



HomER

A Graphical Interface for Functional NIRS Analysis



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Overview:

HomER is a graphical user interface designed to help analyze functional Near-Infrared Spectroscopy (NIRS) data. HomER provides tools for filtering and signal processing, averaging and linear regression, and also contains image reconstruction capabilities. HomER is designed to work with NIRS data from most source and experimental set-ups, allowing the user full control of the measurement configuration and probe properties.



HomER is available for download to the research community at:
<http://www.nmr.mgh.harvard.edu/PMI/resources/>

System Requirements:

HomER is distributed as a stand-alone application for Windows[®]. It utilizes the Matlab Run-time Component [Mathworks Inc. Natick, MA USA].

| Operating System | Processor | Disk Space | RAM |
|---------------------------------------|--|---------------------------------|--------------------------------|
| Windows [®] XP (SP 1 or 2) | Pentium III, IV, Xeon, Pentium M, AMD Athlon, Athlon XP, Athlon MP | Matlab Runtime Component: 175Mb | 256 MB 512 MB (recommended) |
| Windows [®] 2000 (SP 3 or 4) | | HomER: 15Mb | |
| Windows [®] NT (SP 5+) | | Total = 190 Mb | |

Data Format:

HomER accepts raw data files saved in Matlab (.mat) format. This allows the user flexibility to analyze data from virtually any existing NIRS system with only minor pre-processing. Both the probe geometry and experimental design are specified by the user, allowing for greater versatility.

Input Variables:

- Data (d)** – This variable contains raw light intensity versus time data for each NIRS source-detector combination.
- Measurement List (ml)** – This lists all the combinations of source-detector pairs. The user can specify any number of measurements. The measurement list can be pruned within HomER to remove channels with low signal-to-noise ratios.
- Stimulus (s)** – This allows the user to specify the timing for functional stimulus. HomER allows both blocked and event-related experimental designs. Multiple stimulus types can be specified within a single data file.
- Source-Detector Geometry (SD)** – The user can describe any probe geometry by specifying the spatial positions of each optode in the probe.
- Lambda (SD.Lambda)** – Any combination of wavelengths can be used in analysis (depending on the NIRS measurement hardware).

Data Export:

HomER allows export of analyzed data into both ASCII and Matlab (.mat) formats for further processing. This is done easily by pop-up menus on each plotted data window. Figures can also be created and saved into a variety of formats (JPEG, TIFF etc).
 Data from HomER can also be saved into movie (MPEG) files for future presentations. Movies of either optical-density or hemoglobin concentration can be created for viewing the hemodynamic response changes over time.

Features:

Signal Processing:

HomER contains tools for filtering time-courses with band-pass filters. Principle component analysis can be applied for motion artifact correction and systemic fluctuation (physiology) removal.

Callouts for Signal Processing features:

- Display of various time-course data variables
- Visual display of optode probe. Data is selected by clicking on optode positions
- Full control over how many and which wavelengths were recorded
- Low and High pass filtering options
- Principle Component Filtering Options (Zhang Y, et al. 2005, J. Biomed. Optics, 10(1))
- Load multiple experimental data-sets and subjects

Response Processing:

HomER contains a number of tools for analyzing functional hemodynamic responses. Both blocked design and event-related paradigms are supported, in addition to multiple condition (parametric) experimental designs. Responses are analyzed at the single experimental run and session level. Region-of-interest based analysis can be performed across subjects and sessions.

Callouts for Response Processing features:

- Task timing is overlain on the raw time-courses. Epochs can be manually rejected from the analysis to remove motion or other artifacts
- Hemodynamic response curves can be re-displayed according to their corresponding optode locations for easy visualization of localized activity
- Data can be exported to Matlab or ASCII file formats
- The hemodynamic response can be displayed for each source-detector pair averaged within and across data files.
- Controls allow the user to set the response averaging window. Either block averaging or linear regression can be performed

Other Features:

- Linear regression allows for multiple condition/Event-related experimental designs.
- Independent regressors, such as auxiliary recording of blood pressure or cardiac can be included to remove systemic fluctuations
- ANOVA and Effects statistics can be displayed for each channel.
- Blocks of time-points or individual channels can be selected to be disregarded in analysis allowing for rejection of motion or other artifacts

Image Reconstruction:

HomER offers a number of options for basic image reconstruction including back-projection and other regularized inversion techniques. HomER uses the PMI toolbox (also available to download at www.nmr.mgh.harvard.edu/PMI) to generate forward models using semi-infinite (homogenous) slab geometries. Spectral priors can be used to reconstruct images of concentration [Li et al. 2005 Applied Optics 44(10)].

Callouts for Image Reconstruction features:

- Features allow for movies to be created and saved as MPEG files
- Absorption and scattering coefficients can be specified for each wavelength
- Slide bar allows control of the response time to reconstruct
- Both optical density and hemoglobin concentration images can be reconstructed. The latter uses spectral priors during reconstruction
- Voxel sizes and reconstruction depths are user-defined

Image Reconstruction Methods:

- (weighted) Back-projection
- Regularized Inversion

$$Y = S \cdot A^T \cdot X_{src,det}$$

$$Y = R \cdot A^T \cdot (A \cdot R \cdot A^T + \lambda \cdot C)^{-1} \cdot X_{src,det}$$

User selects from a choice of regularization parameters to define the R and C variables.

Region-of-Interest Analysis:

Region-of-interest analysis can also be carried out with HomER. ROI averages can be calculated for individual subjects or group averages. Either effects or ANOVA statistics can be used to define regions of interest. This can be done by source-detector channel or within the reconstructed images.

Callouts for Region-of-Interest Analysis features:

- Region-of-interest averages can be calculated for individual subjects or group averages across multiple sessions
- Region-of-interest can be selected based on:
 - Response effects statistics
 - ANOVA analysis
 - In channel or image space

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