create Slice Animation	
	Overlay on MRI Image	
	Click any image slice to allow a pixel-based time series view associated with the selected slice.	



Selecting a Hemoglobin State

Use the 'Hb State:' pull-down menu to specify the hemodynamic variable you wish to view. For example, selecting Hbdeoxy causes the (default) Hboxy image to be replaced with the Hbdeoxy image, as shown in the updated GUI below.







Selecting the View Direction

Below the 'Hb State:' pull-down menu is a second pulldown menu that provides you with the ability to choose which of the three principal axis directions shall be the = line of sight, if a time series of 3D images is being viewed. (If the images are 2D, then the functionality described here will be disabled.) The following figure shows the result after the 'Coronal View (Front to Back)' is selected for the Hboxy images.

> Axial View (Top to Bottom) Axial View (Top to Bottom) Sagittal View (Right to Left) Coronal View (Front to Back)





The corresponding result after selection of 'Sagittal View (Right to Left)' is:



Orthogonal View

The Orthogonal View function allows you to display a specific image in the form of three mutually orthogonal planes that intersect at a single, user-specified point.

Clicking on the **Orthogonal View** button brings up a second image-display window (*i.e.*, a child GUI), in which three mutually orthogonal sections (axial, sagittal, and coronal) through the 3D target medium are displayed. (If the images are 2D, then the functionality described here will be disabled.) The new window contains a set of crosshairs. You can use it to select any point in any of the 2D sections, by clicking with the left/primary mouse button. Upon doing so, a new set of orthogonal 2D sections will be drawn, all intersecting at the user-selected point. The crosshairs will remain active, allowing you to change the intersection point at will, until you press the right/secondary mouse button to disable them.





Changing Display Grid

NAVI employs FEM technology for its time series image reconstructions. Therefore, in order to view these images, it is necessary to interpolate the image values from the (geometrically irregular) nodes of the FEM mesh to a regular 2D or 3D Cartesian grid. We have set up 40x40 (2D Image) or 40x40x40 (3D Image) as the default number of Cartesian grid points per dimension. If you prefer to use a different gridding, the 'Change Display Grid' function allows you to implement the change.

Clicking the **Change Display Grid** button brings up a new dialog window that allows you to set parameters for your display grid.

	Display Options:
	Time (frame): 222
	Hb State: Hboxy
	Orthogonal View
-	Change Display Grid
	Rescale Image
	Create Slice Animation
	Overlay on MRI Image
	Click any image slice to allow a pixel-based time series view associated with the selected slice.

- 1 -	ietDisplayGrid
	Set Parameters for Display Grids
	Select from Grid-Dim Library: 40x40x40
	Generate a new grid, and add It to library:
	X Grid-Dimension 40
	Y Grid-Dimension
	Z Grid-Dimension:
	OK QUIT

Select from Grid-Dim Library

This selection (default) allows you to specify a set of grid dimensions from the existing griddimension library. The available sets of grid dimensions are listed in the pull-down menu that is next to the 'Select from Grid-Dim Library:' checkbox. In the example considered here, there are two sets of grid dimensions for the FEM model: $20 \times 20 \times 20$ and (the default) $40 \times 40 \times 40$.

:DisplayGrid	
Set Parameters f	or Display Grids
Select from Grid-Dim Library:	40x40x40
	40x40x40
Generate a new grid, and add It to libration	rary. Kun
X Grid-Dimension	40
Y Grid-Dimension	40
	1
Z Grid-Dimension:	40
ок	QUIT

Note: The Grid-Dim Library is a group of files that contains pre-calculated parameters associated with different sets of grid dimensions that are used for interpolating an image having an irregular grid (*e.g.*, FEM mesh) onto one with a regular grid. Any FEM model used by NAVI has its own unique Grid-Dim Library that accompanies the model. You can find the library in the same folder location where the FEM model is stored. Whenever parameters for a new set of grid dimensions are specified, the library is automatically updated with the new information, for later use.

Generate a new grid and add it into library

If none of the sets of grid dimensions available in the grid-dimension library meets your requirements, you can generate a new one by through the following steps.

Step 1: Check the 'Generate a new grid and add it into library' checkbox to enable the components for generating a new grid: the **Run** button and the 'X Grid-Dimension', 'Y Grid-Dimension' and 'Z Grid-Dimension' text fields.

🕼 SetDisplayGrid	
Set Parameters for Dis	splay Grids
Select from Grid-Dim Library.)x40x40
Generate a new grid, and add It to library	Run
X Grid-Dimension	40
Y Grid-Dimension	40
Z Grid-Dimension:	40
ОК	QUIT

Step 2: Change the numbers in three text fields to the desired grid dimensions, such as $30 \times 30 \times 30$. (The three numbers do *not* have to all be the same.)

📣 SetDisplayGrid	
Set Parameters for E)isplay Grids
Select from Grid-Dim Library:	40×40×40
Cenerate a new grid, and add It to library	Run
X Grid-Dimension	30
Y Grid-Dimension	30
Z Grid-Dimension:	30
ОК	QUIT

Step 3: Click the **Run** button to start calculation of the interpolation parameters for the specified set of grid dimensions. While the computation is underway, a progress bar will be displayed. Following completion of the computation, the new grid dimensions are exported into the Grid-Dim Library.



Step 4: Select the desired grid from the pull-down menu, for example $30 \times 30 \times 30$.

- 1 S	SetDisplayGrid	<u> </u>
	Set Parameters for Display Grids	
	Select from Grid-Dim Library	
	Generate a new grid, and add It to library	
	X Grid-Dimension 30	
	Y Grid-Dimension	
	Z Grid-Dimension:	
	OK QUIT	

OK or Quit

After you have specified a desired set of grid dimensions, click the **OK** button to close the pop-up window and update the image display GUI. Otherwise, click the **Quit** button to abort the process of selecting a new set of grid dimensions. The figure below shows the updated GUI corresponding to the newly generated $30 \times 30 \times 30$ grid, for the 122^{nd} image in the Hboxy time series, with the Axial View 2D sectioning option.



Changing the Image Color Scale

By default, each image in a time series is independently scaled, with the minimum image value corresponding to the deepest blue color and the maximum image value corresponding to the deepest red. However, you may wish to zoom in on a limited range of image values, and/or enforce a common scale on all images in a time series. The **Rescale Image** function allows you to accomplish either goal.



Clicking on the **Rescale Image** button brings up a pop-up window titled 'Specify Scales for Image View', as shown here:

🛃 Specify Scales for Image View 📃 🗖 🔀
Minimum Value of Amplitude (using "auto" to reset the scale:
-2.2289e-007
Maximum Value of AMPlitude (using "auto" to reset the scale):
2.3435e-007
OK Cancel

The default values in the two text fields are the minimum and maximum image values, across all time frames, for the hemodynamic variable being viewed. You may directly type your desired minimum and maximum values (*e.g.*, -2e-8 and 2e-8) in the text fields. Then click the OK button to update the image view with the new color scale.

📣 Specify Scales for Image View		×
Minimum Value of Amplitude (default is "auto"):		_
Maximum Value of AMPlitude (default is "auto"):		
2e-008		
	OK Cance	

If you subsequently wish to return to the default scaling method, click the Rescale Image button a second time, enter "auto" in both text fields as shown below, and click the OK button.

Specify Scales for Image View	×
Minimum Value of Amplitude (default is "auto"): auto	
) Maximum Value of AMPlitude (default is "auto"):	
auto	
	OK Cancel

Slice-Based Animation View

The Create Slice Animation function allows you to generate an animation showing the temporal evolution of the displayed hemodynamic variable in a selected 2D section of the medium.

Click the **Create Slice Animation** button to activate a set of crosshairs, as illustrated below:





Simply place the crosshairs' intersection point anywhere inside the desired section, and press the primary mouse button to open a pop-up window titled 'Specify Time Range for Creating Movie'.

ovie	×
ОК	Cancel
	ovie OK

The default minimum and maximum values are 1 and the length of image time series, respectively. If you want, you can specify different starting and ending time frames in the text fields. Then click the OK button to show the animation, for the selected 2D section over the specified range of time frames. Note that the animation may play in a continuous loop, but the frame counter stops after one complete cycle.



Overlay on MRI Image

The Overlay function allows you to display a specific NAVI-based image that overlays on an MRI Image template. Currently, NAVI provides this function only for the models included in its brain model library. Otherwise, this function will be disabled.

Click the **Overlay on MRI Image** button to activate a set of crosshairs, then place the crosshairs' intersection point anywhere inside the desired section, and press the primary mouse³ button to open a child GUI for overlaying the NAVI-based image onto a 3D MRI image template.





Automated Anatomical Labeling

The Anatomical Labeling function allows you to label the brain anatomy of a small sphere, whose default radius is 10 mm, centered at a user-specified position.



Pixel Time Series View

Beyond providing a GUI for viewing images one at a time, the NAVI Image View module also provides a GUI for viewing the temporal evolution of hemodynamic variables in selected image pixels.

Place a mouse cursor on one of the 2D image sections in the View Hemodynamic Images parent GUI and click the primary mouse button. This action will open a child GUI similar to the one used for viewing detector-channel Hb-state time series. The default pixel has (x,y) coordinates (20,20) on the specified slice. In the example shown below no time series is displayed, because the default pixel coordinates lie outside the <u>boundaries</u> of the model used for image reconstruction.





The principal difference between the Detector View and Image Pixel View GUIs is that in the former the source-detector geometry map is replaced by a small reproduction of the selected 2D section, with controls for specifying which pixel's time series (and corresponding PSD) to display:



Detail from Detector Time Series Viewer GUI

Detail from Hemodynamic Image Viewer GUI

Specify Pixel by Graphics

This function allows you to specify the display pixel in the selected slice. Click the **Specify Pixel by Graphics** button to activate a set of crosshairs. Place the crosshairs over any pixel of the selected image slice in the upper right corner of the GUI.



Next, click the primary mouse button to display the chosen pixel time series and its PSD. The following example shows these plots for a selected pixel, whose coordinates are (26,19,23). As shown in the figure below, the location of the chosen pixel is labeled with a small white square in the image section.



As an alternative to the 'Specify Pixel by Graphics' crosshairs, the user can enter the coordinates of a pixel directly into the 'Specify ROI (X, Y)' field.



As in the detector-channel display case, the image-pixel GUI allows you to produce a simultaneous display of multiple hemoglobin states, for one pixel at a time. The following figure shows an example of this capability.



Note: A difference from the detector-channel display case is that the image-pixel child GUI does not allow you to switch from one Hb state to another when the 'Single Hb State' radio button is checked. To view time series for a different Hb state, you must return to the parent GUI.



Data Processing Info Viewer

The **Data Processing Info Viewer** module provides a GUI with the functionalities for displaying information that has been previously recorded in a dataInfo file.





<u>Outline</u>

This shows you an outline of the dataInfo file contents, which includes: the imager type and experimental data group name; a listing of which data processing steps have and have not, so far, been performed; and the folder path and name of the dataInfo file. Clicking on the **Outline** button brings up a temporary text file called 'diary', containing the desired information. The figure below shows an example of output file produced by this function.

🖟 diary - Notepad	\mathbf{X}
File Edit Format View Help	
USER SPECIFIED dataInfo FILENAME IS: keith_dataInfo.mat	^
USER SPECIFIED VIEW OPTION IS: Outline View	
INTRODUCTION: THE CONTENTS DISPLAYED IN THE TEXT FILES ARE EXTRACTED FROM THE USER_SPECIFIED dataInfo file ACCORDING TO THE USER_DEFINED VIEW OPTION, IN WHICH, 1. Imager Type : 1 - Breast; 3 - Rat; 4 - Limb; 5 - Baby; 6 - Phantom; 7 - Pigs 2. Data Type : 1 - Detector Data; 2 - Image Data 3. Hemoglobin State : 1 - Hboxy; 2 - Hbdeoxy; 3 - Hbtot; 4 - HbO2Sat	;
DESCRIPTION: The Outline View option provides users the general information stored in the user-specified dataInfo file that has been created during the application of the NAVI Software Package.	
Beginning of Search Results	
dataInfo =	
ImagerType: 1 BatchProcessing: 0 FilteringProcessed: 1 CVProcessed: 1 ReconstructionProcessed: 1 PCA_SavedResults_N: 0 MSA_SavedResults_N: 0 GLA_SavedResults_N: 0 COD_SavedResults_N: 0 COLS_SavedResults_N: 0 COLS_SavedResults_N: 0 COLS_SavedResults_N: 0 COLS_SavedResults_N: 0 BADS_SavedResults_N: 0 Area_SavedResults_N: 0 BADS_SavedResults_N: 0 RawDataInfo: [1x1 struct] Reconstruction: [1x1 struct] dataInfo_file: [1x52 char]	
dataInfo_file =	
C:\NAVI2p1\work\left_motor_cortex\keith_dataInfo.mat	
Find of sourch Deculty	
	×

The meaning or significance of the items included in this window is:

"ImageType: 1" – the target medium was a human brain
"FilteringProcessed: 1" – the detector data have been frequency filtered.
<i>"CVProcessed: 1" – baseline CVs have been calculated, and have been used to exclude</i>
noisy data channels from further processing
"NormalizationProcessed: 1" – the detector data have been normalized
"ReconstructionProcessed: 1" – hemoglobin-state images have been reconstructed
"PCA_SavedResults_N: 0" – no recorded results for PCA (Principal Component Analysis)
"MSA_SavedResults_N: 0" – no recorded results for MSA (Molgedey-Schuster Analysis)
"ICA_SavedResults_N: 0" – no recorded results for ICA (Independent Component Analysis)
"GLM_SavedResults_N: 0" – no recorded results for GLM (General Model Method)
"RawDataInfo: $[1 \times 1 \text{ struct}]$ " – data structure used to store raw data information
"PreProcessing: $[1 \times 1 \text{ struct}]$ " – data structure used to store data preprocessing information
"Reconstruction: $[1 \times 1 \text{ struct}]$ " – data structure used to store image reconstruction information
"dataInfo_file: $[1 \times 52 \text{ char}]$ " – a string used to identify the name and location of the dataInfo file

<u>Raw Data</u>

Activation of this function displays information pertaining to the quantity of data collected and the measurement rate: how many wavelengths, source fibers, and detector fibers were used; total number of time frames, and number of frames per second; the folder path and names of the DYNOT-generated files in the experimental data group. Also identifies the geometry model used for image reconstruction, and contains a table indicating which optical fibers were used as both a source and a detector, and which were detector-only. Click the **Raw Data** button to get the following information:

📕 diary - Notepad	
File Edit Format View Help	
USER SPECIFIED dataInfo FILENAME IS: keith_dataInfo.mat	^
USER SPECIFIED VIEW OPTION IS: Raw Data Info	
INTRODUCTION: THE CONTENTS DISPLAYED IN THE TEXT FILES ARE EXTRACTED FROM THE USER_SPECIFIED dataInfo FILE ACCORDING TO THE USER_DEFINED VIEW OPTION, IN WHICH, 1. Imager Type : 1 - Brain; 2 - Breast; 3 - Rat; 4 - Limb; 5 - Baby; 6 - Phantom; 7 - 2. Data Type : 1 - Detector Data; 2 - Image Data 3. Hemoglobin State : 1 - Hboxy; 2 - Hbdeoxy; 3 - Hbtot; 4 - Hbo2sat	Pigs
DESCRIPTION: The Raw Data View option provides users the Raw Data information stored in the user-specified dataInfo file that has been generated during the first use of the NAVI Software Package for a particular user-specified measurement.	=
Beginning of Search Result5	
<pre>SamplingRate: 2.1500 waveLength_N: 2 source_N: 25 detector_N: 25 channel_N: 650 time_point_N: 628 raw_data_files: {4x1 cell} source_detector_key: [25x2 double] gain_setting_file: 'c:\NAVI2p1\work\left_motor_cortex\keith.set' ModelFilePath: 'c:\NAVI2p1\models\brains\Left_Motor_cortex\S25D25\'</pre>	

\diamond raw_data_files: shows the location and the file names for wavelength-dependent Raw Data sets.	
'C:\NAVI2p1\work\left_motor_cortex\keith.wl1' 'C:\NAVI2p1\work\left_motor_cortex\keith.wl2' 'C:\NAVI2p1\work\left_motor_cortex\keith.set' 'C:\NAVI2p1\work\left_motor_cortex\keith_config.txt'	
\diamond source_detector_key: shows the relationship between detector-index and source-index.	
D-Index S-Index 1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 11 11 12 12 13 13 14 14 15 15 16 16 17 17 18 18 19 19 20 20 21 21 22 22 23 23 24 24 25 25 End of Search Results	

Preprocessing

This displays information pertaining to the frequency-filtering and normalization operations applied to the detector data: filter type, cutoff frequency, width of roll off, and size of filter window; the threshold for the baseline CV computation; the reference signal used for normalization; the folder path and names of the NAVI-generated processed detector-data files. Also contains a table indicating which source-detector combinations are excluded from subsequent processing steps. Click the **Preprocessing** button to display the following information.

```
📕 diary - Notepad
                                                                                                                                                                          File Edit Format View Help
                                       USER SPECIFIED dataInfo FILENAME IS: keith_dataInfo.mat
                                       USER SPECIFIED VIEW OPTION IS: PreProcessing
INTRODUCTION: THE CONTENTS DISPLAYED IN THE TEXT FILES ARE EXTRACTED FROM THE USER_SPECIFIED
dataInfo FILE ACCORDING TO THE USER_DEFINED VIEW OPTION, IN WHICH,
1. Imager Type : 1 - Brain; 2 - Breast; 3 - Rat; 4 - Limb; 5 - Baby; 6 - Phantom; 7 - Pigs
2. Data Type : 1 - Detector Data; 2 - Image Data
3. Hemoglobin State : 1 - Hboxy; 2 - Hbdeoxy; 3 - Hbtot; 4 - Hbo2Sat
DESCRIPTION: The Preprocessing view option provides users the Detector Preprocessing information stored in
the user-sepcified dataInfo file that has been generated during the use of Filter Data and
Normalization Modules.
 -----Beginning of Search Results------
PreProcessing:
     SetFilterParameterProcessed: 1
filter_parameters: [1x1 struct]
filtered_data_file: [1x55 char]
goodChannels: [650x5 double]
good_channel.index: [1x596 double]
CV_parameters: [2x650 double]
normalized_data_file: [1x57 char]
          stilter_parameters: shows the user-defined parameters used for the detector preprocessing.
     filter_type: {'BAND_PASS'}
SamplingRate: 2.1500
cutoff_frequency: [0.0200 0.3000]
widthdrop; [15 15]
cv_threshold: 25
Cv_baseline_segment: [2x1 double]
normalization_type: 3
baseline_segment: [2x1 double]
detrend_option: 0
detrend_option: 0
              detrend_params: []
filter_length: 100
Asseline time segments selected in frames (columns 1&2) and in seconds (columns 3&4)
baseline segment =
       1 54
                       0
                                25
ormalized_data_file: shows the location and file name for the filtered-normalized detector data sets.
C:\NAVI2p1\work\left_motor_cortex\Detectors\n_f_keith.NAV
<> goodChannels: shows the useful information for source-detector channels used for the experiment.
                      C-all C-good C-flag
                D
1
                                            11111
       1111
                          67
                 6
                                   5
                 8
                          89
       1
1
                                   89
               10
                        10
                       617
               17
     589
590
591
592
593
594
595
596
0
0
                                            111111
               18
19
20
21
22
23
24
25
26
                       618
619
620
621
622
623
624
625
0
                                             000
                       -----End of Search Results-----
```

Reconstruction

This displays information related to the process of image reconstruction from the detector data: the number of images reconstructed, and the starting and ending time frames; dimensions of the interpolation grid; the number of singular values retained and the corresponding cumulative percentage of the singular-value sum. Also contains a table indicating the minimum and maximum values, over all time frames and FEM mesh nodes, of the reconstructed hemodynamic variables.

```
📕 diary - Notepad
                                                                                                                                                                             File Edit Format View Help
                                         USER SPECIFIED datainfo FILENAME IS: keith datainfo mat
                                        USER SPECIFIED VIEW OPTION IS: Reconstruction
INTRODUCTION: THE CONTENTS DISPLAYED IN THE TEXT FILES ARE EXTRACTED FROM THE USER_SPECIFIED
dataInfo FILE ACCORDING TO THE USER_DEFINED VIEW OPTION, IN WHICH,
1. Imager Type : 1 - Breain; 2 - Breast; 3 - Rat; 4 - Limb; 5 - Baby; 6 - Phantom; 7 - Pigs
2. Data Type : 1 - Detector Data; 2 - Image Data
3. Hemoglobin State : 1 - Hboxy; 2 - Hbdeoxy; 3 - Hbtot; 4 - Hbo2Sat
DESCRIPTION: The Reconstruction View option provides users the Image reconstruction information stored in the user-specified dataInfo file that has been generated during the use of Reconstruction Module.
 Reconstruction:
                                       image_N: 628
StartTimePoint: 1
EndTimePoint: 628
     EndTimePoint: 628

maxTimePoint_N: 512

repeating_N: 1

restTimePoint_N: 116

NodeCoordinate: [5460x4 double]

TSVD_N: 54

sv_CP_used: 97

imageScale: [6x2 double]

reconstructed_img_file: {1x4 cell}

Grid_Lib_N: 1

SetReconstructionParameterProcessed: 1

ModelGeometrySize: [3x2 double]
                                  ModelGeometrySize: [3x2 double]
  *****
imageScale: shows the minimum and maximum values for Hboxy and Hbdeoxy image series.
        Min
                              Мах
 -1.9785e-007
                    2.571e-007
 -1.5673e-007 1.7871e-007
-1.2052e-007 1.8791e-007
0.6817 0.6943
  -0.00033808 0.00040142
-0.00030587 0.00046487
 ModelGeometrySize: shows the minimum and maximum cordinates for model geometry.
Min(cm)
12.7376
                    Max(cm)
                    21.0186 23.4385
   28478
 3.28478
17.4028
                     25.2932
 reconstructed_img_file: sthe loacation and the file names for Hboxy and Hbdeoxy image sets.
       'C:\NAVI2p1\work\left_motor_cortex\Images\i_n_f_keith_hboxy.NAV
'C:\NAVI2p1\work\left_motor_cortex\Images\i_n_f_keith_hbred.NAV
'C:\NAVI2p1\work\left_motor_cortex\Images\i_n_f_keith_wll.NAV'
'C:\NAVI2p1\work\left_motor_cortex\Images\i_n_f_keith_wl2.NAV
                          -----End of Search Results-----
```

<u>Block Average Data</u>

The **Block Average Data** push button, combined with the data type option, is designed to display information related to the results derived from **Data Generation** module in the **Data Analyzer** portal. You can get the desired information presented in a text file called "diary" by clicking the Block Average Data button. You can also find a similar operation that achieves the same goal in the Data Generation module (see Chapter 7: Block Averaging).

<u>Multivariate Analysis</u>

The **Multivariate Analysis** push button, combined with its analysis-option function (PCA, MSA, ICA and GLM), is designed to display information related to the results derived from the **Multivariate Analysis** functions in the **Data Analyzer** portal. Click the Multivariate Analysis button to get the specified information. You can achieve the same goal by using a similar function built into the Multivariate Analysis module (see Chapter 8: Feature Extraction).

Spectral Analysis

The **Spectral Analysis** push button, combined with its analysis-option function (PSD, CSD, Cross Correlation and Coherence), is designed to display information related to the results derived from the **Spectral Analysis** functions in the **Data Analyzer** portal. Click the Spectral Analysis button to get the specified information. You can also achieve the same goal by using a similar function built into the Spectral Analysis module (see Chapter 8: Feature Extraction).

<u>Event Analysis</u>

The **Event Analysis** push button, combined with its analysis-option function (Slope, Time Delay, Area under the Curve), is designed to display information related to the results derived from the **Event Analysis** functions in the **Data Analyzer** portal. Click the Event Analysis button to get the specified information. You can also achieve the same goal by using a similar function built into the **Event Analysis** module (see Chapter 8: Feature Extraction).

Block Averaging

Introduction

This section describes how to generate block-averaged data sets, using tools and modules built into the **Data Analyzer** portal of NAVI. Note that even if you do not want to block-average a given set of time series, it is necessary to carry out the following sequence of steps in order to enable use of the functionalities in the **Feature Extraction** module (Chapter 8).

Data Analyzer
Load dataInfo From File System 💌
Data Type Specification
Data Generation Get Dataset for Analysis
Feature Extraction Multivariate Analysis
Set Parameters for PCA

Step 1: Click the **Load dataInfo** button in the Data Analyzer portal, then specify and load a dataInfo file. This action will enable the **Get Dataset for Analysi**s button.

Load dataInfo
Data Type Specification
Image 💽 Hboxy 💽
Data Generation
Get Dataset for Analysis
Feature Extraction
Feature Extraction Multivariate Analysis
Feature Extraction Multivariate Analysis

Step 2: Specify a data type in the **Data Type Specification** panel, using the pull-down menus illustrated in the following figure, before attempting to generate block-average data.



Step 3: Click on the **Get Dataset for Analysis** button in the **Data Generation** panel, which will open the dialog window illustrated in the following figure. Specify the time range of interest (units are measurement frames), whose default value is the entire time period for the specified data set.

🛃 Specify time frame rang for data generation 🔳 🗖 🔀
Starting time (frame):
a
Ending time (frame):
628
OK Cancel

Following this, click on the OK button in order to open a data-type-dependent child GUI (examples are shown in the following section). The child GUI contains functionalities that allow you to view the specified original data and to define, confirm and save new, block-averaged data sets that can be used for further feature extraction.
GUI for Image Selection

Illustrated below is the GUI that is associated with selection of the 'Image' data type. In this figure, colored rectangles are used to delineate the major components of the GUI, which are described in the following pages.



View the original information: The components in the RED region are designed to allow you to view information associated with original data set and with the block segments that you will specify. The figure on the right side is the FEM model used for image reconstruction. The figure on the left side contains a plot of the spatial mean time series (amplitude vs. time) of the selected hemodynamic variable, averaged over the originally specified data set.

Define a new block average data set: The components in the YELLOW region are designed to specify the parameters (*e.g.*, starting time, ending time, block size) of a new block-averaged data set. Three methods are provided for you to define the new block average; use the three radio buttons to select the method that you want to use. The default option is **Type through Keyboard**, with a single block segment, defined as the entire time series, specified.

Specify and view an existing block average data set: The components in the GREEN region allow you to examine and view any previously generated and saved block-average results.

View, save and confirm a block average data set: The components in the BLUE region are designed to view, save or confirm a desired block average for uses of further data analysis. Initially, the plotted curves in the blue and red regions are the same; this is a consequence of the default setting described above (*i.e.*, one block segment, consisting of the entire time series).

Methods for Specifying Parameters of a New Block Average Data Set

NAVI provides three options for block average specification through three radio buttons, which are

- Type through Keyboard
- Specify through Event File (.evt)
- Specify Graphically Using Mouse

Each of these is appropriate to certain circumstances and experimental protocols, and you will select the one that fits your needs.

Type through Keyboard

This option is designed primarily for the case where a stimulus is repeatedly applied or a task is repeatedly performed during the course of a measurement, with a fixed time course and amplitude for all repetitions. The derived block-average data is the average of all applied stimulus or task episodes.

Please take the following steps to generate a block average data set:

- 1. Select the time unit using the pull-down menu located in the same row as the **Type through Keyboard** radio button. In the example shown on p. 3, the specified time unit is 'seconds'.
- 2. Type a string with format 'starting_time: time_ interval: ending_time' in the text field next to the time-unit pull-down menu. For example, '25:31:289' means that, starting at 25 seconds and ending at 289 seconds, sequential 31-second time intervals are marked off.
- 3. Press the **Enter** button on your keyboard to start the block averaging computation.

The following figures show the results for the preceding block average generation, which is based on a experimental data set collected by a UTA research group led by Dr. Hanli Liu.



The figure below shows the same result with time expressed in units of frames.



Specify through Event File (.evt)

This option is designed primarily for the case where the stimuli applied during a measurement session have been recorded in a DYNOT- or NIRScout-based event file during data collection with the following format:

frame no	pin1	pin2	pin3	pin4	pin5	pin6	pin7	pin8
54	0	0	1	0	0	0	0	<pre>0 Event starts with 1 in pin3 0 continue</pre>
56	1	0	0	0	0	0	0	
121	1	0	0	1	0	0	0	<pre>0 Event ends with 1 in pin4</pre>
121	0	0	1	0	0	0	0	0 Event starts with 1 in pin3
123	1	0	0	0	0	0	0	0 continue
188	0	0	0	1	0	0	0	0 Event ends with 1 in pin4
188	0	0	1	0	0	0	0	0
120	1	0	0	0	0	0	0	0
255	1	0	0	1	0	0	0	
255	0	0	1	0	0	0	0	
157	1	0	0	0	0	0	0	
322	1	0	0	1	0	0	0	
322	0	0	1	0	0	0	0	
224	1	0	0	0	0	0	0	
389	0	0	0	1	0	0	0	
389	1	0	0	0	0	0	0	
391	1	0	1	0	0	0	0	
456	0	0	0	1	0	0	0	
456	1	0	1	0	0	0	0	
458	1	0	0	0	0	0	0	
523	0	0	0	1	0	0	0	0

Please take the following steps to generate a block average data set:

- 1. Specify the time unit using the pull-down menu described above.
- 2. Select the **Specify through Event File (.evt)** radio button to bring up a new window, which displays the spatial mean time series over the originally specified data set, with the starting and ending times of the block segments extracted from the event file indicated. The same window also shows the values of the block segments in a text field. You may add, delete or modify the extracted block segments in the edit text field, if necessary.
- 3. Click the **Finish** button to start the process of block average data generation. After a successful completion, a new block average data set with the defined block segments will replace the previous one to be shown on the main GUI.

The examples presented below illustrate the preceding process for a block-average generation derived from an experimental data set and a manually generated event file.





Specify Graphically by Mouse

This option is designed primarily to allow you to define arbitrary block segments. The sequence of steps to follow in order to use this option are:

- 1. Specify the time unit using the pull-down menu described above.
- 2. Select the **Specify Graphically by Mouse** radio button to bring up a new user interface, which provides the functions and tools for you to specify, edit or clear block segments.
- 3. Click the **Finish** button to start the process of generating the specified block-average data. After successful completion, a new block-average data set with the defined block segments will replace the one previously displayed in the main GUI.

The examples presented below illustrate the preceding process of block-average data generation associated with a deoxyHb image time series derived data collected from a dynamic human head phantom.



The default main GUI for the specified dataInfo file, with deoxyHb images selected.





How to View a Block-Average Result

There are two ways to view a block-average result, using the functions in the **Block Average Results** section of the GUI.

1. View the spatial mean block-average result (default option), as shown below.



2. View either the individual images in the block-average result, or the mean image averaged across the entire block. Use the pull-down menu next to the **View** button to select an option, as illustrated in the following figure:



Clicking on the **View** button with the **Individual Block Average Image** option selected brings up the following child GUI:





Similarly, clicking the **View** button with the **Temporal Mean of Block Image** option selected brings up the following GUI:



How to View Previously Generated Block-Average Results

Existing Block Average Results
View Existing Block Averaged Results Graphically
Parameter Info O View Result 1 Note: 1 saved result is determined.

NAVI automatically determines and displays the number of existing (*i.e.*, previously generated) results whenever you launch the **Data Generation** GUI. If saved previously generating results are found, a text note will tell you how many such results there are.

To view previously generated results, select either the **Parameter Info** or **View Results** radio button, and type a desired result number in the text field next to the **View Result** radio button. If **Parameter Info** is selected, then clicking on the **View Existing Block Average Results** button opens a new text file that contains the information regarding the parameter settings for all existing **Block Average Results**, including the one you have specified. If **View Result** is selected, clicking on the **View Existing Block Average Results** button displays the specified existing block average result in the main GUI.

How to Confirm and Save a Block-Average Result



For a newly generated block-average result, 'Not Save' is NAVI's default setting. If you prefer to save the result into the local NAVI database, you should select 'Save' instead of 'Not Save'. Then the results will be automatically saved, and the relevant components on the main GUI will be updated to show the changes. You can view any saved results as described above.

If you want to use a block-average data set for further data analysis (*e.g.*, for correlation analysis or GLM, as described in Chap. 8), simply click on the **Confirm** button shown in the upper right corner of the preceding figure. This will automatically close the main Block Average Images Generator GUI, and will enable the **Feature Extraction** modules. A previously generated block-average result also can be confirmed for use with the feature-extraction modules. Note that it is not necessary to save a block-average data set in order to confirm it.

GUI for Detector Selection

If you select 'Detector' in the **Data Type Specification** module (see p. 2), clicking on the **Get Dataset for Analysis** button brings up the following GUI:



The GUI for detectors is similar to one for images, but it has some important differences.

Difference 1: In the upper right corner, the **FEM Model** image is replaced by **S-D Geometry** and a display of the detector array. Using the tools in the S-D Geometry module (the slider, detector buttons and the text field, whose operations are the same as those described in Chap. 6), you can view the time series associated with any source-detector pair by clicking on the numbered buttons to specify a detector and typing a source number in the text field, or by moving the slider.

Difference 2: In the **Block Average Results** panel, the functions used for image viewing have been replaced by ones used for a generating colored contour surfaces that summarize the detector responses (see p. 17). The differences between the image and detector **Block Average Results** panels are illustrated in the following figures:

Functions for detector view

Functions for image view



The following figure shows a block-average result for the specified detector data set, using the same block parameters as were used for the corresponding image data.



Block average time series related to source 1 and detector 13, based on the specified block segments.



View Block Average Detector Map with a single source (Source 1) specified

View Block Average Detector Map with all sources (*i.e.*, averaged across all source locations)





Feature Extraction

Introduction

The current NAVI package has three **Feature Extraction** modules (*i.e.*, Multivariate Analysis, Spectral Analysis and Event Analysis) that apply mathematical functions to a user-defined block-averaged data set in order to extract its intrinsic features. They become enabled only after you confirm a user-defined block-average data set through the GUI of the **Data Generation** module.

You can access each of these modules through the **NAVI** main screen, as shown here.

Feature Extraction	Multivariate Analysis
Set Parameters Multivariate Analysis	E vent Analysis
Start PCA 💌	

Multivariate Analysis: This module provides a suite of functionalities—PCA, MSA, ICA and GLM. You can use them for estimating the number of distinct physiological rhythms or event-related responses, and for determining their spatial distributions, within a specified set of time series data.

Spectral Analysis: This module provides a suite of functionalities—PSD, CSD, Coherence, and Cross Correlation. You can use them for identifying the frequency structure of a specified set of time series data, and for determining the spatial distributions of spectral features.

Event Analysis: This module provides a suite of functionalities—Slope, Time Delay and Area under Curve. You can use them for identifying the rate and magnitude of event-related responses in a set of time series. These types of information are important in, for example, studies of functional connectivity between different regions of tissue.

Multivariate Analysis



The "Multivariate Analysis" module contains three components:

- Function Specification (a pull-down menu)
- Set Parameters for (a push button)
- **Start** (a push button)

Function Specification

Use the pull-down menu to specify an operation, which can be PCA, MSA, ICA, or GLM.

PCA — This function performs principal component analysis (PCA) on the specified data set or on a user-specified subset of the data. The displayed results include the time courses and spatial distributions of the derived principal components.

MSA — This function takes a user-selected subset of principal components as its input, and then performs an extended temporal decomposition, with the algorithm of Molgedey and Schuster (M-S). The displayed results include the time courses and spatial distributions of the derived M-S components.

ICA — This function is still under construction. We will notify you when an upgraded NAVI version containing this functionality becomes available.

GLM — This function performs a general linear model (GLM) computation on the user-specified data set or subset, with any number of user-specified model functions in the design matrix. The GLM module automatically supplements these models with terms that account for constant offsets and linear and quadratic trends (drifts) in the data. The displayed results include the model functions and the spatial distributions associated with the corresponding GLM coefficient, t-statistics and p-values, and percentage of variance accounted for.

Setting Parameters

Clicking on the Set Parameters button	brings up a new	GUI window.	You can use it for	setting values of
control parameters.				

SetSSAParameters	
Set Parameters for Multivariate Analysis	
Specify Parameters for PCA, MSA and ICA	
Number of PCA (ICA) Components for Generating: 30 Spatial ICA C Temporal ICA	
Number of PCA (ICA) Components for Displaying: 6 ICA Algorithm: Informax	•
Select PCA Components for MSA: 123456 Max Number of ICA Training Steps: 1024	-
Specify Model Function for General Linear Modelling	
• Use Spatial Average of Specified Data as Model Function	
C Use User-defined Model Function	
Save & Exit Exit Without Saving	

This window contains two panels with the labels:

- Specify Parameters for PCA, MSA and ICA
- Specify Model Function for General Linear Modeling

Here we describe how you can use each of the preceding feature extraction methods.

Specify Parameters for PCA, MSA and ICA

The parameters in this panel define functions for PCA, MSA and ICA

- Number of Principal (Independent) Components to Generate
- Number of Principal (Independent) Components to Display
- Select PCA Components for MSA

Specify Parameters for PC	A, MSA and ICA
Number of PCA (ICA) Components for Generating: 30	Spatial ICA C Temporal ICA
Number of PCA (ICA) Components for Displaying: 6	ICA Algorithm: Informax
Select PCA Components for MSA: 123456	Max Number of ICA Training Steps: 1024

The first user-specified parameter is the number of principal components you want to calculate (and save). The default value is 30 and the theoretical maximum value is either the number of data time frames, or the number of FEM mesh nodes (for image data) or good detector channels (for detector data), whichever is smaller. You can replace the default setting by typing a desired number in the text edit field provided.

The second user-specified parameter is the number of principal components you want to display. The default value is 6, and the maximum permitted value is the number of components defined by the first parameter. You can replace the default setting by typing a wished number through the provided text edit.

The third parameter pertains only to MSA computations. The number in this field is the subset of principal components to use as the starting point for the MSA procedure. The default setting is [1 2 3 4 5 6], which means that MSA will use the first six PCs as input for further decomposition. You can pick any desired subset of PCs, such as [1 3 5] or [2 3 10 11]. However, the number of entries in this field cannot be larger than the number specified in the "Number of Components" parameter field. You should also avoid any repeated selections.

The parameters shown in the right-side column pertain only to ICA computations. The ICA module is still under construction, and the user's guide will include information on its use once an upgraded NAVI version with the ICA utility is available.

Specify Model Function for General Linear Modeling

You can use this panel to define a model function for GLM. Two methods are available for specifying a model function.

- Use Spatial Average of Specified Data as Model Function (default)
- Use User-defined Model Function



The first choice means that you select the spatial mean time series as the model function for the GLM computation. Unselecting and then reselecting the Use Spatial Average of Specified Data

as Model Function radio button opens a pop-up window in which the spatial mean time series is plotted. An example of this is shown in the figure below.



Checking the **Use User-Defined Model Function** radio button allows you to load other model functions, which should satisfy the following rules:

- The model functions and the specified data set should have same number of time frames, if they have the same sampling rate.
- Save the models in an ASCII-format file, with each column constituting one model function.

Once the user-defined model function is ready, check the Use User-Defined Model Function radio button in order to open an additional panel, shown below, in the Specify Model Function for General Linear Modeling GUI. The additional edit text fields allow you to specify the model function sampling rate and the number of data columns in the external file.

Specify Model F	Function for General Lin	ear Modelling				
O Use Spatial Average of Specified I	C Use Spatial Average of Specified Data as Model Function					
Use User-defined Model Function						
Load Model Function	with Sampling Rate:	2.15				
	with Model Number:	1				

Clicking on the **Load Model Function** button brings up a browser window that allows you to navigate to the folder containing the user-defined model function file. You will be able to view



the user-defined model function(s) after the file is loaded, as in the example shown in the figure below.

<u>Save & Exit</u>

Click on the **Save and Exit** button to commit to all settings you have made and to close the **Set Parameters for Multivariate Analysis** window with all parameters saved into a temporary file found in the current working space.

Note: You can start the **Set Parameters** operation before or after you specify which featureextraction method you wish to perform. But you must use **Set Parameters** at least once for each dataInfo file that you load. Otherwise, NAVI will automatically stop and the Help Dialog message shown below will pop open, to remind you of this requirement.



Exit without Saving

Click on the **Exit without Saving** button to abandon all parameter settings you have made and to close the **Set Parameters for Multivariate Analysis** window without making any changes to the working project and its dataInfo file.

Starting PCA

Selecting the "PCA" through the pull-down window in the **Feature Extraction:** Multivariate Analysis module, and then clicking on the **Start** button, brings up the following user interface for PCA.

🛃 startDataAnalysis	
PCA Analysis	_
View Existing Results	
Parameter Info C Result 0	
Note: 0 result is determined.	
Get a New Result]
Next result is labeled as	
Not Save	
Quit	_

You can use the interface to view previously generated PCA results associated with the specified project, or to compute a new PCA result from the confirmed block-average data set. You can choose whether or not to save the new result, by checking the appropriate radio button before starting the process. (Note that "Not Save" is the default.) NAVI automatically labels each results file with a numerical index that increases by a single unit after each computation. However, you can manually set the numerical index value for a new results file. If the number that you type in the "Next result is labeled as" field matches the number assigned to a previously created file, then the new file will overwrite the old one.

After clicking on the **Get a New Result** button, a progress-bar window will pop up, and will track the computational progress. When PCA concludes successfully, the progress bar will automatically close, and two figures will pop open to present the PCA results. The first figure shows the:

- Position-dependent temporal mean (left top sub-figure)
- Time-dependent spatial mean (right top sub-figure);
- Singular value spectrum (left bottom sub-figure);
- Cumulative percentage of singular values (right bottom sub-figure).



The second figure includes thumbnail images of:

- The time courses of the computed principal components that you chose to display (top row)
- The spatial distributions of the computed principal components (the second row)



Clicking on one of the thumbnail images in the first row causes another figure to pop open, displaying an enlarged plot of the selected time series.

Click one of the figures in the second row to bring up an image-viewer GUI, which is similar to the one used for viewing the reconstructed hemoglobin images, with a few components disabled in the **Display Options** field. In addition, you can find identifying information in the title bar of the GUI. The example reproduced below, for instance, is the time series and spatial distribution for Principal Component 1.







If you have checked the "Save" radio button in the PCA Analysis GUI, NAVI's file manager will automatically record the PCA process into the corresponding dataInfo file and save the result in its tree structure.

The following is an example of the output-file tree structure with three PCA results recorded for the data set described in the previous chapters.



Starting MSA

Select "MSA" in the pull-down window in the **Feature Extraction:** Multivariate Analysis module, and then click the **Start** button to bring up the **MSA Analysis** user interface.

🛃 startDataAnalysis	
MSA Analysis	
View Existing Results	
Parameter Info C Result 0	
Note: 0 result is determined.	
Get a New Result	
Next result is labeled as 1	
Not Save	
Quit	

The procedure for performing MSA, and the output produced, are fully analogous to those for PCA.

Similarly, if the "Save" option is checked in the **MSA Analysis** interface, the project file structure will have an MSA sub-folder under the AnalyzedResults folder, as in the following example:



Starting GLM

Select "GLM" through the pull-down window in the **Feature Extraction:** Multivariate Analysis module, and then click the **Start** button to bring up the **MSA Analysis** user interface.

🤣 st	artDataAnaly	sis			
		GLM /	Analysi	is	
		View Exis	ting Resul	ts	
	۲	Parameter Info	C Result	0	
		Note: 0 result is d	etermined.		
				1	
		Get a N	lew Result		
		Next result is labeled as	S	1	
		Not Save		C Save	
		Qu	ıit		

As in the cases of PCA and MSA, you can either view previously generated GLM results, or compute a new one using the **GLM Analysis** interface. After clicking on the **Get a New Result** button, a progress bar pops open during the GLM process, and indicates the computational progress.

A successfully completed GLM application will produce one GUI that contains the following results:

- Model function(s) (Column 1)
- GLM coefficients (Column 2)
- t-statistics (Column 3)
- p-values, which are displayed on a logarithmic scale (Column 4)
- percentage of variance accounted for by the model functions (Column 5)

Clicking on one of the thumbnail images in the first column causes an additional figure to pop open, displaying an enlarged plot of the selected model function. Clicking on one of the figures in the second through fifth columns will bring up an image-viewer GUI similar to the one used for viewing the reconstructed hemodynamic images, but with the **Time (frame)**, **Hb State** and **Create Slice Animation**

options disabled in the **Display Options** field. If the "Save" option is selected in the **GLM Analysis** interface, the project file structure will have a GLM sub-folder under the AnalyzedResults folder.



SPECTRAL ANALYSIS

Feature Extraction		
Set Parameters Spectral Analysis	•	PSD CSD
Start	•	Cross Correlation Coherence

The "Spectral Analysis" module contains three components, which are

- Function Specification (a pull-down menu)
- Set Parameters for (a push button)
- **Start** (a push button)

Function Specification

Use the pull down-menu to specify a function, which can be PSD (power spectral density), CSD (cross spectral density), Cross Correlation, or Coherence.

PSD – Power spectral density is a function used to describe how the power (or amplitude) per unit frequency in a time series is distributed across frequencies. In NAVI, this function returns PSD estimates for each channel or pixel time series in the specified data set, using Welch's averaged periodogram method. It also provides options for you to record the processing information into the NAVI file management system, and to visualize results in either the temporal or spatial domain.

CSD – Cross spectral density is a function used to describe how the power (or amplitude) per unit frequency, common to two different time series, is distributed across frequencies. In NAVI, this function returns CSD estimates between a user-defined seed time series and each channel or pixel time series in the specified data set, via Welch's method. It also it provides options for you to record processing information into the NAVI file management system, and to visualize results in either the temporal or spatial domain.

Coherence – Coherence is a function, with values between 0 and 1, used to indicate how tightly coordinated two time series are at each frequency. In NAVI, , this function returns coherence estimates between a user-defined seed time series and each channel or pixel time series in the specified data set, via Welch's method. It also provides options for users to record processing information into the NAVI file management system, and to visualize results in either the temporal or spatial domain.

Cross Correlation – Cross correlation is a function, with values between -1 and 1, used to estimate the degree of similarity between two time series for different values of time shift (lag time). In

NAVI, the cross correlation function estimates the correlation between a user-defined seed time series and each channel or pixel time series in the specified data set. It also provides options for users to record processing information into the NAVI file management system, and to visualize results in either the temporal or spatial domain.

Setting Parameters

Clicking on the **Set Parameters** button in the **Spectral Analysis** module brings up a GUI window. You can use it for setting values of control parameters.

J SetSAParameters
Set Parameters for Spectral Analysis
Specify Parameters for PSD, CSD and Coherence
Length of FFT: 512 Detrend Flag: Linear
Window: hamming Overlap Sample No.: 0
Specify Parameters for Cross Correlation Max Lag: 512 Scale Option: None
Specify Parameters for Wavelet Transform
Lower Carrier Frequency: 0.01 Higher Carrier Frequency: 0.2 Number of Carrier Frequencies: 150
Wavelet Filters: Complex Morlet wavelets
Save & Exit Exit without Saving

The window contains three panels with the labels:

- Specify Parameters for PSD, CSD and Coherence
- Specify Parameters for Cross Correlation
- Specify Parameters for Wavelet Transform [under construction at this time]

Specify Parameters for PSD, CSD and Coherence

Specify Parameters for PSD, CSD and Coherence						
Length of FFT:	512	Detrend Flag: Linear	•			
Window:	hamming 💌 512	Overlap Sample No.:	0			

Use this panel to set the following parameters for PSD, CSD and Coherence:

- Length of FFT
- Window
- Detrend Flag
- Over Sampling No

The *Length of FFT* parameter defines the number of successive time frames used in each FFT (fast Fourier transform) computation. Its default value is either 512 time frames or the total number of time frames in the data set, whichever is smaller.

The *Window* parameter specifies a data windowing function and its length. Using a window will improve your ability to resolve spectral features that are close to each other in frequency. The window length can not be larger than the length of FFT.

The *Detrend Flag* parameter specifies a detrending option, which can be 'linear', 'mean' or 'none'. Selection of 'mean' will remove the DC component from the PSD, while 'linear' corrects for the effects of linear drifts in the data time series.

The *Overlap Sampling No* parameter specifies the number of time frames by which the sections of data used in the FFT computation will overlap. It must be an integer smaller than the window length. The default value of 0 produces data sections with no overlap.

Specify Parameters for Cross Correlation

Specify Parameters for Cross Correlation					
Max Lag:	512	Scale Option:	None		

This panel is used for setting the following parameters for cross correlation:

- Max Lag
- Scale Option

The *Max Lag* parameter is the largest time-shift value that you want NAVI to include in it computation of the cross-correlation function.

The *Scale Option* defines a manner that normalizes the correlation to the specified scale option listed as follows:

_	'none'	_	no scaling (this is the default).
_	'biased'	_	scales the raw cross-correlation by the length of the specified data set .
_	'unbiased'	_	scales the raw correlation by an amount proportional to the time-

shift value.

'coeff'
 normalizes the cross-correlation so that the auto-correlations at zero time-lag are identically 1.0.

<u>Save & Exit</u>

Click on the **Save & Exit** button to commit to all the settings you have made and to close the **Set Parameters for Spectral Analysis** window with all parameters saved into a temporary file located in the current workspace.

Exit without Saving

Click on the **Exit without Saving** button to abandon all parameter settings you have made and to close the **Set Parameters for Spectral Analysis** window without any changes to the working project and its dataInfo file.

Starting PSD

Select "PSD" through the pull-down window in the **Feature Extraction:** Spectral Analysis module and then click the **Start** button to start the computation. The **PSD Analysis** interface shown below will pop open.

artDataAnalysis	
PSD Analysis	
View Existing Results	
Parameter Info C Result 0	
Note: 0 result is determined.	
Get a New Result	
Next result is labeled as	
Not Save	
Quit	
Quit	

With the **PSD Analysis** interface, you can either view previously generated PSD results or compute new ones. Clicking the **Get a New Result** button brings up a progress bar that tells how close the calculation is to completion.

When the PSD computation is completed, GUIs will open to display the spatial distribution of PSD as a function of frequency, and the power-spectral density in each pixel or channel. These GUIs are similar to ones described in Chapter 6 for displaying hemodynamic images and individual-pixel time series.

If the "**Save**" option is selected, a tree-structure and output files will be created to store the PSD results, in a similar manner as described above for other functions in the Data Analyzer portal.







The parameters in this panel also become disabled. They are controlled by the parent GUI for the corresponding image display.

pixel time series used for PSD

parameters are disabled.

analysis. Note that the indicated

Starting CSD

	CSI) Analy:	SIS		
	View	Existing Res	ults		
·	Parameter Info	C Result		0	
	Note: 0 result	is determined.			
	Get	a New Resu	lt		
	Next result is labele	ed as	1		
	G Not Source		<u> </u>	ve	

Select "CSD" through the pull-down window and then click the **Start** button to bring up the GUI window for CSD analysis.

Clicking on the **Get a New Result** button brings up another window that allows you to specify a seed time series (i.e., a single time series that all those in the image-dataset will be compared to) for the CSD computation.

4 Specify Seed	Time Series For CSD Analysis	
÷.		Specify Seed
- P		Specify by Graphics (ROI by Clicking -
9		ROI (X, Y, Z):
•		
2		Start CSD
Specify a Seed Time Series

The GUI provides three ways to specify a seed time series through a pull-down window next to the "Specify by" push-button inside the **Specify Seed** box.

Graphics (ROI by Clicking 💌
Graphics (ROI by Typing)
Graphics (ROI by Clicking)
User-Defined Data

Selecting the "Graphics (ROI by Typing)" option enables the "ROI (X, Y, Z)" text field, which allows you to type in the (X, Y, Z) coordinates of an image pixel. The corresponding time series will automatically be displayed in a pop-up window.



If the "Graphics (ROI by Clicking)" option is selected, then clicking the "Specify by" button activates a set of crosshairs. Place the crosshairs over any pixel of the selected image slice in the GUI and then click the left mouse button. The coordinates of the selected pixel will automatically appear in the "ROI (X, Y, Z)" field, and the corresponding time series will be displayed in a pop-up window.



If the "User-Defined data" option is selected, clicking the **Specify by** button will open a browser window that you can use to navigate to a file containing the user-defined seed time series (in a ASCII-format file, containing a single column of numbers). After this file is selected, the seed time series is loaded and then displayed in a pop-up window.

Starting CSD

Clicking the **Start CSD** button will start the specified CSD computation. When the computation is completed, the results are displayed in GUIs similar to those for a PSD computation.



If the **Save** option is checked in the **CSD Analysis** window, an output file structure and results files will be created, analogous to those produced by the other functions in the Data Analyzer portal.

Starting Cross Correlation

The steps taken to perform a Cross Correlation analysis parallel those used to perform a CSD analysis. The only difference is that "Cross Correlation" is selected from the pull-down menu of the "Spectral Analysis" module, prior to clicking the **Start** button. Saved results are stored in a sub-folder named "COR" within the project-specific file structure.



Starting Coherence

The steps taken to perform a Coherence analysis parallel those used to perform either a CSD or Cross Correlation analysis. The only difference is that "Coherence" is selected from the pull-down menu of the "Spectral Analysis" module, prior to clicking the **Start** button. Saved results are stored in a sub-folder named "COH" within the project-specific file structure.





Event Analysis

Feature Extraction	
Set Parameters Event Analysis	
Start Slope Analysis	► Slope Analysis Delay Analysis Area under Curve

The "Event Analysis" module contains two components, which are

- Function Specification (a pull-down menu)
- **Start** (a push button)

Note that the **Set Parameters** button is intentionally disabled in the **Feature Extraction** module when "Event Analysis" is selected. Use the block-average data generator to select the time interval(s) that you are interested in for performing the Event Analysis operations. The figures below illustrate the use of the **Get Dataset for Analysis** functionality to select time intervals for slope analysis (left screenshot) or for delay analysis and area-under-curve computation (right screenshot).



Function Specification

After **Confirm**ing the time interval selection in the block-average image (or detector signals) generator, use the pull-down menu to specify an operation, which can be Slope, Time Delay or Area under Curve.

Slope Analysis – This utility computes the average slope, within the user-defined time interval, for each channel or pixel time series in the specified data set. The spatial distribution of slope

values for all channels or pixels, and the cumulative distribution function for the computed slopes, are displayed.

Delay Analysis – This functionality computes the time required for each channel or pixel time series to reach its maximum (absolute) value, following the start of a user-specified time interval. The spatial distribution of time-delay values for all channels or pixels, and the cumulative distribution function for the time delays, are displayed.

Area under Curve – This utility computes the area between the time axis and each channel or pixel time series. The spatial distribution of area-under-curve values for all channels or pixels, and the cumulative distribution function for the time delays, are displayed.

Starting Slope Analysis

Select "Slope Analysis" from the pull-down menu in the "Event Analysis" module, and then click the **Start** button to begin the computation.

After the Slope computation is completed, a GUI will automatically pop up, displaying the results. An example is shown below. The image in the left-hand side of the GUI is the spatial distribution of the computed slopes, while the x-y plot on the right-hand side is the corresponding cumulative distribution function.



Clicking on the image on the left-hand side of the results GUI opens a child GUI, similar to one used for the PCA image display, that will allow you to view 2D sections of the spatial distribution of slopes, overlay them onto a structural image, and use the orthogonal-planes 3D image viewer, as shown in the figures below.

If the "Save" option is selected in the **Slope Analysis** window, prior to clicking the **Get a New Result** button, a file structure similar to those for the other functions in the Data Analyzer portal will be created to store the computed-slope results, in a sub-folder named "Slope".

Export

Close



• back

(Slope)

front 🖪

Slice: 21

Starting Delay Analysis

Select "Time Delay" from the pull-down menu in the "Event Analysis" module, and then click the **Start** button to begin the computation.

After the Time Delay computation is completed, a GUI similar to the one generated by the Slope functionality will automatically pop up, displaying the results.

If the "Save" option is selected in the **Delay Analysis** window, prior to clicking the **Get a New Result** button, a file structure similar to those for the other functions in the Data Analyzer portal will be created to store the computed-slope results, in a sub-folder named "Delay".

Starting Area under Curve

Select "Area under Curve" from the pull-down menu in the "Event Analysis" module, and then click the **Start** button to begin the computation.

After the Area under Curve computation is completed, a GUI similar to the one generated by the Slope functionality will automatically pop up, displaying the results.

If the "Save" option is selected in the **Area under Curve** window, prior to clicking the **Get a New Result** button, a file structure similar to those for the other functions in the Data Analyzer portal will be created to store the computed-slope results, in a sub-folder named "Area".

9

FEM Model Generator

Introduction

The **FEM Model Generator** module in the **Utilities** portal provides the functionality for you to reconfigure an existing FEM model to match a user-defined source-detector geometry. The module also provides visualization utilities to explore important features associated with an existing or newly generated FEM model (for example, S-D configuration, mesh parameters, weight matrix coefficients, and reference detector readings.

Launching FEM Model Generator

Take the following steps to launch the **FEM Model Generator** module:

First, select the "FEM Model Generator" option through the pull-down menu built in the Utilities portal, as shown below:



Next, click the **Start** button to open a GUI for FEM model generation. The module, illustrated in the next figure, contains six basic components:

- The Load function, which is used to specify and load an existing FEM model
- Two **Set** functions, which are used to set source and detector positions to fit your measurement conditions
- The **Generate** function, which produces a new weight function and new reference-medium detector readings
- The **View** function, which allows the user to display an existing (*i.e.*, previously generated) FEM model and the newly generated model.
- The Forward FEM Model Running Status window

Load	FEM Model Information
Set	Source Positions Graphically Set
Set	Detector Positions Graphically Set
Generate	Reference Medium Detector Readings and Weight Function
View	FEM Model Information
Forward FEM Model R	unning Status: n file first

The following sections show you step-by-step how to generate an FEM model for a user-specified source-detector arrangement.

Loading and Viewing Existing Model

The first step in generating a new FEM model is to load an existing, pre-calculated FEM model through its modelInfo file. Similar to a dataInfo file, a modelInfo file is model-specific, and has a filename ending with '_modelInfo.mat'. It contains the information about how the model has been generated.

Clicking the **Load** button allows you to specify and load a modelInfo file through a browser window. As an example, let us specify the following modelInfo file that is associated with the basic (9×7) model in the 'models\brains\Right_Motor_Cortex_9x7' folder.

Select a modell	nfo file					? 🛛
Look in:	Bight_Motor_	Cortex_9x7	•	Þ 🗈 I	•	
My Recent Documents	head_box15_E	94132_gid_modelInfo.mat				
Desktop						
My Documents						
My Computer	File name:	head_box15_D4T32_gi	d_modelInfo.ma	ət	•	Open
<u>~</u>	Files of type:	*_modelInfo.mat			•	Cancel

A successful modelInfo load operation enables the **Set** buttons and the **View** button for further processing.

Set Source Positions Graphically Set
Set Detector Positions Graphically Set
Generate Reference Medium Detector Readings and Weight Function
View FEM Model Information

GUI for generating FEM model, before an existing model is loaded.

We strongly recommend that you view the loaded FEM model by clicking the **View** button before you do anything else. This gives you an opportunity to verify if the model you have specified is appropriate for creating a new model with your experimental source-detector arrangement. You can find a detailed description of the use of the model viewer function in the "Viewing Models" section (p. 10) of this chapter.

Defining New S-D Configuration

You should first define the source and detector positions for a new FEM model generation. There are two ways available for you to do so.

Set	Source Positions	Graphically Set
		Graphically Set Load Source Config. File
Set	Detector Positions	Graphically Set

The first method allows you graphically set the source/detector configuration by using the GUI that we have developed for that purpose. The second method is to complete the specification of source and detector locations by loading pre-generated source/detector configuration files, in which the positions of sources/detectors are saved in a matrix. You can manually generate the source/detector configuration files using any available editor. The configuration files must be saved into the project folder containing the raw data sets, with file names conforming to the following filename syntax:

[raw data file name prefix] +_Config_source.txt (for the source configuration file)

[raw data file name prefix] +_Config_detector.txt (the detector configuration file)

Setting Source Positions

First, you should specify an option from the pull-down menu next to the top (*i.e.*, Source Positions) Set button. Depending on which of the preceding options you selected, follow the steps in the corresponding section below.

"Graphically Set" Option

Step 1: Clicking the **Set** Source Positions button brings up a new GUI titled 'Graphically Set Source Positions'. The GUI, shown in the figure below, contains the following components:

- The **Set** button
- The **Clear** button
- The **Save & Close** button
- The **Close** button
- An image of the original FEM model, with the original source configuration displayed
- The **Source Positions** panel for displaying the new source arrangement
- A text field for typing a **Number of New Sources**
- A pull-down menu for specifying view orientation



Tip: If the sources are not all visible in the default "x-y plane," you can change the view orientation to "x-z plane" or "y-z plane" via the pull-down menu in the upper right corner of the GUI.

Step 2: Type the number of source fibers used for the experimental protocol in the **Number of New Sources** text field, which is located in the upper middle area of the GUI. Its default value is the number of sources in the original FEM model.

Tip: If the new source configuration is the same as the original configuration, click the **Save & Close** button in the lower left corner to complete the source position setting.

Step 3: Click on the **Set** button in the upper left corner and move the mouse cursor into the **Source Positions** panel to enable the crosshairs. Then move the crosshairs onto the circle corresponding to the first experimental source position and click the left/primary mouse button. Repeat this process for the other source locations, until all sources for the new model are specified.

The figure below shows an example of graphically set source positions, where there are 30 source positions to be set, the first twenty two sources have been specified, and the crosshairs are moved onto the twenty third source position.



Tip: If you make a mistake while setting the source positions and want to abort the procedure, just click the right/secondary mouse button to make the crosshairs disappear. Then click the **Clear** button located under the **Set** button, and repeat steps 1-3 to set the source position again.

Tip: If a source position is selected twice, the second selection will be ignored. However, if a source position is specified more than twice, the source setting process will automatically terminate. You can reset the source positions by clicking the **Clear** button and starting over again.

Step 4: Click the **Save & Close** button in the lower left corner to save your source configuration settings, after all source positions have been specified for the new model.

"Load Source Config. File" Option

Click the **Set** Source Positions button on the **Generate Forward FEM Model** main interface. This brings up the browser window shown below to allow for navigating to and specifying a source configuration file that has been pre-generated and saved in the project folder.

Select a Source	• Configuration	file			? 🛛
Look in:	Bight_Motor_	Cortex_9x7	•	🗢 🗈 💣 📰 •	
My Recent	Config_source	.txt 30d30			
Desktop					
My Documents					
My Computer	File name:	Config_source.txt		•	Open
	Files of type:	source.txt		•	Cancel

The source configuration file contains a matrix, in which each element stands for one of the source positions contained in the original FEM model. The value of the element is the label of the source located at that position, in the new model being generated. If the value of an element is 0, then there is no source at that position in the new model.

The following matrix shows an example of a source configuration file for a new model design, based on the original model that has the maximal 9×7 source/detector arrangement.

0	0	0	0	0	0	0	0	0
0	0	25	26	27	28	29	30	0
0	0	19	20	21	22	23	24	0
0	0	13	14	15	16	17	18	0
0	0	7	8	9	10	11	12	0
0	0	1	2	3	4	5	6	0
0	0	0	0	0	0	0	0	0

The source position setting for the new model is complete after the specified source configuration file is loaded.

Setting Detector Positions

The procedures for setting detector positions are the same as those for setting the source positions, except that you use the **Set** button and the pull-down menu design on the 'Detector Positions' line of the GUI. Completion of the detector-position setting process enables the **Generate** button in the main **Generate Forward FEM Model** GUI.

Click the **Set** Detector Positions button open the GUI for setting detector positions:



An example of a result for the detector positions setting procedure is shown in the following figure:



Successful specification of both the source and detector locations enables the **Generate** button in the parent GUI.

Load	FEM Model Information
Set	Source Positions Graphically Set
Set	Detector Positions Graphically Set
Generate	Reference Medium Detector Readings and Weight Function
View	FEM Model Information

Generating a New Model

Click the **Generate** button on the main 'Generate Forward FEM Model' GUI to start the mesh generation process with the specified source/detector configuration. During the operation, a pop-up window will open to allow you to specify a folder in which to save the new model. You can use the default folder name generated by NAVI, for example, 'Right_Motor_s30d30',

🛃 Please spec 🖡	
Name of folder to save n Right Motor s30d30	ew model:
ОК	Cancel

or you can define a name you prefer (provided that the name has <u>no</u> blank spaces and that it <u>does</u> contain one of the key words 'Right_Motor', 'Left_Motor', 'Frontal_Cortex', or 'Occipital_Cortex'), for example, 'Right_Motor_experiment1'.



Click the OK button to start the process of generating the new model. A successful application of the **Generate** button produces a new model, which is located either in a user-defined subfolder or in the NAVI-generated default folder.

Folders	×	Name	Size	Туре
🖃 🦳 models	~	⊮.FEM	36,617 KB	FEM File
🗏 🦳 brains		sd_coords.FEM	4 KB	FEM File
Erontal Cortex	الأ coords التي mri_nir الأ det.FE الم head_t	Coords.FEM	216 KB	FEM File
Left Motor Cortex 9x7		mri_nirx01.dat	4,231 KB	DAT File
Occipital Contex		det.FEM	16 KB	FEM File
Bight Motor Cortex 9x7		head_box021.jpg	7 KB	JPEG Image
Right_Motor_s30d30		FEMModel.jpg	7 KB	JPEG Image

Viewing Models

You can view the original model or the newly generated one using the **View** button included in the **Generate Forward FEM Model** main GUI. Clicking the button brings up a child GUI with the following four functions:

- **Outline** (this is the default mode)
- FEM Mesh & S/D
- Detector Reading
- Weight Function

Outline

Clicking on the **Outline** button displays four types of FEM model information in the model information window:

- FEM Mesh
- Source/Detector Configuration
- Forward FEM Model
- Forward FEM Model (S/D configuration changed)

View FEM Model		
Model Information	Model Information: OUTLINE	
Outline	FEM Mesh:	
FEM Mesh & S/D	Dimension of Mesh: 3D Number of Nodes: 4211 Number of Elements: 18049 Format of Mesh File: GID Format Mesh File: Diversivono01/emselveaddatabase15/box15_9x7/bead_box15_D4T32_oid_msh	
Weight Function	Source/Detector Configuration: Number of Sources: 63 Number of Detectors: 63 Source File: C:\users\yongxu\navi01\models\brains\Right_Motor_Cortex_9x7\box15_sdcoords_9x7 Detector File: C:\users\yongxu\navi01\models\brains\Right_Motor_Cortex_9x7\box15_sdcoords_9x7	
	Forward FEM Model:	
	Detector Readings: C:\users\yongxu\navi01\models\brains\Right_Motor_Cortex_9x7\\det.FEM Weight Function: C:\users\yongxu\navi01\models\brains\Right_Motor_Cortex_9x7\\w.FEM	
	Forward FEM Model (S/D configuration changed): Number of Sources: 30 Number of Detectors: 30	
Close	Source File: C.:usersiyongxunavi01/models/brains/kight_Motor_cortex_9xr/box15_scdcoords_9xr_new Detector File: C.:usersiyongxunavi01/models/brains/Right_Motor_Cortex_9x7/box15_sdccoords_9x7_new Detector Readings: C:!usersiyongxunavi01/models/brains/Right_Motor_Cortex_9x7/Right_Motor_s30d30/wiFEM Weight Function: C:!usersiyongxunavi01/models/brains/Right_Motor_Cortex_9x7/Right_Motor_s30d30/wiFEM	

FEM Mesh & S/D

This function allows you to view the model geometry and the source/detector positions for the original FEM model, or for the newly generated FEM model, and gives you a choice of viewing planes.

Tip: It is important to make sure the source/detector positions you have set exactly match your experimental source/detector configuration. Performing the following steps, you can conveniently check if your setting is right: 1) Click the **FEM Mesh & S/D** push-button; 2) Click the **Changed** radio button; 3) (if necessary) Choose the most advantageous viewing plane. You will see all source and detector positions you have set, as shown in the figures below. Then you can carefully check to see if all sources and detectors are located at the right positions.

Examples of the use of the viewer function, as applied to both the original model and the newly generated one, are shown below.





Detector Reading

This function allows you to view the reference medium detector readings. Click the **Detector Reading** button to produce a plot of reference medium detector readings in the **View FEM Model** interface.

The upper figure is a contour-surface plot of detector readings, and the lower figure is a plot of detector readings, on a logarithmic scale, for the detectors associated with a specific source. You can select a different source position using the scroll bar located at the bottom of the GUI. You also can toggle between the original and changed FEM models by checking either the **Original** or **Changed** radio button on the left side of the GUI.



Weight Function

Click the **Weight Function** button to produce a graphical display of the weight function, for either the original or the newly generated FEM model.

The upper figure shows the weight function matrix; the nearly uniform appearance is a consequence of the large range (6-9 orders of magnitude) of weight values in the model, with only a few elements in the matrix having weights on the order of unity while the great majority of weight values are orders of magnitude smaller. The bottom figure is a plot of the weight function for one S/D channel, in all FEM mesh nodes. You can select a different S/D channel by using the slider at the bottom of the window. Also, you can choose to show the weight function for either the original or the newly generated FEM model by checking either the **Original** or **Changed** radio button on the left side of the GUI.



Raw Data Editor

Introduction

The **Raw Data Editor** module in the **Utilities** portal supports editing of a DYNOT or NIRScout data file group that cannot (for reasons presented subsequently) be analyzed directly by NAVI, into one or more subsets that can be. Editing capabilities include:

- 1) Selection of desired time segments from a larger time series
- 2) Apply a time-averaging process to an existing raw data set, or to a subset derived from item (1)
- 3) Sort raw data from multisite measurements into subsets corresponding to distinct regions (*e.g.*, left and right motor cortex), enabling analysis of the daughter files by NAVI
- 4) Access the FEM Model Generator module to create site-based FEM models in support of site-based image reconstruction

Multi-Site Measurement Setup

A. Different sites with concurrent source illumination.

Figure 1 shows an example of the optical-fiber layout from a DYNOT measurement intended to explore multiple regions simultaneously. In practice this can be achieved by using optode designs available from NIRx that divide the optical power to two or more transmitting bundles. The considered example explores the effect of a table tilt maneuver on a subject lying in the supine position, while the subject's forehead, left and right forearms, and left gastrocnemius muscle were simultaneously monitored using the indicated illumination-detection geometry. Similar measurements can, for example, involve data collected from the left and right foretal and parietal regions of the head. For the particular case considered here, data were collected by simultaneously illuminating each site using a time-multiplexing scheme and optodes that support co-located measurements. [We encourage readers to explore this data as a reminder of the importance that subject orientation can have on data collection. A description of the precise protocol applied can be found at the end of this chapter.]

The Original Raw Data Files:

In the considered measurement, the DYNOT imager generated raw data files that contain information from all four sites. Direct processing of the original raw data set using NAVI would result in a mixing of information from all sites. To avoid this it is necessary to sort the data in accordance with the optode arrangement for each site. In the example here, the original files are named:

- 1. Doug_Tilt_Study1.wl1
- 2. Doug_Tilt_Study1.wl2
- 3. Doug_Tilt_Study1.set
- 4. Doug_Tilt_Study1_config.txt

In 'Doug_Tilt_Study1_config.txt', we find the following information:



Figure 1. Diagram of a four-site measurement setup and its site-based source-detector arrangement. Note that each optode serves both as a source and a detector.

Preparation of the site-based information

To successfully use the **Raw Data Editor** module to separate the original data into multiple site-related subsets, the user needs to provide the correct optode information for the particular experimental setup. Table 1 is an example of the user-prepared site-based information identified from the setup shown in Figure 1 and from the contents of the 'Doug_Tilt_Study1_config.txt' file.

 Table 1. The relationship among source groups, source / detector indexes and the measured sites.

Source	Source / Detector Indexes			
Group	Site 1 (S / D)	Site 2 (S / D)	Site 3 (S / D)	Site 4 (S / D)
1	1 / 1	1 / 2	1 / 3	1 / 4

2	2 / 5	2 / 6	2 / 7	2 / 8
3	3 / 9	3 / 10	3 / 11	3 / 12
4	4 / 13	4 / 14	4 / 15	4 / 16
5	5 / 17	5 / 18	5 / 19	5 / 20
6	6 / 21	6 / 22	6 / 23	6 / 24
7	7 / 25	7 / 26	7 / 27	7 / 28
8	8 / 29	8 / 30		
Total Source/Detector No.	8 / 8	8 / 8	7/7	7/7

Launching Raw Data Editor

Take the following steps to lunch the **Raw Data Editor** module:

First, use the pull-down menu in the **Utilities** portal to select the 'Raw Data Editor' option, as shown in Figure 2:



Figure 2. The NAVI GUI components for launching the Raw Data Editor

RawDataEditor DYNOT-Based Raw Data Editor Parameter Setup	Figure 3. The Raw Data Editor child GUI, which is launched when the Load button in Fig. 2 is pressed.
Specify a DYNOT-based raw experimental dataset: Browser	
↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓	Parameter Setup
MultiSite Study? No Ves Set Parameters	
Specify the time range(s) for the new subdataset(s): 1 1000	
Specify the average window size for the new subdataset(s):	
Execution	
There are no multi-site-based subdatasets created yet at this moment.	
Generate New Subdataset(s)	Execution

Next, click on the **Start** button to open the Raw Data Editor GUI. Components of the GUI are divided into two panels, **Parameter Setup** and **Execution**, as shown in Figure 3.

Step by Step Data Editing Process

Step 1: Specify a raw dataset through the config.txt file

Click the **Browser** button in the Raw Data Editor GUI shown in Figure 3 to specify and load a userdesired raw data set through its config.txt file. Following this operation, the Raw Data Editor module will automatically show the user which config.txt file has been selected and where the corresponding raw data group files are located. Also listed are default values for two editable fields corresponding to the time range (by default, the first and last time frames in the time series) and the window size for time averaging the data (by default, 1). Figure 4 shows an example of the GUI after a raw data is specified through the Browser button.

RawDataEditor	- • •				
DYNOT-Based Raw Data Editor					
Parameter Setup					
Specify a DYNOT-based raw experimental dataset: Browser					
C:\TEMP\demodata\test\MultiSite4\Doug_Tilt_Study1_config.txt					
MultiSite Study? O No O Yes Set Parameters	_				
Specify the time range(s) for the new subdataset(s): 1 5500					
Specify the average window size for the new subdataset(s):					
Execution					
There are no multi-site-based subdatasets created yet at this moment.					
Generate New Subdataset(s)					

Figure 4. The Raw Data Editor GUI

The dataset specified is located in 'C:\TEMP\demodata\test\MultiSite4', the file name root is 'Doug_Tilt_Study1', and there are 5500 recorded time frames in the data time series.

Step 2: Set parameters for separation of multi-site raw data

Parameters associated with source-detector arrangement

The Raw Data Editor module provides two methods for users to specify the parameters associated with the optode arrangement employed during data collection. In one method, the user can directly type the desired parameter values through a GUI developed for setting the data-editing parameters. In the other, the user can edit the original config.txt file by introducing additional information about the site-related optode arrangement. NAVI will then extract the site-related information and transfer the relevant information to various data fields of the GUI. The config.txt file containing the site-based information can be either generated manually (current) after data collection, or automatically (under construction) during data collection.

While both editing features can achieve the same outcome, data editing through the GUI affords additional flexibility. For instance, in cases where data are collected from a single site, it can nevertheless be of interest to explore a selected ROI. This can be achieved by simply identifying the optode subset of interest. Alternatively, editing of the config.txt file can be most efficient in cases where data truly are collected from distinct sites.

An example of the format used for editing the config.txt file is:

```
%The updated Doug_Tilt_Study1 _config.txt file:
%-----The original information-----The original information-----
_____
                            _____
raw_data_name='Doug_Tilt_Study1';
SamplingRate=7.94;
waveLength_N=2;
source_N=8;
detector N=30;
time point N=5500;
source_detector_key=[1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
20 21 22 23 24 25 26 27 28 29 30;...
                  1 1 1 1 2 2 2 2 3
                                   3
                                      3
                                         3
                                            4
                                               4
                                                 4
                                                    4
                                                       5
                                                          5
                                                             5
          6 7 7 7 7 8 8];
5
  6 6 6
%-----The updated information-----
_____
multi site N=4;
source_detector_key_site1=[ 1 5 9 13 17 21 25 29;...
                        1 2 3
                                 5
                              4
                                   б
                                      7
                                         8];
source_detector_key_site2=[ 2 6 10 14 18 22 26 30;...
                                 5 6 7 8];
                        12
                            3
                              4
source_detector_key_site3=[ 3 7 11 15 19 23 27;...
                        1 2
                            3
                               4
                                 5
                                    67];
source_detector_key_site4=[ 4 8 12 16 20 24 28;...
                            3
                               4
                                  5
                                    6
                        1 2
                                      7];
```

Clicking on the 'Set Parameters' button in Figure 4 will bring up the child GUI shown in Figure 5, which contains fields for the user to specify the desired number of sites (up to four), to input the site-based optode indices (source-detector arrangement) corresponding to the original raw data, to define site-based folder/file names for storing the separated subsets, and also to launch the FEM Model Generator for generating site-based FEM models, if necessary. If the config.txt file has been updated with the muti-site

information, the site-based parameter values can be extracted from it and used to specify the number-ofsites and optode-index information shown in Fig. 5. Otherwise, a similar GUI will appear with the default values shown in Figure 6, where, the number of sites has the default value of 1 (the top panel) and only the optode indices belonging to original config.txt file are listed.

MultiSitesSDArrangement				
Source-Detect	or Arrangem	ent and FEM Model	Generation for Mult	i Site Measurement
	— Site Number —— The multi site	information is found in the spec	ified config file.	
	How many sit	tes are included in the specified	iraw dataset: 4	
Site-Related Parameters	and Computational	Models		
Source Ir Site 1	ndexes:	Detector Indexes:	Name for New Subdataset	FEM Model for Images
Site 2				
1 2 3 4 5	678	2 6 10 14 18 22 26 30	Site2	Generate FEM Model
Site 3	567	3 7 11 15 19 23 27	Site3	Generate FEM Model
Site 4	567	4 8 12 16 20 24 28	Site4	Generate FEM Model
	0	Confirm	Close	

Figure 5. The GUI used for parameter setup when the muti-site information is recorded in the modified config.txt file.

Site Info There is through How m	no multi site-based information four the GUI or close the window and p any sites are included in the specifie	id in the config file. You can manu repare it using the configure file. ed raw dataset? 1	ally specify it
-Related Parameters and Cor Source Indexes: - Site 1	nputational Models Detector Indexes: 3 3 1 2 3 4 5 6 7 8	Name for New Subdataset	FEM Model for Images
Site 2		Site2	Generate FEM Model
Site 3		Site3	Generate FEM Model
Site 4		Site4	Generate FEM Model

Figure 6. The default GUI used for parameter setup when muti-site information is not included in the config.txt file.

To subdivide the raw data in the second case, you should first change the default number of sites from 1 to 4, which will result in a change in the appearance of the GUI, as shown in Figure 7a.

MultiSitesSDArrangement
Source-Detecor Arrangement and FEM Model Generation for Multi Site Measurement
Site Info There is no multi site-based information found in the config file. You can manually specify it through the GUI or close the window and prepare it using the configure file. How many sites are included in the specified raw dataset?
Ste-Related Parameters and Computational Models
Site 1 Site 1 Site 1 Generate FEM Model
Site 2Site2Generate FEM Model
Ste 3 Generate FEM Model
Site 4 Site4 Generate FEM Model
Confirm Close

Figure 7a. The updated GUI after the site number is modified to 4 from the default value shown in Figure 6.

Next, you should manually type the site-based source and detector indices into the blank source- and detector-index fields seen in Figure 7a. The result is shown in Figure 7b. Note that this arrangement is identical to that in Figure 5, where these parameter values were extracted from the config.txt file directly.

MultiSitesSDArrangement
Source-Detecor Arrangement and FEM Model Generation for Multi Site Measurement
Site Number — The multi site information is found in the specified config file. How many sites are included in the specified raw dataset:
Site-Related Parameters and Computational Models Source Indexes: Detector Indexes: Name for New Subdataset FEM Model for Images
1 2 3 4 5 6 7 8 1 5 9 13 17 21 25 29 Site1 Generate FEM Model
1 2 3 4 5 6 7 8 2 6 10 14 18 22 26 30 Site2 Generate FEM Model
Site 3 Generate FEM Model 1 2 3 4 5 6 7 3 7 11 15 19 23 27 Site 3 Generate FEM Model
Site 4 Generate FEM Model 1 2 3 4 5 6 7 4 8 12 16 20 24 28 Site 4 Generate FEM Model
Confirm Close

Figure 7b. The updated GUI after the site-based source and detector indexes are typed in.

Step 3: Create site-based FEM models

It is emphasized that it is not necessary to execute this step in order to separate the site-based raw data. However, the **Generate FEM Model** buttons seen in Figs. 5-7 provide a convenient access to NAVI's FEM Model Generator module, if it is needed (see Chap. 9). The site-based FEM models must be available for subsequent analysis of the separated data with NAVI, especially for image reconstruction.

Clicking on the **Generate FEM Model** button for any site GUI shown in Figs. 5-7 will bring up the FEM Model Generator GUI. As described in Chap. 9, this module also can be accessed through the main NAVI GUI.

📣 Generate Forward FEM Model					
Generate Forward FEM Model					
Load	FEM Model Information				
Set	Source Positions	Graphically Set	•		
Set	Detector Positions	Graphically Set			
Generate	Reference Media and Wei	ım Detector Readings ight Function			
View	FEM Model In	formation			
Forward FEM Model Ru	nning Status:				
Please "Load" FEM model information f	file first!		T T		
Exit		Help			

Figure 8. The FEM Model Generator GUI.

For the particular data set described in this chapter we select the 'Frontal_Cortex' brain model, as an example to show how site-based models can be generated from the pre-existing models in our model library. So far, most of our FEM model library development efforts have been focused on analysis of data collected from brain studies. In practice, analysis of the particular data set considered here would need to

proceed from segmented anatomical priors obtained from the corresponding body sites (*i.e.*, head, forearm, leg).

The parent model and the derived sub-models are presented in Figure 9a-f. Please consult Chapter 9 of the NAVI User's Guide to learn details about the use of the FEM Model Generator.





The FEM Model for Site 1: Site1_s8d8 (Figure 9b)



The FEM Model for Site 2: Site2_s8d8 (Figure 9c)

The FEM Model for Site 3: Site3_s7d7 (Figure 8d)





The FEM Model for Site 4: Site4_s7d7 (Figure 9e)

The parent model and its site-based sub-models in the file system (Figure 9f)



Step 4: Confirm the parameter specifications.

The parameter setup will not be completed until you click on the **Confirm** button at the bottom of the GUI shown in Figs. 5-7. Following this operation, that GUI will automatically close, the Execution panel of the Raw Data Editor GUI will be updated, and the **Generate New Subdataset**(s) button will be enabled, as shown in Figure 10.

wDataEditor	
DYNOT-Based Raw Data Editor	
- Parameter Setup	
Specify a DYNOT-based raw experimental dataset: Browser	
C:\TEMP\demodata\test\MultiSite4\Doug_Tilt_Study1_config.txt	
MultiSite Study? No Set Parameters	
Specify the time range(s) for the new subdataset(s): 1 5500	
Specify the average window size for the new subdataset(s):	
- Execution	
There are no multi-site-based subdatasets created yet at this moment.	
Generate New Subdataset(s)	
Generate New Subdataset(s) Close	

Figure 10. The Raw Data Editor GUI following confirmation of the specified parameter values.

Step 5: Specify the desired time range and/or the average window size

You can use the GUI shown in Figure 10 to modify the default time range in order to remove undesired time segment. You also can specify an average window size of N > 1, and NAVI will apply a time averaging process to generate a new data set smaller than the original one (*i.e.*, data down-sampling), by averaging successive groups of N consecutive raw data values for each channel. For the particular example described in this chapter, we keep the default values and do not change either of these two parameters.

Step 6: Generate New Site-Based Subdatasets

Click on the **Generate New Subdataset**(s) to start the process of separating the original raw data files and generating the site-based data files. Following completion of this operation, the GUI will be updated as shown in Figure 11.

RawDataEditor	- • •
DYNOT-Based Raw Data Editor	
Parameter Setup	
Specify a DYNOT-based raw experimental dataset: Browser	
C:\TEMP\demodata\test\MultiSite4\Doug_Tilt_Study1_config.txt	
MultiSite Study? No Yes Set Parameters Specify the time range(s) for the new subdataset(s): 1 5500 Specify the average window size for the new subdataset(s): 1	
Execution	
4 subdatasets have been created in C:\TEMP\demodata\test\MultiSite4\	
Generate New Subdataset(s)	

Figure 11. The Raw Data Editor GUI after the user-defined subsets have been created and saved to the file system.

Figures 12a-e show how the original raw dataset and the derived site-based subsets are named and stored in the file system.

The original raw data:

C:TEMP\demodata\test\MutltiSite4\Doug_Tilt_Study1*** (Figure 12a)

		<u>s</u>	end Feedback	
CO Computer > OS (C:) > TEMP > demodata > test > MultiSite4 > v 4 Search MultiSite4				
Organize 🔻 New Folder Include in library 💌	Share with 👻		!≡ ▼ [1 0
D 🛃 Videos	 Name 	Date modified	Туре	Size
 Computer Computer Computer Solution MHWGuides MATLAB Memusage MININT PerfLogs Program Files Fresources richyao SmartDraw 2009 TEMP demodata Ieft_motor_cortex multiSite test models Breasts Breasts Horses 	Doug_Tilt_Study1.wl2 Doug_Tilt_Study1.wl1 Doug_Tilt_Study1.config Doug_Tilt_Study1.set Site1 Site2 Site3 Site4	6/24/2009 3:33 PM 6/24/2009 3:33 PM 6/28/2009 12:40 PM 6/24/2009 3:33 PM 6/24/2009 10:22 PM 6/24/2009 10:22 PM 6/24/2009 10:22 PM	WL2 File WL1 File Text Document SET File File Folder File Folder File Folder File Folder	15,0: 15,0:
8 items				

Figure 12a. Raw Data file and the newly created folders for 4 sites

The derived subdataset for Site 1:

C:TEMP\demodata\test\MutltiSite4\Site1\Doug_Tilt_Study1_Site1*** (Figure 12b)

			<u>s</u>	end Feedback	• 🗙
	TEMP 🕨 demod	lata ▶ test ▶ MultiSite4 ▶ Site1	✓ Search Site1		Q
Organize 🔻 New Folder Include in	library 👻 Sl	hare with 🔻		!≡ ▼ [
Documents	^	Name	Date modified	Туре	Size
Initial Products		Doug_Tilt_Study1_Site1.set	6/24/2009 10:21 PM	SET File	
Videos		Doug_Tilt_Study1_Site1.wl1	6/24/2009 10:22 PM	WL1 File	6,19
-		Doug_Tilt_Study1_Site1.wl2	6/24/2009 10:22 PM	WL2 File	6,19
👰 Computer		Doug_Tilt_Study1_Site1_config	6/24/2009 10:21 PM	Text Document	
 OS (C:) HWGuides MATLAB Memusage MININT PerfLogs Program Files resources richyao SmartDraw 2009 TEMP demodata left_motor_cortex multiSite test models 	E				
iii Brains	+ •	•			•
4 items					

Figure 12b. The new experimental-like files for Site 1
The derived subdataset for Site 2:

C:TEMP\demodata\test\MutltiSite4\Site2\Doug_Tilt_Study1_Site2*** (Figure 12c)

			2	end Feedback	
Computer > 0	OS (C:) 🕨 TEMP 🕨 demo	odata 🕨 test 🕨 MultiSite4 🕨 Site2	✓ ⁴ → Search Site2		Q
Organize 👻 New Folder	Include in library 🔻	Share with 🔻		8== ▼	
Documents	*	Name	Date modified	Туре	Size
Pictures		Doug_Tilt_Study1_Site2.set	6/24/2009 10:21 PM	SET File	
Videos		Doug_Tilt_Study1_Site2.wl1	6/24/2009 10:22 PM	WL1 File	6,1
		Doug_Tilt_Study1_Site2.wl2	6/24/2009 10:22 PM	WL2 File	6,1
👰 Computer		Doug_Tilt_Study1_Site2_config	6/24/2009 10:21 PM	Text Document	
GS (C:) HWGuides MATLAB Memusage MININT PerfLogs PerfLogs resources richyao SmartDraw 2009 TEMP	E				
demodata left_motor_cortex multiSite test models Brains 		٠ [111		,
4 items					

Figure 12c. The derived experimental-like group files for Site 2

The derived subdataset for Site 3:

C:TEMP\demodata\test\MutltiSite4\Site3\Doug_Tilt_Study1_Site3*** (Figure 12d)

			<u>2</u>	end Feedback	
Computer > OS (C:) > TEMP	▶ dem	odata 🕨 test 🕨 MultiSite4 🕨 Site3	✓ 4 Search Site3		Q
Organize 💌 New Folder Include in libra	ry 👻	Share with 💌		= -	
Documents	*	Name	Date modified	Туре	Size
Music		Doug_Tilt_Study1_Site3.set	6/24/2009 10:21 PM	SET File	
Videos		Doug_Tilt_Study1_Site3.wl1	6/24/2009 10:22 PM	WL1 File	4,8
-		Doug_Tilt_Study1_Site3.wl2	6/24/2009 10:22 PM	WL2 File	4,8
🖳 Computer		Doug_Tilt_Study1_Site3_config	6/24/2009 10:21 PM	Text Document	
🚣 OS (C:)					
HWGuides	-				
MATLAB Memusade	-				
MININT					
PerfLogs					
🌗 Program Files					
i resources					
SmartDraw 2000					
TEMP					
lemodata					
left_motor_cortex					
JunultiSite					
u test					
models Brains					
-	~	•			- F
4 items					

Figure 12d. The derived experimental-like group files for Site 3

The derived subdataset for Site 4:

C:TEMP\demodata\test\MutltiSite4\Site3\Doug_Tilt_Study1_Site4*** (Figure 12e)

			2	iend Feedback	-	×
G v limit → Computer → OS (C:) → TEMP → c	lemo	data ▶ test ▶ MultiSite4 ▶ Site4	✓ ✓ Search Site4			Q
Organize 🔻 New Folder Include in library 🕶		Share with 🔻			•	?
Documents	*	Name	Date modified	Туре		Size
Music Pictures		Doug_Tilt_Study1_Site4.set	6/24/2009 10:21 PM	SET File		
Videos		Doug_Tilt_Study1_Site4.wl1	6/24/2009 10:22 PM	WL1 File		4,8
		Doug_Tilt_Study1_Site4.wl2	6/24/2009 10:22 PM	WL2 File		4,8
🖳 Computer		Doug_Tilt_Study1_Site4_config	6/24/2009 10:21 PM	Text Docur	nent	
🚢 OS (C:)						
HWGuides						
MATLAB	=					
MININT						
PerfLogs						
Program Files						
resources						
📕 richyao						
SmartDraw 2009						
demodata						
left motor cortex						
\mu multiSite						
🌗 test						
models						
Brains -	-	•	11			+
4 items						

Figure 12e. The derived experimental-like group files for Site 4

Another Type of Measurement Setup

Different sites explored using single source illumination with time multiplexing.

Figure 13 shows an example of a two-site measurement setup and its site-based source-detector arrangement. The particular arrangement was achieved using a DYNOT 264 system (32 sources, 64 detectors) with half of the available optodes. Here our goal is to separate the data into left and right regions of the head.



Figure 13. Diagram of a two-site measurement setup and its site-based source-detector arrangement.

The Original Raw Data Files:

In the considered measurement, the DYNOT imager generated raw data files that contain information from both sites. The files are named:

- 1. chris.wl1
- 2. chris.wl2
- 3. chris.set
- 4. chris_config.txt

In 'chris_config.txt', we find the following information:

```
%----- twoSitesData_config.txt-----
raw_data_name='chris';
SamplingRate=;
waveLength N=2;
source N=16;
detector_N=30;
source_detector_key=[1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
20 21 22 23 24 25 26 27 28 29 30;...
                  1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
                                                        0 0
                                                              0
0
  0
     0 0
          0
            0
                0
                  0 0 0 0];
```

Subsequently, the config.txt was manually modified to:

```
%The updated chris config.txt file:
%-----The original information-----
raw_data_name='chris';
SamplingRate=7.94;
waveLength_N=2;
source N=16;
detector N=30;
source_detector_key=[1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
20 21 22 23 24 25 26 27 28 29 30;...
                  1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
                                                      0 0
                                                             0
  0 0 0 0 0 0 0 0 0 0];
0
%-----The updated information-----
multi_site_N=2;
source_detector_key_site1=[1 2 3 4 5 6 7 8 17 18 19 20 21 22 23;...
                       1 2 3 4 5 6 7 8 0
                                         0
                                           0
                                              0
                                                   0
                                                0
                                                      0];
source_detector_key_site2=[9 10 11 12 13 14 15 16 24 25 26 27 28 29
30;...
                       9 10 11 12 13 14 15 16
                                              0 0
                                                    0
                                                       0
                                                          0
                                                             0
0];
```

Preparation of the site-based information

Table 2 is an example of the user-prepared site-based information identified from the experimental setup shown in Figure 13 and from the corresponding modified config.txt file.

Source	Source/Det	tector Indexes
Group	Site 1	Site 2
	1/1	-
2	2/2	-
3	3/3	-
4	4/4	-
5	5/5	-
6	6/6	-
7	7/7	-
8	8/8	-
9	-	9/9
10	-	10/10
11	-	11/11
12	-	12/12
13	-	13/13
14	-	14/14
15	-	15/15
16	-	16/16
0	0/17	-
0	0/18	-
0	0/19	-
0	0/20	-
0	0/21	-
0	0/22	-
0	0/23	-
0	-	0/24
0	-	0/15
0	-	0/26
0	-	0/27
0	-	0/28
0	-	0/29
0	-	0/30
Total Source/Detector No.	8/15	8/15

Table 2. The relationship among	ource groups and source/detector indice	s for the Fig. 13 measurement sites
. ~		

11

naviSPM

Introduction

The **naviSPM** module in the **Utilities** portal uses functionalities found in the SPM (<u>Statistical Parametric</u> <u>Mapping</u>) freeware package to extend the capability of NAVI to fit users' needs for statistical analysis of hemodynamic image time series. Several of the currently favored techniques for interpretation of neuroimaging data collected during designed experiments are available at this time, for both Level-1 (within-session and within-subject) and Level-2 (across multiple sessions or subjects) analyses. The functions currently available include: Level-1 general linear model (GLM) analysis of fNIRS hemodynamic time series images, to evaluate the position-dependent relationships between image values and user-specified temporal models; and Level-1 and Level-2 assessment of the statistical significance of the GLM model-fitting coefficients (t-test, ANOVA), or of user-defined contrasts of two or more models.

Launching naviSPM

Select the 'naviSPM' option from the drop-down menu in the Utilities portal (lower-right corner of the NAVI main GUI),



and then click the **Start** button to launch the main naviSPM GUI. An annotated screenshot of the GUI is shown in the next figure.



Level-1 Analysis with naviSPM

The following steps are carried out using the functions and utilities in the 'SPM: Level 1 (within-subject)' module.

Step 1: Specify, edit, and save a NAVI-based detector/image data set.

• In the 'Single Data Specification' sub-module, use the drop-down menus in the 'Data type:' line to specify your choice of detector or image data and your hemoglobin isoform selection.

SPM: Level 1 (within-subject) SPM: Level 1 (within-subject)				
Single Data Specification	Single Data Specification			
Data type: Image 🔹 Hb-oxy 👻	Data type: Image 👻 Hb-oxy 🔽			
Specify *** Detector	Specify ***_dataInfo.mat Hb-oxy			
No file has been Image	No file has been specified yet. Hb-deoxy			
	Hb-total			

• From the drop-down menu next to the 'Specify' button, select '***_dataInfo.mat' (the default option) to read in a dataset that has not already been processed with naviSPM. Select 'pre-defined Hb dataset' if you want to review or perform additional analysis on a dataset that was processed with naviSPM on a previous occasion.

- SPM: Level 1 (within-subject)						
Single Data Specification						
Data type:	Image 👻	Hb-oxy 👻				
Specify **	*_dataInfo.mat					
No file has b	*_dataInfo.mat					
P	re-defined Hb dataset					

- To generate a new NAVI-based data set for GLM analysis (*i.e.*, you are using the '***_dataInfo.mat' option):
 - Press the 'Specify' button, causing a navigator window to pop up. Navigate to the folder containing the main NAVI-generated dataInfo file for your dataset. Select that file and press the 'Open' button in the window's lower right corner.

🛃 Specify DataIr	Specify DataInfo File								
Look in:	<u> k</u> eith			-	← 🗈	d 📅			
Recent Places Desktop Doug Computer Network	Name AnalyzedR conditionf Detectors Images Left_Motor naviSPM old Akeith_data	Date modif esults iles r_s25d25 info.mat	Туре	Size					
	File name: Files of type:	keith_dataInf DataInfo File	io.mat s (*_dataInfo.ma	t)		•	Open Cancel		

• If you selected 'Image' from the 'Data type:' drop-down menu, then the preceding pop-up window will be replaced by a new one, containing two text fields. Enter the first and last time frame that you want to include in your GLM analysis; the default settings are 1 and the last time frame in your dataset. Press the 'OK' button.

🛃 Specify ti 💶 💷 💻 🏹				
Starting time (frame):				
1				
Ending time (frame):				
628				
OK Cancel				

• The preceding pop-up window will be replaced by either the **Image Data Editor** or **Detector Data Editor** GUI, depending on which data type you selected. Other than their title lines, these GUIs are the same as the ones described in Chap. 7: Block Averaging. Please refer to that chapter, if necessary, for explanation of how to use the Data Editor GUIs. Press the **Confirm** button when you are ready to proceed.



• The preceding action will cause a navigator window to pop up; naviSPM will generate a default name for the file that will be created, which the user is permitted to modify. At the same time, naviSPM will specify a default location for the file, which also is modifiable by the user. Note that the default file location is a folder called 'navi_data', which is a sub-folder of 'naviSPM', which is located in the same folder as the dataInfo file. If the ...\naviSPM\navi_data path does not already exist, naviSPM will create it at this time. Press the 'Save' button in the lower right corner to save the file and close the pop-up window and Data Editor GUI. At the same time, the 'Single Data Specification' sub-module will automatically update to show the path and name of the dataInfo file that you selected.

	📣 Save navi dat	a as	1				×
l	Save in:	🔋 navi_data			• •	➡ 📰 🕶	
	Recent Places	Name Name Name	Date modified ge_Hboxy.mat	Туре	Size		_
	Desktop Doug Pfeil Computer						
		File name: Save as type:	keith_image_Hbo MAT-files (*.mat)	xy.mat		• •	Save Cancel
		Single Data Spe Data type: Specify ** N: \navimanual\	cification Image *_dataInfo.mat keith\keith_dataInf	fo.mat	Hb-oxy	•	

- To load a pre-existing NAVI-based data set for GLM analysis (*i.e.*, you are using the 'pre-defined Hb dataset' option):
 - Press the 'Specify' button, causing a navigator window to pop up. Navigate to the folder containing a naviSPM-generated data file for your dataset. If the default file name and path settings were used when the file was created (as described under the preceding set of bullet points), then it will be located in a ...\naviSPM\navi_data folder, and the name syntax will be '***_[detector|image]_Hb[deoxy|oxy|tot].mat', where '***' is the name that the user originally gave to the raw data files.

Single Data Spec	cification ———							
Data type:	Image	-	Hb-oxy	•				
Specify Pre	Specify Pre-defined Hb dataset							
No file has been specified yet.								
		L						

Specify a pre-	Specify a pre-generated navi dataset									
Look in:	\rm 📗 navi_data	navi_data 🛛 🚽 🖨 🛗 🎹 🔻								
Recent Places Desktop Doug Pfeil Computer	Name Akeith_imag	Date modif e_Hboxy.mat e_Hboxy2.mat	Туре	Size						
Network	File name: Files of type:	keith_image_ MAT-files (*.r	Hboxy.mat nat)			•	Open Cancel			

Select the .mat file for the dataset that you wish to process and press the 'Open' button in the window's lower right corner. The pop-up window will close, and the 'Single Data Specification' sub-module will automatically update to show the path and name of the dataInfo file that you selected.

Single Data Spe	cification ——			
Data type:	Image	-	Hb-oxy	-
Specify Pr	e-defined Hb d	ataset		•
N: Inavimanual	(eith\naviSPM\r	havi_data\ke	eith_image_Hbo	xy.mat

Step 2: Specify a GLM design matrix, hemodynamic response function, and other parameters for Level-1 GLM analysis.

• In the 'Model specification, review and estimates' sub-module, press the 'Specify' button to launch the 'Parameter Setup for GLM Analysis (Level 1)' GUI. (Note that the 'Review' button will remain grayed out throughout the naviSPM session, as its functionalities are still under construction at this time.)

└─ Model specification, revi	iew and estimates -	
Specify	Review	Estimate
	\downarrow	

Data Info Type: Hb State: Sampling Freq:: Scans: Mesh Node No.: Image Hboxy 2.15 628 3487 NIRS data file with the directory: Nt Inavimanual/keith/naviSPM/navi_data/keith_image_Hboxy.me Directory for GLM results: Nt Inavimanual/keith/naviSPM/nspm_results/ • Model Specification • Inspecify unit for design scans BF Parameter Specification 1. Specify unit for design scans BF Parameter Specification 2. Specify basis function: none 616 1 1 6 0 30 View BF 3. Specify (multiple) conditions: Create a condition file? Create Load a pre-defined file? none View Convolution Model(s) 4. Temporal filtering? none Highpass frequency cutoff (s): 128 View DCT Set 5. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
Data info Type: Hb State: Sampling Freq.: Scans: Mesh Node No.: Image Hboxy 2.15 628 3487 NIRS data file with the directory: NthavimanualkethhaviSPM/navi_data/keth_image_Hboxy.ms Directory for GLM results: Nthavimanual/keth/naviSPM/spm_results/ Model Specification Model Specification 1. Specify unit for design scans BF Parameter Specification 2. Specify basis function: none 3. Specify (multiple) conditions: Load a pre-defined file? 4. Temporal filtering? 9. Temporal autocorrelation? 9. Temporal autocorrelation? 9. Temporal autocorrelation? 9. Temporal autocorr
NIRS data file with the directory: N: Inavimanual/keith/naviSPM/navi_data/keith_image_Hboxy.ms Directory for GLM results: N: Inavimanual/keith/naviSPM/spm_results/ Model Specification Model Specification NAVI-based procedu Confirm Model Specification 1. Specify unit for design scans BF Parameter Specification 2. Specify basis function: none BF Parameter Specification 3. Specify (multiple) conditions: Create a conditon file? Create Load a pre-defined file? none View Convolution Model(s) 4. Temporal filtering? none Highpass frequency cutoff (s): 128 View DCT Set 5. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
Directory for GLM results: N: \navimanual\keith\naviSPM\spm_results\ Model Specification Model Specification NAVI-based procedu Confirm Model Specification Specify unit for design scans BF Parameter Specification Specify basis function: none BF Parameter Specification Specify (multiple) conditions: Create a conditon file? Create Load a pre-defined file? none View Convolution Model(s) Load a pre-defined file? none Highpass frequency cutoff (s): 128 View DCT Set S. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): View Filter Matrix
Model Specification Image: Specification Image: Specify unit for design scans Image: Specify basis function: none Image: Specify basis function: none Image: Specify (multiple) conditions: Image: Specify (multiple) conditions: Image: Create a condition file? Image: Load a pre-defined file? Image: Image: Image: Specification? Image:
3. Specify (multiple) conditions: Create a conditon file? Create Load a pre-defined file? none View Convolution Model(s) 4. Temporal filtering? none Highpass frequency cutoff (s): 128 View DCT Set 5. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
Load a pre-defined file? none View Convolution Model(s) 4. Temporal filtering? none Highpass frequency cutoff (s): 128 View DCT Set 5. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
4. Temporal filtering? none Highpass frequency cutoff (s): 128 View DCT Set 5. Temporal autocorrelation? Pre-coloring: none ✓ Gaussian FVVHM (s): 4 View Filter Matrix
5. Temporal autocorrelation? Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
Pre-coloring: none Gaussian FVVHM (s): 4 View Filter Matrix
Pre-whitening: none View Filter Matrix (W)
SPM-based procedu Start Model Specification

• The 'Data Info' module has several fields containing (grayed out) information extracted from the .mat file that was specified in **Step 1**. Examine the contents of these fields to confirm that you have selected the dataset that you intended.

Type: Image	Hb State: Hboxy	Sampling Freq.: 2.15	Scans: 628	Mesh Node No.: 3487
IRS data file with	n the directory:	V: \navimanual\keith\naviS	PM\navi_data\ke	ith_image_Hboxy.ma
	I requite:			

In the 'Directory for GLM results:' line of the 'Data Info' module, naviSPM supplies a default location for the output of the computations that will be carried out. If you want the output to go somewhere else, select the 'user-defined' option from the drop-down menu. Selecting 'user-defined' causes a 'Browse for Folder' window to pop up, which you can use either to navigate to an existing folder or to create a new one.

Type:	Hb State:	Sampling Freq.:	Scans:	Mesh Node No.:
Image	Hboxy	2.15	628	3487
RS data file with	n the directory:	l: \navimanual\keith\naviS	PM\navi_data\ke	ith_image_Hboxy.ma
irectory for GLN	1 results: N: \navin	nanual\keith\naviSPM\spr	m_results\	-
	N: \navir	manual\keith\naviSPM\sp	m_results\	
lodel Specificatio	onuser-de	efined		
	Browse For Fo	older ory		
		navimanual		

AnalyzedResults
 conditionfiles
 Detectors
 Images
 Left_Motor_s25d25
 naviSPM

- 📗 navi_data spm_results ⊳ 📗 old 📙 src_modelgenerator_05102011_p som results Folder: Cancel Make New Folder OK The 'Model Specification' module provides two methods for specification of design matrices 0 and other user-defined parameters. These are the (default) 'NAVI-based procedure' and the 'SPM-based procedure'. Either one produces a .mat file that holds all the information about the specified dataset and about the GLM computation. The information is stored in a MATLAB structure array based on the SPM data structure, and it is stored in a userdesignated folder. The default location for the name syntax for the file is [the folder containing the dataset's primary dataInfo file]\naviSPM\ spm results. The default filename syntax is 'naviSPM' pre-pended to the name of the file that was generated (**** dataInfo.mat' option) or specified ('pre-defined Hb dataset' option) in Step 1.
 - The principal difference between the 'NAVI-based procedure' and 'SPM-based procedure' methods is that the former provides capabilities for the user to explicitly explore models and parameters before their selection is finalized, and the latter does not.

- Model Specification	
NAVI-based procedu Confirm M	lodel Specification
1. Specify unit for design scans	BF Parameter Specification
2. Specify basis function: none	616116030 View BF
3. Specify (multiple) conditions:	Create a conditon file? Create
Load a pre-defined file? none	View Convolution Model(s)
4. Temporal filtering? none 💌 Highp	bass frequency cutoff (s): 128 View DCT Set
5. Temporal autocorrelation?	
Pre-coloring: none 💌 Gauss	sian FWHM (s): 4 View Filter Matrix
Pre-whitening: none	w Filter Matrix (W)
SPM-based procedu Start Model	Specification

Method 1: Specify the model and other parameters using NAVI-based procedure

1) Select either 'scans' (the default) or 'seconds' from the 'Specify unit for design' drop-down menu.



2) Select a hemodynamic response function (HRF) from the 'Specify Basis Function:' drop-down menu. The 'HRF Parameter Specification' field and 'View BF' button, which are grayed out under the default 'none' selection, become enabled when you select any of the other options from the menu.¹ Press the 'View BF' button to open a pop-up window containing a plot of the HRF that you have selected.

¹ The purpose of using an HRF is to account for the empirical fact that the hemodynamic correlates of a change in neural activity are not perfectly synchronized with that activity. Thus if a subject is, for example, presented with a brief visual stimulus (flash of light), the subject's primary visual cortex activity will increase immediately but the resulting inrush of oxygenated blood to that region typically will begin 1-2 seconds later, peak ~6 sec after stimulus onset, and persist for a few tens of seconds. Therefore it is recommended that you select an HRF option other than 'none' for your data analyses. (However, you may find that 'none' is useful for testing, training and demonstration purposes.)



The number of user-adjustable parameters is different for different HRF types. When you make a selection, the significance of each parameter is displayed in the MATLAB command window. For example, if you select the 'hrf' option (or 'hrf (with time derivative)' or 'hrf (with time and dispersion derivatives)'), there are seven parameters whose default values can be modified:

```
>>
```

```
p =
p(1) - delay of response (relative to onset); p(2) - delay of
undershoot (relative to onset); p(3) - dispersion of
response; p(4) - dispersion of undershoot; p(5) - ratio of
response to undershoot; p(6) - onset (seconds); p(7) - length
of kernel(seconds);
```

The numerical values assigned to the parameters affect the shape of the plotted function, influencing features such as the time to maximum and minimum value and the dispersion (width) of the positive- and negative-going peaks. Because of interactions between the parameters' effects, the first five do not correspond directly to specific features of the HRF such as the time-to-peak or the peak width. Even so, each parameter has a primary role in shaping the overall response function. These are:

- p(1). The principal determinant of the time (in seconds) at which the response reaches its maximally positive value, with respect to the onset of the experimental condition (e.g., the beginning or the end of a stimulus block that the hemodynamic variables are responding to). Increasing P1 increases the time-to-peak.
- p(2). The principal determinant of the time (sec) at which the response reaches its maximally negative value, with respect to the onset of the experimental condition. Increasing P2 increases the time-to-peak.
- p(3). The principal determinant of the width (sec), or "dispersion," of the positive-going peak.
- p(4). The principal determinant of the dispersion (sec) of the negative-going peak.

- p(5). Approximately equal to the ratio (dimensionless) of the maximum positive value to the (absolute value of the) maximally negative value; the approximation improves as the time lag between the maximum and minimum values increases.
- p(6). The time lag (sec) between the change in experimental condition and the beginning of the associated hemodynamic response,
- p(7). The total duration (sec) of the response function. Note that this does not guarantee that the response will have decayed away by this number of seconds, only that it will not be evaluated at longer times. Remember to visually inspect the HRF to ensure that it has the properties you expect!



The HRFs corresponding to several of the other menu options, with the default parameter values selected in every case, are shown in the next figure. You will notice that in some cases a plot contains more than one curve. In these cases, naviSPM will separately convolve each of the plotted functions with the experimental design models that you will specify in the next step.





3) In this next step you will use one of the functionalities available under 'Specify (multiple) conditions:' to generate a measurement-specific design matrix for GLM. The design matrix has the same number of rows as the number of data time frames in the dataset, and a number of columns equal to the number of different patterns of hemodynamic variation that you think may be present in the image or detector data. A simple demonstrational example of a design matrix is:

$$\mathbf{X} = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 1 & 0 & 0 & 1 \\ 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix},$$

where the alternating 1s and 0s in the first three columns indicate the time frames when an experimental condition (*e.g.*, a sensory stimulus, motor task, or cognitive challenge) was present (1 = "on") or absent (0 = "off"). Models of this type are commonly referred to as "boxcar functions." Note, however, that experimental-condition models are <u>not</u> required to be periodic, or to have "on" and "off" periods of equal duration, or to have only two states. For example, if a task has more than one difficulty level, the corresponding column of the design matrix might use values of 0, 1, 2, ... to denote the different levels (0 = "off," 1 = "easy," 2 = "more difficult," ...).

Alternatively, the design matrix could have a distinct column for each task level, each having the sort of binary off/on structure as depicted above.

The fourth, constant-value column in the preceding design-matrix example is analogous to the intercept in the general formula for a straight line. Its purpose is to account for the non-zero time-average value that may be present in the image or detector time series. In contrast to the experimental design models considered in the preceding paragraph, this model accounts for a phenomenon that likely is present in the data (*i.e.*, different mean values in different pixels or channels) but probably will not be of interest to you. It is included in the design matrix in order to "soak up" a percentage of the data variance that, if not accounted for in this way, could negatively impact your ability to see the true effects of the experimental-design conditions. In order to account for an even larger percentage of the uninteresting data variance, the design matrix also may include linear, quadratic, and higher-order trend terms in addition to the constant. However, if it is not convenient for you to specify these yourself, naviSPM has the ability to generate them for you, as is subsequently described.

A third type of model that sometimes is included in a design matrix is a column of numbers proportional to an external physiological (*e.g.*, blood pressure) or physical (*e.g.*, accelerometer or other macroscopic-motion detector) measurement that was performed at the same time as the fNIRS measurement. These time series are considered because they also may account for some percentage of the data variance, in a manner that is unrelated to the direct effects of the experimental design. If you want to include models of this type in the design matrix, it is necessary to read them into naviSPM from an external ASCII file;² naviSPM is not able to generate them, and at present they can not be represented in either the .mat-file or the .evt-file format described below.

If correctly formatted experimental design time series already are present in a file, then use the 'Load a pre-defined file?' drop-down menu to select type of file that you are using. The three file types that are available in the menu are:

• 'user-defined stimulus design matrix (*.dat)'. The design matrix is stores in an ASCII text file have the extension '.dat'. It has as many rows as there are time frames in the fNIRS dataset. The number of columns in the file is equal to the sum of the number of experimental conditions, the number of ancillary measurements, and the number of trend terms (constant, linear, etc.) that you choose to explicitly specify. Each column specifies a numerical value for the corresponding model, at every time frame.

3. Specify (multiple) conditions	: Create a conditon file
Load a pre-defined file?	none View Conv
4. Temporal filtering? none 5. Temporal autocorrelation?	none user-defined condiftion file (*.mat) experimental event file (*.evt) user-defined stimulus design matrix (*.dat)
Pre-coloring: none	e
	\downarrow

 $^{^{2}}$ NIRx imaging systems offer you the ability to record ancillary data collected simultaneously with your fNIRS measurements in the .evt file that is part of the output of every recording session, and to synchronize the external data streams with the fNIRS time frames.

🚺 Select an pre-	ready file conta	ining simulus d	esign matrix						×
Look in:	Conditionfile	s		•	¢	£	ď		
Ca.	Name	Date modif	Туре	Size					
Recent Places	a boxcar.dat								
									- 1
Desktop									
Doug									
Computer									
L 🖉									
Network									
	File name:	boxcar.dat					•	0	pen
	Files of type:	ASCII-file (*.e	lat)				•	Са	ncel

This data-entry option is the one that you must use if there will be more than two levels (off/on) in the experimental-condition columns of the design matrix. Note that naviSPM will automatically generate the constant-valued design-matrix column, so you should <u>not</u> explicitly include one in your ASCII file.

• 'experimental event file (*.evt)'. The starting and ending time frames for the time intervals in which the experimental condition is "on" are specified in the experimental .evt file, in a manner similar to that used to indicate the starting and ending time frames for block averaging (Chapter 7). *The naviSPM .evt-file option is still under construction at this time, and will be made available in a future release of NAVI.*

3. Specify (multiple) conditions:	Create a conditon file
Load a pre-defined file?	none View Conv
4. Temporal filtering? none	none user-defined condiftion file (*.mat)
5. Temporal autocorrelation?	experimental event file (*.evt)
Pre-coloring: none	user-defined stimulus design matrix (*.dat)

- 'user-defined condition file (*.mat)'. Parameters sufficient to fully characterize one or more design-matrix columns of the boxcar type are contained in a MATLAB binary file, in three cell arrays named 'durations', 'names' and 'onsets'. For the demonstration dataset considered in this user's guide, the contents of these fields are:
 - \circ durations {1} = 31 31 31 31 31 31 31 31 31
 - \circ names {1} = Left Finger tapping
 - \circ onsets {1} = 54 123 192 261 330 399 468 537

NAVI User's Guide

	3. Specify (multiple)) conditions:		Create a	a conditon file	
	Load a pre-def	ined file? no	ne	-	View Convo	
	4. Temporal filtering	I? none us	ne er-defined condifi	tion file (*.mat)		
	5. Temporal autoco	rrelation?	perimental event f er-defined stimulu	file (*.evt) ıs design matrix	(*.dat)	
	Pre-coloring:	none			e	
			\downarrow			
🛃 Select an u	ser-defined condit	ftion file (*.ma	t)			×
Look	in: 🚺 conditionfile	es			≝ 🖬	
œ.	Name	Date modif	. Туре	Size		
Recent Place	condition_	scans.mat				
Necenii Hace.	° 🔄 condition_	seconds.mat				
Desktop						
Doug						
Computer						
2						
Network						
	File name:	condition_s	cans.mat		•	Open
	Files of type:	MAT-files (.mat)		•	Cancel

One way to generate a file having the correct format is to use the 'Create a condition file?' functionality of naviSPM, as described below. Alternatively, if you are a proficient in MATLAB you can generate a cell array having the indicated format at the MATLAB command window (<u>http://www.mathworks.com/help/techdoc/ref/cell.html</u>). When you do, make certain that you use the same time unit [frames (scans), in the preceding example]

If you do not have a file containing correctly formatted experimental design time series, then press the 'Create' button next to 'Create a condition file?' to launch the 'Condition File Setup for GLM' pop-up window, as shown in the following figure.

Specify (multiple) conditions:		Create a c	conditon file?	Create
Load a pre-defined file?	user-defined condiftio 👻] [View Convolu	tion Model(s)
	\downarrow			

	condition_scans.mat
Directory for condition file:	N:\navimanual\keith\conditionfiles\
Sampling frequency (Hz No. of condition	t): 2.15 Unit for design: O scans Is: 1 O seconds
Condition(s) Specification—	
Specify	Confirm
Spcified condition(s)	
Spcified condition(s)	

In the 'Condition File' module, you may:

- Accept the default 'Condition file name:' or change it to one that you prefer.
- Accept the default location for the conditions file, or else select 'user-defined' from the dropdown menu adjacent to 'Directory for condition file:'. The latter action will launch a 'Browse For Folder' window, which you can use to navigate to the folder where you want to store the conditions file, or else create a new folder for that purpose.
- Select the time unit you want for the 'durations' and 'onsets' cell arrays, using the radio buttons adjacent to 'Unit for design:'. (In some cases you may subsequently need to convert between frames and seconds. To assist you in this, the data sampling rate read from the dataInfo file is shown in the 'Sampling Frequency (Hz):' field, but it is not editable.)
- In the text field adjacent to 'No. of conditions:', indicate the number of boxcar-type model function that you want to include in the design matrix.

After making your selections, press the 'Specify' button in the 'Condition(s) Specification' module to launch the 'Specify condition 1' pop-up window shown in the following figure.

Specify condition 1
Name
condition1
Onset(s)
[1,10,30]
Duration(s)
[5,5,5]
OK Cancel

Here you may:

- Accept the default 'Name:' or change it to one that you prefer.
- In the 'Onset(s)' field, specify the correct starting time frames (or time in seconds, depending on which unit you selected in the 'Condition File' module) for each boxcar segment (*e.g.*, each presentation of a particular stimulus) associated with the experimental condition.
- In the 'Duration(s)' field, specify the correct starting time (frames or seconds, depending on which unit you selected in the 'Condition File' module) for each boxcar segment associated with the experimental condition.

Press the 'OK' button at the bottom of the window. If you entered a number larger than 1 in the 'No. of conditions' field, the window will refresh and the title will change to 'Specify condition 2'. Repeat the preceding sequence of steps for each remaining experimental condition. The window will automatically close when you press 'OK' for the final condition.

Press the 'Confirm' button in the 'Condition(s) Specification' module to save the conditions file with the file name and location that you specified in the 'Condition File' module; the 'Condition File Setup for GLM' window will automatically close. Alternatively, press the 'Close' button to exit without saving any of the changes you have made.

After you either load a conditions-defining file or use naviSPM to create one, the 'View Convolution Model(s)' will be enabled, as shown here:

3. Specify (multiple) conditions:		Create a c	conditon file?	Create	
Load a pre-defined file?	user-defined condiftio	•	View Convolut	ion Model(s)	

Press that button in order to launch the two windows shown in the following figure. The first one contains plots of the time series that show the state (*e.g.*, present or absent, difficulty level) of each experimental condition as a function of time, before (blue curve) and after (green) they have been convolved with the HRF (the simple 'hrf' model was used for the example depicted here). Also shown is the spatial mean time series (red curve) for the hemodynamic variable you are analyzing, so that you can directly see whether there is good temporal alignment between the data and the design-matrix models. The second window is a graphical depiction of the design matrix, after the experimental conditions have been convolved with the HRF. In this second window, shades of gray are used to represent the numerical values that are shown along the y-axis in the first window. Note that, as indicated above, naviSPM automatically generates the constant-value

term (last column) of the design matrix. (Note that these graphics windows will not automatically close, but must be closed manually.)



The next figures show the convolved models and design matrix for the case of 'hrf (with time and dispersion derivatives)', which is the HRF used to generate results shown in subsequent figures.



4) If you want naviSPM to generate design-matrix columns to account for data variance unrelated to the experimental design, select 'DCT' (<u>discrete cosine transform</u>) from the 'Temporal Filtering?' drop-down menu. This will enable the adjacent 'Highpass frequency cutoff (s):' text field and the 'View DCT Set' button.

4. Temporal filtering?	none 👻	Highpass frequency cutoff (s): 128 View DCT Set
5 Temporal autocorrel	none	
	DCT	
		\downarrow
		v
4. Temporal filtering?	DCT 👻	Highpass frequency cutoff (s): 128 View DCT Set

Press the button to launch the two windows shown in the following figure. The curves shown in these figures (overlaid colored x-y plots in the first, separated gray-scale surface map in the second) are additional design-matrix columns that define sinusoidal rhythms having different frequencies. Their purpose is to "soak up" temporal variability in the hemodynamic data that is not related to the experimental conditions.



The significance of the number in the 'Highpass frequency cutoff (s):' field is that fluctuations with periods longer than the indicated value will be suppressed (*i.e.*, partially accounted for by the sinusoidal models), while shorter-period fluctuations will be regarded as part of the signal you are trying to account for with the experimental-condition models. You may enter a number smaller than the 128-seconds default value if you also want to suppress shorter-period fluctuations, and press the 'View DCT Set' button again to view the result. (Note that these graphics windows will not automatically close, but must be closed manually.)



5) In order to maximize the accuracy of the statistical inferences that you will draw from the GLM computations, it is important to account for the fact that the value of a hemodynamic variable at one time frame is correlated with the values it has at the frames immediately preceding and following it, and that the correlation falls off as the lag between two time frames increases. This phenomenon is called "serial correlation."

Two methods for dealing with serial correlation are available in the 'Temporal autocorrelation?' step. One approach is known as pre-coloring, which means that the data are assumed to have serial correlations, and the GLM formulation includes a mathematical term that explicitly models the dependence of the correlation on the time interval between two data values. The other approach is known as pre-whitening, which means that before the GLM computation is

performed the data time series are mathematically pre-treated using an algorithm that attempts to remove the influence of each data value on the ones that come after it in time.

To apply pre-coloring to your data, select either the 'Gaussian' or the 'hrf' option from the 'Pre-coloring:' drop-down menu. If you select 'Gaussian', you will have the option of specifying a FWHM (<u>full-width at half-maximum</u>; for a Gaussian, 1 FWHM ≈ 2.355 standard deviations) that is different from the 4-second default value (the FWHM value that you use will presumably be based on independent estimates you have made on the duration of the serial correlation).

5. Temporal autocorrelation?
Pre-coloring: none Gaussian FWHM (s): 4 View Filter Matrix
Pre-whitening Gaussian View Filter Matrix (W)
\downarrow
5. Temporal autocorrelation?
Pre-coloring: Gaussian 🗸 Gaussian FWHM (s): 4 View Filter Matrix

If you select 'hrf', then the GLM computation will proceed under the assumption that the serial correlation is proportional to the value of the hemodynamic response function, adjusted so that the maximum serial correlation occurs when the time lag is zero (since every data value is perfectly correlated with itself).

5. Temporal autoco	rrelation?		
Pre-coloring:	hrf 🥃 Gaussia	n FVVHM (s): 4	View Filter Matrix
Pre-whitening	none Gaussian	Filter Matrix (W)	
		\checkmark	
5. Temporal autoco	rrelation?		
Pre-coloring:	hrf 🚽 Gaussia	an FWHM (s): 4	View Filter Matrix

Press the 'View Filter Matrix' button to open a window in which the serial correlation matrix is displayed as a color-scale map, as shown in the following figure.



To pre-whiten your data, select 'AR(1)' (<u>autoregression</u> of order <u>1</u>; this is the only option available at this time) from the 'Pre-whitening:' drop-down menu.

5. Temporal autocorrelation?
Pre-coloring: none Gaussian FVWHM (s): 4 View Filter Matrix
Pre-whitening: none View Filter Matrix (W)
SPM-based pro AR(1) Model Specification
\downarrow
5. Temporal autocorrelation?
Pre-coloring: none Gaussian FWHM (s): 4 View Filter Matrix
Pre-whitening: AR(1)

For every pixel or channel time series in your dataset, the AR(1) algorithm fits the data to a model of the form $x(t_i) = a + b \cdot x(t_{i-1})$, and it finds those values for the coefficients *a* and *b* that minimize the difference between $x(t_i)$ and $a + b \cdot x(t_{i-1})$. The GLM computation subsequently operates upon the residual, $r(t_i) = x(t_i) - a - b \cdot x(t_{i-1})$, which has substantially less serial correlation than the original data. Press the 'View Filter Matrix (W)' button to open a window that displays a color-scale map showing which data values are used as predictors for each subsequent one, as shown in the following figure. (Note that, since only order-1 autoregression is used at present, what is seen is a simple identity matrix.)



6) Press the 'Confirm Model Specification' button at the top of the 'Model Specification' module, to generate a design matrix incorporating the experimental conditions, HRF, and more advanced options that you have specified. During this process a graphics pop-up window will open, showing a gray-scale map of the columns of the design matrix that are related to experimental conditions (and also the constant term, but not the sinusoidal trend terms that you may have specified).





Method 2: Specify the model and other parameters using SPM-based procedure

The SPM-based procedure is still under construction at this time, and will be made available in a future release of NAVI.

- 1) Select the 'SPM-based procedure' radio button located at the bottom of the 'Model Specification' module.
- 2) Press the 'Start Model Specification' button, then follow the program requests in order to generate the GLM model function(s), HRF, detrending options and serial correlation correction options that are analogous to those described above.

Step 3: In the 'Model specification, review and estimates' sub-module, press the 'Estimate' button to start the process of solving the GLM equation: $Y = X\beta + E$.

- Model specification, revie	w and estimates -	
Specify	Review	Estimate

The variables in the GLM equation are:

- Y is the matrix of hemodynamic data. Its dimensions are $N_t \times N_s$, where N_t is the number of measurement time frames and N_s is the number of pixels (for image data) or channels (for detector data).
- X is the design matrix that was generated in Step 2. Its dimensions are $N_t \times N_m$, where N_m is the total number of models (including the constant and any terms that you may have included to account for subject motion or other sources of variance not related to the experimental design).
- β is a $N_m \times N_s$ matrix of numbers that, when multiplied by **X**, produces linear combinations of design-matrix columns that are the maximally accurate approximations to the hemodynamic time series. This matrix is the unknown quantity that is solved for in the GLM computation; hence it is referred to as the "GLM-parameter matrix" or "GLM-coefficient matrix."
- E is the "error term" or "residual term." It has the same dimensions as Y and is the quantity that the GLM algorithm seeks to minimize (*i.e.*, the more accurately $X\beta$ approximates to Y, the smaller E becomes). The E matrix also is useful for evaluating whether theoretical assumptions that underlie the GLM technique are violated: for example, ideally every column of E will have the same standard deviation, the correlation between any two columns of E will be zero, and the elements of E will be normally distributed.

For estimation of β , naviSPM uses a SPM-based algorithm called ReML (restricted maximum likelihood) to compute a least-squares solution to an overdetermined system of linear equations. Under ideal conditions the ReML solution is the same as the solution obtained with any other method for solving systems of linear equations. But ReML is more robust than other methods to non-ideal effects, such as the presence of uncontrolled sources of variance in the measurement data.

In practice, you should notice that the estimation process runs quickly if you used a pre-coloring option to correct for serial autocorrelation (or if you did not use either method). In contrast, if you used the pre-whitening option, then naviSPM will resort to an iterative nonlinear optimization algorithm to solve the GLM equation. The optimization algorithm frequently converges, *but convergence is not guaranteed*. If it fails to converge for the dataset you are analyzing, you will need to re-generate the conditions file using a different serial correlation correction.

When the GLM computation is complete, a Help dialog pop-up will open, displaying the path an name of the output file.

🛃 Help Di	alog
	The estimated results are stored in N:\navimanual\keith\naviSPM\spm_results\naviSPM_keith_image_Hboxy.mat and can be viewed using "naviViewer" or "spmViewer" with naviSPM. OK

Step 4: Display the results of the GLM computation

- Use NAVI Viewer to display results from your analysis of reconstructed image time series.
 - Press the 'NAVI Viewer' button in the 'Results Visualization' sub-module to launch the 'NAVI-Based SPM Result Viewer' GUI shown in the following figure.

Results Visualization	
NAVI Viewer	SPM Viewer

naviSPM_resultsViewer		
NAVI-Based SPM	Result Vie	wer
└── View SPM results		
Specify SPM Result (*.mat) < Please spe	ecify an existing SPM	result file first.
View Beta Image	Beta:	1
Specify Contrast (SPM Contrast Manager)	p-value:	0.05
Specified Contrast:]	
Save the specified resuts. ASCII Format	• ?	

• Press the 'Specify SPM Result (*.mat)' button in the 'NAVI-Based SPM Result Viewer' GUI. This will open a navigator pop-up window, as illustrated here. Navigate to and select the naviSPM_***.mat file for your dataset (recall that default location is the [raw data path]\naviSPM\spm_results' sub-folder). The path and file you select will appear in the text field adjacent to the 'Specify SPM Result (*.mat)' button. A new text line also will appear in the GUI, to remind you of how many GLM coefficients were computed in **Step 3** (*i.e.*, number of models in the design matrix).

Pick an NAVI-I	based SPM resu	lt file					×
Look in:	spm_results	;		•	de 🔁	di 🗐	
(Han	Name	Date modif	Туре	Size			
Recent Places	🖻 naviSPM_k	eith_image_Hb	oxy.mat				
Desktop							
Doug							
Computer							
L 💐 -							
Network							
	File name:					-	Open
	Files of type:	MAT-files (*.r	mat)			•	Cancel
<u> </u>							

NAVI-Based SPM F	Result View	wer
- View SPM results-		
Specify SPM Result (* mat)	SDM)som resultsin	aviSDM keith image k
Speerry of Minesuk (max)	SPM/spm_results in	aviorim_kelui_image_i
There are 4 GLM coefficients (betes) found in the specif	iad SDM raculto	
There are 4 GLM coefficients (betas) found in the specif	ied SPM results.	
There are 4 GLM coefficients (betas) found in the specif	ied SPM results. Beta:	1
There are 4 GLM coefficients (betas) found in the specif	ied SPM results. Beta:	1
There are 4 GLM coefficients (betas) found in the specif	ied SPM results. Beta: p-value:	1
There are 4 GLM coefficients (betas) found in the specif	ied SPM results. Beta: p-value:	1
There are 4 GLM coefficients (betas) found in the specif View Beta Image Specify Contrast (SPM Contrast Manager) Specified Contrast:	ied SPM results. Beta: p-value:	0.05
There are 4 GLM coefficients (betas) found in the specif View Beta Image Specify Contrast (SPM Contrast Manager) Specified Contrast: Save the specified results ASCII Format	ied SPM results. Beta: p-value:	0.05

• From the drop-down menu adjacent to the 'View' button, select the GLM-related parameter that you want to view. The available menu selections, as shown in the following figure, are:

aviSPM_results	Viewer									
NAVI-Based SPM Result Viewer										
View SPM results Specify SPM F There are 4 GLM	View SPM results Specify SPM Result (*.mat) N:\navimanual\keith\naviSPM\spm_results\naviSPM_keith_image_F There are 4 GLM coefficients (betes) found in the specified SPM results									
View	View Beta Image Beta: 1									
Specify C	Beta Image Contrast Image	p-value:	0.05							
Specified Contr	ResMS Image SPM{t} Image									
Save the sp	SPM{t} Image Thresholded SPM{F} Image SPM{F} Image Thresholded	• ?								

- 'Beta Image': A "beta" (*i.e.*, Greek letter β) is one of the coefficients that the GLM model uses to explain fluctuations in the image data in terms of the temporal models in the design matrix. This is expressed mathematically as y(t) = β₁•x₁(t) + β₂•x₂(t) ... + β_M•x_M(t), where y(t) is the time-varying image value in a given image voxel, and x₁(t), x₂(t), ..., x_M(t) are the models included in the design matrix. The ReML algorithm finds the specific values for β₁, β₂ ..., β_M that make the two sides of the preceding equation as nearly equal as possible.
- 'Contrast Image': A contrast is a weighted sum of one or more models from the design matrix, embodying a biological hypothesis that you wish to evaluate. For example, suppose that the models $x_1(t)$ and $x_2(t)$ tell you when two different experimental stimuli

(*e.g.*, a low-pitched sound and a high-pitched sound) were presented to the subject, and you want to know if the second induces a larger hemodynamic response than the first does. The resulting contrast image will show you the value of the difference $\beta_2 - \beta_1$, which is close to zero in voxels where the two experimental conditions have comparable effects, positive in voxels where the second has a larger <u>absolute</u> effect that the first, and negative in voxels where the first has a larger <u>absolute</u> effect that the second.

- 'ResMS Image': The term 'ResMS' is an abbreviation for "<u>res</u>idual <u>mean square</u>"; in other words, a ResMS image shows you the spatial distribution of values in the E matrix described above (see **Step 3**). Inspection of this image, which ideally will show little if any spatial structure, can assist you in deciding how well your design matrix satisfies the theoretical assumptions underlying the GLM analysis.
- 'SPM{t} Image': Interpretation of beta and contrast values can be difficult, because they are determined by two distinct factors: 1) how closely the time-varying GLM models approximate the time-varying hemodynamic image values; 2) the magnitude or amplitude of the fluctuations in each voxel. To allow for an unambiguous assessment, naviSPM can compute a t-statistic that simultaneously considers both of the preceding factors. The t-statistic is a normalized, dimensionless number. Let us continue to use the hypothetical example considered in the 'Contrast Image' item. Then the SPM{t} image has positive values in voxels where the second experimental condition has a larger relative effect that the first, and is negative in voxels where the first has a larger relative effect that the second.
- 'SPM{t} Image Thresholded': For the preceding menu option, the displayed image will show you the t-statistic values in <u>all</u> image voxels. But the computed value of a t-statistic will rarely be exactly zero, even in voxels where the hemodynamic effects of the two experimental conditions really do have the same amplitude. If you choose the 'SPM{t} Image Thesholded' option, the displayed image will have non-zero values in only the voxels where the t-statistic is statistically significant and is positive-valued. (To see which voxels have statistically significant negative t-statistic values, it is necessary to specify another contrast that reverses the algebraic signs of the first contrast.)
- 'SPM{F} Image': Some biological hypotheses involve comparisons of three or more experimental conditions. For example, you may want to know if there are any differences among the hemodynamic responses elicited by three auditory stimuli, that is, whether or not β₁, β₂ and β₃ are all the same. Other hypotheses involve comparisons among two or more contrasts, for example, if β₂ β₁ is different from β₃ β₂. These types of comparisons can be performed by using the F-test capability of naviSPM. The F-statistic is a dimensionless quantity that has large values if the experimental conditions induce different hemodynamic responses (which in turn give rise to different beta values or contrasts of beta values).
- 'SPM{F} Image Thresholded': If you choose the 'SPM{F} Image' option, the displayed image will show you the F-statistic values in all image voxels. If you choose the 'SPM{F} Image Thesholded' option, the displayed image will have non-zero values in only the voxels where the F-statistic is statistically significant.
- Example for viewing a beta image:

• Select 'Beta Image' from the drop-down menu.



- Enter a model number (*i.e.*, design-matrix column) in the 'Beta:' text field.
- Press the 'View' button. The spatial distribution of the GLM coefficient you have selected will be displayed in a GUI having the same appearance and functionalities as the GUI for viewing reconstructed images (Chapter 6).





- Example for viewing a contrast image:
 - Select 'Contrast Image' from the drop-down menu. This will disable the 'Beta:' field and enable the 'Specify Contrast (SPM Contrast Manager)' button.

View	Contrast Image	•						
Specify (Specify Contrast (SPM Contrast Manager)							
Specified Con	trast:							

 Press the 'Specify Contrast (SPM Contrast Manager)' button to launch the 'SPM contrast manager' GUI.

View	Contrast Image
Specify C	ontrast (SPM Contrast Manager)
Specified Cont	rast:

Press the 'Define new contrast...' button in the 'SPM contrast manager' window. This will launch the '*define contrast...*' utility. In the '*name*' field, enter a name for the contrast you are going to define. In the '*type*' field, select the 't-contrast' radio button.

SPM contra	ast manager			
_ show	Select	contrasts		
• t-co	ontrasts	 F-contrasts) all	
#### {ty	pe}:name			
noTo	contrasts defi	ned	*	no contrast(s)
				Design matrix
	efine new contr	rast Reset	Done	parameter estimability
		Selected 0 c	ontrasts.	?

• For this demonstration, we will consider the hypothetical example described above: the models $x_1(t)$ and $x_2(t)$ tell you when two different experimental stimuli (*e.g.*, a low-pitched sound and a high-pitched sound) were presented to the subject, and you want to know if the second induces a larger hemodynamic response than the first does. Place the cursor in the '*contrast*' field and type "-1 1", then press the '...submit' button. (A value of 0 is automatically assigned to all models that follow the last one that you explicitly

assigned a value to. If you were interested in the difference between the first and <u>third</u> GLM models, then you would type "-1 0 1" in the '*contrast*' field.)

SPM contrast manager	
define contrast	
lowpitchhighpitch	contract(s)
type • t-contrast • F-contrast	
contrast weights weights uecht -1 1 -1 1 - (right padded with 2 zeros) Reset Cancel OK	Design matrix
name defined, contrast defined	?

• Examine the graphical display of the contrast you have defined, in the right-hand side of the 'SPM contrast manager' window, to ensure that it is what you intended. When you are satisfied, press the 'OK' button near the bottom of the window. Then press the 'Done' button near the bottom of the 'SPM contrast manager' window.

SPM contrast manager	
name define contrast	
type t-contrast F-contrast	contrast(s)
contrast ueidt: ueid	Design matrix parameter estimability
name defined, contrast defined	?
\downarrow	

SPM contrast manager		
Select c	ontrasts	
● t-contrasts	F-contrasts all	
#### {type} : name		contrast(s)
001 {T} : lowpitchhighp	bitch 🔺	
		Design matrix
Define new contras	st Reset Done	parameter estimability
Selecte	ed 1 contrast, press "Done" wh	en finished.

 Press the 'View' button in the 'NAVI-Based SPM Result Viewer' window. Proceed as in the 'Beta Image' case.

	V	ïew	Contrast I	mage		•	
		Specify Co	ontrast (SP	M Contrast	Manage	r)	
	Spec	ified Contr	ast:	T-con	trast		
			\downarrow				
🛃 ImageView (C	ontrast Image:[-1 🛛	1 0 0])					□ X
	Insert Tools D	estop Window	Help Others			Display Option	ns: pns: pns: pns: pns: pns: pns: frid e frid e frid e frid e frid frid e frid
3	-8.34e-008	9.58e-0		3.20e-007		FEM Model:	

• **NOTE:** Although you can go through the motions of defining an F-contrast instead of a t-contrast, you will get the following warning dialog pop-up when you press the 'View' button. At this time naviSPM is not set up to display F-contrast values directly.



- Example for viewing a ResMS image:
 - Select 'ResMS Image' from the drop-down menu.

View	ResMS Image	-

• Press the 'View' button, and proceed as in the 'Beta Image' case.

🚺 Ir	mageVi	iew (RE	sMS Im	age: err	or estimate))						
File	Edit	View	Insert	Tools	Desktop	Window	Help	Others			 	
												Display Options:
								1		-		Time (frame) ◀►
				a i		Alter						Hb State: Hboxy 🗸
				ł.		2 :		4				Axial View (Top to Bottom)
												Orthogonal View
				8		4						Change Display Grid
				1								Rescale Image
			3	ŧ.		4		\$				Create Slice Animation
			- 5	ð.,		362		1				Overlay on MRI Image
						*		All.				This is the image corresponding to the one you have selected to be viewed.
	a.					3		J				FEM Model:
				<u> </u>		•						17
	N.C.			ł.		\$						
			1.49	e-029		8.04e-()15		1.	81e-014		6

- Example for computing and viewing a SPM{t} image:
 - Select 'SPM {t} Image' from the drop-down menu. This will enable the 'Specify Contrast (SPM Contrast Manager)' button.
| View | SPM{t} Image | | |
|---|--------------|--|--|
| Specify Contrast (SPM Contrast Manager) | | | |
| Specified Contrast: T-contrast | | | |

 Press the 'Specify Contrast (SPM Contrast Manager)' button to launch the 'SPM contrast manager' GUI.

View	I{t} Image
Specify Contra	ist (SPM Contrast Manager)
Specified Contrast:	T-contrast
SPM contrast manager	
Select contrast	<i>s</i>
t-contrasts F-contrasts	o ali
#### {type} : name 001 {T} : lowpitchhighpitch	no contrast(s)
	Design matrix
Define new contrast	eset Done parameter estimability
Select	ied 0 contrasts.

- Proceed as in the 'Contrast Image' case.
 - If you want to generate a t-statistic map for a single model, you can enter a single "1" in the '*contrast*' field. Enter "1" to get a t-statistic map for the first model, "0 1" for the second model, "0 0 1" for the third, etc.

SPM contrast manager	
name define contrast	
type • t-contrast F-contrast	contrast(s)
contrast weithts wector	
1 <- (right padded with 3 zeros)	Design matrix
Reset Cancel	OK parameter estimability
name defined, cont	rast defined ?

SPM contrast manager		
Select contrasts		
t-contrasts F-contrasts all]	
#### (type) : name	1	contrast(s)
001 {T} : lowpitchhighpitch	1	
002 {T} : tstatsinglemodel		
		Design matrix
	_	
Define new contrast Reset Done		parameter estimability
Selected 1 contrast proce "Dono" with	an fir	niched La
	ion ni	<u>IIIIIII</u>
	_	
I		
\checkmark		
View SPM(t) Image		•

View SPM{t} Image			
Specify Contrast (SPM Contrast Manager)			
Specified Contrast: T-contrast			



- Example for computing and viewing a thresholded SPM {t} image:
 - Select 'SPM{t} Image Thresholded' from the drop-down menu. This will enable the 'Specify Contrast (SPM Contrast Manager)' button and the 'p-value:' text field.

View SPM{t} Image Thresholded	Beta:	1
Specify Contrast (SPM Contrast Manager)	p-value:	0.05

• Enter a statistical significance level in the 'p-value' field. For example, if you enter "0.05," the resulting plot will show you the t-statistic values in all voxels where the contrast is statistically significant at the p<0.05 level (one-side t-test, not corrected for multiple tests). In all other voxels, the original t-statistic values will be changed to zero.

View SPM{t} Image Thresholded	Beta:	1
Specify Contrast (SPM Contrast Manager)	p-value:	0.05

- Press the 'Specify Contrast (SPM Contrast Manager)' button to launch the 'SPM contrast manager' GUI.
- Proceed as in the 'Contrast Image' case.

	Image	View (Th	resholded SPM{t]	Image: p-value =	: 0.05)			
F	ile Edi	t View	Insert Tools I	Desktop Window	Help Others			ע
								Display Options:
				.	-	. 💓		Time (frame) 1
				·	-	- - 1	¥	Hb State: Hboxy - Axial View (Top to Bottom)
L								Orthogonal View
			1 () 1	E.B.o.	_			Change Display Grid
				- *				Rescale Image
						1.1		Create Slice Animation
				1	-			Overlay on MRI Image
				-	-			This is the image corresponding to the one you have selected to be viewed .
			a'	-				FEM Model:
			* [
			0.00e+000	2.08e+	000	4.69e+000)	6

- To change the p-value threshold, simply enter the new value in the 'p-value' field and press the 'View' button. It is <u>not</u> necessary to repeat the contrast specification process.
- Example for viewing a SPM{F} image:
 - Select 'SPM{F} Image' from the drop-down menu. This will enable the 'Specify Contrast (SPM Contrast Manager)' button.

View SPM{F} Image		
Specify Contrast (SPM Contrast Manager)		
Specified Contrast:	T-contrast	

 Press the 'Specify Contrast (SPM Contrast Manager)' button to launch the 'SPM contrast manager' GUI.

View SPM{F} Image			
Specify Contrast (SPM Contrast Manager)			
Specified Contrast:	T-contrast		

Press the 'Define new contrast...' button in the 'SPM contrast manager' window. This will launch the '*define contrast...*' utility. In the '*name*' field, enter a name for the contrast you are going to define. In the '*type*' field, select the 'F-contrast' radio button.

SPM contrast manager	
Select contrasts	
t-contrasts F-contrasts all	
#### {type} : name 001 {T} : lowpitchhighpitch 002 {T} : tstatsinglemodel	no contrast(s)
Define new contrast Reset Done	parameter estimability
Selected 0 contrasts.	?

For this demonstration, we will consider the hypothetical example of three distinct experimental auditory stimuli: there may be a difference between the hemodynamic responses associated with the first and <u>second</u>, and there may be a difference between the hemodynamic responses associated with the first and <u>third</u>, and you want to know whether there is a significant <u>difference between the differences</u> anywhere in the brain. Place the cursor in the '*contrast*' field and type either "1 -1 [Enter key] -1 0 1" or "1 -1 0 0; -1 0 1 0". Then press the '...submit' button.

🛃 SPM contrast manager	
name define contrast threestimuli	
type • F-contrast	contrast(s)
<pre> I -1 contest i -1 0 1 weight reduced design i -1 <- (right padded with 2 zeros) + 1 0 1 <- (right padded with 1 zero) </pre> Reset Cancel OK	Design matrix
name defined, contrast defined	1 ?

• Examine the graphical display of the contrast you have defined, in the right-hand side of the 'SPM contrast manager' window, to ensure that it is what you intended. When you are satisfied, press the 'OK' button near the bottom of the window. Then press the 'Done' button near the bottom of the 'SPM contrast manager' window.



 Press the 'View' button in the 'NAVI-Based SPM Result Viewer' window. Proceed as in the 'Beta Image' case.

科 ImageView (SI	PM{F} Image: F-sta	atistic map)			
File Edit View	Insert Tools	Desktop Window H	elp Others		۲
					Display Options:
•					Time (frame) 1 ∢
					Hb State: Hboxy
			- - 4		Axiai View (Top to Bottom)
	100				Orthogonal View
					Change Display Grid
<u></u>					Rescale Image
					Create Slice Animation
			-	_	Overlay on MRI Image
					This is the image corresponding to the one you have selected to be viewed.
			-		FEM Model:
	3.41e+000	6.49e+001		1.42e+002	6

- Example for viewing a thresholded SPM{F} image:
 - Select 'SPM{F} Image Thresholded' from the drop-down menu. This will enable the 'Specify Contrast (SPM Contrast Manager)' button and the 'p-value:' text field.

View SPM{F	Image Thresholded 🔍	Beta:	1
Specify Contrast	(SPM Contrast Manager)	p-value:	0.05
Specified Contrast:	F-contrast		

• Enter a statistical significance level in the 'p-value' field. For example, if you were to enter "1e-12," the resulting plot would show you the F-statistic values in all voxels where the contrast is statistically significant at the p<1e-12 level (not corrected for multiple tests). In all other voxels, the original F-statistic values will be changed to zero.

View	SPM{F} Image Thresholded	•	Beta:	1
Specify Co	ontrast (SPM Contrast Manager)		p-value:	1e-12

 Press the 'Specify Contrast (SPM Contrast Manager)' button to launch the 'SPM contrast manager' GUI.



Proceed as in the 'SPM{F} Image' case.



- If you specify a contrast matrix containing only one row, then the resulting F-test will be equivalent to a <u>two</u>-sided t-test performed on the same contrast. The reason is that in this special case, the F-statistic value for any voxel is the square of the t-statistic value for that same voxel. That is, F-statistic values are always non-negative, whereas t-statistics may be either positive or negative. Thus the thresholded SPM{F} will have non-zero values in all voxels where the F-statistic is statistically significant, whether the contrast value is positive or negative.
- To change the p-value threshold, simply enter the new value in the 'p-value' field and press the 'View' button. It is <u>not</u> necessary to repeat the contrast specification process.
- Use NAVI Viewer to display results from your analysis of detector-channel time series. *The* NAVI Viewer utility for detector time-series data is still under construction at this time, and will be made available in a future release of NAVI.
- Use SPM Viewer to display results from your analysis of reconstructed image time series. *The* **SPM Viewer** *is still under construction at this time, and will be made available in a future release of NAVI.*

Level-2 Analysis with naviSPM

The following steps are carried out using the functions and utilities in the 'SPM: Level 2 (between-subject) module.

Step 1: Specify and load multiple SPM Level-1 data sets.

• In the 'Multiple Data Specification' sub-module, enter the number of groups in the 'Number of groups:' field, and the numbers of subjects in each group in the 'Number of subjects:' field.

	NaviSPM Statistical Parametric Mapping (DYNOT-Based Neuroimaging Analysis) Help Quit SPMt.Level 1 (within-subject) Single Data Specification Data type: mage Hb-oxy Specify **_dataInfo.mat No file has been specified yet. Model specification, review and estimates Specify Review Results Visualization NAVI Viewer SPM Viewer	
Specify the number of groups.	Results Visualization NAVI Viewer SPM Viewer SPM Level 2 (between-subject) Multiple Data Specification Cecify Arrange data order: No Yes Number of groups: 2 Number of subjects: [5, 5] Contrast specification, result visualization Specify NAVI Viewer	Specify the number of subjects in each group.

• Press the 'Specify' button to launch a navigator window, as shown in the following figure. Use it to navigate to and select a naviSPM_***.mat file containing previously generated Level-1 results, for each subject in turn.

Specify	Arr	ange data order: 🥛	No OYe:
Number of groups:	2	Number of subject	s: [2, 2]
ontrast specification	n, result	visulization	1
Specify	0	NAVI	Viewer
- opoon)			nonor



- So that you won't lose your place during the process of loading multiple datasets, the title bar initially reads 'Specify Group1 Subject1 NAVI-based SPM result file', and after the first file is loaded this changes to 'Specify Group1 Subject2 NAVI-based SPM result file', etc. After the file for the last subject in the first group has been loaded, the title changes to 'Specify Group2 Subject1 NAVI-based SPM result file', etc.
- However, naviSPM does not compare the names of the files that you load to ensure that they are all of the same data-type field ("_image_" vs. "_detector_") or the same hemoglobin isoform field ("_Hbdeoxy" vs. "_Hboxy" vs. "_Hbtot"), or to ensure that you haven't loaded the same file more than once. Carefully examine the name of each file before pressing the 'Open' button, to ensure that you are loading the correct one.
- If the design matrices for different subjects don't all have exactly the same ordering of experimental conditions, then it is necessary for you to re-arrange the columns of the design matrices so that they do all have the same condition order. To do this, select the 'Yes' radio button adjacent to 'Arrange data order:'. This will launch a user interface that allows you to permute the design-matrix columns for selected data sets, in a convenient way.

• Identify which dataset(s) need re-sequencing of design-matrix columns, by entering the group number in the 'Group:' field and the subject number(s) in the 'Subject(s):' field. Note that if

two or more subjects in a single group have the same incorrect ordering of design-matrix columns, you may permute the columns of all of their design matrices in one operation.

- Specify Data &	Order		
Specify Data	a: Group:	1	
	Subject(s):	[2]	
Specify Orde	• 		
Old Co	ndition Order:	[1 2 3 4 5 6 7]	
New Co	ndition Order:	[1623457]	

• In the 'New Condition Order:' field, enter the sequence in which you want to arrange the design-matrix columns, so that they will match the ordering of columns in the other datasets' design matrices.

Specify Data & Order	
Specify Data: Group:	1
Subject(s):	[2]
Specify Order:	
Old Condition Order:	[1 2 3 4 5 6 7]
New Condition Order:	[1623457]

o Press the 'Confirm' button the implement the re-ordering that you have specified.

Specify Data & Order	
Specify Data: Group:	1
Subject(s):	[2]
pecify Order:	
Old Condition Order:	[1 2 3 4 5 6 7]
New Condition Order:	[1623457]

 Press the 'Adjust more data' button if there are additional datasets with inconsistently ordered design-matrix columns, or 'Close' to close the 'Adjust Order of Conditions in Loaded Data' window.

Specify Data & Order	
Specify Data: Group:	1
Subject(s):	[2]
Specify Order:	
Old Condition Order:	[1 2 3 4 5 6 7]
New Condition Order:	[1623457]

Step 2: Specify the F-test contrast matrix or t-test contrast matrix.

• Press the 'Specify' button in the 'Contrast specification, result visualization' sub-module. This will launch the 'SPM contrast manager' GUI.

Specify	Arrange data order: 🚫 No 💿 Yes
Number of group:	s: 2 Number of subjects: [2, 2]
ontrast specificat	tion, result visulization —

Selec	ct contrasts	•	
 5/1000 1-contrasts 	⊙ F-contrasts	Gal	
#### {type} : name			
no F contrasts (defined	-	no contrast(s)
		3	Design matrix
Define new c	ontrast Rese	t Done	

- Press the 'Define new contrast...' button in the 'SPM contrast manager' window. Proceed in the same manner as described above for generating Level-1 SPF{F} images or Level-1 SPF{t} images.
 - The type of biological hypothesis that you will most commonly be evaluating is that an experimental condition, or some combination of conditions, elicits a different hemodynamic response in one group of subjects than in another group. For example, suppose that:
 - Models $x_1(t)$ and $x_2(t)$ tell you when a low-pitched and a high-pitched sound, respectively, were presented to the subjects.
 - One subject group comprises people who play musical instruments professionally, while the other group consists of control subjects who work in other fields.
 - You want to know if the difference between the hemodynamic responses to the two sounds is larger in the first subject group than in the second.
 - The design matrix for each subject also includes three other temporal models that are not relevant to this hypothesis.
 - You would test the preceding hypothesis by specifying

	Des for :	ign m subjec	atrix n t grou	nodels p 1	_	I f	Design r or subje	natrix	model up 2	s	Constant term in composite (2-group) design matrix
1^{st} contrast \rightarrow	$\begin{bmatrix} -1 \end{bmatrix}$	1	0	0	0	0	0	0	0	0	0
2^{nd} contrast \rightarrow	0	0	0	0	0	1	-1	0	0	0	0

as the F-contrast matrix.

• Note that it is also permissible to specify a contrast (*i.e.*, an individual row of the contrast matrix) that includes information from both groups. For example, suppose that the biological hypothesis you want to evaluate is that there is a difference between the inter-

group response differences for experimental condition 3 and for experimental condition 4. You can test that hypothesis by specifying

 $\begin{bmatrix} 0 & 0 & 1 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix}$

as the F-contrast matrix.

• If you are testing a hypothesis involving a simple comparison between two conditions, it may be more appropriate to perform a t-test. For example, suppose that the biological hypothesis you want to evaluate is that there is a difference between the two groups' hemodynamic responses to condition 5. You can test that hypothesis by specifying

 $\begin{bmatrix} 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 \end{bmatrix}$

as the t-contrast matrix.

• When you press the 'Done' button in the 'SPM contrast manager' window, a pop-up window will open asking if you want to save the contrast-generation results (default answer is 'yes'), and suggesting a name for the results file. If you wish, you can modify or replace the file name. Pressing the 'OK' button will simultaneously close the pop-up window and launch a navigator window, which you can use to select a folder in which to save the results (default is the current directory of MATLAB).

Step 3: Viewing a SPM{F} image, or a thresholded SPM{F} image.

• Press the 'NAVI Viewer' button in the 'Contrast specification, result visualization' sub-module. This will launch the 'NAVI-based SPM Result' GUI.

Multiple Data Specification
Specify Arrange data order: O No O Yes
Number of groups: 2 Number of subjects: [2, 2]
Contrast specification, result visulization Specify NAVI Viewer
↓
🛃 naviSPM_resultsViewer_L2
NAVI-Based SPM Result Viewer
View SPM(F) Image p-value: 0.05
Save ASCII Format Close

- Select an option ('SPM{F} Image', 'SPM{F} Image Thresholded', 'SPM{t} Image', 'SPM{t} Image Thresholded') from the drop-down menu that is adjacent to the 'View' button.
 - Press the 'Load' button to launch a navigator window. Use it to locate and select a file containing the Level-2 contrast that you want to view, and press the 'Open' button to load it.
 - The only exception to the preceding would occur if you are still in the same naviSPM session in which you generated the Level-2 contrast you want to view, and it is the most recently generated contrast, and you have selected the correct contrast type (*i.e.*, F or t) from the drop-down menu. In this case, you can bypass the 'Load' operation and simply press the 'View' button.
 - If you selected one of the 'Thresholded' items from the drop-down menu, enter your choice of significance level in the 'p-value:' field.
- Press the 'View' button. The spatial distribution of the t- or F-statistic you have selected will be displayed in a GUI having the same appearance and functionalities as the GUI for viewing reconstructed images (Chapter 6).



• If you chose either the 'SPM{F} Image' or the 'SPM{t} Image' option, the displayed image will show you the statistic values in all image voxels. If you chose either the 'SPM{F} Image Thesholded' or the 'SPM{t} Image Thesholded' option, the displayed image will have non-zero values in only the voxels where the statistic is statistically significant.

Appendix: Monkey Brain Atlas



Introduction

We have developed a rhesus-monkey brain atlas, for DYNOT/NIRScout users whose research interests include 3D optical image reconstruction and functional mapping of the monkey brain. The atlas is based from two MRI maps: a whole-head image obtained from a single animal, and a group-average brain-only image derived from scans of 112 animals. For our atlas, we replaced the brain elements of the whole-head image with the group-brain image. The resulting hybrid atlas will be representative of a larger number of individual animals.

Hybrid Monkey Map & Segmentation

In order to produce the hybrid rhesus monkey atlas, it was necessary to merge a highresolution 3D MR image of a rhesus monkey head (healthy, young, male) and a populationaverage MRI-based rhesus macaque brain atlas (112 monkeys: 80 males, 32 females [D.G. McLaren *et al.*, *NeuroImage* **45**, 52 (2009)]). By carefully measuring the dimensions of the single-animal brain and the group-average brain along their principal axes and executing an affine transformation, we substituted the group brain for the individual brain to produce the hybrid monkey atlas. Figures A1-A3 show the individual rhesus monkey head, the groupaveraged brain and the hybrid rhesus monkey head MR images, respectively.



Figure A1. Individual rhesus macaque MRI



Figure A2. Group-averaged rhesus macaque brain MRI



Figure A3. Hybrid rhesus macaque head MRI

The hybrid monkey head has been segmented into six tissue types: skin, muscle, skull, cerebrospinal fluid (CSF), gray matter, and white matter. Figure A4 shows a representative segmented 2D axial section, where skin is color-coded white, muscle is light blue, skull is blue, CSF is yellow, gray matter is red, and white matter is green.



(a) Hybrid MRI map

(b) Segmentation of hybrid MRI map

Figure A4. Segmentation of hybrid rhesus macaque atlas

FEM Mesh & Models

Based on the segmentations of the hybrid monkey head, we have generated 3D finite element method (FEM) meshes for numerically solving the diffusion equation constituting the forward problem of diffuse optical tomography (DOT). Taking the characteristics of optical imaging (*e.g.*, light penetration depth of several centimeters) into account, the whole monkey head is divided into several optical imaging regions/pieces, and then a segmented FEM mesh was generated for each region. Axial, coronal and sagittal views of one of the region meshes is shown in Figure A5.



Figure A5. Segmented FEM mesh of an optical imaging region

In order to reconstruct the 3D optical images of monkey brain, we need to load into NAVI the FEM model that matches the experimental imaging region and source/detector configuration. A FEM model contains reference detector readings and weight functions that can be obtained by numerically solving the DOT forward problem. The monkey brain FEM models for each of the imaging regions have been computed and saved in a FEM model database.

As an example, Figure A6 illustrates a monkey-brain FEM model that has 64 sources and 64 detectors on the skull surface. The imaging region for this model is shown in Figure A5. The FEM model is saved in ...\NIRXpackage\NIRX_NAVI\navi_models\monkey_brain_64x64\'.



Figure A6. A monkey FEM model with 64 sources and 64 detectors

FEM Model Generator

You can use the 'FEM Model Generator' module in the **Utilities** portal of NAVI to generate a monkey brain model that matches the user-defined source/detector geometry. The steps are detailed in Chapter 9 of NAVI User's Guide. The 'FEM Model Generator' GUI is illustrated in the following figure:

Load	FEM Model Int	formation
Set	Source Positions	Graphically Set
Set	Detector Positions	Graphically Set
Generate	Reference Mediu and Wei	m Detector Readings ght Function
View	FEM Model In	formation
Forward FEM Model R	u <mark>nning Status:</mark> n file føstl	

Image Reconstruction & Functional Mapping

The steps involved in using NAVI to reconstruct monkey brain optical images are the same as those that are described in detail in Chapters 1-6 of the NAVI User's Guide. When you use NAVI's Hemodynamic Image Viewer to display reconstructed 3D monkey brain images, the viewer will overlay the optical images onto the hybrid monkey brain MRI if you click the 'Overlay on MRI Image' button and select a sliced image by mouse (see Chap. 6 for a complete description of this functionality). Figures A7 and A8 show an example, in which the Hemodynamic Image Viewer is used to view images reconstructed from experimental data collected from a dynamic phantom monkey head, and to overlay the optical image information onto the structural MR image.



Figure A7. Images reconstructed from monkey-phantom experimental data.



(a) Axial view

(b) Sagittal view



(c) Coronal view

Figure A8. Images reconstructed from monkey-phantom experimental data overlaid onto the hybrid monkey brain MRI.



FEM Brain Model Generator User's Manual



Software and documentation developed by the Optical Tomography Group (<u>http://OTG.downstate.edu</u>) of SUNY Downstate Medical Center (450 Clarkson Ave., Brooklyn, NY, 11203; <u>http://www.downstate.edu</u>)

FEM Brain Model Generator

Introduction

Brain Model Generator is a MATLAB-based, interactive FEM model-generation tool. It allows users to modify and customize the FEM brain models that are supplied with NAVI, to match novel experimental source/detector geometries.

Installation

The system requirements for the current release of ModelGenerator include having a MATLAB 7.x release installed on your computer, and that you have the Image Processing Toolbox in addition to basic MATLAB.

To install the p-file version (*i.e.*, code that is executable but not editable) of ModelGenerator, please follow these steps:

- 1. Place the installation CD/external hard disk in your computer, and navigate to a directory called 'src_modelgenerator_p'.
- 2. Copy the entire folder and save it in your computer's NAVI workspace. For example, if NAVI is located in a folder called 'C:\NIRXpackage', then you would create a subfolder called 'C:\NIRXpackage\NIRX_BrainModelGenerator' and copy the src_modelgenerator_p files into it. The resulting file structure will contain a sub-folder that is called

'C:\NIRXpackage\NIRX_BrainModelGenerator\src_modelgenerator_p'.

- 3. Add the newly created folder to the MATLAB search path by doing the following:
 - Launch MATLAB by double-clicking the MATLAB icon on your desktop.
 - Select 'Set Path...' from the File menu, or type "pathtool" at the MATLAB prompt. This will open the Set Path dialog box, which is used to view and modify the MATLAB search path.
 - Navigate to the src_modelgenerator_p folder in your computer by clicking on the 'Add with Subfolders...' button. This will cause the Browse for Folder window, containing a searchable directory tree, to pop up. Locate the src_modelgenerator_p folder and then click on the OK button to place src_modelgenerator_p and all its subfolders into the MATLAB search path.
 - Save the changes you have made for later use by clicking on the Save button in the Set Path dialog box. Then click on the Close button, after which you may exit from MATLAB.

Launching FEM Brain Model Generator

Type "brainmodel" at the MATLAB command prompt and press the Enter key. The main interface for FEM Brain Model Generator, shown in the following figure, will open.

Load	Brain Model Information	Rotating Image On Off	EEG 10-20 System clear
Locate	DOT Imaging Region	······	
Manua	ally Setting		
Measu Data F	Format none		
Set	Detector Positions		
Set	Source Positions		
Generate	FEM Brain Model		
View	Generated FEM Model	Y	
Load	FEM Model Information		

Loading Brain Model Information

Clicking on the **Load** button shown at the top of the preceding figure will open the popup window shown in the following figure. You can use this 'pick Brain model information file' window to specify an existing file containing brain-model information. The appropriate file will be located in the '...\NIRX_Brain_Library\BrainModelbase\' folder that comes bundled with NAVI (see Chap. 1, p. 1), and it will have the name 'brain_modelsInfo.mat'.

Look in:	📕 BrainMoo	lelbase		٠.	
0	🍌 box1	Ja Fei	MLibs	🗾 box8_boxInfo	
and the	🍶 box10	💌 bo	x10_boxInfo	📰 brain_modelsInfo	
Recent Items	🌛 box11	😿 bo	x11_boxInfo	🗊 brain_modelsInfo_0	
	box12	🔝 bo	x12_boxInfo	🗃 brain_modelsInfo_V6	
-	퉬 box13	📰 bo	x13_boxInfo	brain_modelsInfo_v7	
	🍶 box14	💌 bo	x14_boxInfo	🗊 brain_modelsInfo_v71	
Desktop	🌙 box15	📰 bo	x15_boxInfo		
	box2	🔝 bo	x1_boxInfo		
	퉬 box3	🕅 bo	x2_boxInfo		
	🍶 box4	🔝 bo	x3_boxInfo		
My	🌛 box5	🔝 bo	x4_boxInfo		
Documents	🍌 box61	🔝 bo	x5_boxInfo		
n 🔊	🌙 box62	🔝 bo	x61_boxInfo		
	🌙 box71	🔝 bo	x62_boxInfo		
Computer	box72	🔊 bo	x71_boxInfo		
	퉬 box8	🕅 bo	x72_boxInfo		
	File name:	brain_modelsInfo	o.mat		Open

As illustrated in the following figure, successful loading of the brain_modelsInfo.mat file enables several buttons that initially were "grayed out" (see p. 1). These buttons are used to perform the next set of processing steps.



In order to accurately locate the DOT imaging region and optode positions, an extended EEG 10-20 system is overlaid onto our image atlas, as shown in the preceding figure (green dots, yellow text labels). The original coordinates of the 10-20 system were obtained from EEGLAB (<u>http://sccn.ucsd.edu/eeglab/</u>) and were co-registered with our image atlas via an affine transformation.

The definition of the extended 10-20 system is shown in the following figure. The labels Nz, Iz, T9, and T10 (circled) denote the nasion, inion, left and right pre-auricular points, respectively; these are commonly used reference-voltage points for scalp EEG measurements.



Locating DOT Imaging Region

The Generator provides you with two ways to locate a DOT imaging region: **Manually Setting** and **Measured S/D Coordinates**. Click on one of the radio buttons below the **Locate** button to indicate your choice of method.

1. Manually Setting option

Manually Setting is the default method for locating the imaging region.

Step 1: Click the **on** button located in the upper right portion of the GUI, next to the words "Rotating Image." Move the mouse cursor onto the meshed 3D head image, press and hold down the primary mouse button, and rotate the head image by moving the mouse. The purpose of rotating the image is to bring the aspect of the head that you are interested in (*e.g.*, the occipital cortex region) into view.

🚺 xyBrainModels_v65	Name of Concession, Name of Street, or other		_ 0 <mark>_ ×</mark>
	FEM Bra	ain Model Generator	
Load	Brain Model Information	Rotating Image on off	EEG 10-20 System clear
Locate	DOT Imaging Region	25	
⊚ Manual ⊙ Measur Data F	Ily Setting ed S/D Coordinates ormat none +	20 - 50 05 102 00 00 00 00 00 00 00 00 00 00 00 00 0	CCEDREP COEDREPCT
Set	Detector Positions	5 CFU5 CP3 PCF 15 5 CF5 5 CF5 PCP5 5 CF5 PCP53	P3+1 ^{H3-2}
Set	Source Positions		PO3 PO1PQHY20 PO3 CFC 55 «OPO1PH98
Generate	FEM Brain Model	СССУЗ Р7 Р0 РТ9 РСР9Р07 Т9гр9ро Р09	7 ∗O1 *O2 *020 9 *OI1 *O2 9 *OI1 *O2
View	Generated FEM Model FEM Model Information		91 "12
		10 15 20 20	15 10 5
		T Generator Rt Please first LOAD the brain model information file Please LOCATE the DOT imaging Region.	Inning Status from the FEM brain model database.
Exit	Help		•

Step 2: Click on the **Locate** button that is inside the DOT Imaging Region box, move the mouse cursor onto the head region that you want to specify, and click the primary mouse button.

In the example shown below, a user is specifying the occipital cortex as the DOT image region.



Clicking the primary mouse button causes four images to appear in the GUI, as shown in the following figure. The upper-left sub-figure shows the position that you specified as a red dot, and the other three sub-figures are the three pre-defined DOT imaging regions that are closest to the selected point.



Step 3: Move the mouse cursor onto one of the three DOT image regions that have appeared in the GUI, and click the primary mouse button to select it as your DOT imaging region.

As illustrated in the following figure, selection of an imaging region enables the two **Set** buttons, which previously were grayed out. In addition, a magnified representation of the DOT imaging region you selected will appear in the GUI.



Proceed to the next step, Setting Source and Detector Positions, on page 13.

2. Measured S/D Coordinates option

You also can locate the DOT imaging region by loading the measured source/detector coordinates from a file that contains that information. In order to register the source/detector positions on our FEM brain model, you first have to measure the coordinates of fiducial points on the subject's head surface, then measure the source/detector positions. At this time, the generator is configured to accept fiducial data from the Polhemus Patriot 3D Tracking System (http://polhemus.com) or a specific format of measured data that is called user-defined format data. The capability for accepting fiducial data from other surface rendering systems is under construction.

There are thirteen 10-20 system positions on the head surface that are selected as fiducial points. The locations, names, and measuring order of the points are shown in the following figure.



Fiducial Points: Definition and measuring order

```
1. Nz
          (Nasion)
 2. Lpa
          (Left pre-auricular)
 3. Rpa
          (Right pre-auricular)
 4. Iz
          (Inion)
 5. Cz
          Length (Nz,Cz) = 0.5L_1, Length (Lpa,Cz) = 0.5L_2
 6. Fpz
         Length (Nz, Fpz) = 0.1L_1
 7. Fz
         Length (Nz, Fz) = 0.3L_1
 8. Pz
          Length (Nz, Pz) = 0.7L_1
 9. Oz
         Length (Nz, Oz) = 0.9L_1
10. Т7
          Length (Lpa, T7) = 0.1L_2
11. C3
          Length (Lpa, C3) = 0.3L_2
12. C4
          Length (Lpa, C4) = 0.7L_2
13. Т8
         Length (Lpa, T8) = 0.9L_2
      [L_1 = Length(Nz, Iz), L_2 = Length(Lpa, Rpa)]
```

If you use the Polhemus Patriot 3D Tracking System to digitize points, the system must be have two sensors: a stylus and a receiver. The stylus is used to digitize points, and the receiver is rigidly fixed to the subject's head as a reference point during digitization, and is used for moving error correction. The Appendix to this chapter contains a detailed description of how to save the data recorded using a Patriot system in a format that the brain model generator can read.

If you use a different 3D tracking systems to digitize the points, you may send us your measured data and our software developers will add a new feature to the brain model generator to allow you to load your digitized data. Alternatively, if you edit and save your measured data in a text (ASCII) file having the format summarized in the following table, the current version of the brain model generator can load it. You must arrange the digitized data in a table of space-separated numbers, with each row containing the X, Y, and Z coordinates for one digitized point. Note that all fiducial points and source and detector positions must be digitized in the same reference frame and in units of centimeters.

	Х	Y	Z
Point 1	X ₁	y 1	z_1
Point 2	X2	y ₂	Z ₂
÷	:	:	:
Point n	X _n	y _n	Zn

|--|

In our product CD or external hard disk, there are two demonstration sets of digitized data saved in a folder called

...\NIRXpackage\NIRX_BrainModelGenerator\digitizing_demodata\. One of the demo data sets was obtained using a Polhemus Patriot, while the other is in the above-described user-defined format. You can open the latter file in any text editor (e.g., Notepad, WordPad) or spreadsheet program (e.g., Excel) in order to examine the data format.

Use the following sequence of steps to locate the DOT imaging region:

Step 1: Click the **Measured S/D Coordinates** radio button, and then select one of the listed data formats from the Data Format pull-down menu. For example, the Polhemus Patriot Format was selected here.



Step 2: Click the **Locate** button that is in the DOT Imaging Region box. This action will open a pop-up window, which you will use to navigate to the folder where the files containing the measured source/detector coordinates are stored. Load the measured fiducial-point coordinates file first, then the detector coordinates file, and finally the source coordinates file.



				-
Look in:	🌗 patriot_1		•]	
Ecent Items	detector_c	<mark>oords</mark> ints_coords ords		
Desktop				
E				
My Documents				
My Documents (Computer				
My Documents	File name:	detector_coords.txt		Open

Look in:	patriot_1		•]	🖻 📸 🥅 🗐	
Secent Items	detector_c	oords ints_coords ords			
Desktop					
My Documents					
Computer					
Computer	File name:	source_coords.txt			Open

After the three measured coordinate files are successfully loaded, the measured source/detector coordinates will be registered onto the corresponding DOT imaging region of the standard FEM brain model, and the model source/detector positions will be located automatically. The imaging region and measured source/detector positions are shown in the GUI, as illustrated below.


Proceed to the next step, Generating FEM Brain Model, on page 19.

Setting Source and Detector Positions

To generate a new FEM model, you should first define the source and detector positions. The Generator allows you to graphically set the source/detector configuration, using a "child" GUI developed for that purpose.

1. Setting Detector Positions

Step 1: Clicking the **Set** button next to the words "Detector Positions," as illustrated here, brings up a new GUI titled Graphically Set Detector Positions.





Step 2: If necessary, rotate the imaging region to make sure that you are able to see all of the possible detector positions (the pink dots in the preceding figure). To do this, click the **on** button next to the words "Rotating Image," move the mouse cursor onto the meshed image, press and hold down the primary mouse button, and rotate the image by moving the mouse. A result of this type of rotation is shown in the next figure:



- **Step 3:** Type the number of detectors used to collect imaging data in the Number of Detectors text field located in the left middle area of the Graphically Set Detector Positions GUI.
- **Step 4:** Click the **Set** button in the upper left corner, move the mouse cursor onto the first detector position, and click the primary mouse button. Then move the cursor onto the next detector position and click the primary mouse button again. Repeat this process until all detectors are specified for the new model.

If you make a mistake during setting the detector positions and want to delete a detector location you already have set, click the **Clear** button under the **Set** button to delete the most recently set detector. Then click the **Set** button again to continue setting detector positions.

Step 5: Click the **Save & Close** button in the lower left corner of the Graphically Set Detector Positions GUI to save your detector configuration setting after all detector positions have been specified for the new model.

Shown here is an example of a completed detector-positions setting, where there were 24 detector positions to be set.



2. Setting Source Positions

The steps for setting source positions are parallel to those given above for setting detector positions.

Step 1: Clicking the **Set** button next to the words "Source Positions" in the parent GUI, as illustrated in the next figure, brings up a new GUI titled Graphically Set Source Positions.





For guidance, the detector positions you already have specified are shown in the imaging region.

Step 2: If necessary, rotate the imaging region to make sure that you are able to see all of the possible source positions (the pink dots in the preceding figure). To do this, click the **on** button next to the words "Rotating Image," move the mouse cursor onto the meshed image, press and hold down the primary mouse button,



and rotate the image by moving the mouse. A result of this type of rotation is shown in the next figure.

- Step 3: Type the number of sources used to collect imaging data in the Number of Sources text field located in the left middle area of the Graphically Set Sources GUI
- Step 4: Click the Set button in the upper left corner, move the mouse cursor onto the first source position, and click the primary mouse button. Then move the cursor onto the next source position and click the primary mouse button again. Repeat this process until all sources are specified for the new model.

If you make a mistake during setting the source positions and want to delete a source location you already have set, click the **Clear** button under the **Set** button to delete the most recently set source. Then click the **Set** button again to continue setting source positions.

Step 5: Click the **Save & Close** button in the lower left corner of the Graphically Set Source Positions GUI to save your source configuration setting after all source positions have been specified for the new model.

Shown here is an example of a completed source positions setting, where there were 12 source positions to be set.



Once the source/detector configuration is successfully set, the **Generate** button in the parent GUI will be enabled. Both the detector and source positions you have set will be labeled, as shown in the following figure, with detector positions marked by green dots, source positions by red dots, and co-located source/detector positions (if there are any) by pink dots.



Generating FEM Brain Model

Click the **Generate** button in the FEM Brain Model Generator GUI to start the process of generating forward-problem solutions for the selected FEM model and source/detector configuration. During the operation, a progress bar will pop up to show you how the calculations are proceeding.



Upon completion of the model generation step, a new window will open, with a text field in which you can specify a folder where you want to save the new model. You can either use the default folder name suggested by the Generator, or define a name you prefer; note, however, that any name you enter may *not* contain any blank spaces, and *must* contain the default key word (this is the 'box1', 'box2', ..., or 'box72' prefix in the suggested name). For example, 'box8_experiment1' is a permissible user-defined folder name. Then click the OK button to store the FEM model in the specified folder.

Please specify the name	of folder to save new m	odel 🛛 🔀
Name of folder to save generated r box8_S12D24	nodel:	
	ок	Cancel

After the saving, a warning dialog box will open. The complete path for the folder where the generated FEM model was saved is shown in the box.



A successful FEM model generation enables the **View** button for further processing.

Viewing Generated FEM Model

You can view either pre-existing models or a newly generated one using the **View** button inside the Generated FEM Model box in the FEM Brain Model Generator GUI. Clicking on the **View** button brings up another GUI, as shown in the next figure, with the following four functions:

- **Outline** (this is the default)
- Detectors
- Sources
- D & S

1. Outline

Clicking the **Outline** button displays four types of FEM model information in the model information window:

- **FEM Mesh:** numerical information about the mesh
- **Source/Detector Configuration:** numerical information about the sources and detectors, and names of the files containing the new coordinates
- Forward FEM Model: names of generated files containing output from the forward-problem computations

	Generated FEM Model Information	
lodel Information		
Outline		
Detectors	Model Information: OUTLINE	
	EEM Mesh:	
Sources	Number of Nodes: 4256	
D&S	Number of Tetrahedrons: 18393	
	Number of Surface Triangles: 2532	
	Mesh Dimension in cm: [11.0147 4.7462	5.987]
	Source/Detector Configuration:	
	Number of Sources: 12	
	Number of Detectors: 24	
	Source Coordinates: SourCoords.FEM	
	Detector Coordinates: DetcCoords.FEM	
	Forward FEM Model:	
	Detector Readings: det.FEM	X7XM
	Weight Function: w.FEM	
	Model saved in: N:\Shared_Folders\Yong_Xu\BrainModelbas	e\FEMLibs\box8_S12D24

2. Detectors

This function allows you to review the model geometry and detector positions.



If you generated the FEM model from measured source/detector coordinates, the **Detectors** function will show the detector indices on the located DOT imaging region and the corresponding original detector indices from your experimental configuration. The original detector indices are shown within parentheses. An example of this case (which happens to have an exact match between the original and mapped detector-position indices) is shown in the following figure.



3. Sources

This function allows you to review the model geometry and source positions.



If you generated the FEM model from measured source/detector coordinates, the **Sources** function will show the source indices on the located DOT imaging region and the corresponding original source indices from your experimental configuration. The original source indices are shown within parentheses. An example of this case (which happens to have an exact match between the original and mapped source-position indices) is shown in the following figure.



4. D & S

This function allows you to view the model geometry and the detector and source positions simultaneously.



Appendix: Brief Manual for Polhemus (http://www.polhemus.com) Patriot System

1. Installing the Patriot Host Software

- a. The Patriot host software PiMgr is intended for installation on a computer running Windows 2000, Windows XP or Win7.
- b. See <u>Install the Host Software</u> on page 6 of the Patriot User Manual for instructions.

2. Setting and Powering up the Patriot

- a. Detailed instructions for setting up the Patriot system are presented on pages 1-5 of the Patriot User Manual.
- b. Set up the Patriot system close to your host computer and away from large metal objects such as file cabinets, metal desks, etc., and away from the floor and walls.
- c. Usually, there are four steps to powering up the Patriot:
 - i. First ensure that the power switch on the back panel of the Patriot is in the OFF (Down) position and that the power supply is not plugged in;
 - ii. Plug in the source and two sensors (Stylus into sensor receptacle 1 and the other sensor into receptacle 2);
 - iii. Plug in the desired I/O cable (USB or RS-232);
 - iv. Plug in the power supply and turn the Power Switch to the ON (Up) position.

On startup, the power indicator will blink red for 5-10 seconds to indicate the system's performance of an initialization and self-test routine. System operation is not possible during this time. At the completion of this routine, the power indicator will change from a flashing red state to a steady green state.

3. Collecting Measurement Data from the Patriot System by Using the Polhemus PiMgr GUI

The instructions for using the Polhemus PiMgr GUI can be found on pages 6-8 of the Patriot User Manual. The usual steps for collecting measurement data from the Patriot by using the GUI are:

a. Power up the Patriot;

- b. Open the Polhemus PiMgr GUI on your computer;
- c. Create a connection and set Tracker and Station Configurations through the Polhemus PiMgr GUI Device menu:

```
Device \rightarrow Track Configuration \rightarrow General: Measurement Unit (CM);
\rightarrow Connection: Type (RS-232 or USB);
Device \rightarrow Toggle Connection;
```

Device \rightarrow Toggie Connection,

Device \rightarrow **Station Configuration** \rightarrow **Hemisphere**: e.g., (0,0,-1) for Z-; \rightarrow **Stylus**: Point/Track

d. Select data recording type through the Polhemus PiMgr GUI Motion menu:

Motion \rightarrow Recording \rightarrow Toggle Record;

- e. Move the stylus to the position you want to locate;
- f. Type 'p' or 'P' anywhere on the PiMgr window. This will cause PiMgr to request a single data frame from the Patriot system;
- g. Repeat steps (e) and (f) until you locate all positions of interest.

4. Saving the Measured Data

There are two steps to save your measured data as a text file.

a. Stop the data recording through the Polhemus PiMgr GUI Motion menu:

Motion \rightarrow Recording \rightarrow Stop

b. Export the data through the Polhemus PiMgr GUI File menu:

File \rightarrow **Export Motion Recording** (save as a text file: *.txt)

5. Useful Range

An X, Y, or Z position value exceeding Patriot's useful range of **60 inches** (**152 cm**) will be output as zero.

6. Hemisphere of Operation

The theory of the hemisphere of operation is described in detail in the Patriot User Manual.

Because of the symmetry of the magnetic fields generated by the source, there are two mathematical solutions to each set of sensor data processed. Therefore, only half of the total spatial sphere surrounding the source is practically used for any measurement. This is referred to as the current hemisphere. The current hemisphere is defined by a LOS (Line of Sight) vector from the source through a point at the zenith of the hemisphere, and is specified by the LOS direction cosines. For example,

X+ hemisphere: (1,0,0); Y+ hemisphere: (0,1,0); Z+ hemisphere: (0,0,1) X- hemisphere: (-1,0,0); Y- hemisphere: (0,-1,0); Z- hemisphere: (0,0,-1).

The figure below shows an example. There are two possible candidates for the hemisphere operation, Z- and X+. X+ is not a good choice for the operational hemisphere because the subject is at the edge of the hemisphere, close to the YZ plane. The best choice for the operational hemisphere in this case is Z-.



7. Definitions of 13 Fiducial Points and Their Measurement Order



Fiducial Points: Definition and measuring order

```
1. Nz
         (Nasion)
 2. Lpa (Left pre-auricular)
 3. Rpa (Right pre-auricular)
 4. Iz
         (Inion)
 5. Cz
         Length (Nz, Cz) = 0.5L_1, Length (Lpa, Cz) = 0.5L_2
 6. Fpz Length (Nz, Fpz) = 0.1L_1
 7. Fz
       Length (Nz, Fz) = 0.3L_1
 8. Pz
         Length (Nz, Pz) = 0.7L_1
 9. Oz
       Length (Nz, Oz) = 0.9L_1
10. T7 Length (Lpa, T7) = 0.1L_2
11. C3
       Length(Lpa,C3) = 0.3L_2
12. C4
       Length (Lpa, C4) = 0.7L_2
13. Т8
         Length (Lpa, T8) = 0.9L_2
      [L_1 = Length(Nz, Iz), L_2 = Length(Lpa, Rpa)]
```

Fiducial Points:



NIRS-based Dynamic Causal Modeling (DCM)

User's Manual



Software and documentation developed by the Optical Tomography Group (<u>http://OTG.downstate.edu</u>) of SUNY Downstate Medical Center (450 Clarkson Ave., Brooklyn, NY, 11203; <u>http://www.downstate.edu</u>)

User's Guide: NIRS-based Dynamic Causal Modeling (DCM)

A. Components of the NIRS-DCM application

1. NIRS-DCM source code. The essential files for the application are located in the SourceCodes folder, as shown in Fig. 1. In the installation that is illustrated here, it was convenient to place the SourceCodes folder as a subfolder of the MATLAB 'work' folder. However, it is <u>not</u> essential for you to place SourceCodes in that same location. You may place it anywhere in your folder structure that is convenient for you.



Figure 1. NIRS-DCM source code files, with the primary user interface file highlighted.

When you are ready to run NIRS-DCM, start MATLAB and then select one of the following alternatives: a. Make the SourceCodes folder you current directory, as illustrated in Fig. 2. If you choose this option, you must confirm that SourceCodes is the current directory before every use of NIRS-DCM.

Figure 2	. Selection	of SourceCodes	folder as the	MATLAB	current directory.
----------	-------------	----------------	---------------	--------	--------------------

_				_	
	$Current \; Director\underline{Y};$	C:\Program Files\MATLAB\R2007b\work\SourceCodes	-		Ē

b. Add the SourceCodes folder to your MATLAB search path, as illustrated in Fig. 3, in which case you will be able to run the code from any current directory location. You will need to do this only one time. If you choose this option, however, it is recommended that you place the SourceCodes folder at the top of the search path. This will eliminate any possibility of conflicts between the NIRS-DCM source code files and other files having the same names but located in different folders.

Figure 5. Au	ung SourceCodes folder to the MATLAB search pat	1.
📣 Set Path		
All changes take effect imme	diately.	
	MATLAB search path:	
Add Folder	🗀 C:\Program Files\MATLAB\R2007b\work\SourceCodes	
Add with Subfolders	C:\Documents and Settings\Harry\My Documents\MATLAB C:\src_NAVI3132008	
Move to Top	C:\src_NAVI3132008\FEMLibs	
Move Up	C:\src_NAVI3132008\FEMLibs\FEMIib_breasts\Left	
Move Down	C:\src_NAVI3132008\FEMLibs\FEMIib_breasts\Left\GiD	
Move to Bottom	C:\src_NAVI3132008\FEMLibs\FEMIib_breasts\Right\GiD	
Remove	C:\src_NAVI3132008\FEMLibs\Occipital_Cortex_3x10	T
Save Close	Revert Default	Help

Figure 3. Adding SourceCodes folder to the MATLAB search path.

2. Demonstration data set. To aid in understanding the use of the NIRS-DCM code and to facilitate your gaining practical experience, we have provided a set of files, as shown in Fig. 4, that specify values for all of the quantities needed to carry out a sample NIRS-DCM computation. These will be used during the remainder of this user's guide.

i igui e ii Demonstration	data mes r	er runde blenn.	
😂 C:\Program Files\MATLAB\R2007b\work	DemoData		- 🗆 🗵
<u>F</u> ile <u>E</u> dit <u>V</u> iew F <u>a</u> vorites <u>T</u> ools <u>H</u> elp			
🚱 Back 🔹 🕥 👻 🏂 🔎 Search 🞼	Folders	🗉 🔏 🔏	× »
Address 🛅 C:\Program Files\MATLAB\R2007b\wc	ork\DemoData	•	🔁 Go
Folders ×	Name 🔺	Size Type	
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E Colbox	🛃 A1.dat	1 KB DAT File	
🗉 🧰 uninstall	🛃 BO.dat	1 KB DAT File	
🗆 🦳 work	🛃 🛃 🛃 🛃 🛃	1 KB DAT File	
🔁 DemoData 💻	🛃 CO.dat	1 KB DAT File	
	🛃 C1.dat	1 KB DAT File	
	🗐 LFOs.txt	1 KB Text Docu	iment
🕀 🫅 Microsoft	📃 NVCP.txt	1 KB Text Docu	iment
1 Dicrosoft ActiveSync	🛃 u.dat	541 KB DAT File	
🕀 🧰 Microsoft CAPICOM 2.1.0.2 🖵	🖉 v_1.dat	541 KB DAT File	
	•		Þ
10 objects (Disk free space: 30.2 GB)	1.05 MB	🧕 My Computer	

Figure 4. Demonstration data files for NIRS-DCM.

The demo data are derived from an experiment originally described in 1997 by Büchel and Friston,¹ who used BOLD fMRI to study interactions among components of the visual system. Several years later the same data were used as demonstrational input for a BOLD-signal-based DCM application.² DCM is based upon a particular mathematical model of how the neural activity of one brain region is influenced by exogenous inputs (*e.g.*, stimuli), as well as by the activity in other brain regions (which also are being influenced by exogenous inputs, as well as by ..., *ad infinitum*; see <u>Appendix 1</u> for more detailed description of the DCM model). The output of a DCM computation includes numerical estimates of the effective coupling parameters (*i.e.*, the inter-regional interaction strengths) associated with the mathematical model. The 'A1.dat', 'B1.dat', 'C1.dat' and 'NVCP.txt' files seen in the preceding figure contain the results of one such calculation,^{*} while 'u.dat' contains the numerical values of the exogenous inputs.[†]

A functionality offered by NIRS-DCM is the ability to evaluate the DCM effective connectivity model in the "forward direction." What this means is that if you enter coupling-parameter information such as that found in the 'A1.dat', 'B1.dat', 'C1.dat' and 'u.dat' files, NIRS-DCM will calculate the corresponding neural activity time series. However, fNIRS measurements are not direct recordings of neural activity, but rather of its vascular correlates. Therefore, NIRS-DCM takes the calculated neural activity, and the information contained in the NVCP.txt file, and supplies them as input to the "balloon model" of neurovascular coupling described in Friston *et al.*³ (See <u>Appendix 2</u> for more detailed description of the neurovascular coupling model) The model's equations were numerically solved, thereby generating idealized deoxyhemoglin (deoxyHb)

^{*} In particular, the 'A1.dat' file contains the **A** matrix described in Refs. 2 and 3 (and <u>Appendix 1</u>), while 'B1.dat' and 'C1.dat' contain the non-zero elements of the **B** and **C** matrices, respectively. Numerical values for the parameters in the neurovascular coupling model (<u>Appendix 2</u>) are found in 'NVCP.txt'.

[†] The 'u.dat' file holds the time-varying values of the **u** vector described in Refs. 2 and 3 (and <u>Appendix 1</u>). For the example considered here, all of the inputs are dichotomous in character. Accordingly, every element of **u** is either a 1 (the input is present) or a 0 (the input is absent).

and venous blood volume time series. The computed hemodynamic time series can subsequently be used as a model for the types of data that can be obtained from a measurement carried out with a DYNOT or NIRScout imager.

An important role served by the demonstration data set (and by any other that you may subsequently generate using the forward-problem solver[‡]) is that it gives you *a priori* knowledge of the correct answer to the question "What is the effective connectivity network that gave rise to this data?" Thus you will be able to know whether NIRS-DCM selects the correct network from among the set of alternative hypotheses that you give it to choose from. As described below, you also will be able to "corrupt" the idealized data in various ways so that the computed time series will exhibit features that can be expected to occur in data from real experiments: noise, dynamic fluctuations that are unrelated to the experimental design paradigm, and location-dependent error in the amplitudes of time-varying signals extracted from different brain regions. This will allow you to determine how large any of these effects can be before the ability of NIRS-DCM to select the correct network is impaired.

B. Launching the NIRS-DCM application

1. Please note that the NIRS-DCM application clears the MATLAB workspace and closes all open figure windows upon startup, in order to maximize the amount of available RAM. Therefore, it is important that you remember to save any variables or figures that you will want to work with again, <u>before</u> you start the NIRS-DCM application. {Future code revisions will give the user an opportunity to "bail out" before clearing and closing.}

2. Ensure that the MATLAB current directory is one from which the NIRS-DCM user interface file can be accessed (using either option A.1.a or option A.1.b, as described above). Then enter 'NIRSDCM' at the command window prompt.

Command Window
>> NIRSDCM

3. The following messages will be displayed in the command window:

im =

You will now be guided through the user-input process.

Are the external inputs located in a file (f), or will you enter them interactively (i)? (f|i [f]):

[‡] or by using a laboratory test-bed that includes a programmable dynamic phantom

The program then pauses until you reply to the question in the second message.

Exogenous inputs are time series that indicate the presence or absence of experimental conditions (e.g., see Fig. X, below). For some paradigms the inputs have more than one level (e.g., degree of difficulty of a task), and the exogenous inputs time series will also contain level-vs.-time information.

The notation 'fli' means that you are being asked to enter either the letter 'f' (meaning that the exogenous-input data are located in a <u>fi</u>le that you have already generated, such as the 'u.dat' file included in the demo data set) or the letter 'i' (meaning that you will use the capability that NIRS-DCM provides to generate the exogenous-input data interactively) in response.

The notation '[f]' means that 'f' is the default option, so that if you simply press the Enter key it will be understood that the exogenousinput data are located in a file.

We have attempted to anticipate the sorts of data-entry errors that are likely to occur, and have equipped NIRS-DCM to recover gracefully from them without "crashing." As an example, if you inadvertently enter any text other than 'i' or 'f' (or just the Enter key) in response to the first question:

Are the external inputs located in a file (f), or will you enter them interactively (i)? (f|i [f]): x

Then you will see the following message:

em =

Please enter either an 'i' or an 'f' (or simply press the Enter key)

and then you will be given another opportunity to respond to the question. In order to work with the demonstration data set, select the 'f' option and proceed to Section C of this user's guide (use of the 'i' option will be covered in Section \underline{D}).

C. Loading Exogenous-Input Information from a File

1. After you indicate that the exogenous inputs are located in an external file, the user interface will respond with the next question in the input sequence:

Are the external inputs located in a file (f), or will you enter them interactively (i)? (f|i [f]): f Name of external-inputs file? For the demo data set, the exogenous inputs are located in a file named 'u.dat', which is located in the DemoData folder. Accordingly, in response to the question enter the file name, including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory):

Name of external-inputs file? ..\DemoData\u.dat

If the specified folder does not contain a file with the specified name, or if there is a file but it does not have the required format (*i.e.*, a matrix of real numbers, with no headings or other text characters {Future code revisions will give the user greater format flexibility.}), then you will see the following message:

em = The specified folder has no file with that name, or the file format is not correct. Please try again.

Following this, you will be given another opportunity to specify a file.

2. After an exogenous-inputs file is specified, NIRS-DCM responds with the next question in the input sequence:

Number of external input functions [default value (3) is the number of rows in the 'u.dat' file]?

Note that NIRS-DCM has read the contents of the specified file, and knows that it contains, in this case, three rows of data. It interprets each row as a time series of exogenous-input data. If your exogenous-input data are arranged in columns instead of rows, then NIRS-DCM automatically transposes the contents of the file after loading it. (It is assumed that the matrix dimensions will be unequal, with the smaller dimension representing the number of exogenous-input time series and the larger dimension representing the number of measurement time frames.)

To account for the possibility that the specified file contains more time series than you want to explicitly consider in your DCM analysis, the software asks you to specify how many rows of data you want to retain. The default value (all of the rows in the file, 3 in this example) can either be entered explicitly, or by simply pressing the Enter key.

The following message will be displayed if you enter something other than a single positive integer:

You entered something other than a single positive integer. Please try again.

After this, you will be given another opportunity to accept the default value or to specify a positive integer less than or equal to the default.

The following message will be displayed if you enter a positive integer larger than the default value:

Number of external input functions [default value (3) is the number of rows in the 'u.dat' file]? 5 em = The number you entered, 5, is too large. Reducing it to 3.

If you wish to retain fewer rows than the permissible maximum, then enter the correct number. For example, if you wish to use only two of the three rows of data in the 'u.dat' file in a DCM computation, then you would enter '2' in response to the 'Number of external input functions' question:

Number of external input functions [default value (3) is the number of rows in the 'u.dat' file]? 2

NIRS-DCM will reply by asking which two rows of data in the file are the ones you want to keep:

Which rows of 'u.dat' are the inputs (e.g., '[1 2 4]' or '2:3')?

A contiguous subset of the available inputs can be indicated by entering either '[1 2]' or '1:2' (likewise, either '[2 3]' or '2:3') in reply to the question. For a non-contiguous subset, it is necessary to enter '[1 3]'.

3. In order to work with the demonstration data set, accept the default value of 3 exogenous inputs:

Number of external input functions [default value (3) is the number of rows in the 'u.dat' file]? 3

NIRS-DCM will open a figure window containing plots of the exogenous-input functions that you have selected, which for this example are:



Figure 5. Exogenous-input time series loaded from an external file and plotted by NIRS-DCM.

At the same time, the following question will be posted to the MATLAB command window:

Are these the correct external inputs? (y|n [y]):

If the plotted exogenous-input time series are <u>not</u> the ones that you meant to use, then enter 'n' in reply to the question. This will bring up the following response from NIRS-DCM:

Are these the correct external inputs? (y|n [y]): n
Do you want to:
 A) Pick different functions from this file, or
 B) Load a different file? (A|B [A]):

The answer that you enter will return you to an appropriate earlier point in the input sequence, either:

Do you want to: A) Pick different functions from this file, or B) Load a different file? (A|B [A]): A Number of external input functions [default value (3) is the number of rows in the 'u.dat' file]?

or:

```
Do you want to:
A) Pick different functions from this file, or
B) Load a different file? (A|B [A]): B
Are the external inputs located in a file (f),
or will you enter them interactively (i)? (f|i [f]):
Do you want to:
A) Pick different functions from this file, or
B) Load a different file? (A|B [A]): x
em =
Please enter either a 'B' or an 'A' (or simply press the Enter key)
Are the external inputs located in a file (f),
or will you enter them interactively (i)? (f|i [f]):
```

where 'x' stands for any reply other than 'A' or 'B'.

or:

4. If the plotted exogenous-input time series <u>are</u> the ones that you meant to use, then enter 'y', or just press the Enter key, in reply to the 'Are these the correct external inputs?' question. This will bring up the following response:

Are these the correct external inputs? (y|n [y]): y Do you want to load a file of time series derived from experimental data (e), or to carry out a forward-problem simulation (s)? (e|s [s]):

In order to work with the demonstration data set, select the 's' option and proceed to Section <u>E</u> of this user's guide (use of the 'e' option will be covered in Section <u>F</u>).

D. Entering Exogenous-Input Information Interactively [Go back to **B.3**]

1. After you indicate that you want to enter the exogenous-input time series interactively, the user interface will respond with an information message and then with the next question in the input sequence:

Are the external inputs located in a file (f), or will you enter them interactively (i)? (f|i [f]): i

im =

Input functions of either the 'event' or 'boxcar' type can be conveniently entered interactively. Please use a text file to specify more complex types of external inputs.

Do you wish to continue? (y|n [y]):

[The time series plotted in Fig. 5 are "boxcar" functions; each of them has a value of 1 at every time frame in which the input is on/present, and 0 at every time frame in which it is off/absent. An "event" function is a limiting special case of a boxcar, in which every presentation of the input has a duration of only one time frame, and is zero at all other time frames. For example,

boxcar: 0 0 0 1 1 1 1 0 0 0 1 1 1 1 0 0 0 event: 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0

represents a pair of interacting inputs, with each presentation of the second occurring at a different position within the cycle of the first.]

Entering 'n' in response to the 'Do you wish to continue?' question will return you to an earlier point in the input sequence:

Do you wish to continue? (y|n [y]):n
im =
Resetting...
Are the external inputs located in a file (f),
or will you enter them interactively (i)? (f|i [f]):

2. Entering 'y' in response to the 'Do you wish to continue?' question will bring up the next question in the input sequence:

Do you wish to continue? (y|n [y]):y Number of external input functions?

Indicate the number of exogenous-input functions, and the user interface will ask for the overall length of the time series that NIRS-DCM will generate. For example:

Number of external input functions? 3

Length of the external input functions (i.e., number of time frames being modeled)?

Enter the number of time frames, for example:

Length of the external input functions (i.e., number of time frames being modeled)? 1000

At this point NIRS-DCM will create an array with (in the example presented here) 3 rows and 1000 columns, with every element having a value of 0. The user interface will guide you through the process of specifying which elements will have their values changed from 0 to 1. For example:

Please enter the time frames for the onset of input #1: [101 401 701]

Please enter the durations (in numbers of time frames) of input #1: [90 90 90] Please enter the time frames for the onset of input #2: [201 501 801]

Please enter the durations (in numbers of time frames) of input #2: [90 90 90]

Please enter the time frames for the onset of input #3: [301 601 901]

Please enter the durations (in numbers of time frames) of input #3: [90 90 90]

In the preceding example, we generated "boxcar" representations for three non-overlapping exogenous inputs. (If, say, the three functions represent presentations of a task with three difficulty levels, then this is the sort of temporal relation we would expect.) The first one is present during time frames 101-190, 401-490 and 701-790; the second is present during time frames 201-290, 501-590 and 801-890; and the third is present during time frames 301-390, 601-690 and 901-990.

Once all the onset and duration information is entered,[§] NIRS-DCM will open a figure window containing plots of the exogenous-input functions that you have generated, which for this example are:



Figure 6. Exogenous-input time series loaded from an external file and plotted by NIRS-DCM.

At the same time, the following question will be posted to the MATLAB command window:

```
Are these the correct external inputs? (y|n [y]):
```

If the plotted exogenous-input time series are <u>not</u> the ones that you were trying to design, then enter 'n' in reply to the question. This action will automatically return you to an earlier point in the input sequence:

Are these the correct external inputs? (y|n [y]): nAre the external inputs located in a file (f), or will you enter them interactively (i)? (f|i [f]):

3. If you are satisfied with the plotted exogenous-input time series, then enter 'y', or just press the Enter key, in reply to the 'Are these the correct external inputs?' question. This will bring up the following response:

[§] From this point on, this guide does not explicitly describe the messages that appear in the user interface if the user makes a mistake during data entry. Please be assured that NIRS-DCM will alert you, and let you gracefully recover from, occurrences such as entering non-integer or non-positive values for either an onset or a duration, a mismatch between the number of onsets and the number of durations, or requesting an onset-plus-duration combination that exceeds the specified overall length of the exogenous-input time series.

Are these the correct external inputs? (y|n [y]): yDo you want to load a file of time series derived from experimental data (e), or to carry out a forward-problem simulation (s)? (e|s [s]):

To generate simulated measurement data with the forward-problem solver, select the 's' option (see Section E of this user's guide). To load real measurement data, select the 'e' option (see Section <u>F</u>).

E. Generating Measurement Data with a Forward-Problem Simulation [Go back to C.4]

1. When you answer 's' in reply to the preceding question, the next question in the input sequence will appear in the user interface:

Do you want to load a file of time series derived from experimental data (e), or to carry out a forward-problem simulation (s)? (e|s [s]): s

Number of cortical regions in your model?

For the demonstration data set supplied with NIRS-DCM, the correct answer is 3. (It is a coincidence that in this example the number of cortical regions is equal to the number of exogenous inputs. This is <u>not</u> a general requirement for DCM computations.)

2. Entering '3' in answer to the 'Number of cortical regions' question brings up the next input-sequence question:

Number of cortical regions in your model? 3 Are the intrinsic connectivities in a file (f), or will you enter them interactively (i)? (f|i [f]):

For the demonstration data set, the intrinsic connectivities are located in a file named 'A1.dat', which is located in the DemoData folder. Accordingly, enter 'f', or just press the Enter key, in reply to the preceding question. (For information on interactive entry of the intrinsic connectivities, skip to Subsection $\underline{E.18}$.)

3. The next question in the input sequence is:

Are the intrinsic connectivities in a file (f), or will you enter them interactively (i)? (f|i [f]): f Name of intrinsic connectivities file? In response, enter the file name including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory).

Name of intrinsic connectivities file? .. \DemoData \A1.dat

NIRS-DCM will load the file, display its contents in the MATLAB command window, and ask you to confirm that these are the connectivities that you wanted to specify.

0

A = -1.55360.8959 0.5020 -1.0858 -0.2159 0 0.5186 -0.8960

Is the preceding the correct intrinsic connectivity matrix? $(\nabla |n| \nabla |)$:

If the displayed information were not the intrinsic connectivity matrix you wanted, you would enter 'n' to return to the input-sequence position indicated in Subsection E.2. However, for the demonstration data set the indicated numbers are the correct intrinsic connectivity values. Accordingly, enter 'y' or just press the Enter key.

4. When you accept the preceding intrinsic connectivity values, NIRS-DCM displays an information message regarding the modulatory connectivities, followed by the next question in the input sequence:

> Is the preceding the correct intrinsic connectivity matrix? (y|n [y]): yim = The modulatory connectivity structure is a 3-by-3-by-3 array. Usually this 3D array is sparse, so it will be initialized to all zeros, and then you will indicate which elements have non-zero values. Is the modulatory connectivity information in a file (f), or will you enter it interactively (i)? (f|i [f]):

[Note that in the example considered here, the reason why the dimensions of the modulatory connectivity array are $3 \times 3 \times 3$ is that there are 3 cortical regions and 3 exogenous inputs. In general, if the number of cortical regions is M and the number of inputs is N, then the dimensions of the modulatory connectivity array will be $M \times M \times N$.]

For the demonstration data set, the modulatory connectivities are located in a file named 'B1.dat', which is located in the DemoData folder. Accordingly, enter 'f', or just press the Enter key, in reply to the preceding question. (For information on interactive entry of the intrinsic connectivities, skip to Subsection $\underline{E.19}$.)

5. After you indicate that you are loading the modulatory connectivities from a file, NIRS-DCM displays an information message regarding the expected file structure, followed by the next question in the input sequence:

Is the modulatory connectivity information in a file (f), or will you enter it interactively (i)? (f|i [f]): f im = Each row in the data file should contain just four numbers: The row, column and layer indices (each a positive integer, and a connectivity coefficient value.

Name of modulatory connectivities file?

In most cases only a small percentage of the elements in the modulatory-connectivity array will have non-zero values. For the demonstration data set, for example, only 2 out of 27 entries in the $3 \times 3 \times 3$ are not zero. Therefore it is more efficient to structure the B1.dat file, and other files of the same type, so that they include only information about the small number of non-zero elements.

6. In response to the preceding question, enter the file name including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory).

Name of modulatory connectivities file? ..\DemoData\B1.dat

NIRS-DCM will load the file, display its contents in the MATLAB command window, and ask you to confirm that these are the connectivities that you wanted to specify.
Bedit =	:			
2.0	000	1.0000	2.0000	0.8657
2.0	000	1.0000	3.0000	0.2595

Is the preceding information correct? (y|n [y]):

What the 'Bedit' array is telling you is that there are 2 non-zero elements in the $3 \times 3 \times 3$ modulatory-connectivity array. One is located in (row 2, column 1, layer 2) with a numerical value of 0.8657, and the other is located in (row 2, column 1, layer 3) with a numerical value of 0.2595.

If the displayed information were not the modulatory connectivities that you wanted, you would enter 'n' to return to the input-sequence position indicated in Subsection $\underline{E.4}$. However, for the demonstration data set the indicated numbers are the correct modulatory connectivity values. Accordingly, enter 'y' or just press the Enter key. In response, the complete modulatory-connectivity array will be displayed in the MATLAb command window, thereby giving you an additional opportunity to ensure that the non-zero elements are in the correct locations:

B(:,:,1) =Ο B(:,:,2) =0.8657 Ο B(:,:,3) =0.2595

Is the preceding information correct? ($\forall \mid n \; [\forall]): \; \forall$

The user interface will then request a final confirmation:

Is the preceding the correct modulatory connectivity array? ($y \mid n ~[y]$):

As this is the correct modulatory-connectivity array for the demonstration data set, enter 'y' in reply to the question (replying 'n' will return you to the input-sequence position indicated in Subsection $\underline{E.4}$).

7. After you confirm the modulatory connectivities, NIRS-DCM displays an information message regarding the direct-effects file structure (*i.e.*, direct effects of the exogenous inputs on the cortical regions' neural activities), followed by the next question in the input sequence:

Is the preceding the correct modulatory connectivity array? (y|n [y]): y
im =
The direct effects structure is a 3-by-3 array.
Usually this matrix is sparse, so it will be initialized to all zeros,
and then you will indicate which elements have non-zero values.
Is the direct effects information in a file (f),

or will you enter it interactively (i)? (f|i [f]):

As indicated, the direct-effects file is structured similarly to the modulatory-connectivities file, in that it contains information about only the nonzero elements of the direct-effects matrix.

For the demonstration data set, the direct effects are located in a file named 'C1.dat', which is located in the DemoData folder. Accordingly, enter 'f', or just press the Enter key, in reply to the preceding question. (For information on interactive entry of the direct effects, skip to Subsection $\underline{E.20}$.)

8. When you indicate that you are loading the modulatory connectivities from a file, NIRS-DCM displays an information message regarding the expected file structure, followed by the next question in the input sequence:

```
Is the direct effects information in a file (f),
or will you enter it interactively (i)? (f|i [f]): f
im =
Each row in the data file should contain just three numbers:
The row and column indices (each a positive integer,
and a connectivity coefficient value.
```

Name of direct effects file?

Enter the file name including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory). NIRS-DCM loads the file, displays its contents in the MATLAB command window, and asks you to confirm that these are the direct effects that you wanted to specify:

Name of direct effects file? ..\DemoData\C1.dat Cedit = 1.0000 1.0000 1.7152

Is the preceding information correct? (y|n [y]):

What the 'Cedit' array is telling you is that there is 1 non-zero element in the 3×3 direct-effects array. It is located in (row 1, column 1) with a numerical value of 1.7152.

If the displayed information were not the direct effects that you wanted, you would enter 'n' to return to the input-sequence position indicated in Subsection $\underline{E.7}$. However, for the demonstration data set the indicated number is the correct direct-effects value. Accordingly, enter 'y' or just press the Enter key. In response, the complete direct-effects array will be displayed in the MATLAb command window, thereby giving you an additional opportunity to ensure that the non-zero elements are in the correct locations:

Is the precedir	ng information	correct?	(y n	[7]):	Σ
C =					
1.7152	ο	0			
0	0	0			
0	0	0			

The user interface will then request a final confirmation:

```
Is the preceding the correct direct-effects matrix? (y|n [y]):
```

As this is the correct direct-effects array for the demonstration data set, enter 'y' in reply to the question (replying 'n' will return you to the inputsequence position indicated in Subsection $\underline{E.7}$).

9. Confirming the direct effects brings up the next question in the input sequence:

```
Is the preceding the correct direct-effects matrix? (y|n [y]): y
What is the time interval between successive data frames (default value = 0.1 s)?
```

You may recall that when the exogenous-input time series were loaded or generated, no physical unit was assigned to the time interval Δt between successive time frames. In contrast, the elements of the intrinsic-connectivity, modulatory-connectivity, and direct-effects arrays all have physical units of s⁻¹ (see <u>Appendix 1</u>). In order to obtain accurate results from the DCM forward-problem computation, it is necessary to specify the correct Δt between successive time frames.

For the demonstration data set, the exact inter-frame time interval is 0.100625 s, a value that differs only slightly from the default 0.1 s. Therefore press the Enter key to accept the default value:

```
What is the time interval between successive data frames (default value = 0.1 s)?
You specified dt = 0.1, and the number of external-input time frames is 11520.
This corresponds to a measurement period of 1152 s, or 19.2 m.
Do you approve? (y|n [y]):
```

[The total measurement period would be 7.2 s longer if you were to use the exact Δt instead of the default value.] Enter 'y' or press the Enter key to accept the time-unit assignment:

10. Confirming the time-unit assignment brings up the next question in the input sequence:

```
Do you approve? (y|n [y]): y
```

```
Do you want to add a stochastic element to the neural-activity equation? (y|n [n]):
```

The fully deterministic DCM equation (Eq. (12)) described in <u>Appendix 1</u> will be solved if you choose not to add a stochastic, or random, term to the equation. Adding a stochastic term (Eq. (13)) is a simple way of extending the DCM model to include a non-deterministic effect that can be expected to occur in biological effective connectivity networks. For the demonstration considered here, however, our first goal is to examine the behavior of the deterministic model. Accordingly, enter 'n' or press the Enter key in reply to the preceding question. (For information on use of the 'y' option, skip to Subsection <u>E.21</u>.) NIRS-DCM performs the forward-model computation, and then opens a figure window containing plots of the resulting neural-activity time series, which for this example are:





At the same time, the following question will be posted to the MATLAB command window:

Do you wish to proceed to computation of the hemodynamic variables? (y|n [y]):

The reason why the magnitudes of the functions plotted in Fig. 7 vary over time is that they are principally determined by <u>how many</u> inputs are present at a given time (inspection of the Fig. 5 boxcar functions shows that they partially overlap in time).

The 'Do you wish to proceed...?' question gives you an opportunity to inspect the forward-problem solution, in order to ensure that it is free of the oscillatory artifact that can occur if the you specified a too-large value for the Δt between successive time frames. An example of this artifact is shown in the next figure, where we set up the problem exactly as indicated above, except that we specified $\Delta t = 0.79$ s (for even longer time intervals, the amplitudes of the oscillations increase rapidly with increasing Δt):

Figure 8. Neural-activity time series computed by NIRS-DCM, using exogenous inputs plotted in Fig. 5, the connectivity information in the A1.dat, B1.dat and C1.dat files, and $\Delta t = 0.79$ s.



If you were not satisfied with the result of the neural-activity computation, you would enter 'n' to return to the input-sequence position indicated in Subsection $\underline{E.9}$. As it happens, there is no problem in the result plotted in Fig. 7; therefore enter 'y', or press the Enter key, in response to the 'Do you wish to proceed...?' question:

11. When you indicate that you are ready to proceed, NIRS-DCM displays an information message regarding the expected file structure for the parameters of the neurovascular coupling model (see <u>Appendix 2</u>), followed by the next question in the input sequence:

```
Do you wish to proceed to computation of the hemodynamic variables? (y|n [y]): y
im =
There are 5 numerical parameters you must specify for the neurovascular coupling model.
Values must be specified for all of them, in each of the 3 cortical regions.
Are the parameters in a file (f), or will you enter them interactively (i)? (f|i [f]):
```

For the demonstration data set, the neurovascular coupling parameters are located in a file named 'NVCP.txt', which is located in the DemoData folder. Accordingly, enter 'f', or press the Enter key, in reply to the preceding question. (For information on interactive entry of the neurovascular coupling parameters, skip to Subsection <u>E.22</u>.) NIRS-DCM responds with the next question in the input sequence:

Are the parameters in a file (f), or will you enter them interactively (i)? (f|i [f]): f

Name of the neurovascular-coupling parameters file?

To work with the demonstration data set, enter the file name including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory). NIRS-DCM loads the file, displays its contents in the MATLAB command window, and asks you to confirm that these are the coupling parameters that you wanted to specify:

Name of the neurovascular-coupling parameters file? ..\DemoData\NVCP.txt disp = 'alpha = [0.32257219 0.32440402 0.31754959]' 'gamma = [0.24539545 0.2875248 0.2553348]' 'kappa = [0.91111855 0.9254821 0.99167867]' ' rho = [0.36170081 0.35458101 0.35242145]' ' tau = [1.810595 1.6049656 1.5917432]'

Is the preceding the correct matrix of neurovascular coupling parameters? (y|n [y]):

Notice that there are 5 rows of numbers (one for each of the five parameters— α , γ , κ , ρ , τ —described in <u>Appendix 2</u>), with 3 numerical values in each row (one for each of the three cortical regions discussed in <u>Appendix 1</u>). If the parameters displayed were not the ones that you want to use, you would enter 'n' to return to the 'Are the parameters in a file...?' question.

12. The neurovascular coupling parameters shown in Subsection E.11 are the correct ones for the demonstration data set. Therefore enter 'y', or press the Enter key, in reply to the preceding question. Using the parameters and the previously computed neural-activity time series as input, NIRS-DCM numerically solves the "balloon model" equations and then opens a figure window containing plots of the resulting deoxyhemoglobin and blood volume time series, which for this example are:



Figure 9. Deoxyhemoglobin (blue) and blood volume (red) time series computed by NIRS-DCM, using the neural activities plotted in Fig. 7.

13. After producing the preceding plots, NIRS-DCM gives you the option of adding one or more "real world effects" to the hemodynamic time series. The next question asked by the user interface is:

Do you want to add measurement noise to the computed hemoglobin content and blood volume? (y|n [n]):

Whereas the stochastic-element option in the neural activity computation is intended to model non-deterministic behavior of the biological <u>system</u> being studied, this measurement noise option is meant to model random noise in the measurement <u>device</u>. If you enter 'y' in response to the preceding question, NIRS-DCM will add normally-distributed (zero-mean) random numbers to all of the hemodynamic time series. You will be prompted to supply standard deviations for the normal distributions. For example:

Do you want to add measurement noise to the computed hemoglobin content and blood volume? (y|n [n]): y

Do you want to use a single set of measurement-noise standard deviations for both the hemoglobin content and blood volume variables? (y|n [y]): n

Please enter a standard deviation (SD) value for the deoxyhemoglobin measurement noise in each of the 3 cortical regions. If you want to use a single SD value for all regions, then you can enter just a single numerical value. [.05 .06 .03]

mnsd1 =

```
0.0500 0.0600 0.0300
```

```
Do you approve the preceding SD values? (y|n [y]): y
Please enter a standard deviation (SD) value for the venous blood volume measurement noise
in each of the 3 cortical regions. If you want to use a single SD value for all regions,
then you can enter just a single numerical value. [.1 .12 .06]
mnsd2 =
    0.1000   0.1200   0.0600
Do you approve the preceding SD values? (y|n [y]): y
Do you approve the plotted noise-added results? (y|n [y]): y
```

produces the following output:



Figure 10. Deoxyhemoglobin (blue) and blood volume (red) time series, with normally-distributed additive noise.

If you should change your mind about adding measurement noise, or inadvertently start the process by pressing the Enter key in response to the 'Do you want to add measurement noise...?' question, you can abort the process without terminating NIRS-DCM. To do this, simply specify a value of 0 for the noise standard deviations:

```
Please enter a standard deviation (SD) value for the measurement noise in each of the
3 cortical regions. If you want to use a single SD value for all regions,
then you can enter just a single numerical value. 0
mnsd1 =
0
Do you approve the preceding SD values? (y|n [y]):
im =
By entering only zero SD values, you are aborting the measurement-noise procedure.
```

14. The second "real world effects" option that NIRS-DCM provides is:

Do you want to add low-fequency oscillations (LFOs) to the computed hemoglobin content and blood volume? (y|n [n]):

The option of adding low-frequency oscillations (LFOs) to the hemodynamic time series is provided as a way of modeling "background phenomena," that is to say, other phenomena that cause the hemoglobin content and blood volume to fluctuate but are not related to the exogenous inputs. If you indicate that you do want to add LFOs, the next question in the input sequence is:

Do you want to enter oscillation parameters from a file (f), or interactively (i)? (f|i [f]):

The demonstration data set includes a file called 'LFOs.txt' that contains frequency, amplitude and phase information for a number of LFOs. Accordingly, enter 'f', or press the Enter key, in reply to the preceding question. (For information on interactive entry of the frequency, amplitude and phase parameters, skip to Subsection <u>E.23</u>.) NIRS-DCM responds with the next question in the input sequence:

```
Do you want to enter oscillation parameters from a file (f), or interactively (i)? (f|i [f]): f
Name of LFO-parameters file?
```

To work with the demonstration data set, enter the file name including the path for navigating to DemoData from the current directory (here we are assuming that SourceCodes is the current directory). NIRS-DCM loads the file, displays its contents in the MATLAB command window, and asks you to confirm that these are the LFO parameters that you wanted to specify:

```
Name of LFO-parameters file? ..\DemoData\LFOs.txt
disp =
    'q, region 1: f = 0.003 Hz, ampl. = 0.1, phase = 20 degrees'
    'q, region 1: f = 0.001 Hz, ampl. = 0.2, phase = 38 degrees'
    'q, region 2: f = 0.003 Hz, ampl. = 0.15, phase = 54 degrees'
    'q, region 3: f = 0.001 Hz, ampl. = 0.25, phase = 173 degrees'
    'v, region 1: f = 0.003 Hz, ampl. = 0.2, phase = 200 degrees'
    'v, region 1: f = 0.001 Hz, ampl. = 0.4, phase = 218 degrees'
    'v, region 2: f = 0.003 Hz, ampl. = 0.3, phase = 334 degrees'
    'v, region 3: f = 0.001 Hz, ampl. = 0.5, phase = 353 degrees'
```

Do you approve these LFO parameter values? (y|n [y]):

You may recall (see <u>Appendix 2</u>) that the symbols 'q' and 'v' denote the deoxyhemoglobin content and the venous blood volume, respectively. Thus the displayed information tells you that for cortical region 1, two LFOs will be added to each of the hemodynamic time series, while one LFO will be added to the time series for each hemodynamic variable, for each of the other two cortical regions. Enter 'y', or press the Enter key, to indicate your approval of these LFO parameters. (If you want to specify different LFO parameters, you may either use the interactive entry method described in Subsection <u>E.23</u>, or use a text editor to modify a copy of the LFOs.txt file.) In response, NIRS-DCM will open a figure window containing plots of the resulting deoxyhemoglobin and blood volume time series:



Figure 11. Deoxyhemoglobin (blue) and blood volume (red) time series, with added low-frequency oscillations.

Note that in order to produce the sample output in the preceding figure, we answered 'n' to the 'Do you want to add measurement noise...?' question and 'y' to the 'Do you want to add low-frequency oscillations...?' question. If we also had added noise, then the time series would show the net result of both effects.

If you should change your mind about adding LFOs, or inadvertently start the process by pressing the Enter key in response to the 'Do you want to add low-frequency oscillations...?' question, you can abort the process without terminating NIRS-DCM. To do this, indicate that you want to specify the LFO parameters interactively, then enter 'n' in reply to all of the 'Ready to enter a set of parameters...?' questions:

```
Do you want to enter oscillation parameters from a file (f), or interactively (i)? (f|i [f]): i
Ready to enter a set of parameters for variable 'q', cortical region 1? (y|n [y]): n
Ready to enter a set of parameters for variable 'q', cortical region 2? (y|n [y]): n
Ready to enter a set of parameters for variable 'q', cortical region 3? (y|n [y]): n
Ready to enter a set of parameters for variable 'v', cortical region 1? (y|n [y]): n
Ready to enter a set of parameters for variable 'v', cortical region 1? (y|n [y]): n
Ready to enter a set of parameters for variable 'v', cortical region 2? (y|n [y]): n
Ready to enter a set of parameters for variable 'v', cortical region 2? (y|n [y]): n
meady to enter a set of parameters for variable 'v', cortical region 3? (y|n [y]): n
meady to enter a set of parameters for variable 'v', cortical region 3? (y|n [y]): n
meady to enter a set of parameters for variable 'v', cortical region 3? (y|n [y]): n
```

By not entering any LFO parameters, you are aborting the LFO procedure.

15. The third "real world effects" option is:

Do you want to add amplitude distortions to the computed hemoglobin content and blood volume? (y|n [n]):

What this means is that you may multiply each hemodynamic time series by a different constant factor, as a way of modeling positional variability in the quantitative accuracy of the recovered hemoglobin-content and blood-volume information. You will be prompted to supply a set of multiplicative constants. For example: Do you want to add amplitude distortions to the computed hemoglobin content and blood volume? (y|n [n]): y

```
Do you want to use a single set of amplitude-distortion factors (ADFs) for both the hemoglobin content and blood volume variables? (y|n [y]): y
```

Please enter an ADF for each of the 3 cortical regions. If you want to use a single ADF for all regions, then you can enter just a single numerical value. [1.1 .9 1.5]

adf1 =

```
1.1000 0.9000 1.5000
```

Do you approve the preceding ADFs? (y|n [y]): y

produces the following output:



Figure 12. Deoxyhemoglobin (blue) and blood volume (red) time series, with amplitude distortions.

Note that in order to produce the sample output in the preceding figure, we answered 'n' to the 'Do you want to add measurement noise...?' and 'Do you want to add low-frequency oscillations...?' questions, and 'y' to the 'Do you want to add amplitude distortions...?' question. If we also had included one or both of the others, then the time series would show the net result of all of the modeled effects.

If you should change your mind about adding amplitude distortions, or inadvertently start the process by pressing the Enter key in response to the 'Do you want to add amplitude distortions...?' question, you can abort the process without terminating NIRS-DCM. To do this, simply specify a value of 0 for the amplitude-distortion factors:

Please enter an ADF for each of the 3 cortical regions. If you want to use a single ADF for all regions, then you can enter just a single numerical value. 0 adf1 = 0 Do you approve the preceding ADFs? (y|n [y]): im =

By entering only zero ADFs, you are aborting the amplitude-distortion procedure.

16. You will be asked to specify the name of a folder, into which the output files of the NIRS-DCM forward-problem solver will be stored (if the folder that you name does not already exist, NIRS-DCM will create it):

Enter the file path for the folder where the output files will go:

For this demonstration, we will specify a folder called 'OutputFiles', which will be located in the MATLAB 'work' folder, at the same level as the SourceCodes and DemoData folders (here we are assuming that SourceCodes is the current directory):

Enter the file path for the folder where the output files will go: .. \OutputFiles

After the output is saved, NIRS-DCM automatically proceeds to run the inverse-problem solver (Section \underline{G}). After the inverse-problem computation is completed, the final input-sequence question is displayed in the MATLAB command window:

Do you want to process another data set? (y|n [y]):

If you enter 'y' or press the Enter key, NIRS-DCM will bring you to the starting point of the data-input sequence (see Subsection $\underline{B.3}$), so you can prepare another data set for processing with the DCM inverse-problem solver. For this demonstration, enter 'n' at this time, in order to end the NIRS-DCM session:

Enter the file path for the folder where the output files will go: .. \OutputFiles

Do you want to process another data set? (y|n [y]): n

17. The newly created (for this example) folder, and the output files it contains, are shown in Fig. 13, below. You will notice that all of the files have '_1' as part of the file name. This indicates that they are the results from the first forward-problem simulation carried out in the current NIRS-DCM run. If we had entered 'y' in response to the 'Do you want to process another data set?' question and performed a second simulation, then ' 2' would be part of the file name for the second simulation's output files.

Files having names that start with the letter 'z' contain computed neural activity time series. Files with names that start with the letter 'q' contain deoxyhemoglobin time series, and files with names that start with the letter 'v' contain blood-volume time series. The 'q_1.dat' and 'v_1.dat' files contain the hemodynamic time series <u>prior to</u> the inclusion of any of the "real world effects," as shown in Fig. 9. The 'q_1.dat' and 'v_1.dat' files contain the hemodynamic time series <u>after</u> inclusion of the amplitude-distortion effect, as shown in Fig. 12.

If we had added measurement noise to the computed hemodynamic time series, then the output folder also would contain files named 'qn_1.dat' and 'vn_1.dat'. If we had added low-frequency oscillations to the computed hemodynamic time series, then the output folder also would contain files named 'qo_1.dat' and 'vo_1.dat'. Please recall that the noise, LFO and distortion effects are <u>cumulative</u>. That is, if the folder has both a 'vn_1.dat' file and a 'vo_1.dat' file, then data in the former will include <u>only</u> the measurement-noise effect (since this is the first effect that NIRS-DCM gives you the option of adding), but the latter will include <u>both</u> the measurement-noise <u>and</u> LFO effects.

😂 C:\Program Files\MATLAB\R2007b\w	ork\OutputFile	es		_ 🗆	×
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📄 SourceCodes					
🛅 Messenger	-				
					►
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Figure 13. Folder and files containing output of the NIRS-DCM forward-problem solver.

18. [Go back to E.2] After you specify that you want to enter the intrinsic connectivities interactively,

Number of cortical regions in your model? 3 Are the intrinsic connectivities in a file (f), or will you enter them interactively (i)? (f|i [f]): i

NIRS-DCM will respond by prompting you for the connectivity values:

Enter the 3-by-3 intrinsic connectivity matrix:

(The user interface asks for a 3×3 matrix, in this example, because we entered '3' in reply to the 'Number of cortical regions...?' question.) When entering numbers that form an array, it is necessary to somehow indicate each number's correct <u>position</u> in the array, in addition to its numerical value. This is accomplished as shown in the following example:

Enter the 3-by-3 intrinsic connectivity matrix: [-1.5 .9 0; .5 -1 -.2; 0 .5 -.9]

where the square brackets indicate "everything inside these brackets is part of the array," and the semicolons mean "skip to the next row." In response, NIRS-DCM will display the numbers that you entered in the conventional 2D matrix form, allowing you to confirm that the numerical values and locations in the array are correct:

A =

0	0.9000	-1.5000
-0.2000	-1.0000	0.5000
-0.9000	0.5000	0

Is the preceding the correct intrinsic connectivity matrix? (y|n [y]):

19. [Go back to $\underline{E.4}$] When you specify that you want to enter the modulatory connectivities interactively,

Is the modulatory connectivity information in a file (f), or will you enter it interactively (i)? (f|i [f]): i

NIRS-DCM will respond by asking you for the number of non-zero values in the $M \times M \times N$ (3×3×3, in this example) modulatory-connectivity array:

How many array elements are non-zero? :

After you answer the preceding question, you will be prompted for the array locations and numerical values of the non-zero elements:

How many array elements are non-zero? :2

Enter the row, column, layer and coefficient information for element #1:

Use the following syntax for entering the array-position and numerical-value information:

Enter the row, column, layer and coefficient information for element #1: [2 1 2 .9]

Enter the row, column, layer and coefficient information for element #2: [2 1 3 .3]

In response, NIRS-DCM will display the complete 3D modulatory-connectivity array, allowing you to confirm that the numerical values and locations of the non-zero elements are correct:

B(:,:,1) =	•		
0	0	0 0	
U	U	0	
B(:,:,2) =	•		
C)	0	0
0.9000)	0	0
C)	0	0
B(:,:,3) =			
C)	0	0
0.3000)	Ο	0
C)	0	0

Is the preceding the correct modulatory connectivity array? (y|n [y]):

20. [Go back to E.7] When you specify that you want to enter the direct effects interactively,

Is the direct effects information in a file (f), or will you enter it interactively (i)? (f|i [f]): i

NIRS-DCM will respond by asking you for the number of non-zero values in the $M \times N$ (3×3, in this example) direct-effects array:

How many array elements are non-zero? :

After you answer the preceding question, you will be prompted for the array locations and numerical values of the non-zero elements:

How many array elements are non-zero? 1

Enter the row, column and coefficient information for element #1:

Use the following syntax for entering the array-position and numerical-value information:

Enter the row, column and coefficient information for element #1: [1 1 1.7]

In response, NIRS-DCM will display the complete 2D direct-effects array, allowing you to confirm that the numerical values and locations of the non-zero elements are correct:

C = 1.7000 0 0 0 0 0 0 0 0

Is the preceding the correct direct-effects matrix? (y|n [y]):

21. [Go back to <u>E.10</u>] If you want to incorporate a simple model of non-determinism into the DCM forward-problem solver, enter 'y' in response to the 'Do you want to add a stochastic element...?' question:

Do you want to add a stochastic element to the neural-activity equation? (y|n [n]): y

The effect of invoking the stochastic-element option is that, in each simulated time frame, NIRS-DCM will add normally-distributed (zero-mean) random numbers to the computed neural-activity changes. You will be prompted to supply standard deviations for the normal distributions. For example:

Please enter a standard deviation (SD) value for the random fluctuation in each of the 3 cortical regions. If you want to use a single SD value for all regions, then you can enter just a single numerical value. [.5 .6 .3]

NIRS-DCM displays the standard-deviation values that you have specified, and asks you to confirm that these are the ones you want.

sesd = 0.5000 0.6000 0.3000

Do you approve the preceding SD values? (y|n [y]):

If you want to change one or more of the standard deviations that you specified, enter 'n' to repeat the 'Please enter a standard deviation...' step. If you change your mind about including a stochastic element, you can abort the procedure by entering 0 for the standard deviations:

Please enter a standard deviation (SD) value for the random fluctuation in each of the 3 cortical regions. If you want to use a single SD value for all regions, then you can enter just a single numerical value. 0 sesd = 0 Do you approve the preceding SD values? (y|n [y]): im = By entering only zero SD values, you are aborting the stochastic-element procedure.

Otherwise, enter 'y', or press the Enter key, to start the neural-activity computation. NIRS-DCM performs the forward-model computation and opens a figure window containing plots of the neural-activity time series, as shown in Fig. 14 (black curves). For comparison, the results that

would be obtained for the fully deterministic model also are computed and are plotted as overlays in the same figure (red curves). An accompanying information message, as shown below, is displayed in the MATLAB command window:

```
Do you approve the preceding SD values? (y|n [y]): y
im =
The red and black curves in the neural activity plots are
the fully deterministic and deterministic-plus-stochastic cases,
respectively.
```

Figure 14. Neural-activity time series computed by NIRS-DCM, with (black curves) and without (red curves) a stochastic element included in the forward-problem model. Compare to Fig. 7 in Subsection E.10.



In Figure 15 we show an expanded view of a portion of the computed time series from Fig. 14, order to convey a more complete understanding of the expected effects of the stochastic term.



Figure 15. Same neural-activity time series as in Fig. 14, after zooming in on the 360-600 s time interval.

22. [Go back to $\underline{E.11}$] In order to interactively enter the parameters of the neurovascular coupling model, start by entering 'i' in reply to the question that asks you to choose a method for specifying those model parameters:

There are 5 numerical parameters you must specify for the neurovascular coupling model. Values must be specified for all of them, in each of the 3 cortical regions.

Are the parameters in a file (f), or will you enter them interactively (i)? (f|i [f]): i

NIRS-DCM will respond by prompting you for the model-parameter values:

Enter the 5-by-3 matrix of neurovascular coupling parameters:

(The first matrix dimension will always be 5, which is the number of distinct model parameters. The second matrix dimension is 3, in this example, because we previously answered '3' to the 'Number of cortical regions...?' question.) When entering numbers that form an array, it is necessary to indicate each number's correct <u>position</u> in the array, in addition to its numerical value. This is accomplished as follows:

Enter the 5-by-3 matrix of neurovascular coupling parameters: [.32 .32 .32;.25 .29 .26;.91 .93 .99;.36 .36 .35;1.8 1.6 1.6]

The square brackets indicate "everything inside these brackets is part of the array," and the semicolons mean "skip to the next row." In response, NIRS-DCM will display the numbers that you entered, with text labels indicating which parameter corresponds to each row of the array, allowing you to confirm that the locations and numerical values are correct:

disp =

'alpha = [0.32 0.32 0.32]'
'gamma = [0.25 0.29 0.26]'
'kappa = [0.91 0.93 0.99]'
' rho = [0.36 0.36 0.35]'
' tau = [1.8 1.6 1.6]'

Is the preceding the correct matrix of neurovascular coupling parameters? (y|n [y]):

23. [Go back to $\underline{E.14}$] In order to interactively enter the parameters for low-frequency oscillations (*i.e.*, frequency, amplitude, phase), start by entering 'i' in reply to the question that asks you to choose a method for specifying those model parameters:

Do you want to add low-fequency oscillations (LFOs) to the computed hemoglobin content and blood volume? (y|n [y]): y Do you want to enter oscillation parameters from a file (f), or interactively (i)? (f|i [f]): i

NIRS-DCM will respond by prompting you for the model-parameter values. The hemodynamic variables and cortical regions are considered in a systematic order. First, you will be asked if you want to add a LFO to the 'q' (*i.e.*, deoxyhemoglobin-content) variable, for the first cortical region:

Ready to enter a set of parameters for variable 'q', cortical region 1? (y|n [y]):

If you enter 'n' in reply, NIRS-DCM will proceed to ask you the same question about cortical region 2. If, instead, you enter 'y' or press the enter key, then you will be prompted for the frequency, amplitude and phase information:

Frequency (in Hz)? .003 Amplitude? .1 Phase (in degrees)? 20

Next, you will be asked if you want to add a second LFO to the region-1 deoxthemoglobin time series:

Ready to enter another set of parameters for variable 'q', cortical region 1? (y|n [y]): y Frequency (in Hz)? .001 Amplitude? .2 Phase (in degrees)? 38

NIRS-DCM does not impose a limit on how many LFOs you can add to a hemodynamic-variable time series. It will repeat the 'Ready to enter another set...?' question until you enter 'n' as your answer, and then it will proceed to the next cortical region:

Ready to enter another set of parameters for variable 'q', cortical region 1? (y|n [y]): n

Ready to enter a set of parameters for variable 'q', cortical region 2? (y|n [y]): y

After you finish entering the LFO-parameter information for the 'q' variable for the last cortical region, NIRS-DCM will automatically proceed to the 'v' (*i.e.*, venous blood volume) variable:

Ready to enter another set of parameters for variable 'q', cortical region 3? (y|n [y]): n

Ready to enter a set of parameters for variable 'v', cortical region 1? (y|n [y]): y

After you finish entering the LFO-parameter information for the 'q' variable for the last cortical region, NIRS-DCM will automatically proceed to the next step in the data-input sequence.

F. Loading Measurement Data from a File [Go back to C.4 D.3]

1. If you enter 'e' in response to the 'Do you want to load a file of time series derived from experimental data...?' question (Subsection <u>C.4</u>), NIRS-DCM will respond by prompting you for the name of the file containing your measurement-based data:

Do you want to load a file of time series derived from experimental data (e), or to carry out a forward-problem simulation (s)? (e|s [s]): e

Name of file containing experimental data-derived time series?

2. Reply to the preceding question by entering the name of the file (including the path) that contains the data you want to process. For demonstration purposes, we will use a file that is included in the DemoData folder (here we are assuming that SourceCodes is the current directory):

Name of file containing experimental data-derived time series? ..\DemoData\v 1.dat

3. Note that the file that is loaded contains a <u>single</u> hemodynamic time series for <u>each</u> cortical region that will be considered in the DCM inverseproblem computation (Section G). That is, NIRS-DCM expects that you have already processed your reconstructed-image data, to reduce it from a (number of time frames)-by-(number of image pixels) array down to a (number of time frames)-by-(number of cortical regions) array. This operation is not performed by the current version of the NIRS-DCM code {but it is planned that it will be included in a future revision of the NIRx data processing and analysis suite}.

4. In addition to the exogenous inputs and experimental data, it is necessary for you to specify a hypothesis for the network of effective connectivity, as described in <u>Appendix 1</u>. In practical terms, this means that you need to tell NIRS-DCM which elements of the **A B** and **C** matrices are permitted to have non-zero values. For the demonstration data set, the appropriate <u>patterns</u> of intrinsic connectivity, modulatory connectivity and direct effects are stored in the DemoData folder, in files named 'A0.dat', 'B0.dat' and 'C0.dat', respectively.

After the experimental data are loaded, NIRS-DCM will prompt you for information on the pattern of intrinsic connectivity, which can be loaded from a file or entered interactively. To load a file, follow the steps in Subsection E.3, but specify the 'A0.dat' file instead of 'A1.dat'. To enter the information interactively, follow the steps in Subsection E.18, but enter only values of '1' and '0', in order to indicate which matrix elements do and do not have non-zero values, respectively.

After the intrinsic-connectivity pattern is specified, NIRS-DCM will prompt you for information on the pattern of modulatory connectivity, which can be loaded from a file or entered interactively. To load a file, follow the steps in Subsections E.4-E.6, but specify the 'B0.dat' file instead of 'B1.dat'. To enter the information interactively, follow the steps in Subsection E.19, but enter only the row-index, column-index and layer-index values, in order to indicate which array elements have non-zero values.

After the modulatory-connectivity pattern is specified, NIRS-DCM will prompt you for information on the pattern of direct effects, which can be loaded from a file or entered interactively. To load a file, follow the steps in Subsections E.7-E.8, but specify the 'C0.dat' file instead of 'C1.dat'. To enter the information interactively, follow the steps in Subsection E.20, but enter only the row-index and column-index values, in order to indicate which array elements have non-zero values.

5. NIRS-DCM loads the specified file, then automatically proceeds to run the inverse-problem solver (Section G). After the inverse-problem computation is completed, you will be asked if you have another data set to process:

Do you want to process another data set? (y|n [y]):

If there are additional data sets that you want to proces with NIRS-DCM, then enter 'y', or press the Enter key, to return to the starting point of the data-input sequence (see Subsection $\underline{B.3}$).

G. Inverse Problem Solver [Go back to E.16]

1. When you either run a simulation or load data time series from a file, NIRS-DCM automatically creates and saves the files that the DCM inverse-problem solver requires as its <u>input</u>. Then the inverse-problem solver automatically is called, and the inverse-problem computation begins. {Future code revisions will give the user increased control over when to run the inverse-problem module and over the inverse-problem solver's input and output file names.}

2. As the present revision of NIRS-DCM makes use of SPM8 source code files for computing solutions to the inverse problem, the SPM8 'System Identification' window illustrated in the following figure will open at the start of the inverse-problem computation. An iterative nonlinear optimization algorithm is used to estimate values of the effective-connectivity and neurovascular-coupling parameters that provide the best fit to the data time series. After each iteration, the plots in the System Identification window will be updated.





3. When the inverse-problem computation is complete, a set of information having the following form will be displayed in the MATLAB command window (and also saved in an output file, so it is not necessary for you to manually record anything).

ans =

a: [3x3 double] b: [3x3x3 double] c: [3x3 double] d: [3x3x0 double] U: [1x1 struct] Y: [1x1 struct] v: 360 n: 3 options: [1x1 struct] M: [1x1 struct] Ce: [3x1 double] Ep: [1x1 struct] Cp: [52x52 double] Pp: [1x1 struct] Vp: [1x1 struct] H1: [32x3x3 double] K1: [32x3x3 double] R: [360x3 double] y: [360x3 double] T: 0 F: 537.2809 ID: 182.4857 AIC: 1.9136e+003 BIC: 1.8805e+003

For the purpose of comparing two or more hypothesized effective-connectivity networks (see Appendix 1), the most relevant quantity is the 'F' parameter near the bottom of the list. The network having the largest value of F is the most likely one, among the set that were considered.

References

¹ C. Büchel and K.J. Friston, "Modulation of connectivity in visual pathways by attention: Cortical interactions evaluated with structural equation modelling and fMRI," *Cerebral Cortex* **7**, 768-778 (1997).

² "Dynamic Causal Modeling for fMRI," Chapter 32 in: J. Ashburner et al., SPM8 Manual (2010). <u>http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf</u>.

³ K.J. Friston, L. Harrison, and W. Penny, "Dynamic causal modelling," NeuroImage 19, 1273-1302 (2003).

Appendix 1. Dynamic Causal Modeling of Effective Connectivity [Go back to A.2 E.9 E.10 E.11 F.5]

1. The physical or structural interconnectivity of the brain, mediated by white-matter tracts that permit communication between physically separated regions, is well known. So too is the fact that many cognitive processes entail the participation of multiple areas of the brain. Thus it is appropriate to apply methods developed in the subject area of network theory,⁴ of which DCM is one particular flavor, to NIRS neuroimaging data in order to see if they can help us to interpret the data in terms of how the different regions interact.

An underlying premise of the DCM strategy is that the connectivity among brain regions is <u>effective</u> in nature, which means that changes in neural activity^{**} in one region actively induce corresponding changes in others, as implied by the yellow arrows in the following cartoon:



Figure A1.1. Cartoon depiction of an effective-connectivity network [reproduced from Ref. 5]. Blue regions have been identified as participating in the neural response to a stimulus or task, for example by GLM analysis of NIRS functional neuroimaging time series. Red arrow indicates the site where the exogenous inputs have their direct effects. Yellow circles indicate that the identified regions are hypothesized to participate in a network of effective connectivity, while the yellow arrows show the hypothesized pattern of inter-regional influences.

The DCM theory distinguishes effective connectivity from merely <u>functional</u> connectivity. The latter term refers to temporally correlated activity in distinct regions, without regard to whether or not any causal influence flows from one to another (*e.g.*, even in the case of a complete commissurotomy, an auditory stimulus simultaneously delivered to both ears would result in functional, but not effective, connectivity between the left and right primary auditory cortices). This raises the question of how is it possible to distinguish one type of connectivity from the other. The answer is that they cannot be distinguished by analytical strategies that are entirely based on examination of the neuroimaging data: a requirement of DCM is that we supply an a priori <u>hypothesis</u> as to the structure of the effective-connectivity network.

^{**} For a NIRS measurement, the only data available are the hemodynamic correlates of changes in neural activity. Consequently, in NIRS-DCM as in BOLD fMRI-based DCM [2,3], the term "neural activity" is intentionally left vague and defined in dimensionless relative units.

2. The yellow arrows in the preceding cartoon are meant to indicate an effective-connectivity hypothesis involving the four highlighted cortical regions. It should be noted that the arrows are <u>not</u> meant to imply that we are postulating direct anatomical connections between them (*e.g.*, via white matter tracts), or that these connections, even if present, necessarily are the pathways by which one region influences another in a given instance.

It cannot be overemphasized that DCM does <u>not</u> have the ability to tell us whether the effective-connectivity network embodied in a usersupplied hypothesis corresponds to the network that really is present in the brain. Rather, it performs a mathematical estimation of the likelihood that the hypothesized network of effective connectivity could produce the observed data. If the same computation is carried out for multiple hypothesized networks of effective connectivity, for example the one depicted in Fig. A1.1 and the three alternatives in Fig. A1.2, then a conclusion can be drawn as to which one is most likely, given the particular imaging data. However, the possibility that none of the hypotheses considered is the correct one cannot be definitively excluded.^{††}





3. Identification of which brain regions to include ordinarily is based on the use of functional NIRS imaging tools of the sort provided by the NAVI and naviSPM packages (and on prior biological knowledge): detector pre-processing + image reconstruction + GLM or another post-reconstruction feature-extraction algorithm. From that point on, it is not necessary to be concerned with details of the neuroanatomy. Instead, hypotheses regarding the effective interactions among the regions can be conveniently represented by a simplified diagram, as shown in the following figure. The depiction in Fig. A1.3 (where, for convenience, we have lowered the value of M from 4 to 3) is useful for illustrating a number of basic features of the DCM approach to network analysis:

a. The entities that lie within the light green layer are unknown quantities, not directly observable via functional NIRS measurements. In contrast, those that lie above or below that layer are known quantities, either because they are directly user-controlled (the inputs) or because they are experimentally measured (the *y* outputs).

b. The black arrows have the same significance as the yellow arrows in Figs. A1.1 and A1.2: they indicate the manner in which each region's activity is influenced by the activity in other regions.

^{††} An additional caveat is that comparison of computed likelihoods cannot be used to choose between networks comprising different sets of brain regions, but only for choosing among two or more networks interconnecting a fixed set of regions.

c. The orange arrows indicate the tendency of each region to have an inhibitory effect (emphasized by the '-' signs) on its own activity. Whether or not these have real anatomical correlates in every part of the brain, they have the mathematically necessary effect of stabilizing the neural activity computation (*i.e.*, they ensure that the computed activities will not "blow up" in the presence of exogenous inputs [and that they trend toward zero in the absence of inputs]).

Figure A1.3. Simplified representation of an effective-connectivity network [reproduced from Ref. 6]. Here the distinction between direct and modulatory inputs is made explicit.



d. There are two classes of exogenous input. The "driving input" $u_1(t)$ directly induces a change in neural activity in one or more brain regions. The "modulatory input" $u_2(t)$ exerts its effect in a more indirect way, by temporarily changing (*i.e.*, modulating) the magnitude of the connectivity between at least one pair of regions. It should be noted that in the preceding cartoon, the depicted modulatory input is a "boxcar" function while the direct input is of the "event" type, as described in Section D.1.

An even more compact (and hence more convenient to work with), 2D representation of an effective-connectivity network is:



Figure A1.4. Even more simplified representation of an effective-connectivity network. Cortical regions and inputs associated with the DemoData files are explicitly labeled.

where the intra-regional inhibitory connectivities no longer are explicitly shown (since it is a given that they always are present), and where we have explicitly labeled the exogenous inputs that were used in the experiment reported in Ref. 1: the "Photic" driving input was a set of white dots projected onto a screen; the "Motion" modulatory input was present during epochs when the dots were moving and absent when they were stationary; and the "Attention" modulatory input was present during epochs when the subject was given the instruction to look carefully at the moving dots and to count the number of times their velocities changed.^{‡‡} The labels on the three cortical regions—V1 = primary visual cortex, V5 = middle temporal visual area, PPC = posterior parietal cortex—indicate the three areas that were identified, through GLM analysis of BOLD fMRI image time series, as showing hemodynamic behavior most directly related to the three exogenous inputs. As to the locus of action of the modulatory inputs: as already indicated, it is not possible to establish these with certainty. The specific network depicted in Fig. A1.4 is one among many that have been suggested as hypotheses for the situation that is present in the brain.²

However, if the specific network shown in Fig. A1.4 is used as input for the DCM forward-problem solver, then the resulting computed neural-activity time series are necessarily the output of that network and no other, and we know the correct answer to the effective connectivity question *a priori*. Thus the forward-problem data serves a function analogous to the role played by phantom object for evaluating image reconstruction algorithms.

4. Formally, the DCM equation for neural activity is a system of ordinary differential equations, which specifies how the neural activity of each brain region <u>changes</u> over time, under the influence of the present neural activities and the present values of the exogenous inputs. Before proceeding to the general form, it is instructive to consider some special cases.

a. A single brain region, where the <u>rate of change</u> of neural activity is proportional to the present neural-activity value, and having neural activity of z_0 at t = 0. The mathematical equation describing this situation is:

$$\frac{dz}{dt} = az \quad (z(0) = z_0). \tag{1}$$

Many readers will recognize that the solution is:

$$z = z_0 e^{at} \tag{2}$$

^{‡‡} The velocity never actually varied. However, every subject claimed to have seen changes in velocity.

from which it follows that the parameter *a* must be a negative number, a < 0, in order to guarantee that the value of *z* will not "blow up" with the passage of time.

b. In Eq. (1), there is no explanation for how z acquired a non-zero initial value. For a somewhat more realistic special case, we'll add a positive-valued exogenous driving input:

$$\frac{dz}{dt} = az + c \quad (z(0) = 0, \quad c > 0).$$
(3)

The solution to the new differential equation is:

$$z = -\frac{c}{a} \left(1 - e^{at} \right) = \frac{c}{|a|} \left(1 - e^{at} \right).$$
(4)

As in the previous case, the requirement that the solution not "blow up" implies that a < 0. Consequently, the ratio -c/a is a <u>positive</u> number, and the solution is an exponential that increases from an initial value of zero to the final limiting value of c/|a|.

What if the value of the driving input should suddenly change at some time: for example, if c = 1 for $t \le T$, and c = 0 for t > T? In that case, the form of the solution also changes, from Eq. (4) for $t \le T$ to Eq. (2) for t > T.

c. Next, we consider a case of <u>two</u> cortical regions, where the rate of change of each region's activity is affected not only by the exogenous input and by <u>its own</u> present activity, but also by the present activity in the <u>other</u> region. For convenience, we will assume that the driving input has a direct effect on only one of the regions, as in the networks depicted in Figs. A1.3 and A1.4. Thus the differential equation in Eq. (3) generalizes to:

$$\frac{dz_1}{dt} = a_{11}z_1 + a_{12}z_2 + c$$

$$\frac{dz_2}{dt} = a_{21}z_1 + a_{22}z_2$$

$$(z_1(0) = z_2(0) = 0, \quad c > 0)$$
(5)

A mathematically equivalent but more compact way of writing Eq. (5) is:

$$\begin{bmatrix} dz_1/dt \\ dz_2/dt \end{bmatrix} = \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} \begin{bmatrix} z_1 \\ z_2 \end{bmatrix} + \begin{bmatrix} c \\ 0 \end{bmatrix}$$
(6)

while an even more compact (and still equivalent) way is:

$$\dot{\mathbf{z}} = \mathbf{A}\mathbf{z} + \mathbf{c}. \tag{7}$$

Just as Eq. (5) (or (6), or (7)) is formally similar to Eq. (3), the form of its solution is similar to Eq. (4):

$$z_1 = \alpha e^{s_1 t} + \beta e^{s_2 t} + \gamma \tag{8}$$

$$z_2 = \delta e^{s_1 t} + \varepsilon e^{s_2 t} + \zeta \tag{6}$$

The parameters s_1 and s_2 in the exponents are numbers that mathematicians call the <u>eigenvalues</u> of the **A** matrix, while the ratios α/δ and β/ε are governed by **A**'s eigenvectors. The expressions for the solution parameters do not matter here; what is important is that inspection of Eq. (8) allows us to derive the stability criterion for systems of two or more interacting regions: every eigenvalue of **A** must be a negative number. (Complex-number eigenvalues are permissible, in which case the requirement becomes that they all must have negative real parts.)

As in the one-region case, if the value of the exogenous driving input changes at t = T, then the solution will still have the mathematical form shown in Eq. (8), but the specific numerical values of α , β , γ , δ , ε and ζ will change. However, s_1 , s_2 , α/δ and β/ε will not change, since **A** is not affected by driving inputs

d. Finally, what is the effect of an exogenous modulatory input? The answer is that it is equivalent to changing the values of one or more elements of **A** at specific times! For example, Eq. (6) might become:

$$\begin{bmatrix} dz_1/dt \\ dz_2/dt \end{bmatrix} = \begin{cases} \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} \begin{bmatrix} z_1 \\ z_2 \end{bmatrix} + \begin{bmatrix} c \\ 0 \end{bmatrix}, \quad t \le T \\ \begin{bmatrix} a_{11} & a_{12} + b_{12} \\ a_{21} & a_{22} \end{bmatrix} \begin{bmatrix} z_1 \\ z_2 \end{bmatrix} + \begin{bmatrix} c \\ 0 \end{bmatrix}, \quad t > T \end{cases}$$
(9)

(For convenience, we have assumed that the driving input does not change.) Since an element of **A** is changing at time *T*, its eigenvalues and eigenvectors also will change at that time. While the mathematical form of the solution will still be given by Eq. (8), but the parameter values will change. What distinguishes this from the previously considered case of a driving input that changes at time *T* is that a modulatory input can also affect $s_1, s_2, \alpha/\delta$ and β/ε .

5. Generalizing from the preceding example, the DCM differential equation that corresponds to the Fig. A1.4 network is:

$$\begin{bmatrix} dz_{V1}/dt \\ dz_{V5}/dt \\ dz_{3}/dt \end{bmatrix} = \begin{bmatrix} a_{V1\leftarrow V1} & a_{V1\leftarrow V5} & 0 \\ a_{V5\leftarrow V1} + b_{V5\leftarrow V1}^{Motion} + b_{V5\leftarrow V1}^{Attention} \cdot u_{Attention} & a_{V5\leftarrow V5} & a_{V5\leftarrow PPC} \\ 0 & 0 & a_{PPC\leftarrow V5} & a_{PPC\leftarrow PPC} \end{bmatrix} \begin{bmatrix} z_{V1} \\ z_{V5} \\ z_{PPC} \end{bmatrix} + \begin{bmatrix} c_{V1}^{Photic} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} u_{Photic} \\ u_{Motion} \\ u_{Attention} \end{bmatrix}$$
(10)

Eq. (10) can be reduced to a more compact form analogous to Eq. (7), as follows:

$$\begin{bmatrix} dz_{v_1}/dt \\ dz_{v_5}/dt \\ dz_3/dt \end{bmatrix} = \begin{pmatrix} \begin{bmatrix} a_{v_1\leftarrow v_1} & a_{v_1\leftarrow v_5} & 0 \\ a_{v_5\leftarrow v_1} & a_{v_5\leftarrow v_5} & a_{v_5\leftarrow PPC} \\ 0 & a_{PPC\leftarrow V5} & a_{PPC\leftarrow PPC} \end{bmatrix} + u_{Motion} \begin{bmatrix} 0 & 0 & 0 \\ b_{v_5\leftarrow v_1}^{Motion} & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} + u_{Attention} \begin{bmatrix} 0 & 0 & 0 \\ b_{v_5\leftarrow v_1}^{Attention} & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} z_{v_1} \\ z_{v_5} \\ z_{PPC} \end{bmatrix} + \begin{bmatrix} c_{v_1}^{Photic} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} u_{Photic} \\ u_{Motion} \\ u_{Attention} \end{bmatrix}$$
(11)
$$\dot{\mathbf{z}} = \left(\mathbf{A} + u_{Motion} \mathbf{B}^{Motion} + u_{Attention} \mathbf{B}^{Attention}\right) \mathbf{z} + \mathbf{C}\mathbf{u}$$

The final expression in Eq. (11) can be generalized to any effective-connectivity network, involving any numbers of regions and exogenous inputs:

$$\dot{\mathbf{z}} = \left[\mathbf{A} + \sum_{j} u_{j} \mathbf{B}^{(j)} \right] \mathbf{z} + \mathbf{C} \mathbf{u}, \tag{12}$$

which is the fully deterministic DCM equation for neural activity.

6. A stochastic element into the model (see Subsection E.21) by adding one more term to Eq. (12):

$$\dot{\mathbf{z}} = \left[\mathbf{A} + \sum_{j} u_{j} \mathbf{B}^{(j)} \right] \mathbf{z} + \mathbf{C} \mathbf{u} + \begin{vmatrix} N(0, \sigma_{1}^{2}) \\ \vdots \\ N(0, \sigma_{M}^{2}) \end{vmatrix},$$
(13)

where $N(0,\sigma_i^2)$ is a Gaussian random variable with mean value equal to zero and variance equal to (the user-specified value of) σ_i^2 for the *i*th cortical region.

References

⁴ Y. He and A. Evans, "Graph theoretical modeling of brain connectivity," *Current Opinion in Neurology* 23, 341-350 (2010).

⁵ K.E. Stephan, "Causal modeling and effective connectivity," HBM Educational course on advanced MRI, June 6, 2010. http://hbmpresentersdirectory.org/HBM%202010/2010%20Presenters%20Directory/Presentations%20pdf/06-SUNDAY/Advanced%20fMRI/11.20%20-%20Klaas/HBM_AdvfMRI_KES_final.pdf

⁶ K. Friston, "Causal modeling and brain connectivity in functional magnetic resonance imaging," *PLoS Biology* 7, 0220-0225 (2009)

Appendix 2. Mathematical Model of Neurovascular Coupling [Go back to A.2 E.11 E.14]

1. After identifying the brain regions that will be considered in the NIRS-DCM computations, the user must distill the set of image time series within each region into a single time series: this may be accomplished, for example, by computing the volume average, or by computing the first principal component of all the region's time series; or by selecting the image pixel that has the largest amplitude, or is most strongly correlated with the exogenous input function, or lies nearest the centroid of the region. Thus the 4D hemodynamic image time series is reduced to a set of M hemodynamic time series (*i.e.*, these are the y functions depicted in Fig. A1.3). However, the y functions cannot be used directly as input to an algorithm designed to solve Eq. (12) or (13) for A, B and C, because y (hemodynamic variable) is not the same thing as z (neural activity). It is necessary to augment the neural-activity model with a mathematical model of neurovascular coupling.

2. As our neurovascular coupling model, we have used the following previously described system of coupled differential equations,³ which has frequently been employed in DCM analyses of fMRI data. The form of the model for any brain region is:

$$\frac{ds}{dt} = z - \kappa s - \gamma (f - 1),$$

$$\frac{df}{dt} = s,$$

$$\frac{dv}{dt} = \frac{1}{\tau} (f - v^{1/\alpha}),$$

$$\frac{dq}{dt} = \frac{1}{\tau} \left[\frac{1 - (1 - E_0)^{1/f}}{E_0} f - \frac{q}{v} v^{1/\alpha} \right].$$
(14)

The time-dependent variables in Eq. (14) are the vasodilatory signal *s*, associated with neural activity, blood flow *f*, blood volume *v*, and deoxyhemoglobin content *q*. The parameters are the vasodilatory signal decay rate κ , autoregulatory feedback rate constant γ , mean capillary transit time τ , vessel stiffness exponent α , and the capillary resting net oxygen extraction E_0 ; the numerator term $1 - (1 - E_0)^{1/f}$ is a convenient approximation to the flow-dependent oxygen extraction.

In the current implementation of NIRS-DCM, the variable that the inverse-problem solver attempts to match to the experimental or simulated data is the blood volume v. Therefore, the appropriate NIRS image-based parameter to use as input in total hemoglobin, which is proportional to blood volume.



Brief Introduction to NILAB2



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nilab2 Installation

Beginning with the latest (May 2011) revision of the NAVI data analysis package, a separate installation of nilab2 is no longer required. Instead, nilab2 comes bundled with NAVI, and its files will be installed automatically when you install NAVI (see NAVI User's Guide, Chapter 1: Getting Started).

Starting nilab2

Select 'nilab' from the drop-down menu in the Utilities of the primary NAVI GUI (lower-right corner of the GUI), and press the **Start** button.

📣 NIRx Dynamic Imaging Analyzer 1.0					
Near I	NAM — Near Infrared Analysis, Visualization and Imaging				
NIRx Med	NIRx Medical Technologies, Copyright 2006-2011 Exit				
Image Generator	Data Viewer	Data Analyzer			
Load From File System	Load dataInfo From File System 💌	Load dataInfo From File System			
Imager Type: None (Please Choose One)	Detector Time Series Viewer with wavelength dependence data	Data Type Specification			
Detector Preprocessing Run Set Parameters Filter Data Low Pass	Hemodynamic Image Viewer	Data Generation Get Dataset for Analysis			
Normalize Data	Data Processing Info Viewer	Feature Extraction			
Image Reconstruction Run Set Parameters Reconstruct Image	Running Status:	Set Parameters Multivariate Analysis Start PCA			
Data Export		Utilities			
ANALYZE Format		Start nilab FEM Model Generator Raw Data Editor naviSPM			

This will launch the primary GUI of nilab2, shown in the next figure. (At this point you can, if you wish, close the NAVI GUI without terminating nilab2. However, if the amount of RAM available is not an issue, it may be more prudent to minimize NAVI but keep it open.)



Primary GUI of nilab2. At startup, the 'ni' structure is empty

Primary GUI Functions

Here we explain the actions that can be performed by pressing each of the buttons that appear on the left-hand side of the nilab2 GUI:



evalin passes a ni-structure from the MATLAB workspace to the nilab2 GUI

evalout passes a ni-structure from the nilab2 GUI to the MATLAB workspace

clear deletes the contents of all the fields of the ni-structure. This is equivalent to restarting nilab2.

The button deletes all open figures (including NAVI GUIs, if there are any open) except for nilab2 GUIs.

Pressing the button, after highlighting one of the fields of the loaded ni-structure, displays the contents of the highlighted variable, in the black lower portion of the nilab2 main window.

The 'ni' data structure

1. It is a MATLAB structure array that contains the data collected during a measurement session, the results from subsequent data-processing operations, and the values of user-specified parameters supplied during all stages of processing and analysis stages.

2. The number of fields increases during the course of a data-analysis session.

Fields of an empty ni-struct
The naming syntax for all 'ni' fields is 'ni. F ', where $F =$
 IMG: matrix contains image layout, see below IMGinfo: header of IMG IMGlabel: optode label dat: data [dimensions are (the number of measurement time frames) by (the number of detector channels)] file: path and filename data file2save: path and filename data for saving file4cst: path and filename of layout functions: functions executed info: info about executed functions mrk: matrix containing the markers, see below sf: sampling frequency (Hz)
system: used system/hardware wl: wavelength (2 values, high and low)

Loading (demo) data

1. The nilab2 code has the ability to process measurement data collected using a number of different imaging systems from different companies.

2. Accordingly, the need to reconcile a variety of different data-file formats arises.

3. The solution used by nilab2 is that it has *import filters*, which can convert the various imaging systems' file formats into a common single format that we call UNIFORMAT.

4. If you have not yet converted the demo data set to UNIFORMAT, then select 'convert to UNIFORMAT' from the 'file' menu, as indicated in the following figure. (If the conversion had

already taken place, for example during a previous nilab2 session, then you would select 'load data (uniformat)' instead.)



5. The pop-up window shown in the next figure opens:

🛃 u_uniformat		
system		
NIRSCOUT 😽		
get file(s) save to	prefix	
help	t file(s)	5e

For the demo data set provided, select 'NIRSCOUT' from the 'system' drop-down menu. (For data collected using a DYNOT imager, you would select 'NIREX' from the same menu.

6. Press the 'get file(s)' button, then navigate to the 'nilab2\data\Leftmotor' folder, and select the 'NIRS-2011-02-09_002_Left_config.txt' file.

7. Press the 'save to' button to specify a location for the output file; the MATLAB current directory is the default location. If you want, supply a prefix for the output file name in the 'prefix' text field. By default, the name of the output file will be the same as the one you selected, except that the suffix will change from '.txt' to '.mat'.

8. Press the 'convert file(s)' button to perform the data-format conversion. Note that the process will "crash" if your data set has an empty .evt file. If you did not record anything in the .evt file during the measurement, you can create a "dummy" by copying the first line from another measurement's .evt file into the .evt file for this one. Press the 'close' button when the file conversion process is completed.

9. Select 'load data (uniformat)' from the 'file' menu, navigate to the folder containing the *_config.mat file, then highlight and open it. The ni-struct fields will be updated as shown in the following figure:



10. Press the 'evalout' button on the nilab2 GUI. Enter 'ni' at the MATLAB command prompt to view the contents of the ni-structure. When you do you will see that the dataset contains the following fields:

```
ni =
           IMG: []
       IMGinfo: {}
      IMG1abe1: {}
           dat: [1440x128 single]
            file: [1x113 char]
       file2save: []
        file4cst: []
       functions: {'ni=u loaddata(1,ni); % READ NIRSFILE'}
            info: {8x1 cell}
             mrk: [11x2 single]
              sf: 3.4700
          system: 'NIRSCOUT'
              wl: [850 760]
              SD: [8 8]
      columncode: 'column= (S*detector N)-detector N + D
                                                            ; '
            root: [1x123 char]
```

What the fields in the structure tell you is:

- ni.dat: The data comprises 1440 time frames and 128 channels, with columns 1-64 corresponding to the higher wavelength and columns 65-128 to the lower wavelength
- ni.file: The name of the UNIFORMAT file, and its file path (to view the contents of the ni.file field it may be necessary, as in this case, to enter 'ni.file' at the MATLAB command prompt.)
- ni.root: The name of the data file that was converted to UNIFORMAT, and its file path (to view the contents of the ni.root field it may be necessary, as in this case, to enter 'ni.root' at the MATLAB command prompt.)
- ni.functions: The function u_loaddata was applied with 2 inputs: 1 refers to open the GUI while the second argument is the name of the structure (ni) that was processed through the data-loading function. The output variable is again called 'ni', but now it contains the loaded data, while previously it was empty.
- ni.sf: The data sampling rate, or frequency, was 3.47 Hz
- ni.wl: The measurement wavelengths were 850 nm and 750 nm
- ni.SD: There were 8 source optodes and 8 detector optodes
- ni.mrk: Information read in from the .evt file (this is the reason why that file can't be empty!). To view its contents, enter 'ni.mrk' at the MATLAB command prompt:

ans	=		
	69	1	
	208	1	
	347	1	
	486	1	
	625	1	
	764	1	
	903	1	
	1042	1	
	1181	1	
	1319	1	
	1458	1	

The first column refers to the time frames at which a marker occurred, while the numbers in the second column denote to the marker type (there was only one marker type for this experiment; the indicated time frames are the starting times for each data block in a repeated-task paradigm). Thus ni.mrk contains "when" and "what" information on the experimental design.

Load constructionfile

1. Select 'load constructionfile' from the 'file' menu, and navigate to the folder containing the appropriate *configig*.m. (For the NIRScout demo data and the NAVI-bundled version of nilab2, the path is ...\utilities\nilab2\imcon and the file name is 'NIRSconfigifLeftMot.m'.) The *configig*.m file contains the optode layout, which is applied to the measurement data that you loaded in the previous set of steps. (You may subsequently load additional data sets collected using the same optode layout, without having to repeat this 'load constructionfile' step.)

2. After you load the *configig*.m file, you will see that the ni structure array contains information in several fields that previously were empty, as shown in the following figure:



In particular, the header for the layout matrix is in the IMGinfo field:

ni.IMGinfo: {'ChanNr' 'wavelength' 'RowNrTarget' 'ColNrTarget' 'ColNrData' }

The contents of the layout matrix can be viewed by entering 'ni.IMG' at the MATLAB command prompt (after clicking the 'evalout' button again):

>>	ni.IMG				
an	в =				
	1	1	1	2	1
	2	1	1	4	2
	3	1	1	6	10
	4	1	2	1	17
	5	1	2	3	3
	6	1	2	5	26
	7	1	2	7	12
	8	1	3	2	19
			:		
			•		
	16	2	5	4	102
	17	2	5	6	110
	18	2	6	1	117
	19	2	6	3	103
	20	2	6	5	126
	21	2	6	7	112
	22	2	7	2	119
	23	2	7	4	127
	24	2	7	6	128

The matrix contains:

- Column 1: 24 channels for the longer wavelength, followed by 24 channels for the shorter wavelength
- Column 2: wavelength index: 1 or 2

Column 3: layout-matrix row index

Column 4: layout-matrix column index

Column 5: columns of data that will be extracted from the raw-data files

Likewise, the labels assigned to the measurement channels can be viewed by entering 'ni.IMGlabel' at the MATLAB command-window prompt:

```
>> ni.IMGlabel
ans =
    '1-1'
    1-21
     '2-2'
     '3-1'
     1-3'
     '4-2'
     '2-4'
     '3-3'
       :
     '5-6d'
     '6-6d'
     '7-5d'
     '5-7d'
     '8-6d'
     '6-8d'
    '7-7d'
     '8-7d'
     '8-8d'
```

The significance of the channel labels is clarified in the following cartoon,



where it is seen that the notation '3-1' means "the channel comprising source 3 and detector 1," and '6-8' means "the channel comprising source 6 and detector 8."

Interactive assignment of optode layout

If an appropriate *configig*.m file is not available for your data set, an alternative means of specifying the channel locations is available. Use the following sequence of steps:

1. Select 'assign Channels' from the 'file' menu. This will launch the 'u_chanlocs' secondary GUI shown in the following figure:



2. From the 'system' drop-down menu, select the option that combines the correct imager type and optode numbers (for the demo data set, the correct choice is 'NIREX_8_8'). Specify the correct dimensions in the 'gridsize' field (7×7 is correct for this data set¹) and press the 'replot' button, changing the appearance of the u_chanlocs grid to:



¹ For a "checkerboard" optode array containing *M* rows and *N* columns of optodes, the channel grid will have 2M - 1 rows and. 2N - 1 columns In the example considered here, the 8 sources and 8 detectors are arranged in a 4×4 optode array; therefore, the dimensions of the channel grid are 7×7. For guidelines on how to specify a channel grid for optode arrays that are not simple checkerboards, see the appendix to this chapter, starting on p. 63.

3. Enter Source-Detector combinations in the appropriate locations, by double-clicking on the grid cells one at a time to enter or change their field entries. Each selected cell will change color from white to yellow when you select it, and from yellow to orange after you enter the grid-cell label. For the demo data set, the goal is to produce a pattern of channels that looks like the pattern of "sticks" in the ball-and-stick cartoon on p. 10. The final result is:



4. Press the 'save config' button to save the specified optode layout as a *configig*.m file. A navigator window will pop up, which you can use to specify a name and location for the file.

Plot data layout

1. Select Layout from the PLOT menu. This action will open the small GUI in the following figure.



Select any options you may want for the data-trace plots (there are default settings, so it is not necessary to check any of the boxes) and press the 'plot' button. A figure window will open, showing you the optode-layout grid with the channels labeled:

<mark>4</mark> Figure 10	1					
<u>File E</u> dit <u>V</u> i	ew <u>I</u> nsert <u>I</u>	ools <u>D</u> esktop	<u>W</u> indow <u>H</u> e	elp .		¥.
🗅 🚔 🖪		Q Q 🖑] 🗜 🖲			
	1-1		1-2		2-2	
3-1		1-3		4-2		2-4
	3-3		4-3		4-4	
3-5		5-3		4-6		6-4
	5-5		5-6		6-6	
7-6		6-7		8-6		6-8
	7-7		8-7		8-8	

2. Moving the mouse cursor over any of the red squares in the preceding figure causes a second plot window to open (first time you select a grid cell) or be updated (second and subsequent times), containing plots of the data for the selected channel, for both measurement wavelengths:



3. Changing the options selected in the small GUI modifies the quantities plotted on one or both axes





Define stimulation time

Select 'Set Parameter' from the 'FUNs1' menu. A pop-up window opens, that you use to indicate the physical duration of each stimulus episode. Enter the correct value (20 s, for the example in the demo data set) in the 'Stimulusduration [sec]' field and press the 'ok' button.

🛷 u_popparams 📃 🗖	X	📣 u_popparams	. 🗆 🗙
Parameter		Parameter	
Stimulusduration [sec]		Stimulusduration [sec] 20	
cancel hep ok		cancel help ok	

Define marker

1. Select 'Marker' from the 'FUNs1' menu. The event markers from the experiment-specific .evt file are read, and the experimental conditions are separated according to their digital trigger-code values. In cases where more than one marker type is present, you may be interested in only some of them for a particular analysis. (For the demo data set, however, there is only one marker type, as the experiment involved a single condition that was alternately present and absent.)

2. In the 'accepted markers' field, indicate which marker types you are interested in, and click on 'ok'.

📣 u_popmarker			
marker (occu	irence)		
1 N[11]	<u> </u>		
	_		re-copy marker
accepted markers		1	
rename			
can	cel	help	ok

Manual artifact correction

1. If your data contains features that have a high likelihood of being artifacts, such as the high, narrow "spikes" in the data channel shown in the next figure, then you can use the artifact



correction tool of nilab2 to "flatten" them (*i.e.*, to replace the original data values with a linear interpolation between the data values on either side of the artifact).

2. Select 'artefact'² from the 'Plot' menu. This will launch the GUI depicted in the following figure:

 $^{^2}$ This is not a typo; it's the British spelling of 'artifact'



3. Remove the check mark from the 't-all' check-box. After this, by changing the number in the 'wind [dp]' (*i.e.*, the size of the viewing <u>wind</u>ow, in units of <u>data points</u>) text field and using the scroll bar under the text field, you will be able to zoom in on the artifact(s) you wish to remove.



4. Press the 'selection' button (it will turn red when you do). Then place the mouse cursor on the data time series, and a set of crosshairs will appear. Place the vertical hairline at the first data point you want to remove, and press the primary mouse button. Repeat the process for the last data point in the artifact. The interval between the two time values that you selected will become highlighted as shown in the following figure.



5. Repeat the preceding operation for any other artifacts that you want to remove. When you are finished, press the 'selection' button again, to turn off the hairline marker. Then press the 'flatten' button to implement the linear interpolation process:



The effect on the time series plotted on p. 15 is:



6. Press the 'accept' button (lower-right corner of the GUI) if you to continue to use the corrected time series for the remainder of the session. Press 'cancel' to close the GUI without accepting the changes.

Low-pass filtering

Whereas a data set will ordinarily contain a relatively small number of discrete artifacts, highfrequency noise may be present throughout the time series. Also, a set of channel time series may contain features that are not artifacts, but are not relevant for the analysis you want to perform. This class of features includes respiratory and cardiac fluctuations. Notably, the typical frequencies of the rhythms (0.2-0.33 Hz for respiration, 1-1.5 Hz for the heartbeat), and of noise, are substantially higher than the frequency band of most experimental paradigms. Therefore, low-pass filtering can be used to remove them from the data, without appreciably distorting the paradigm-related aspects.

Use the following sequence of steps to low-pass filter data with nilab2:

1. Select 'LowPass Filter' from the 'FUNs1' menu. The pop-up window shown below will open:



2. If you know the cut-off frequency that you want to use, simply enter it in the 'high cutoff frequency' field. Alternatively, if you are not certain what frequency cutoff you should specify, then press the 'select manually' button to graphically choose the cutoff frequency and preview the effect of applying the filter. This will open a figure window containing plots of the data power spectrum, averaged over all channels, at both wavelengths.



3. Use the mouse to select a cut-off frequency. When you press the primary mouse button, you will see the effect of the low-pass filter on the power spectrum):



Note also that the cutoff frequency you choose is displayed at the top of the figure, and is automatically copied into the 'high cutoff frequency' field:

📣 u_popfilter		<u>- ×</u>
	Lov	vPassFilter
high cutoff frequency filter-order	0.30288	elect manually
cancel	help	ok

An additional effect of choosing a cutoff frequency is that it will open another figure window, containing overlaid plots of all the data time series. The original, unfiltered data are plotted in blue, while the low-pass filtered data are colored red.



4. If you want to try a different cutoff frequency, or to explore the effect of changing the filter order (the larger you make it, the sharper the cutoff becomes) press the 'select manually' button again. The second figure window (data time series) will automatically close, and the first one (average power spectrum) will be restored to its original appearance. Repeat Step 3 as many times as you like, and press the 'ok' button when you are satisfied with your selections.

5. You can repeat the 'PLOT \rightarrow Layout' operation described above (pp. 12-14), in order to see the effect of filtering on data for individual channels. (Likewise for any other pre-processing operation.)



High-pass filtering

The light-intensity values recorded in a given channel may slowly change over time, for reasons unrelated to the experimental protocol (*e.g.*, changes in posture or in subject stress/relaxation level) or to phenomena that are associated with the experimental protocol but are not relevant for the analysis you want to perform (*e.g.*, blood volume shifts in response to repeatitive task performance). These slow changes are called "drifts" or "trends," and may affect your ability to discern smaller-magnitude changes in associated with the experimental paradigm. Drifts can be mathematically modeled as fragments of long-period sinusoidal fluctuations having frequencies substantially lower than the frequency band of most experimental paradigms. Therefore, high-pass filtering can be used to remove them from the data, without appreciably distorting the paradigm-related aspects.

Use the following sequence of steps to low-pass filter data with nilab2:

1. Select 'HighPass Filter' from the 'FUNs1' menu. The pop-up window shown below will open:

📣 u_pophpass			<u> </u>
	Highp	assfiltler	
lowCuto	if [sec]	64	
cancel	help	ok	

2. In the 'lowCutoff [sec]' field, specify the cutoff period for the high-pass filter. For example, in the preceding figure, a 64-second cutoff has been specified. This means that all oscillations with periods ≥ 64 seconds (*i.e.*, frequencies lower than 1/64 s⁻¹ ≈ 0.016 Hz) will be suppressed. Pressing the 'ok' button will start the high-pass filter computation.

Note that, in addition to the 'FUNs1 \rightarrow HighPass Filter' function, data can be de-trended at a later data processing step, in the popup window for GLM analysis (p. 31). Therefore, here we will not high-pass filter the demo data set at this point, but instead will press the 'cancel' button to close the popup window without implementing the filter.

Apply modified Beer-Lambert law

The measurement data for each wavelength contains information about both isoforms of hemoglobin: oxygenated (oxy-Hb) and deoxygenated (deoxy-Hb). nilab2 uses the Beer-Lambert law to estimate the average concentrations of oxy-Hb and deoxy-Hb in the portion of tissue that each channel "sees."

1. Select 'BeerLambert' from the 'FUNs1' menu. The pop-up window shown in the next window opens:

<mark>4</mark> u_popLBG		_	
calculate Concentr	ation cha	anges select from spectrum	
inter optode distance [cm]	2.5	[1] W. B. Gratzer	•
N first Datapoints for baseline	all		
	epsilon oxy-h	Hb epsilon deoxy-Hb DPF	
higher WL 850		5.98	
lower WL 760		7.15	
		show DPF	
cancel	help	ok	

2. The items in the 'select from spectrum' drop-down menu are different experimentally measured hemoglobin absorption spectra. When you select one from the menu (even if you want to use the default 'W.B. Gratzer' spectrum, you still must click on it), a figure window containing plots of the spectra will open. For example:

🔥 u_popLBG	
calculate Concent	tration changes select from spectrum
inter optode distance [cm]	2.5 [1] W. B. Gratzer
N first Datapoints for baseline	all [2] J.M. Schmitt
	epsilon oxy-Hb [3] S. Takatani and M. D. Graham [4] older epsylon of ISS [5] older ensylon of IMAG
higher WL 850 lower WL 760	[6] other 7.15
	show DPF
cancel	help ok



The molar extinction coefficients for your spectrum selection, at both measurement wavelengths (nilab2 takes these automatically from the ni-structure) are shown in the red (oxy-Hb) and blue (deoxy-Hb) boxes:

📣 u_popLBG		
calculate Concentr	ation cha	select from spectrum
inter optode distance [cm]	2.5	[3] S. Takatani and M. D. Graham 📃
N first Datapoints for baseline	all	
	epsilon oxy-ł	Hb epsilon deoxy-Hb DPF
higher VVL 850	2.4366	1.8885 5.98
lower WL 760	1.3496	3.9105 7.15
		show DPF
cancel	help	ok

The numbers in the 'DPF' fields (differential pathlength factor) are used to account for the optical pathlength-lengthening effect of tissue light scattering. The experimental data that were used to generate the DPF values can be viewed by pressing the 'show DPF' button.

3. The 'all' default value in the 'N first Datapoints for baseline' field is not always the most appropriate choice. In a typical experimental protocol, there is an initial "rest" time interval that precedes the first stimulus or task epoch, and this constitutes a natural baseline period. For the demo data set the first task epoch began at the 69th time frame (p. 7). Thus we use N = 60:



4. Press the 'ok' button to start the computation. The pop-up window will close automatically when the computation is finished. Use 'PLOT \rightarrow Layout' to view the result:



Cut the session

This operation is used to remove data time frames collected before the start or after the end of the true experimental protocol. If these epochs are lengthy and are not removed, they may have an undesired influence on subsequent GLM computation results. If you want to delete data frames from the beginning or end of the time series, use the following steps:

1. Select 'Cut Session' from the 'FUNs1' menu. This will open the following pop-up window:



2. Click on 'plot marker' to produce plots that will assist in choosing the starting and ending time frames of the data segments that will be retained for subsequent analysis:



The upper plot shows the marker time frames throughout the measurement session (gray vertical lines) and the time course of the first data channel (red curve). The lower 2 plots show expanded views of the initial and final segments of the data time series.³ It can be seen that the experiment started almost immediately after the recording session began, and that it ended immediately after the experiment was completed. Therefore, in this case we will not remove any data from the end of the session. However, we will remove a small number from the starting segment, in order to illustrate the use of the 'cut session' function while still retaining a baseline segment.

³ If the expanded views appear superfluous in this example, that is because the demo data set contains only 1440 time frames. Your experimental time series may be many times longer.

3. In accordance with the preceding considerations, enter '[50 nan]' in the '2 values (DATAPOINTS)' field of the 'cut session' pop-up window, as shown in the next figure. Thus we will keep 50 frames prior to the first marker (equivalently, we are cutting off the initial 18 frames, since initially there were 68 time frames preceding the first marker), but cut none after the last marker.

🔸 u_popcutsession	_ 🗆 🗙
cut session	plot marker
68 dp before FIRST Mrk (> ~19.5965sec -89 dp after <last +="" 20s)="" mrk="" of="" stimdur=""> ~-25.187</last>	3sec
STIMULUSduration: 71dp>>20s	2 values (DATAPOINTS)
input $\{x \ y \ \}$, with $x \ dp$ befor and $y \ dp$ after session to include in session	[50 nan]
cancel help	ok

4. Press the 'ok' button to implement the procedure.

Remove pauses/rests within the session

A long measurement session may include rest periods between successive stimulus or task blocks, to prevent fatigue. Or there may be parts of the session that are especially artifact-rich, or that you want to exclude from your data analysis for some other reason. Then you would want to remove blocks of data frames corresponding to these intervals, so that they cannot influence the results of subsequent GLM computations. To delete data frames from an interior portion of the time series, use the following steps:

1. Select 'Delete Pauses' from the 'FUNs1' menu. This will open the following pop-up window:

샞 u_deletepauses		
delete pauses		plot marker
min time to be defined as a pause [sec]	30	!! SECONDS !!
SECONDS after Block and before next Block to keep	1 1	
show results	help	ok

2. Click on 'plot marker'. The following figure window will open:



The upper plot shows the temporal difference between adjacent markers. We see that there is no variation in the inter-marker intervals (and, again, that there is only one experimental condition, which is alternately present and absent). Therefore, we will not remove any interior segments from *this* data set. However, for data set that *does* contain rest intervals the subsequent steps will be:

3. Enter a number (default value is 30 s) in the 'min time to be defined as a pause [sec]' field of the 'delete pauses' pop-up window (p. 27), in order to indicate that marker pairs with an interval of at least 30 s (or the number that you specify, if you replace the default value) are pauses. That is, the procedure is based on the assumption that the "nuisance" time intervals are *longer than* the true experimental epochs. Note also that *every* inter-marker segment longer than the threshold value you specify here will be affected.

4. Enter a pair of numbers (default values are 1 s and 1 s) in the 'SECONDS after block and before next block to keep' field of the 'delete pauses' pop-up window. This means that the deleted segment will begin 1 second (or the first number that you specify, if you replace the default value) after the start of the long inter-marker time segment, and it will end 1 second (or the second number that you specify, if you replace the default value) before the end of the long inter-marker time segment.

5. Press the 'ok' button in the 'delete pause' pop-up window to start the procedure. After the long inter-marker intervals are removed, nilab2 joins the pairs of "free ends" together using an annealing procedure. Check the 'show results' check-box in the 'delete pause' pop-up window to open a figure window, which will contain plots of the data time series before and after the removal procedure.

Calculate contrasts

Prior to carrying out GLM analysis, it is necessary to define one or more analysis hypotheses. These take the form of *contrasts*, or linear combinations of responses to experimental conditions (*e.g.*, difference between [Condition-1 oxy-Hb] and [Condition-2 oxy-Hb]) that you think may be statistically significant.

1. Select 'Contrast' from the 'FUNs2' menu:

📣 u_popcontras	t	
stimdur [x-y]		
	-x-	contrast
	Marker	1
ALLvsALL Specific ALLvsRest	cancel	e.g. [1 2 3 4 vs 5 6 vs 8] help ok

If you want to modify the previously specified stimulus durations (p. 14), enter your changes in the 'stimdur [x-y]' field.

2. Press the 'ALLvsALL' button to generate an omnibus contrast that you can use to test the (null) hypothesis that all of the conditions produce equivalent responses. Press the 'ALLvsRest' button to generate an omnibus contrast that you can use to test the (null) hypothesis that none of the experimental conditions produce responses different from the resting condition. ('ALLvsALL' and 'ALLvsRest' are equivalent for the demo data set, since there is only one experimental condition, which is alternately present and absent.) For other contrasts, press the 'Specify' button and enter the contrast definition in the resulting text field:

📣 u_popcontrast		
stimdur [x-y]		
	-x-	contrast
	Marker	1
Specific		e.g. [1 2 3 4 vs 5 6 vs 8]
ALLvsRest		
	cancel	help ok

The correct syntax for entering a contrast is shown in the example suggested by nilab2: (1 2 3 4 vs 5 6 vs 8).

3. Press the 'ok' button to generate the contrast. A figure window will open, containing a plot that corresponds to the contrast that you defined, which in our case is:





This procedure is used to estimate how closely each data time series resembles the time course of the experimental conditions. In another words, it evaluates the degree to which knowledge of the experimental conditions allows one to predict each data time series.

1. Select 'GLM' from the 'FUNs2' menu. This will launch the following GUI:

🔥 u_popGLM	
GLM	
HRF Type	HRF parameter
boynton 🔽	5 plot HRF
stimulation cycle or highpass filter [sec]	30
range for timecourses [sec] e.g.[0 20]	0 20
modelbased tiemcourse keep single traces	VES
GLM covariates no covariates	no covariates clear
parse HRFfolded STIMBLOCK 「 YES	
	Peak Detection
chk corr. of FLT and Contrasts YES	Search 4 optimal peak YES
Filt. Treshold (*.18) 0.18	range [e.g2.2]
cancel help	ok

2. Select a HRF (<u>hemodynamic response function</u>) type from the 'HRF Type' drop-down menu (the 'my' type is under construction at this time). This mathematical function is used to account for the time lag between a change in experimental condition and the resulting change in the hemodynamic variables. Press the 'plot HRF' button to produce a graph of the function you have selected. If you want, replace the default value of the 'HRF parameter' (in the case of 'spm_hrf' you may change any or all), and press 'plot HRF' again to see the effect:



3. In the 'stimulation cycle or highpass filter [sec]' field, specify the cutoff period for the GLMimplemented high-pass filter. The value you specify should be at least 2 times the inter-stimulus interval (for the demo data set, the inter-stimulus interval is 40 seconds). Thus we replace the default value (30) with 80, so that all oscillations with periods \geq 80 seconds will be suppressed.

4. The numbers in the 'range for timecourses [sec]' field are the starting and ending times, with respect to the onset of each change in experimental condition, of the data interval that the GLM procedure takes into consideration; data points outside this interval are ignored. For the demo data set, we will set the limits to '-5 35'.

5. If you check the 'yes' box for 'modelbased timecourse', then the GLM computation will isolate responses to different conditions before creating block averages (*i.e.*, removes overlaps between conditions from the block averages; this is not important for the one-condition data set we consider here, but is important for analysis of multi-condition experiments).

6. All other fields and options in the GLM GUI are under construction at this time. Press the 'ok' button to start the computation. This creates several new fields in the ni-structure. One of these is 'ni.GLM', whose contents are:

Here, 'cc' = concentration changes, 'tval' = t-values, 'av' = average time courses, 'va' = variance weighted time-courses, 't' = time-vector, and 'tracelims' = time limits in seconds.

Plot traces and t-values

1. Select 't-values and traces' from the 'PLOT' menu. This opens two secondary GUIs:

📣 u_tvalues			<u>_ </u>
	NIRS-2011-02-09 00	2 Left config	
cond. [1]	▲ ▼	plot Conc change oxy-Hb deoxy-Hb both yslider	close clear figs tilefigs
plot T-value catch figur O Label [on/off]	Min Min Max		

and

📣 u_plotgui	
	NIRS-2011-02-09_002_Left_config
Select Data	parent y-limits smoothing
• VAR	indiv. y-limits width close
U AVG	Parameter hide plots tilefigs
select condition	Oxy-Hb Ocy-Hb Ocy-Hb Ocy-Hb
cond1	barplot
	INDicolor yim Indi on change color
-	Plot linewidth 2 help

2. In the first ('u_tvalues') GUI, press the 'plot T-values' button, to produce:



The plotted quantity is a statistical parameter (t-statistic) produced by the GLM procedure. The larger the (absolute value of) the T-value, the more strongly predictive the experimental time course is of the data time series.

3. Press the 'plot Conc change' button in the 'u_tvalues' GUI, to produce:



which is a plot of the average (Condition present)-minus-(Condition absent) difference in oxy-hb (red) and deoxy-Hb (blue) concentration, for each channel. You may obtain an enlarged view of the plot for a particular channel, by placing the mouse cursor over it and clicking. For example:



4. In the 'u_plotgui' GUI, select 'AVG' in the 'Select Data' module. Then press the 'Plot' button, to produce plots of the block-averaged oxy-Hb and deoxy-Hb time series, as shown in the following figure:



Notice that every plot in the montage has a different range on the y-axis; that is because the default display mode is 'indiv. y-limits' (u_plotgui GUI). Press the 'parent y-limits' button in the u_plotgui GUI to enforce a uniform y-axis range on all the channels:


You may obtain an enlarged view of the plot for a particular channel, by placing the mouse cursor over it and clicking. For example:





The preceding figure window has a row of icons across the top, one of which looks like: Place the mouse cursor on that icon, and click to open the following window:



You can use the preceding window to do the following:

- Click on gray boxes to show/hide the corresponding traces
- Click on colored boxes to change color of the traces
- Click on labels, to change the label text
- Change the line width

Saving data

Select 'save data' from the 'file' menu. This saves the ni-structure, including all of the parameter values that were specified, and with the results of the functions (*e.g.*, frequency filtering, hemoglobin computation) that were applied. A default output file name is supplied, but you are free to change this in any way that you would like.







Multi-Session or Multi-Subject Data Sets

Research designs frequently involve performing measurements on multiple subjects (and there may be more than one recording session per subject), while applying the same experimental protocol each time. Two features are included in nilab2 to facilitate processing of the data sets produced in this type of study:

1: After you process one data set from the study, you can create a MATLAB script that contains all of the parameter values (*e.g.*, stimulus durations, leading and trailing time frames to cut, contrast definitions) that you specified. You can run this script to process the remaining data sets without having to re-enter the parameters each time. During each run, you will be given the option of adjusting parameter values, to accommodate inter-session variations (*e.g.*, the number of leading or trailing time frames is not the same for every measurement session) in the experimental protocol.

2: A level-2, or group-level, data analysis capability is provided, which allows you to evaluate the consistent or variability of experimental results across sessions or across subjects.

For training purposes, we include with nilab2 a sample of data from multi-subject study. During the measurement sessions, the subjects alternately performed finger-tapping with their left and right hands, in a left-rest-right-left-... sequence. Measurements were taken using a NIRScout imager with 16 sources and 16 detectors, which were arranged as shown in the following cartoon. The raw data files are located in the 'nilab2\data\GroupLevel' folder, where you will find two sub-folders named 'Subject1' and 'Subject2'.



A channel grid that corresponds to the depicted optode array, obtained by using the method given in the appendix, is shown in the following screenshot. The associate *configig*.m file, called 'NIRSconfigigGroupLevel.m', is located in the 'nilab2\imcon' folder.



Use the following sequence of steps to carry out multi-subject data processing:

1. Convert *all* subjects' raw data files to UNIFORMAT (pp. 3-5 above).

2. Select *one* subject, and process that subject's data in the manner explained above (pp. 5-32). Here, we select the data in the Subject1 folder. The particular operations and parameter settings that we use are:

- stimulus duration = 10 s (p. 14)
- both markers (default names are '3' and '15', based on the NIRScout trigger channels used by the group that performed the measurements) accepted (pp. 14-15)

— low-pass filtering, with filter order = 3 and high cutoff frequency = 0.21671 Hz (the 'select manually' option was used, to exclude the cardiac and respiratory frequency bands) (pp. 18-21):



- high-pass filtering, with a cutoff of 64 s (p. 22)
- cut the session, keeping 18 time frames before the first marker and 52 after the last marker (pp. 25-27)
- estimate hemoglobin concentration estimation, with inter-optode distance = 3 cm, W. B.
 Gratzer spectra, and all other parameters left at their default settings (pp. 22-25)
- define contrast, selecting ALLvsALL and including both markers (these are the default settings) (pp. 29-30)
- GLM, selecting spm_hrf as the HRF type, 64 s as the high-pass filter cutoff, and '-5 25' as the range for time courses (pp. 30-32).

The result after these processing steps is:



That is, finger-tapping with each hand has the expected spatially localized effect, with the left hand primarily affecting the right side of the head, and vice versa. On each side of the head, there

are statistically significant differences between the hemodynamic effect of left-hand and righthand tapping.

3. Save the selected subject's ni-structure (pp. 37-39). Eventually (see Step 7, below), it will be necessary for you to place the saved ni-structures for all subjects into a single folder. For this example, we will save them into the '...nilab2\data\GroupLevel' folder.

4. Select 'Generate Script' from the 'PostHoc' menu. This action will launch a popup window having the tile 'set gui/window pop up'. Highlight the 'open [default]' option, and press the 'OK' button at the bottom of the window.

📣 nilab2			
file FUNs1 FU	Ns2 PLOT PostHoc I	HELP @intern EXTRAS	plugins 🏻 🔊
	ii. CONmode Masterv Masterv Masterv Masterv Granda Mi. CONstir	Image: Script [2048 2]:d Vork 'allvsall' 'verage 10 ; 1 = 18 52 ; 22 ;	louble ;
evalin 1	ni.FLThp ni.FLTorder ni.GLM ni.GLM_FltcorrCHK ni.GLM_FltcorrTRES	= 64 ; = 0.21671 ; = 3 ; : struct (6 = 0 ; H = 0.18 ;	1) ;
evalout clear 1 2	1. GLM_Reepsinglet 1. GLM_modelbasedt 1. GLM_peaksearch1 1. GLM_peaksearch1 1. GLM_peaksearch1 1. GLMCovariates 1. GLMflthp	Faces = 0; HK = 0; UN = 0; ANGE = -2 2; = (-2 2); = 64;	
	ni.HRFparam ni.HRFtype ni.IMG ni.IMGinfo ni.IMGlabel ni.LBbaseline ni.LBdpf ni.LBepsilon ni.LBepsilon ni.LBepde	= 5 16 = 'spm_hrf' : [102 5]:do = ('ChanNr' : ([102 1]:c = 'all'; = 5.98 : [2 2]:doub = 1 ;	1 1 2000 0 30; ; uuble; 'wavelength' 'RowNrTarget' 'Coll :ell); 7.15; ; le;
1	ni.LBodistance ni.SD 4	= 3 ; = 16 24 ;	▼ ▶
e.(** READ NI ** READ Co ** set n	g. for Fl is 1001, IRSFILE: N:\Shared onstruction-file: parameter	F2 is 1002 Folders\Yong_Xu\r N:\Shared_Folders\	elease_09012012\src_navi_0901201 Yong_Xu\release_09012012\src_nau
** extract ** data 1 ** high ** cut Se ** concer ** creat ** perfor	: marker: 3 15 lowPassfiltered: C ass:64 s ession: 18 52[in tration changes c e contrast: med GLM	.21671Hz; order: 3 datapoints] alculated	
SAVE N	IISdata as: MI\Sha	red_Folders(fong_X	



A MATLAB script will be generated, and a MATLAB editor window containing the script will automatically open. Note that the default name for the script is 'temporary_auto.m', and the default location is the '...\nilab2\essence' folder. Save the file with a name, and in a location, of your choice. Here, we save it in the '...\nilab2\data\GroupLevel' folder, with the name 'TwoSubjectTwoHandFingerTap.m' [but you are free to pick either a different location or a different (shorter) name]:

📝 Edito	r - N:\Shared_Folders\Yong_Xu\release_09012012\src_navi_09012012_p\utilities\nilab2\essence\tempory_auto.m	
<u>Eile E</u> di	it <u>T</u> ext <u>Go</u> <u>C</u> ell T <u>o</u> ols Debug <u>D</u> esktop <u>Wi</u> ndow <u>H</u> elp	X 5 K
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1		
2	SHEETER AUTOMATIC CONFIGETLE HERE	-
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4		
5		
6 -	ni=[]; %clear struct	
7		
8		
9	\$====== [CONTRAST]	
10 -	ni.CONmode=['allvsall'];	
11 -	ni.CONspecific='';	
12 -	ni.CONstimdur=[10];	
13 -	ni.CONstimjit=[1];	
14	&=====================================	_
15 -	ni.Cut=[18 52];	=
16	%= [FILTER]	
17 -	ni.FLThp=[64];	
18 -	ni.FLTlp=[0.21671];	-
19 -	ni.FLTorder=[3];	
20	%======= [General Linear Model]	
21 -	ni.GLM_FltcorrCHK=[0];	
22 -	ni.GLM_FltcorrTRESH=[0.18];	
23 -	ni.GLM_keepsingletraces=[0];	
24 -	ni.GLM_modelbasedtraces=[1];	
25 -	ni.GLM_peaksearchCHK=[0];	
26 -	ni.GLM_peaksearchFUN=[0];	
27 -	ni.GLM_peaksearchRANGE=[-2 2];	
28 -	<pre>ni.GLMcovariates=();</pre>	•
	script	1 Col 1 OVR

📝 Editor - N:\Shared_Folders\Yong	_Xu\release_09012012\9	src_navi_09012012_p\utilities\nilab2'	\essence\tempory_au	to.m	<u>- 0 ×</u>
<u>File E</u> dit <u>T</u> ext <u>Go</u> <u>C</u> ell T <u>o</u> ols De	e <u>b</u> ug <u>D</u> esktop <u>W</u> indow <u>H</u>	<u>t</u> elp			X 5 K
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		<u></u>			
My Netwo	rk File name:	TwoSubjectTwohandFingerTap.m	•	Save	
Flaces	Save as type:	M-files (*.m)	•	Cancel	

5. In the MATLAB main user interface, navigate to the folder containing the script generated in the preceding step. Run the script once for each study session/subject after than the one selected for use in Step 2 above. The complete sequence of processing steps will be executed; in each one, the relevant popup windows will open to give you the opportunity to modify (where appropriate) the parameter values that you selected for the first subject.

a. Enter name of the script file at the MATLAB prompt:

ATLAB 7.5.0 (R2007b)	
File Edit Debug Desktop Window Help	
🎦 🚰 🕉 🐃 🛱 🤊 (° 🚑 🗹 🖹 🎱 Current I	Directory: N:\Shared_Folders\Yong_Xu\release_09012012\src_navi_09012012_p\utilities\nilab2\data\GroupLevel
Shortcuts 🗷 How to Add 💽 What's New	
Current Directory Workspace I+ □ ₹ X	Command Window
🛅 📷 🝓 🤪 🐻 🛛 🕶 Stack: Base 💌	New to MATLAB? Watch this <u>Video</u> , see <u>Demos</u> , or read <u>Getting Started</u> .
Name 🛆 Size Bytes Class	>> TwoSubjectTwohandFingerTap

b. Select the UNIFORMAT data file for the *second* study subject:

Select File to Op	en				? ×
Look in	: 🔁 GroupLevel		•	🗕 🗈 💣 🎟	•
My Recent Documents Desktop My Documents My Computer	Composition Subject1 Subject2 卿 ana_NIRS-20 別IRS-2012-0 卿 NIRS-2012-0	012-07-16_011_config 7-16_011_config 7-17_002_config			
My Network	File name:	NIRS-2012-07-17_002_c	onfig.mat	•	Open
	Files of type:	MAT-files (*.mat)		•	Cancel

c. Select the configuration file:

Select File to Ope	n					? ×
Look in:	imcon		•	← 🗈 💣		
My Recent Documents Desktop My Documents My Computer	 ISSkonfig_INAt NIRSconfigig.m NIRSconfigig_I NIRSconfigigGr NIRSconfigigGr NIRSconfigigLe 	EXP.m 5 S5_steffitest.m roupLevel.m ftMot.m				
My Network	File name:	NIRSconfigigGroupLevel.m		•		Open
Flaces	Files of type:	M-files (*.m)		•		Cancel

d. Set the stimulus duration (the MATLAB script retains the value we selected for the first study subject):



e. Select the markers for the experimental conditions of interest (the MATLAB script retains what we selected for the first study subject):

📣 u_popmarker			
marker (oc 3 N(10) 15 N(10)	:curence)		
accepted markers		3 15	
rename			
	ancel	help	ok

f. Select the cutoff frequency and filter order for the low-pass filter (the MATLAB script retains the values we selected for the first study subject):



g. Select the cutoff for the high-pass filter (the MATLAB script retains the value we selected for the first study subject):

📣 u_pophpass	
Highp	assfiltler
lowCutoff [sec]	64
cancel help	ok

h. Select the numbers of time frames to keep prior to the first marker and after the final marker (the MATLAB script retains the numbers we selected for the first study subject):

🔸 u_popcutsession	
cut session	plot marker
99 dp before FIRST Mrk (> ~28.5303sec	
84 dp after <last +="" 10s)="" mrk="" of="" stimdur=""> ~24.5821</last>	sec
STIMULUSduration: 36dp> >10s	2 values (DATAPOINTS)
input [x y], with x dp befor and y dp after session to include in session	18 52
cancel help	ok

i. Specify parameters for hemoglobin concentration computation (the MATLAB script retains what we selected for the first study subject):

📣 u_popLBG			_ 🗆 🗵
calculate Conce	entration cha	nges select from	spectrum
inter optode distance [cm]	3	[1] W. B. Gratzer	•
N first Datapoints for baseline	all		
	epsilon oxy-H	lb epsilon deoxy-Hb	DPF
higher WL 850	2.5264	1.7986	5.98
lower WL 760	1.4866	3.8437	7.15
		sh	ow DPF
cancel	help	ok	

j. Define contrast for GLM (the MATLAB script retains what we selected for the first study subject):

📣 u_popcontras	t	
stimdur [x-y]		
	-x-	contrast
	Marker	3 15
ALLvsALL Specific ALLvsRest	cancel	e.g. [1 2 3 4 vs 5 6 vs 8] help ok

The resulting model function is displayed in a popup window:



k. Specify parameters for GLM computation (the MATLAB script retains the value we selected for the first study subject):

📣 u_popGLM	_
GLM	
HRF Type	HRF parameter
spm_hrf	5 16 1 1 2000 0 30 plot HRF
stimulation cycle or highpass filter [sec]	64
range for timecourses [sec] e.g.[0 20]	-5 25
modelbased tiemcourse keep single traces	VES
GLM covariates no covariates	Clear Clear
parse HRFfolded STIMBLOCK 🔲 YES	
	Peak Detection
chk corr. of FLT and Contrasts 📃 YES	search 4 optimal peak 📃 YES
Filt. Treshold (*.18)	Function [0,1,2] 0 range [e.g2.2] sec -2.2
cancel	lp ok

1. Select a folder and specify a file name for the processed data file. The default folder and file name are the same as those that we specified for the first study subject. We want the second subject's results to go in the same folder (see Step 7, below), but we do *not* want to overwrite the previous data file! Change the name to one that indicates that these are the second subject's results. A convenient way of doing this is:



Select File to Wr	ite		? ×
Save in:	🗀 GroupLevel	- 🗈 📸 🖬 -	
My Recent Documents	Subject1 Subject2 卿 ana_NIRS-2012-07-16_011_config 卿 NIRS-2012-07-16_011_config 卿 NIRS-2012-07-17_002_config		
Desktop My Documents		Add a prefix, to indicated that this file contains the results of a data <i>ana</i> lysis	
My Computer	File name: ana_NIRS-2012-07-17_000 Save as type: MAT-files (".mat)	2_config.mat S	ave

m. A message indicating successful execution of the script will appear in the MATLAB user interface. If there were additional study subjects, you would repeat Step 5 for each remaining one.

	R2007b)									
Eile Edit Debug Desktop Window Help										
🛅 📸 👗 🐂 🖏 🤊 🥲 🖣 📸 🖹 🥹 Current Directory: N:\Shared_Folders\Yong_Xu\release_09012012\src_navi_09012012_p\utilities\nilab2\data\GroupLevel										
Shortcuts 🕐 How to Add 🕐 What's New										
Current Directory	Wor	kspace	× s ⊡ ≁i	Command Window						
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Name 🛆	Size	Bytes	Class	>> TwoSubjectTwohandFingerTap						
Η model	2049x2	32784	double							
🔚 ni	1x1	2133384	struct	RUN GLM						
🔣 tr	2049x102x2	1671984	single							
				• Bazinga! •						
				>>						

- 6. To view the results of the processing steps carried out for Subject2, do one of the following:
 - If there is a ni-structure resident in the MATLAB memory (*i.e.*, this will be the one most recently computed in the current MATLAB session), press the 'evalin' button on the nilab2 GUI. The latest ni-structure computed in Step 5 will be loaded into nilab2. Alternatively:
 - Select 'load data (uniformat') from the 'file' menu. Select one of the files containing processed data (in this example, one of the files with a 'ana_' prefix). It is not necessary to load the configuration file, because this information is contained in the imported nistructure.



Select 't-values and traces' from the 'PLOT' menu (pp. 32-37) to view the results of the analysis carried out on the data for Subject2. It is seen that the result is similar to that obtained for Subject1 (p. 43), demonstrating inter-subject consistency:





7. To perform level-2 data analysis, select the 'Grandaverage' item from the 'PostHoc' menu. This will open the popup window shown in the next figure:



Press the 'path' button in the popup window, to open a file browser as shown in the next figure. Navigate to the folder containing the processed data files for all subjects, and then press 'OK':

Bro	wse For Folder	? ×
s	elect Directory to Open	
[Description: De	
	🗄 🫅 osa_2012	
	🗄 🧰 pdf01	
	🗉 🛅 Peter_pdf	
	🕀 🧰 rat01	
	🖂 🫅 release_09012012	
	🗉 🚞 src_modelgenerator_09012012_p	
	🖂 🧰 src_navi_09012012_p	
	🗉 🧰 dataanalyzer	
	🕀 🧰 datarelated	
	🕀 🧰 dataviewer	
	🕀 🗀 imagegenerator	
	🖃 🧰 utilities	
	🗉 🧰 batchp	
	🕀 🧰 modelgenerator	
	🕀 🧰 navi2emse	
	🕀 🧰 naviSPM	
	🖃 🧰 nilab2	
	🖃 🚞 data	
	🖽 🧰 data_t01	
	🗉 🧰 DougData	
	🖃 🗀 GroupLevel	
	🖽 🫅 Subject1	
	🗄 🫅 Subject2	T
F	older: GroupLevel	
	Make New Folder OK C	ancel
_		

Press the 'select pbn' button in the popup window, to open a window for choosing files from the selected folder, as shown in the next figure.

📣 u_popavg		_ 🗆 🗙
	Average	
oath select pbn ○ subject show ○ avg	'no subjects'	<u> </u>
drop outs Nr.	close process expo	rt & ROI





With the 'avg' radio button highlighted, press the 'show' button to perform the group-level statistical analysis. Popup windows allowing you to plot the t-statistics and time courses for all channels, similar to those for individual-subject analysis (pp. 32-33) will appear:

📣 u_popa v g			_ _ X
	Avera	ge	
path select pbn Subject avg	'no subjects'		▲ ▼
drop outs Nr.			
	close	process	export & ROI

GUI for level-2 t-statistics:









3-3 5-5 7-7 9-9 11-11 13-13 15-15 5-3 5-7 9-7 9-11 13-11 13-15 -10

GUI for level-2 tine courses:



APPENDIX: How to Generate a Channel-Layout Grid for an Arbitrary Optode Array

For both examples considered in the preceding user's guide, the optodes were arranged in a manner (pp. 10, 40) that corresponded in a rather straightforward way to a simple checkerboard channel layout (pp. 12, 41). However, the arrangement of optodes that is best suited to a particular functional imaging study may have a more irregular character (and a strong point of NIRScout and DYNOT imaging systems is the flexibility they afford users in the positioning of optodes). For concreteness, here we consider a specific example that came from a research group interested in collecting data from a region in the back of the subject's head, overlying the visual cortex. They used 8 sources and 12 detectors, and arranged them in the pattern depicted in the following cartoon:



Here we present a set of steps that can be used to generate a channel layout for the array shown, and that has worked as well for every other array tested so far.

1. Draw line segments connecting all pairs of adjacent source and detector optodes (see Higher-Order Considerations, p. 68). Each line segment represents one measurement channel:



2. Place a mark in the middle of each line segment. These marks indicate the approximate locations of the centers of the volumes of tissue that the channels are sensitive to:



3. Count the number of distinct channel locations in the vertical dimension. This will tell you how many rows to specify in your channel layout:



4. Count the number of distinct channel locations in the horizontal dimension. This will tell you how many columns to specify in your channel layout:



5. Give each channel a numerical label, m-n, where m is the source number and n is the detector number:



6. In nilab2, specify a layout array containing *M* rows and *N* columns (in this example, M = 10 and N = 14):

7. Fill in the channel-layout squares that correspond to the row and column indices identified in Steps 3 and 4. Use the channel labels identified in Step 5:

					1-3			1-8					
		3-3				1-4	1-9				6-8		
			3-4							6-9			
3-6				4-4					6-9				6-11
	4-6				4-1			7-1				7-11	
				4-5					7-10				
						2-5	2-10						
					2-7			2-12					
				5-7					8-12				
						5-2	8-2						

The 7-step method given here also reproduces the checkerboard layout on p. 12 when applied to the optode array sketched on p. 10, and the layout on p. 41 when applied to the array depicted on p. 40.

Higher-Order Considerations

1. Implicit in the instructions presented above is the idea that you will want to define channels for all pairs of nearest-neighbor sources and detectors, and only for these pairs. In our experience the assumption usually is correct, but you may find that for a particular analysis you either don't want to include every possible nearest-neighbor pair, and/or that you do want to include channels defined by optode pairs that are not nearest neighbors. In the former situation, all that is needed is to modify Step 1 on p. 63: instead of connecting *all* possible nearest-neighbor pairs with line segments, connect only the ones that you want to include in your analysis. Then proceed with the remaining steps as written.

The latter situation may require a more careful approach. Suppose, for example, that we decide to add some longer-distance channels to the array we have been considering, as shown in the following figure:



This change does not call for any modification to the sequence of steps given above. However, the number of rows in the channel grid will increase by 2, and the number of columns by 1, as shown next:





					1-3				1-8					
		3-3				1-4		1-9				6-8		
3-6			3-4				1-1				6-9			6-11
	4-6			4-4						7-9			7-11	
					4-1				7-1					
				4-5						7-10				
			4-7				2-1				7-12			
						2-5		2-10						
					2-7				2-12					
				5-7						8-12				
							2-2							
						5-2		8-2						

So the new channels can be incorporated into the method presented here for specifying a channel layout. But there are two significant caveats. First, you might have already noticed that the distance between the source and detector optodes is noticeably larger for the 5 new channels than for the 26 nearest-neighbor channels we had originally. But when you perform a hemoglobin-concentration computation (pp. 22-25), you only get to specify one value for the distance. If you put all 31 channels into a single grid, your only recourse is to pick some average value to use for all of them.

Second, in addition to the 5 long-distance channels we have considered so far, there are 4 others that are easily defined for this optode array, but a new problem is immediately apparent when we try to do so: the central points for the new channels coincide with the central points for 4 of the nearest-neighbor channels. This is shown in the following figure:


Both of these factors (*i.e.*, only one source-detector separation can be specified for the hemoglobin-concentration computation, and overlapping channels) lead us to recommend that if you want to include multiple source-detector separation distances in your data analysis, you should process the same data multiple times with nilab2, each time considering only one class of channels. For the example considered here, there are two classes of channels, nearest-neighbor and longer-distance, and so we would design two layout grids. The layout grid for the 26 nearest-neighbor channels is the one shown on p. 68. The grid for the 9 longer-distance channels is:

4-3		1-1		7-8
4-7		2-1		7-12
	5-5		8-10	
		2-2		

2. The 7-step method (pp. 63-68) for generating a channel layout is straightforward to implement for nearly any optode array. A possible downside is that it can lead you to generate a grid

containing large numbers of rows and columns (10 and 14 for the example on p. 68), with only a small percentage of the grid cells occupied by channels (26 out of 140, or ~19%). Once you have attained proficiency in generating layouts this way, you may want to experiment with collapsing rows and/or columns, on a freehand, case-by-case basis, in order to achieve a smaller grid size (while sacrificing some spatial accuracy in the channel locations). One way in which this sort of grid-size economy can be achieved for the optode array we are considering here would be:



This corresponds to the following 8×6 channel layout, which has channels in more than half of the grid cells:

3-3	1-2	1-4	1-9	1-8	6-8
	3-4			6-9	
3-6	4-4			7-9	6-11
4-6	4-1			7-1	7-11
	4-5			7-10	
	2-7	2-5	2-10	2-12	
	5-7			8-12	
		5-2	8-2		

Likewise, the 7×17 checkerboard grid on p. 41 can be collapsed into a 7×9 one, by merging pairs of adjacent columns:

	2-4	6-4	6-8		10-8	10-12	14-12	
	2-2	4-4	6-6	8-8	10-10	12-12	14-14	
1-2	4-2	4-3	8-6		8-10	12-10	12-14	16-14
1-1	3-2	4-5	7-6	8-9	11-10	12-13	15-14	16-16
3-1	3-5	7-5	7-9		11-9	11-13	15-13	15-16
	3-3	5-5	7-7	9-9	11-11	13-13	15-15	
	5-3	5-7	9-7		9-11	13-11	13-15	