Manual Donders NIRS Batch

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Introduction

The Donders NIRS Batch is a toolbox made to analyze NIRS in a simple way, whilst also giving plenty of options to individualize your analysis. The batch is a collection of scripts that utilises the NIRS_SPM batch, created by Tak et al (Tak & Ye 2014), which is itself based on the SPM toolbox for fMRI analysis (http://www.fil.ion.ucl.ac.uk/spm/).

To run DNB_NIRS on your data, you only need to open 2 Matlab files, one to change settings, dataset-locations, save-destinations etc in. The other one to run the batch.

Before running the batch, please make sure to have raw datafiles, onset information files and MNI coordinate files ready for all subjects. More information on how to construct onset information files and MNI coordinate files can be found in 'The INFO-file' chapter, component 3.

DNB_info

This file is the most important file for running DNB. In this file all settings and locations can be manually changed. If all settings are set right, there is no need to change any of the other DNB scripts.* All settings are explained shortly in the INFO script, but we will explain them a little bit more in detail in 'The INFO-file' chapter.
Advised is to construct separate INFO-files for different trials.

DNB_main_program

This is the main-program from which all the other scripts run. The main-program does not need further alteration after entering the name of the INFO-file constructed before in the script (INFO.infofile). Every step in the batch will be explained briefly in the 'main program' chapter.

* In this phase there still might be some overlooked errors in the data.

The INFO-file

The INFO structure is structured in different components. Each part will be described individually below. When running the batch for the first time, all options should be checked to make a decision on which set of filtering/statistic options will be used for future analysis. When the filtering/statistic options are decided upon, only a few options have to be altered between analyzing different datasets.

The numbers and titles given below can also be found in the INFO file.

1. *DNB: Data selection*
2. *DNB: General options*
3. *DNB: Add data directories*
4. *DNB: Add script directories*
5. *DNB: Data conversion*
6. *DNB: Model specification*
7. *DNB: Filtering*
8. *DNB: Grand average calculation*
9. *DNB: Single subject statistics*
10. *DNB: Group statistics*

1. *DNB: Data selection*
    - Analysisname: Name given to analysis. This is used for naming the report made after the analysis and for naming (if desired) the second level analysis.
    - Subjects: Names/codes of the subject(s) you want to analyse. Subjects should be entered as a cell array containing strings for the subject codes.
    - Taskname: Name of the task you want to analyze. This taskname is used for naming files and for running the adjust_onsets script.

2. *DNB: General options*
    - Overwrite: The batch automatically skips parts of the DNB_script if the results of these steps are already available. When INFO.overwrite='yes', DNB runs the scripts again and overwrites the results. ('yes'/'no').
    - Plots: Should the batch automatically makes plots of every step ('yes'/'no').
    - Extension: File extension of saved plots made by the batch ('.jpg'/'.fig').
    - Stopwhenerror: When running multiple subjects overnight, encountering an error stops the whole analysis process, even when the problem might only be a missing file. To fix this problem, the DNB can skip subjects which generate errors and moves on to the next one. Set this function to 'yes' when troubleshooting ('yes'/'no').
    - Delsteps: Should the batch delete all .mat files generated (except for the final one) when the analysis is finished ('yes'/'no').
    - Firstsecond: The batch has the option to run individual (first level) analysis, group (second level) analysis or both. Note: group level analysis can only be performed when first level analysis has been done before (second level analysis uses GLM calculations from individual subjects) ('first'/'second'/'both').

- SCI.check: The Scalp coupling index is used to check the quality of the NIRS data before analysis. The SCI checks the correlation between HbO and HbR in every channel. These signals should be correlated when the NIRS-signal quality is acceptable. If this script is used, 'bad' channels based on the SCI check are excluded from analysis. Which channels are excluded can be checked later in the report ('yes'/'no').
- SCI.Corrrequired: The minimal correlation between HbO and HbR required for the SCI script to accept a channel. Default is 0.9 (van de Rijt et al. 2016).
- SCI.chanrequired: Number of channels required after deleting not accepted channels using SCI to continue analyzing.

3. *DNB: Add data directories*

Before analysis, the user assigns folders to be used for data storage and data gathering.

The folders used for data storage will be used by the DNB toolbox to store all results and figures, so make sure the chosen folder has enough storage capacity for the data.
Only one directory has to be entered for data storage (INFO.file.dir). DNB will construct a folder structure inside this directory to store all data.

The folders used for data gathering should contain all raw data-files.
The DNB batch needs (at least) three raw types of data-files to be able to analyze:

-The file where the data is stored (named under INFO.file.rawdata_name)
-The file where the onset information is stored (named under INFO.file.conditions_name).
-The file where MNI channel coordinates are stored (named under INFO.file.MNI_file_name).

The rawdata-file is the file directly coming from data acquisition. The system providing the NIRS data should also provide log-files containing the onsets and durations of all trials. The DNB requires a mat-file containing the onset information to analyze the data. This 'onset information file' should consist of three different variables: 'names', 'onsets' and 'durations'.

-Names: a cell array containing strings for the different conditions.
-Onsets: a cell array containing matrices with all the onsets of the trials, matching the names array. For example, when the first cell in 'Names' reads '0back', the first cell of 'Onsets' should contain a matrix (nTrials * 1) with all onsets of the '0back' trials.
-Durations: a cell array containing matrices with all the durations of the trials, matching the names array. For example, when the first cell in 'Names' reads '0back', the first cell of 'Durations' should contain a matrix (nTtrials * 1) with all durations of the '0back' trials.

The 'onset information file' should be made before starting analysis with the DNB.
The MNI channel coordinates of the NIRS optodes should be stored in a matrix with the following structure: 3 x nOptodes, where the first row consists of X-coordinates, the second row consists of Y-coordinates and the third row consists of Z-coordinates.

The DNB batch is designed to run analysis over several subjects at the same time. The INFO.file.rawdata_dir and INFO.file.conditions_dir are therefore designed as matrices in the sample INFO file.

The name of the load directory is entered in four steps: the root directory (rootdir), the extension type (INFO.file.extension_type), the file-name (INFO.file.rawdata_name and INFO.file.conditions_name) and the full directory (INFO.file.rawdata_dir and INFO.file.conditions_dir). Usually, only one MNI-file is used for one experimental set-up. Therefore, INFO.file.MNI_file_name can be entered outside of the subjects loop.

In the sample INFO-file, we used information entered earlier in the 'data selection' section to automatically construct the names of raw-datafiles. To use this algorithm, the names of the raw_datafiles obviously have to match the naming algorithm given in the batch. Using the naming algorithm is not a must, as long as every desired filename/directory is given in the INFO-file, the batch will run.

Alongside the file types necessary for every analysis, the stop-task needs the log and txt file given by the NIRS device to run the adjust_onsets script (see 'The main program, 1.5'). When analyzing stop-task data, add the log and txt files given by the NIRS device to the same folder(s) as the rest of the raw datafiles and give them the same names as the raw data-file. The batch will find these files automatically and use them later on.

- Extension type: The extension of the raw NIRS-file which should be read for analysis. Different manufacturers of NIRS-equipment provide NIRS-files with different extension (for example, the oxymon produces .oxy3 files, while the spectratech produces .csv files).

4. *DNB: Add script directories*

Different scripts are necessary to run the DNB batch. These scripts will be included in the DNB package or can be downloaded online. Only the root directory (INFO.file.scriptdir) and the fieldtrip directory has to be entered by the user (assuming the files inside the DNB package are still in the original folder).

Scripts necessary for running the DNB-batch:

- DNB files
- SPM_nirs files (http://bispl.weebly.com/nirs-spm.html#/)
- SPM files (http://www.fil.ion.ucl.ac.uk/spm/software/spm12/)
- Oxy3convert files (only when using .oxy3 files)
- Fieldtrip files (http://www.fieldtriptoolbox.org/)

5. *DNB: Data conversion*

Information about the raw data files. Some NIRS systems automatically fill in some of these options in the data conversion script, others don't. Some information about this is given in the INFO-file comments. Systems other than the Oxymon are not tested extensively yet.

- System: NIRS system used for the data acquisition. For a list of possible acquisition systems, check the header of the DNB_data_conversion script.
- Samplefrequency: Sampling frequency used during data acquisition. The oxymon will automatically fill in this variable.
- Total channels: Number of channels implemented in the headcap used.
- Dist: Distance between source and detector of the NIRS system. Entered in (cm). The oxymon will automatically fill in this variable.
- Wavelength: Wavelength of the light-source used (perspectively HbO and HbR). The oxymon will automatically fill in this variable.
- DPF: Differential pathlength factor. The oxymon will automatically fill in this variable.
- Ext_coef: Extinction coefficient. Only the NIRX Dynot/Manual OD systems need manual input of this variable.
- Ch_config: channel configuration file. Only the NIRX Dynot/Manual OD systems need manual input of this variable.

To prevent memory issues and decrease storage requirements and calculation time, downsampling and facilitation of the Trace calculation are implemented in the DNB batch.

- Downsampling method: Three different kinds of downsampling can be used. Average downsampling or fieldtrip downsampling/resampling. We advise to use one of either fieldtrip functions as they run a lot more efficiently. If no downsampling should be used on the dataset, type 'none' in INFO.conv.downfs_method. ('ft_downsampling'/'ft_resampling'/' avg_downsampling'/'none')
- Downsampling frequency: The desired sampling frequency the dataset should be downsampled to.
- Stepsize Trace calculation: The trace calculation is the most heavy calculation of the DNB. To unburden the machine doing the calculations, we decided to split the trace calculation in steps. If left empty, the batch will attempt to find a suitable stepsize itself. We found 2000 samples per calculation to be a decent stepsize.

6. *DNB: Model specification*
    - Hb: Hemoglobin type ('HbO'/'HbR').
    - HRF type: Basis function used to model the hemodynamic response. 0='hrf', 1='hrf with time derivative' and 2='hrf with time and dispersion derivative' (see http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf for more information on HRF types).
    - Units: units in which the experimental onsets (from the onset information file) are specified ('scans/'secs')

7. *DNB: Filtering*
    - HPF: High pass filtering method. Options to choose from are Wavelet-MDL detrending (Jang KE, Tak S, Jung J, Jang J 2009), Discrete cosine transformation-based detrending (Tak 2011) or simple detrending (using the Matlab 'detrend' function) ('wavelet'/'DCT'/'detrend'). For DCT, the cut-off value can be entered after the name e.g. 'DCT, 65'. The default value is 128.

- LPF: Low pass filtering method. Options to choose from are an HRF-shaped filter, Gaussian-shaped filter (Friston et al. 1995) or simple low pass filtering (using the Matlab 'butterworth' filter) ('hrf'/'gaussian'/'lpf'). The FWHM value can be changed after Gaussian, the cut-off frequency can be entered after lpf. Defaults are 4 for Gaussian and 0.5 for LPF.
- MARA: Movement artifact removal algorithm. See 1.7 for more explanation about the MARA. The DNB batch can run MARA automatically or interactively ('yes'/'no'/'interactive'). If run interactively, DNB will show data of one channel with and without MARA and give the option to use MARA or not.
    - T: Threshold for artifact detection in MARA, used in the moving standard deviation signal, and expressed in T * mean of the moving standard deviation signal. To prevent MARA from removing useful data, the (T*mean of the moving standard deviation signal) should be high enough to guarantee not removing useful data (see figure 2).
    - L: Length of the moving window to calculate the moving standard deviation (in sec).
    - Alpha: Parameter that defines how much high-frequency information should be preserved by the removal of the artifact (i.e., it corresponds to the length of the LOESS smoothing window).

8. *DNB: Grand average calculation*
   See 1.11 for an explanation on grand averages.

    - Baseline calc: time window before the onset of a task which will be used to calculate the baseline on (sec)
    - Baseline plot: time window before onset of a task which will be plotted (sec).
    - Window size: time window to calculate (and plot) grand averages after onset stimulus (sec).

9. *DNB: Single subject statistics (1st level)*
   The DNB uses linear contrasts to compare activity between different tasks, the General linear model then interpolates the results to a slice of the brain.

    - Contrast names: names of the tasks you are interested in, expressed in a contrast. For example: {'Stopsucces>Stopfail','Gouncert>Gocert'}. Always use either '>' or '<' in the names.
    - Contrast vector: contrast vectors are numeral representations of the contrasts you are interested in. For example, imagine a vector with 4 conditions: '0back, 1back, 2back and 3back'. If you are interested if conditions '3back' produces more brain activity than '0back', '0back' should get a value of -1, while '3back' gets a value of 1. The remainder of conditions gets a value of 0. Therefore, the contrast vector will be: [-1 0 0 1]. Note: the sum of the contrast vector should always be 0.

- Spec_hemi: specific brain slice the user is interested in analyzing/plotting. Including: ‘ventral’, ‘dorsal’, ‘right’, ‘left’, ‘frontal’, ‘occipital’. It is possible to analyze different slices at once (eg. {‘frontal’, ‘left’}).
- Stat: type of statistic method used to see which brain areas are activated. Either T- or F-tests (‘T’/’F’).
- P-value: p-value used for the statistic method.
- Correct-P: P-value correction method. Uncorrected p-values only control type 1 errors for each voxel independently. Since there are many voxels in the brain slice, we are interested to control the type 1 error for the whole brain slice (Li et al. 2012) . NIRS_SPM offers two different correction methods for the p-value (Tak 2011) . Lipschitz-Killing curvature based expected Euler characteristics correction method (Li et al. 2012) and Sun's tube formula correction method (Sun & Loader 1994) (‘EC’/’tube’/’none’).

10. DNB: Group statistics (2nd level)

- Subjects: Subjects which should be used for group analysis. This is a different option from the subjects option in component one. Because of this option, the user can first run first level analysis over x number of subjects, and subsequently run second level analysis over y number of analysis.
- Overlap subjects: number of subjects with valid data on one location required for that location to be included in group analysis.

DNB_main_program

The main program of the DNB is designed to run automatically when the right options in the INFO-file are supplied. After supplying the right info, the following steps will be taken if first level analysis is chosen:

1.1. DNB_pre_loopscript
1.2. DNB_name
1.3. DNB_data_conversion
1.4. DNB_SCI (optional)
1.5. DNB_adjust_onsets
1.6. DNB_downsampling (optional)
1.7. DNB_runMARA (optional)
1.8. DNB_model_specification
1.9. DNB_estimation_batch
1.10. DNB_extract activation
1.11. DNB_grand_averages
1.12. DNB_MNI_coord2render
1.13. DNB_extract_contrast_activation
1.14. DNB_activation_map
1.15. DNB_delete_steps (optional)
1.16. DNB_report

The following steps will be taken if second level analysis is chosen:

2.1. DNB_pre_loopscript
2.2. DNB_name_group
2.3. DNB_estimation_batch_group
2.4. DNB_activation_map_group
2.5. DNB_grand_averages_group
2.6. DNB_extract_contrast_activation_group
2.7. DNB_report

Note: all figures shown in the main_program explanation were generated by the DNB and will be generated for every new experiment (except when the option for generating plots is turned off).

Batch summary

Light red: Steps in the DNB Dark red: Input or output files/figures

1.1. DNB_pre_loopscript.

This script changes some variables supplied in the INFO_file to match with the required format. For example, it adjusts the contrast vector to match the format given in the INFO file.

1.2. DNB_name.

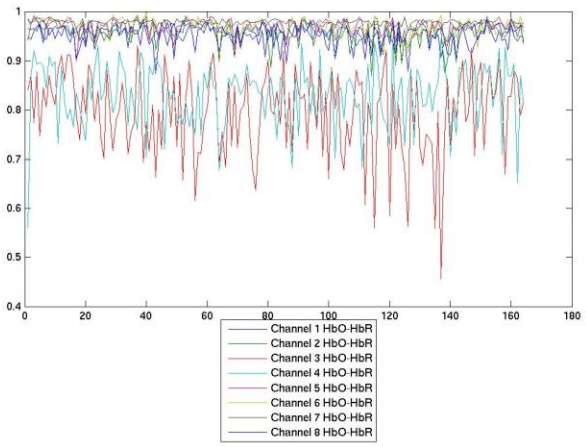
This script constructs file names and directories to use when writing away files. These names are composed from INFOparts (like taskname and subjectname) given earlier.

1.3. DNB_data_conversion

This script converts the raw datasets (e.g. 'oxy3' files) to analyzable '.mat' files.

1.4. DNB_SCI (optional)

This script runs the scalp coupling index over the raw data of all channels. The scalp coupling index is a signal quality measure. The signal for both the HbO and HbR data is bandpass filtered between 0.5 and 2.5 Hz (typical frequency range for heart rate that excludes low-frequency NIRS activity) in the SCI script. The heart rate should influence both channels in the same way, resulting in a strong correlation between both datasets assuming the noise level of the measurement is acceptable. If the noise level of one of the levels is too high (see SCI_correquired), the channel will not be analysed. If more than the number of channels selected in INFO.SCI.chanrequired are removed using the SCI check, the subject will not be analysed (this will be presented later on in the automatic report).



1. Scalp coupling index results. The correlation between HbO and HbR of channel 3 and 4 is less than 0.9. Therefore, these channels are excluded from the analysis.

1.5. DNB_adjust_onsets

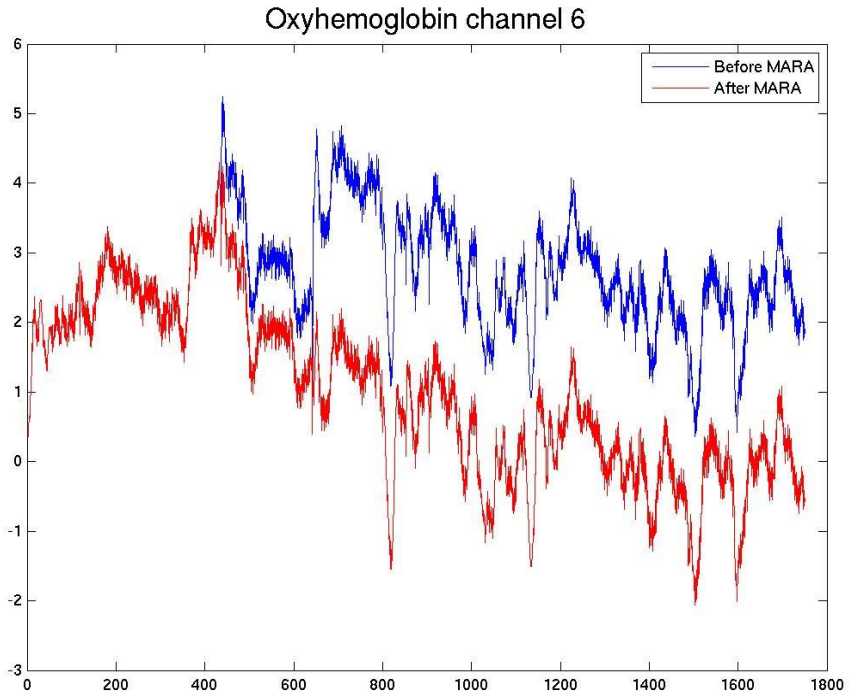
Due to different measurement start times between NIRS acquisition and stimulus presentation , the onsets are offset in time. To fix this offset, an adjust_onsets file has to be made for every task. This script needs to be tailored to each task. Scripts for the 'nback' and 'stop' task are already made.

1.6. DNB_downsampling (optional)

This script downsamples the dataset with one of the three downsampling methods (ft_downsampling, ft_resampling, avg_downsampling) with the downsampling rate chosen in the INFO file.

1.7. DNB_runMARA (optional)

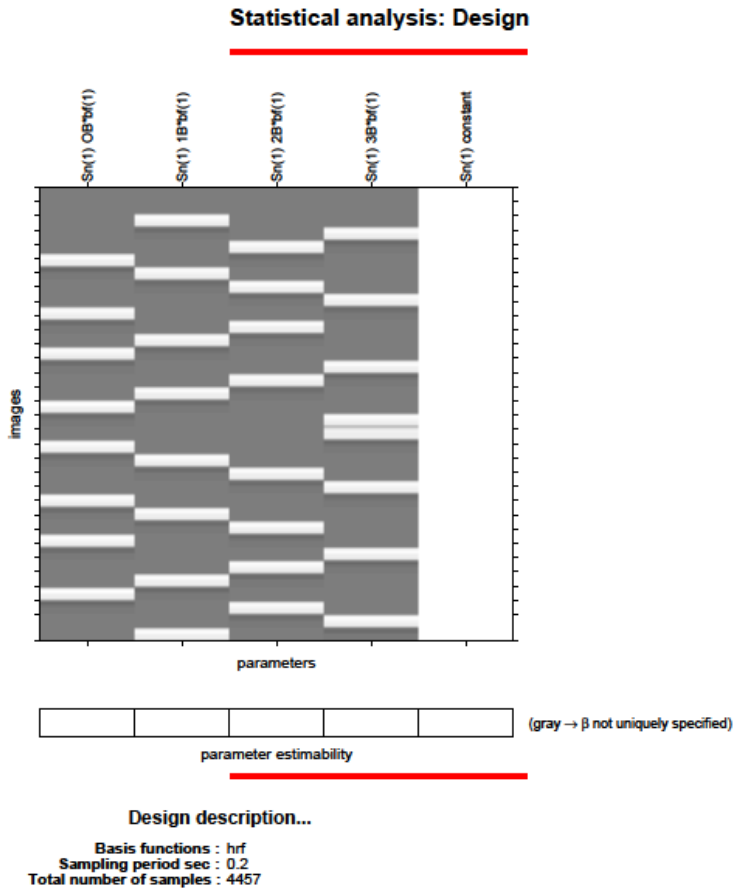
Run MARA (Scholkmann et al. 2010) over the data with the filtering variables given in the INFO file. MARA will attempt to remove spike-like artifacts from the data. These spike-like artifacts can't be removed completely by filtering alone. They can (for example) be generated by movement of the optodes on the head. MARA (Scholkmann et al. 2010) can remove these artifacts. The MARA script will not run if no artifacts found in the data are higher than the threshold (T) given in the INFO-file. However, do not run MARA if you have exceptionally clean data, in that case MARA might remove useful information instead of removing artifacts.



2. MARA results. In the original signal (before MARA), a spike-like artifact is present in the data at approx. 600 ms. MARA finds artifacts by looking for peaks with exceptionally high peaks and removing them from the data. These peaks can't possibly be real data (Oxy/Deoxy concentration does not change as sudden as these peaks). How steep the peaks should be to be considered 'artifact' can be modified in the INFO file (T).

1.8. DNB_model_specification

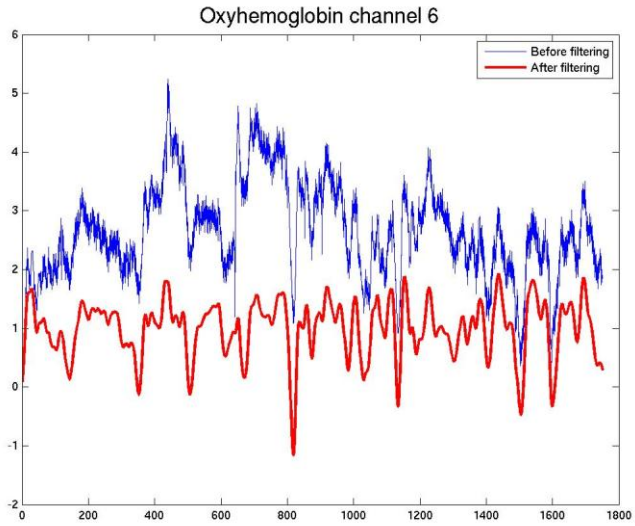
The model specification script specifies the general linear model. It constructs (and plots) the design matrix based on the (altered) onsets and durations of every separate task in an experiment. It also constructs the temporal filters used in the model.



3. Design matrix. The columns represent different conditions, the rows represent samples. Each white block represents one trial.

1.9. DNB_estimation_batch

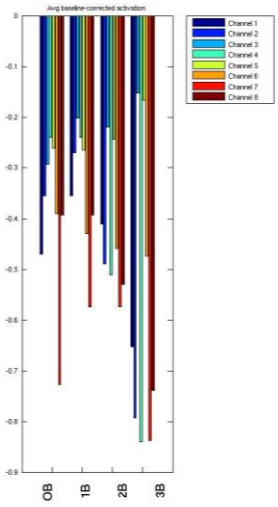
The estimation script runs the GLM estimation process, which estimates the GLM parameters and applies the designed temporal filters on the data.



4. NIRS data before, and after MARA/LPF and HPF filtering.

1.10. DNB_extract activation

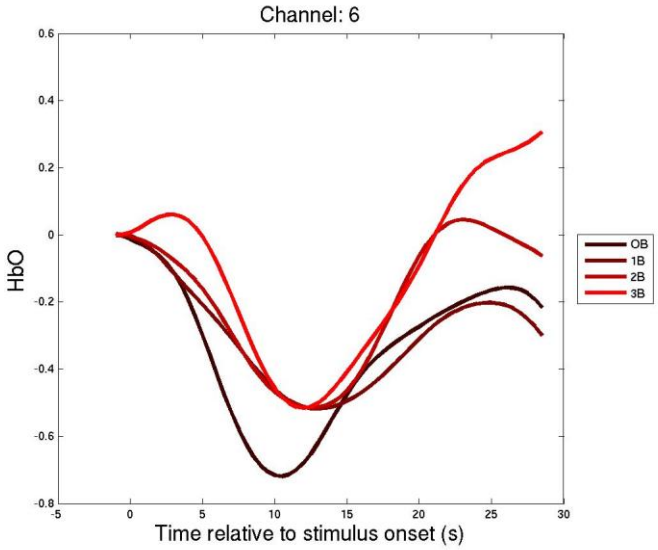
The extract activation script calculates the mean (base-line corrected) NIRS signal for all conditions/channels based on the model specification file (design matrix) and plots them.



5. Mean NIRS signal during all conditions (columns) for all channels (different colors).

1.11. DNB_grand_averages

The grand average script averages the NIRS signal for every trial in every condition, similar to event-related potentials in EEG. For example, experiment A has done 10 '0back' trials. The grand average of the '0back' is the average signal during these 10 '0back' trials. This will be done for all channels separately. Subsequently, the script plots the grand averages for either one task (all channels) or one channel (all tasks) in one figure.



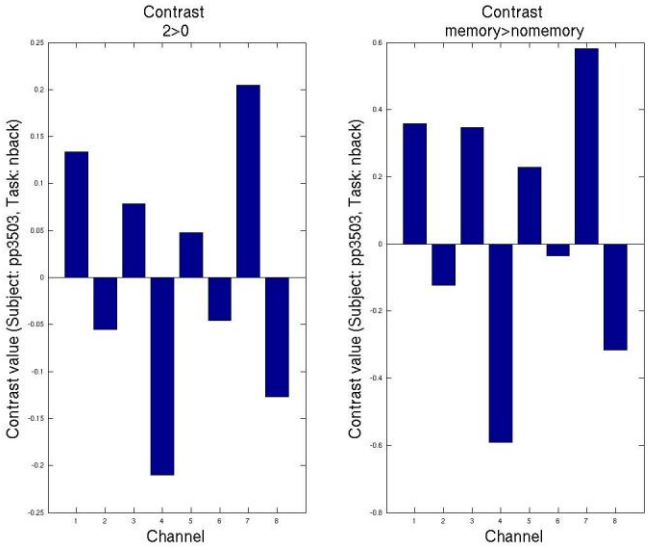
6. Grand average results. Every line is a representation of the resulting HbO response during one task (0back, 1back, 2back or 3back) in one channel mediated over all available repetitions.

1.12. DNB_MNI_coord2render

This script converts the MNI coordinates of the optodes given by the user into real coordinates which can be used to construct brain maps in DNB_activation_map.

1.13. DNB_extract_contrast_activation

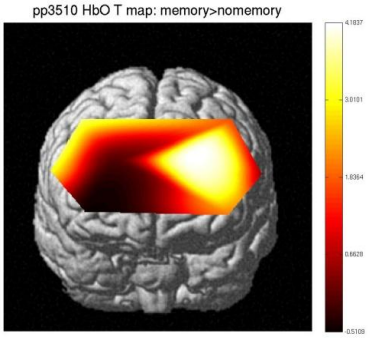
Extract_contrast_activation does the same as extract activation, as it calculates the NIRS signal for every channel. However, instead of plotting every condition, Extract_contrast_activation does a linear multiplication based on the contrastvector to construct one activation-variable that expresses the strength of the contrast. For example, when the contrast '3back>0back' is used, the extracted contrast activation presents the degree to which the '3back' condition led to more NIRS signal than the '0back' condition.



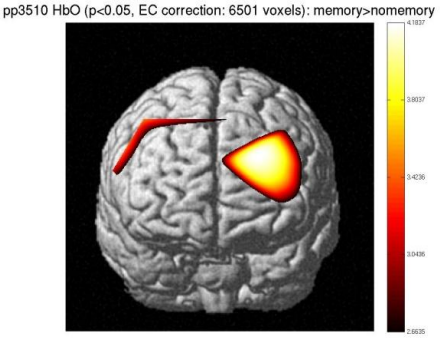
7. Extract contrast activation. In channels 1,3,5 and 7, the 2back contrast is higher than the 0back, and the memory contrast is higher than the no memory contrast. However, in channels 2, 4,6 and 8, results are the other way around.

1.14. DNB_activation_map

This script calculates (and plots) activation maps. One uncorrected activation map is plotted, and one corrected for multiple comparisons. The corrected activation maps uses the variables p-value and correct_p supplied in the INFO file and only presents brain activations where the desired contrasts significantly differ.



8. Uncorrected activation map. All areas of the brain where the color value is higher than 0 represent areas where HbO activation is higher during the memory compared with the no memory conditions (memory>nomemory) in this subject.



9. Corrected activation map. All color blobs in this plot represent areas where HbO activation is significantly higher during the memory compared with the no memory conditions, as calculated with the 'Lipschitz-Killing curvature based expected Euler characteristics' correction method and thresholded at P < 0.05.

1.15. DNB_delete_steps (optional)

Deletes datafiles made after all steps except for the last one and the ones required for group statistics. This way, the analysis costs less overall memory.

1.16. DNB_report

The report script constructs a report-file, which contains some information about the analysis done. For example, the report presents information given in the INFO file, results of the SCI-script (which channels are excluded , which aren't) and which channels are altered by the MARA script.

2.1. DNB_pre_loopscript

See 1.1.

2.2. DNB_name_group

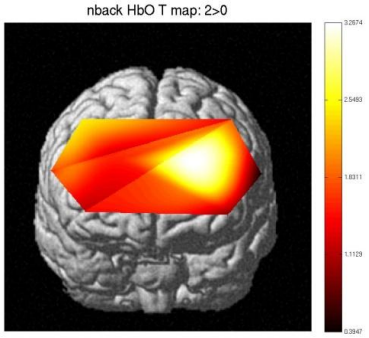
This script constructs names for all figures and files to use during group analysis.

2.3. DNB_estimation_batch_group

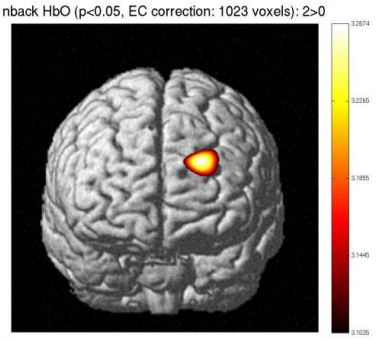
The group estimation script loads in GLM-estimation parameters gained by running the DNB_estimation_batch in separate subjects. These parameters are then converted to parameters for the whole group.

2.4. DNB_activation_map_group

This script has the exact same function as the DNB_activation_map (see 1.14) function. However, it uses the GLM-parameters calculated for a group of subjects (calculated in 2.3) instead of the GLM-parameters for one subject.



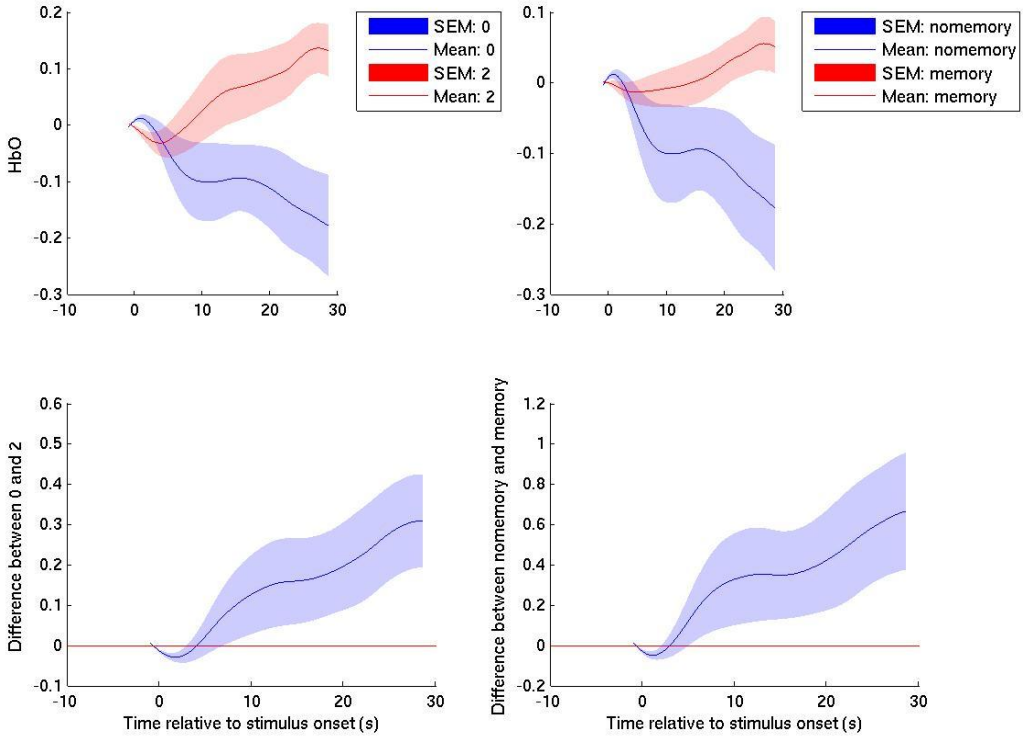
10. Uncorrected activation map. All areas of the brain where the color value is higher than 0 represent areas where HbO activation is higher during the memory condition compared with the no memory condition (memory>nomemory) in this group of subjects.



11. Corrected activation map. All color blobs in this plot represent areas where HbO activation is significantly higher during the memory tasks compared with the no memory conditions, as calculated with the 'Lipschitz-Killing curvature based expected Euler characteristics' correction method and thresholded at P < 0.05.

2.5. *DNB_grand_averages_group*

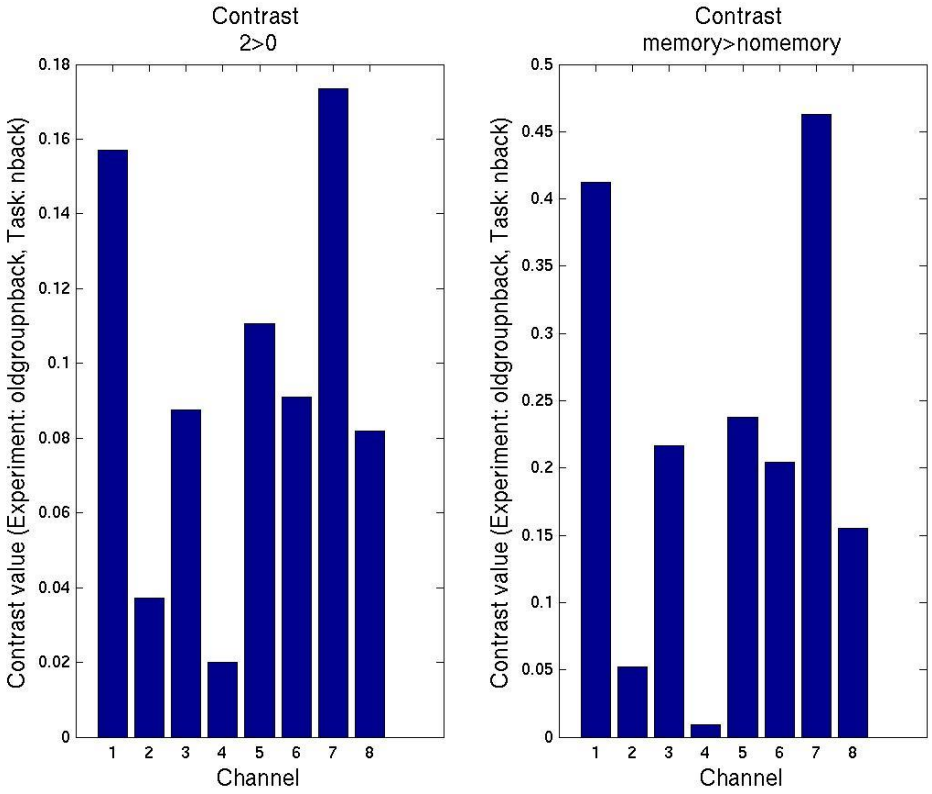
Calculates grand averages in the same way as in 1.11. However, the grand averages are not only mediated over repetitions, but also over subjects. Furthermore, only the contrasts that are interesting for the user (selected using the contrastvalue) are calculated, together with a 'difference' value.



12. Grand average group results. The lines in the upper graph represent mean and SEM of the resulting HbO response during different conditions in one channel mediated over all available trials and all subjects. The lower two graphs represent mean and SEM of the difference between the two lines in the upper graph.

2.6. DNB_ extract_contrast_activation _group

See 1.13. However, as expected, the contrast activation values are mediated over the subjects.



13. Extract contrast activation. In this group analysis, all channels appear to have higher activation values for the 2back/memory tasks than the 0back/nomemory tasks.

2.7. DNB_report

See 1.16.

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