

nirsLAB: A Computing Environment for fNIRS Neuroimaging Data Analysis

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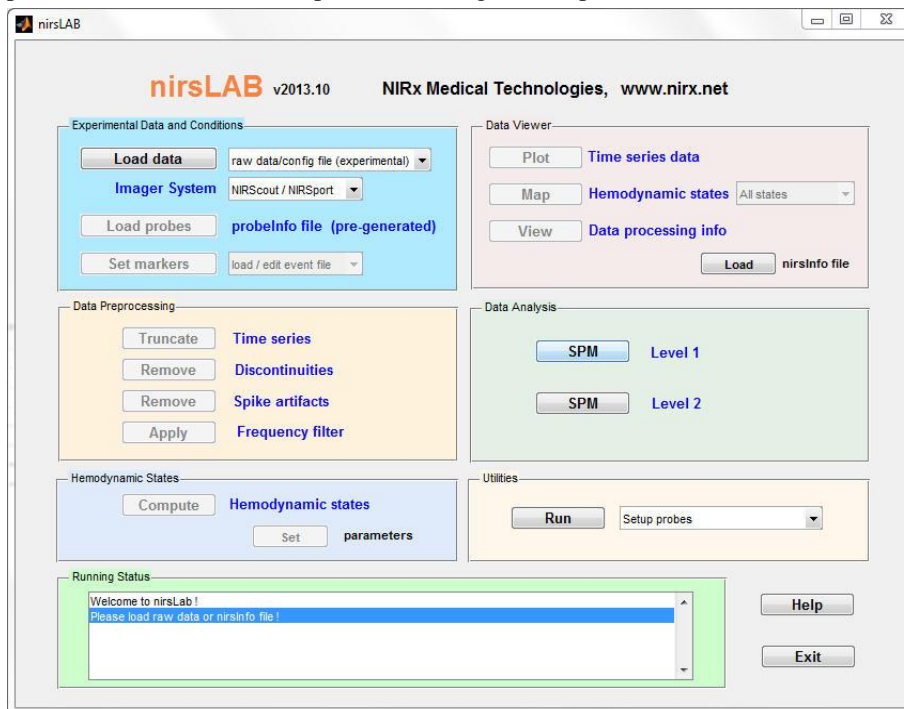
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Abstract. A publicly available MATLAB GUI-based resource for analysis and mapping of near infrared topographic neuroimaging measures is described. The code supports sensor registration, Level 1 and 2 GLM-based statistical parametric mapping and hyperscanning, among other features.

OCIS codes: (170.2655) Functional monitoring and imaging; (200.3050) Information processing; (110.1758) Computational imaging

1. Introduction: Access to well configured computing environments is a key factor necessary to accelerate application development derived from data intensive sensing platforms. In the field of neuroimaging, already well developed are publicly available resources that support processing of EEG [1], MEG [2] and fMRI [3] measures, among other types of data intensive platforms. In recent years commercial devices supporting high density NIRS data have become available, but lagging has been development of well configured computing environments that support data processing by non-domain experts. Several publicly available platforms have been developed including Homer 2 [4], NIRS-SPM [5], NAP [6], NILAB and NAVI [7], each having their strengths and weaknesses. Motivating the configuration of resources available in nirsLAB is consideration of the need for improved resources to facilitate data and event editing, capacity to process more expansive wavelength vectors, improved visualization tools, and access to additional utilities supportive of application development.

Key functionalities include: sensor registration for arbitrary arrays, data and event editing tools, artifact correction, parameter estimation from up to 8 wavelengths of input (instantaneous, canonical event-related responses), display



resources onto planar, scalp and cortical surfaces including block averaging and movies, anatomical structure identification, Level 1 and Level 2 GLM based SMP analysis, data export utilities, recording of history and batch processing, and intersubject comparisons for hyperscanning studies. Also available are utilities to reformat data in support of inter-platform compatibility. Parameter specification can be made through keyboard entry or graphically. Access to other utilities for use of machine learning algorithms and 3D image recovery are in progress.

Figure 1. nirsLAB homepage.

The Home Page:

The nirsLAB environment features processing portals segmented in accordance to principal elements of a pipeline approach. Briefly this is comprised of: (1) registration of optode layout and merging of event protocol; (2) artifact correction and filtering as needed; (3) computation of hemoglobin states; (4) data plotting, editing and topographic viewing; (5) Level 1, 2 GLM based SPM computation; (6) data export and other utilities.

Processing Portals:

Data Loading: Data loading is immediately accomplished using metadata produced by the NIRx line of imagers. Data from other system types can also be processed but require an initial transformation of formats. Also initially loaded are a predefined arbitrary optode layout and a protocol-based event table. The former can be generated using supplied graphical tools or by loading data from a digitizer. Editing tools are supplied for editing of the event file as needed.

Data Preprocessing: This module is intended to correct for the presence of artifacts, deletion of undesired time segments, and perform frequency filtering as needed. Spikes and mean shifts can occur due to changes in optode contact. Disturbances in the channel data can be selected either graphically or using a variance dependent threshold. Data merging following deletion is accomplished by resetting the mean value post artifact to that seen pre-artifact. Correction for mean shifts without deletions is accomplished similarly. Elimination of spikes is accomplished by either substituting affected time intervals with the mean of the nearest neighbor values observed

during the same period, or with assigned random values having a similar variance.

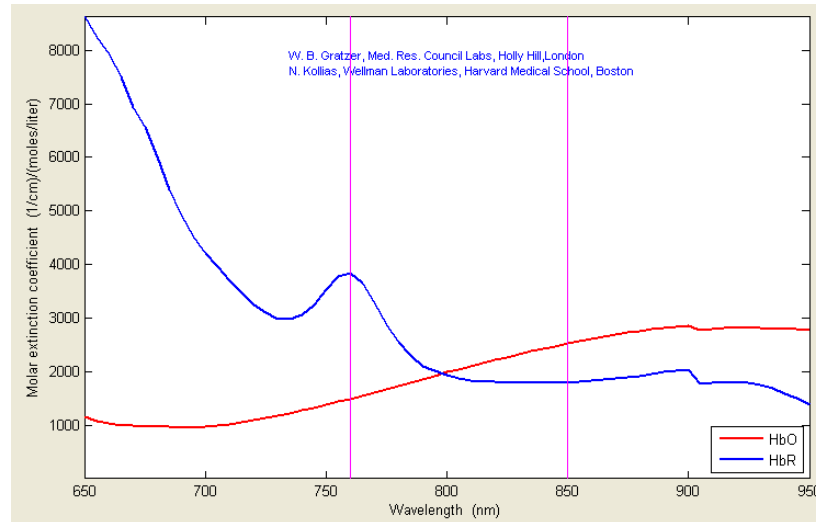


Figure 2: Wavelength selection for computation of Hb states.

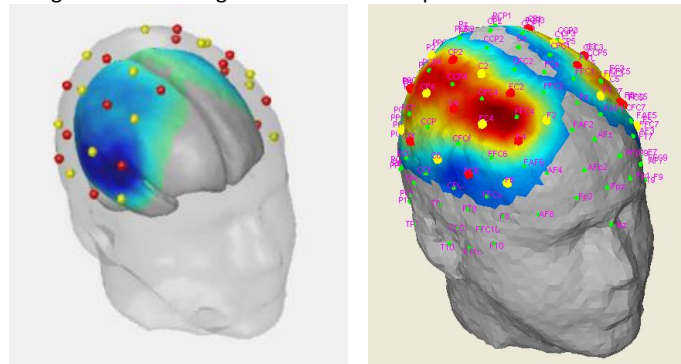


Figure 3. Head model views of Hb response.

Hemodynamic States:

Computation of relative values of hemodynamic states (oxyhemoglobin, deoxyhemoglobin, total hemoglobin and hemoglobin oxygen saturation) is accomplished using a modified Beer-Lambert method corrected for wavelength dependent differential pathlength factor, and estimated values of mixed venous oxygenation and tissue hemoglobin concentration.

Up to eight different wavelengths can be considered ranging from 650-950 nm. Selection of these can be made graphically, as shown in Figure 2, or by entry in a data field. When more than two wavelengths are specified, hemoglobin computation is made based on solving an over-determined system of equations by a least squares method. Also available are options to compute hemoglobin values based on user selected pairs of wavelengths.

Data Viewing: This portal supports viewing of raw and processed data either as an

amplitude-dependent time series or as a composite spatial map viewed in various 2D, scalp or cortical viewing options. To facilitate anatomical views, additional overlays involving sensor positions and EEG landmarks are also available. Shown in Figure 3 is an example of a montage glass-view revealing computed hemoglobin values projected on to the MNI atlas registered within a defined head space. Also seen is a scalp view with additional specification of EEG locations in accordance to the International 10-10 system. Mapping of instantaneous hemoglobin values, movies of selected time segments or movies of block averaged events are available. Also accessible is determination of anatomical features as revealed from registration of the automated anatomical labeling atlas available from SPM [3].

GLM-based Data Analysis: This module is fashioned after the tools originally provided by SPM8 [3]. The drop-down menus provided enable the user to: 1) specify a hemodynamic state for analysis; 2) choose the mathematical form for estimating the hemodynamic response function, and modify the chosen function's parameters; 3) select time series (e.g., stimulus timing records) to use as the primary models in the GLM design matrix; 4) if desired, include additional design-matrix models (e.g., via a discrete cosine transform) to account for hemodynamic fluctuations unrelated to the experimental protocol; 5) implement pre-coloring and/or pre-whitening procedures to account for serial correlations that may be present in the hemodynamic time series.

Connectivity Measures: We have adapted the Dynamic Causal Module of SPM [3] for evaluation of causally directed brain connectivity measures. The module operates on two or more selected ROIs and applies the DCM inverse operation as a basis for model selection.

Hyperscanning: This module supports the loading of data files obtained from two or more subjects engaged in a common task and computes various time dependent metrics based on selected seed vectors. Measures of temporal coherence, cross correlation, and cross spectral density among others are available. Seen in Figure 4 is an example of a computed intersubject cross correlation map.

Utilities: Under development are GUIs that support access to 3D FEM based tomographic imaging resources and to the TU-BCI toolbox developed by Müller and co-workers [8].

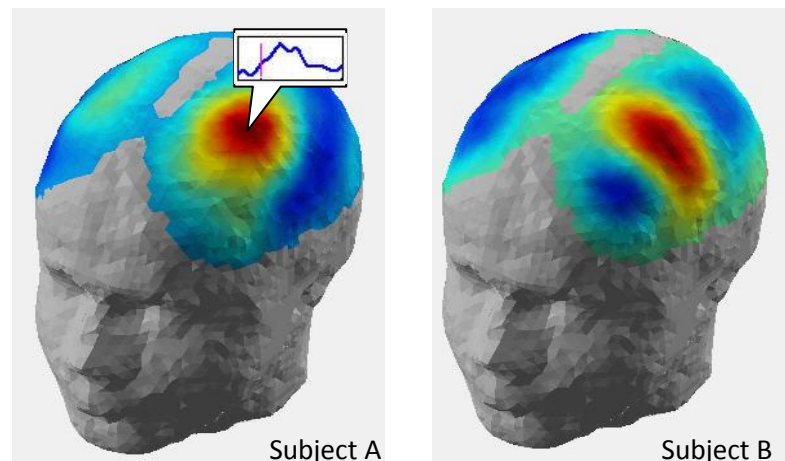


Figure 4: Cross correlation map obtained from subjects undergoing common task.

5. Acknowledgements

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6. References

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- [5] <http://bisp.kaist.ac.kr/NIRS-SPM.html>
- [6] <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0024322>
- [7] http://www.nitrc.org/projects/fnirs_downstate
- [8] <http://bbci.de/toolbox/>