
pynibs Documentation

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pyNIBS is a Python package to work with non-invasive brain stimulation (NIBS) data, foremost from transcranial magnetic stimulation (TMS) experiments.

We created this package to allow the mapping of causal structure-function relationships with TMS. A lot of analyses is based on calculations of the induced electric fields (e-fields) – for this we rely on [SimNIBS](#).

Install **pyNIBS** via [pip](#):

```
pip install pynibs
```

or directly grab from our repository at gitlab.gwdg.de/tms-localization/pynibs

CONTENTS.

1.1 pynibs package

1.1.1 Subpackages

pynibs.congruence package

pynibs.congruence holds the initial congruence factor implementation as described in Weise, Numssen, et al., 2020 [1]. This code is mainly stored here for reproducibility reasons. The current approach (Numssen et al., 2021; [2]) uses the *pynibs.regression* methods.

References

Submodules

pynibs.congruence.congruence module

`pynibs.congruence.congruence.cf_curveshift_kernel(e_curve, mep_curve)`

Curve congruence (overlap) measure for multiple MEP curves per element. Determines the average displacement between the MEP curves. The congruence factor is weighted by `median(E)` and summed up. This favors elements which have greater E, as these are more likely to produce MEPs.

$$dE = \begin{bmatrix} dE_{11} & dE_{12} & \dots & dE_{1n} \\ dE_{21} & dE_{22} & \dots & dE_{2n} \\ \dots & \dots & \dots & \dots \\ dE_{n1} & dE_{n2} & \dots & dE_{nn} \end{bmatrix}$$

-> `congruence_factor ~ np.linalg.norm(dE)/median(E)/n_cond/2`

Parameters

- **e_curve** (*list of np.ndarray of float*) – (n_cond) List over all conditions of electric field values corresponding to the mep amplitudes.
- **mep_curve** (*list of np.ndarray of float*) – (n_cond) List over all conditions of mep values corresponding to the electric field.

Returns

congruence_factor – Congruence factor for the n_cond electric field and MEP curves.

Return type

float

`pynibs.congruence.congruence.cf_curveshift_workhorse(elm_idx_list, mep, mep_params, e, n_samples=100)`

Worker function for congruence factor computation - call from `multiprocessing.Pool`. Calculates congruence factor for $e = (E_{\text{mag}}, E_{\text{norm}}$ and/or E_{tan}) for given zaps and elements. The computations are parallelized in terms of element indices (`elm_idx_list`). `n_samples` are taken from `fitted_mep`, within the range of the [Mep](#).

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for.
- **mep** (list of [Mep](#)) – (`n_cond`) List of fitted Mep object instances for all conditions.
- **mep_params** (*np.ndarray of float*) – (`n_mep_params_total`) List of all mep parameters of curve fits used to calculate the MEP, accumulated into one array.
 - e.g. [`mep_#1_para_#1`, `mep_#1_para_#2`, `mep_#1_para_#3`, `mep_#2_para_#1`, `mep_#2_para_#1`, ...]
- **e** (list of list of *np.ndarray of float*) – [`n_cond`][`n_datasets`][`n_elm`] Tuple of `n_datasets` of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest.
 - `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)
- **n_samples** (*int*, `default=100`) – Number of data points to generate discrete mep and e curves.

Returns

congruence_factor – (`n_roi`, `n_datasets`) Congruence factor in each element specified in `elm_idx_list` and for each input dataset.

Return type

np.ndarray of float

`pynibs.congruence.congruence.cf_curveshift_workhorse_stretch_correction(elm_idx_list, mep, mep_params, e, n_samples=100)`

Worker function for congruence factor computation - call from `multiprocessing.pool` Calculates congruence factor for $e = (E_{\text{mag}}, E_{\text{norm}}$ and/or E_{tan}) for given zaps and elements. The computations are parallelized in terms of element indices (`elm_idx_list`). `n_samples` are taken from `fitted_mep`, within the range of the [Mep](#).

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for
- **mep** (list of [Mep](#)) – (`n_cond`) List of fitted Mep object instances for all conditions.
- **mep_params** (*np.ndarray of float*) – (`n_mep_params_total`) List of all mep parameters of curve fits used to calculate the MEP, accumulated into one array.
 - e.g. [`mep_#1_para_#1`, `mep_#1_para_#2`, `mep_#1_para_#3`, `mep_#2_para_#1`, `mep_#2_para_#1`, ...]
- **e** (list of list of *np.ndarray of float*) – [`n_cond`][`n_datasets`][`n_elm`] Tuple of `n_datasets` of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest
 - e.g.: `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)

- **n_samples** (*int*, *default=100*) – Number of data points to generate discrete mep and e curves.

Returns

congruence_factor – (n_roi, n_datasets) Congruence factor in each element specified in elm_idx_list and for each input dataset.

Return type

np.ndarray of *float*

```
pynibs.congruence.congruence.cf_curveshift_workhorse_stretch_correction_new(mep,
                                                                            mep_params,
                                                                            e,
                                                                            n_samples=100,
                                                                            ref_idx=0)
```

Worker function for congruence factor computation - call from multiprocessing.Pool. Calculates congruence factor for $e = (E_{mag}, E_{norm} \text{ and/or } E_{tan})$ for given zaps and elements. The computations are parallelized in terms of element indices (elm_idx_list). n_samples are taken from fitted_mep, within the range of the *Mep*.

Parameters

- **mep** (list of *Mep*) – (n_cond) List of fitted Mep object instances for all conditions.
- **mep_params** (np.ndarray of *float* [n_mep_params_total]) – List of all mep parameters of curve fits used to calculate the MEP (accumulated into one array)
 - e.g. [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...]
- **e** (np.ndarray of *float*) – (n_elm, n_cond) Electric field in elements.
- **n_samples** (*int*, *default=100*) – Number of data points to generate discrete mep and e curves.

Returns

congruence_factor – (n_elm) Congruence factor in each element specified in elm_idx_list and for each input dataset.

Return type

np.ndarray of *float*

```
pynibs.congruence.congruence.cf_curveshift_workhorse_stretch_correction_sign_new(mep,
                                                                                  mep_params,
                                                                                  e,
                                                                                  n_samples=100,
                                                                                  ref_idx=0)
```

Worker function for congruence factor computation - call from multiprocessing.Pool. Calculates congruence factor for $e = (E_{mag}, E_{norm} \text{ and/or } E_{tan})$ for given zaps and elements. The computations are parallelized in terms of element indices (elm_idx_list). ``n_sample``s are taken from fitted_mep, within the range of the *Mep*.

Parameters

- **mep** (list of *Mep*) – (n_cond) List of fitted Mep object instances for all conditions.
- **mep_params** (np.ndarray of *float*) – (n_mep_params_total) List of all mep parameters of curve fits used to calculate the MEP, accumulated into one array.
 - e.g. [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...]
- **e** (np.ndarray of *float*) – (n_elm, n_cond) Electric field in elements.
- **n_samples** (*int*, *default=100*) – Number of data points to generate discrete mep and e curves.

Returns

congruence_factor – (n_elm, 1) Congruence factor in each element specified in `elm_idx_list` and for each input dataset.

Return type

np.ndarray of float

```
pynibs.congruence.congruence.cf_curveshift_workhorse_stretch_correction_variance(elm_idx_list,
                                                                              mep,
                                                                              mep_params,
                                                                              e,
                                                                              n_samples=100)
```

Worker function for congruence factor computation - call from `multiprocessing.Pool`. Calculates congruence factor for `e = (E_mag, E_norm and/or E_tan)` for given zaps and elements. The computations are parallelized in terms of element indices (`elm_idx_list`). `n_samples` are taken from fitted_mep, within the range of the *Mep*.

Parameters

- **elm_idx_list** (np.ndarray) – (chunksize) List of element indices, the congruence factor is computed for.
- **mep** (list of *Mep*) – (n_cond) List of fitted Mep object instances for all conditions
- **mep_params** (np.ndarray of float [n_mep_params_total]) – List of all mep parameters of curve fits used to calculate the MEP (accumulated into one array)
 - e.g. [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...]
- **e** (list of list of np.ndarray of float) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest
 - e.g.: `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)
- **n_samples** (int, default=100) – Number of data points to generate discrete mep and e curves

Returns

congruence_factor – Congruence factor in each element specified in `elm_idx_list` and for each input dataset

Return type

np.ndarray of float [n_roi, n_datasets]

```
pynibs.congruence.congruence.cf_variance_sign_workhorse(elm_idx_list, mep, mep_params, e)
```

Worker function for congruence factor computation - call from `multiprocessing.Pool`. Calculates congruence factor for `e = (E_mag, E_norm and/or E_tan)` for given zaps and elements.

Parameters

- **elm_idx_list** (np.ndarray) – (chunksize) List of element indices, the congruence factor is computed for.
- **mep** (list of *Mep*) – (n_cond) List of fitted Mep object instances for all conditions.
- **mep_params** (np.ndarray of float) – (n_mep_params_total) List of all mep parameters of curve fits used to calculate the MEP, accumulated into one array), e.g. [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...]
- **e** (list of list of np.ndarray of float) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g.

(*e_mag*, *e_norm*, *e_tan*). Each dataset is a list over all conditions containing the electric field component of interest

- `len(e) = n_cond`
- `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)

Returns

congruence_factor – (*n_roi*, *n_datasets*) Congruence factor in each element specified in *elm_idx_list* and for each input dataset.

Return type

np.ndarray of float

`pynibs.congruence.congruence.cf_variance_workhorse(elm_idx_list, mep, mep_params, e, old_style=True)`

Worker function for congruence factor computation - call from `multiprocessing.Pool`. Calculates congruence factor for *e* = (*E_mag*, *E_norm* and/or *E_tan*) for given zaps and elements.

Parameters

- **elm_idx_list** (np.ndarray) – (*chunksize*) List of element indices, the congruence factor is computed for.
- **mep** (list of *Mep*) – (*n_cond*) List of fitted *Mep* object instances for all conditions.
- **mep_params** (np.ndarray of float) – (*n_mep_params_total*) List of all mep parameters used to calculate the MEP, accumulated into one array).
 - e.g. [*mep_#1_para_#1*, *mep_#1_para_#2*, *mep_#1_para_#3*, *mep_#2_para_#1*, *mep_#2_para_#1*, ...])
- **e** (list of list of np.ndarray of float) – [*n_cond*][*n_datasets*][*n_elm*] Tuple of *n_datasets* of the electric field to compute the congruence factor for, e.g. (*e_mag*, *e_norm*, *e_tan*). Each dataset is a list over all conditions containing the electric field component of interest
 - `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)
- **old_style** (bool, default: True) – True: Weight `var(x_0_prime(r))` with `mean(e(r) * mean(Stimulator Intensity))`, taken from *mep* False: Weight `var(x_0_prime(r))` with `mean(E(r))`, taken from *e*

Returns

congruence_factor – (*n_roi*, *n_datasets*) Congruence factor in each element specified in *elm_idx_list* and for each input dataset

Return type

np.ndarray of float

`pynibs.congruence.congruence.extract_condition_combination(fn_config_cfg, fn_results_hdf5, conds, fn_out_prefix)`

Extract and plot congruence factor results for specific condition combinations from permutation analysis.

Parameters

- **fn_config_cfg** (str) – Filename of .cfg file the permutation study was conducted with
- **fn_results_hdf5** (str) – Filename of .hdf5 results file generated by `00_run_c_standard_compute_all_permutations.py` containing congruence factors and condition combinations.
- **conds** (list of str) – (*n_cond*) List containing condition combinations to extract and plot, e.g. [*'P_0'*, *'I_225'*, *'M1_0'*, *'I_675'*, *'P_225'*]).

- **fn_out_prefix** (*str*) – Prefix of output filenames of *_data.xdmf, *_data.hdf5 and *_geo.hdf5.

Returns

- **<fn_out_prefix_data.xdmf>** (*.xdmf file*) – Output file linking *_data.hdf5 and *_geo.hdf5 file to plot in paraview.
- **<fn_out_prefix_data.hdf5>** (*.hdf5 file*) – Output .hdf5 file containing the data.
- **<fn_out_prefix_geo.xdmf>** (*.hdf5 file*) – Output .hdf5 file containing the geometry information.

pynibs.congruence.ext_metrics module

`pynibs.congruence.ext_metrics.dvs_likelihoood`(*params, x, y, verbose=True, normalize=False, bounds=[(1, 2), (1, 2)]*)

`pynibs.congruence.ext_metrics.e_cog_workhorse`(*elm_idx_list, mep, mep_params, e*)

Worker function for electric field center of gravity (e_cog) computation after Opitz et al. (2013) [1] - call from `multiprocessing.Pool`. Calculates the e_cog for $e = (E_{mag}, E_{norm}$ and/or $E_{tan})$ for given zaps and elements. The electric field is weighted by the mean MEP amplitude (turning point of the sigmoid) and summed up. The computations are parallelized in terms of element indices (*elm_idx_list*).

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for.
- **mep** (list of *Mep*) – (n_cond) List of fitted Mep object instances for all conditions.
- **mep_params** (*np.ndarray of float*) – (n_mep_params_total) List of all mep parameters of curve fits used to calculate the MEP, accumulated into one array.
 - e.g. [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...]
- **e** (*list of list of np.ndarray of float*) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g. (e_{mag} , e_{norm} , e_{tan}). Each dataset is a list over all conditions containing the electric field component of interest
 - e.g.: $\text{len}(e) = n_{cond}$
 - $\text{len}(e[0]) = n_{comp}$ (e.g: $e_{mag} = e[0]$)

Returns

e_cog – (n_roi, n_datasets) RSD inverse in each element specified in *elm_idx_list* and for each input dataset.

Return type

np.ndarray of float

Notes

`pynibs.congruence.ext_metrics.e_focal_workhorse(elm_idx_list, e)`

Worker function to determine the site of stimulation after Aonuma et al. (2018) [1], call from `multiprocessing.Pool`. Calculates the site of stimulation for `e = (E_mag, E_norm and/or E_tan)` for given zaps and elements by multiplying the electric fields with each other. The computations are parallelized in terms of element indices (`elm_idx_list`).

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for
- **e** (*list of list of np.ndarray of float*) – [`n_cond`][`n_datasets`][`n_elm`] Tuple of `n_datasets` of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest
 - `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)

Returns

e_focal – (`n_roi`, `n_datasets`) Focal electric field in each element specified in `elm_idx_list` and for each input.

Return type

np.ndarray of float

Notes

`pynibs.congruence.ext_metrics.rsd_inverse_workhorse(elm_idx_list, mep, e)`

Worker function for RSD inverse computation after Bungert et al. (2017) [1], call from `multiprocessing.Pool`. Calculates the RSD inverse for `e = (E_mag, E_norm and/or E_tan)` for given zaps and elements. The computations are parallelized in terms of element indices (`elm_idx_list`).

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for
- **mep** (list of *Mep*) – (`n_cond`) List of fitted *Mep* object instances for all conditions.
- **e** (*list of list of np.ndarray of float*) – [`n_cond`][`n_datasets`][`n_elm`] Tuple of `n_datasets` of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest
 - `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)

Returns

rsd_inv – (`n_roi`, `n_datasets`) RSD inverse in each element specified in `elm_idx_list` and for each input dataset.

Return type

np.ndarray of float

Notes

pynibs.congruence.stimulation_threshold module

pynibs.congruence.stimulation_threshold.**intensity_thresh**(*mep_curve*, *intensities*,
mep_threshold)

Determines the stimulation threshold of one particular condition (usually the most sensitive e.g. M1-45). The stimulation threshold is the stimulator intensity value in [A/us] where the mep curves exceed the value of *mep_threshold* (in [mV]).

Parameters

- **mep_curve** (*list [1] of np.ndarray of float [n_samples]*) – MEP curve values for every conditions
- **intensities** (*list [1] of np.ndarray of float [n_samples]*) – To the MEP values corresponding stimulator intensities in [A/us]
- **mep_threshold** (*float*) – MEP value in [mV], which has to be exceeded for threshold definition

Returns

stim_threshold_avg – Average stimulation threshold in [V/m] where *c_factor* is greater than *c_factor_percentile*

Return type

float

pynibs.congruence.stimulation_threshold.**mean_mep_threshold**(*elm_idx*, *mep_curve*, *intensities*, *e*,
mep_threshold)

Determines the stimulation threshold by calculating the average electric field over all conditions, where the mep curves exceed the value of *mep_threshold* (in [mV]).

Parameters

- **elm_idx** (*list of np.ndarray of int*) – [n_datasets](n_elements) Element indices where the congruence factor exceeds a certain percentile, defined during the call of *stimulation_threshold()*.
- **mep_curve** (*list of np.ndarray of float*) – [n_conditions](n_samples) MEP curve values for every condition.
- **intensities** (*list of np.ndarray of float*) – [n_conditions](n_samples) To the MEP values corresponding stimulator intensities in [A/us].
- **e** (*list of list of np.ndarray of float*) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g. (*e_mag*, *e_norm*, *e_tan*). Each dataset is a list over all conditions containing the electric field component of interest
 - e.g.: `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)
- **mep_threshold** (*float*) – MEP value in [mV], which has to be exceeded for threshold definition.

Returns

stim_threshold_avg – Average stimulation threshold in [V/m] where *c_factor* is greater than *c_factor_percentile*

Return type

float

`pynibs.congruence.stimulation_threshold.sigmoid_thresh(elm_idx, mep_curve, intensities, e, mep_threshold)`

Determines the stimulation threshold by calculating an equivalent `pynibs.expio.Mep.sigmoid` over all conditions. The stimulation threshold is the electric field value where the mep curves exceed the value of `mep_threshold` (in [mV]).

Parameters

- **elm_idx** (*list of np.ndarray of int*) – [n_datasets](n_elements) Element indices where the congruence factor exceeds a certain percentile, defined during the call of `stimulation_threshold()`.
- **mep_curve** (*list of np.ndarray of float*) – [n_conditions](n_samples) MEP curve values for every condition.
- **intensities** (*list of np.ndarray of float*) – [n_conditions](n_samples) To the MEP values corresponding stimulator intensities in [A/us].
- **e** (*list of list of np.ndarray of float*) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g. (`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest
 - e.g.: `len(e) = n_cond`
 - `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)
- **mep_threshold** (*float*) – MEP value in [mV], which has to be exceeded for threshold definition

Returns

stim_threshold_avg – Average stimulation threshold in [V/m] where `c_factor` is greater than `c_factor_percentile`

Return type

float

`pynibs.congruence.stimulation_threshold.stimulation_threshold(elm_idx_list, mep, mep_params, n_samples, e, c_factor_percentile=95, mep_threshold=0.5, c_factor=None, c_function=None, t_function=None)`

Computes the stimulation threshold in terms of the electric field in [V/m]. The threshold is defined as the electric field value where the mep exceeds `mep_threshold`. The average value is taken over all mep curves in each condition and over an area where the congruence factor exceeds `c_factor_percentile`.

Parameters

- **elm_idx_list** (*np.ndarray*) – (chunksize) List of element indices, the congruence factor is computed for.
- **mep** (*list of Mep object instances*) – (n_cond) List of fitted `Mep` object instances for all conditions.
- **mep_params** (*np.ndarray of float [n_mep_params_total]*) – List of all mep parameters of curve fits used to calculate the MEP (accumulated into one array)
 - e.g. [`mep_#1_para_#1`, `mep_#1_para_#2`, `mep_#1_para_#3`, `mep_#2_para_#1`, `mep_#2_para_#1`, ...]
- **n_samples** (*int*) – Number of data points to generate discrete mep and e curves.
- **e** (*list of list of np.ndarray of float*) – [n_cond][n_datasets][n_elm] Tuple of n_datasets of the electric field to compute the congruence factor for, e.g.

(`e_mag`, `e_norm`, `e_tan`). Each dataset is a list over all conditions containing the electric field component of interest

– e.g.: `len(e) = n_cond`

– `len(e[0]) = n_comp` (e.g: `e_mag = e[0]`)

- **c_factor_percentile** (*float*) – Percentile of the `c_factor` taken into account for the threshold evaluation. Only `c_factors` are considered exceeding this.
- **mep_threshold** (*float*) – MEP value in [mV], which has to be exceeded for threshold definition.
- **c_factor** (*np.ndarray of float*) –
- (**n_roi** –
- **dataset.** (*n_datasets*) *Congruence factor in each element specified in elm_idx_list and for each input*) –
- **c_function** (*function*) – Defines the function to use during `c_gpc` to calculate the congruence factor.
 - `congruence_factor_curveshift_workhorse`: determines the average curve shift
 - `congruence_factor_curveshift_workhorse_stretch_correction`: determines the average curve shift
 - `congruence_factor_curveshift_workhorse_stretch_correction_variance`: determines the average curve shift
 - `congruence_factor_variance_workhorse`: evaluates the variance of the shifting and stretching parameters
- **t_function** (*function*) – Defines the function to determine the `stimulation_threshold`.
 - `stimulation_threshold_mean_mep_threshold`: uses `mep_threshold` to determine the corresponding `e_threshold` over all conditions and takes the average values as the stimulation threshold
 - `stimulation_threshold_pynibs.sigmoid`: Fits a new `pynibs.sigmoid` using all data-points in the `mep-vs-E` space and evaluates the threshold from the turning point or the intersection of the derivative in the crossing point with the `e`-axis

Returns

stim_threshold_avg – Average stimulation threshold in [V/m] where `c_factor` is greater than `c_factor_percentile`.

Return type

float

pynibs.expio package

Submodules

pynibs.expio.Mep module

class `pynibs.expio.Mep.Mep`(*intensities*, *mep*, *intensity_min_threshold=None*, *mep_min_threshold=None*)

Bases: `object`

Mep object.

fun

Function type to fit data with (`pynibs.sigmoid` / `pynibs.exp` / `pynibs.linear`).

Type
function

fun_sig

Best fitting equivalent sigmoidal function (added by `self.add_sigmoidal_bestfit()`).

Type
function

popt

(N_para) Fitted optimal function parameters.

Type
np.ndarray of float

popt_sig

(3) Best fitting parameters `x0`, `r`, and `amp` of equivalent sigmoidal function.

Type
np.ndarray of float

copt

(N_para, N_para) covariance matrix of fitted parameters.

Type
np.ndarray of float

pstd

(N_para) Standard deviation of fitted parameters.

Type
np.ndarray of float

fit

Gmodel object instance of parameter fit.

Type
object instance

x_limits

(2) Minimal and maximal value of intensity data.

Type
np.ndarray of float

y_limits

(2) Minimal and maximal value of mep data.

Type
np.ndarray of float

mt

Motor threshold (MEP > 50 uV), evaluated from fitted curve, added after fitting.

Type
float

calc_motor_threshold(threshold)

Determine motor threshold of stimulator depending on MEP threshold given in [mV].

Parameters
threshold (float) – Threshold of MEP amplitude in [mV].

Notes

Add Attributes:

Mep.mt

[float] Motor threshold for given MEP threshold.

eval(x, p)

Evaluating fitted function with optimal parameters in points x.

Parameters

- **x** (*np.ndarray of float*) – (N_x) Function arguments.
- **p** (*tuple of float*) – Function parameters.

Returns

y – (N_x) Function values.

Return type

np.ndarray of float

eval_fun_sig(x, p)

Evaluating optimally fitted sigmoidal function with optimal parameters in points x.

Parameters

- **x** (*np.ndarray of float*) – (N_x) Function arguments.
- **p** (*tuple of float*) – Function parameters.

Returns

y – (N_x) Function values.

Return type

np.ndarray of float

eval_opt(x)

Evaluating fitted function with optimal parameters in points x.

Parameters

x (*np.ndarray of float*) – (N_x) Function arguments.

Returns

y – (N_x) Function values.

Return type

np.ndarray of float

eval_uncertainties(x, sigma=1)

Evaluating approximated uncertainty interval around fitted distribution.

Parameters

- **x** (*np.ndarray of float*) – (N_x) Function values where uncertainty is evaluated.
- **sigma** (*float, default: 1*) – Standard deviation of parameters taken into account when evaluating uncertainty interval.

Returns

- **y_min** (*np.ndarray of float*) – (N_x) Lower bounds of y-values.
- **y_max** (*np.ndarray of float*) – (N_x) Upper bounds of y-values.

fit_mep_to_function(p0=None)

Fits MEP data to function. The algorithm tries to fit the function first to a sigmoid, then to an exponential and finally to a linear function.

Parameters

p0 (*np.ndarray of float, optional*) – Initial guess of parameter values.

Notes

Additional attributes:

Mep.popt

[np.ndarray of float] (N_para) Fitted optimal function parameters.

Mep.copt

[np.ndarray of float] (N_para, N_para) Covariance matrix of fitted parameters.

Mep.pstd

[np.ndarray of float] (N_para) Standard deviation of fitted parameters.

Mep.fun

[function] Function mep data was fitted with.

Mep.fit

[object instance] Gmodel object instance of parameter fit.

Mep.mt

[float] Motor threshold (MEP > 50 uV).

fit_mep_to_function_multistart (*p0=None, constraints=None, fun=None*)

Fits MEP data to function.

Parameters

- **p0** (*np.ndarray of float, optional*) – Initial guess of parameter values.
- **constraints** (*dict, optional*) – Dictionary with parameter names as keys and [min, max] values as constraints.
- **fun** (*list of functions, optional*) – Functions to incorporate in the multistart fit (e.g. [pynibs.sigmoid, pynibs.exp0, pynibs.linear]).

Notes

Add Attributes:

Mep.popt

[np.ndarray of float] (N_para) Best fitted optimal function parameters.

Mep.copt

[np.ndarray of float] (N_para, N_para) Covariance matrix of best fitted parameters.

Mep.pstd

[np.ndarray of float] (N_para) Standard deviation of best fitted parameters.

Mep.fun

[function] Function of best fit mep data was fitted with.

Mep.fit

[list of fit object instances] Gmodel object instances of parameter fits.

Mep.best_fit_idx

[int] Index of best function fit (fit[best_fit_idx]).

Mep.constraints

[dict] Dictionary with parameter names as keys and [min, max] values as constraints.

```
plot(label, sigma=3, plot_samples=True, show_plot=False, fname_plot="", ylim=None, ylabel=None,
      fontsize_axis=10, fontsize_legend=10, fontsize_label=10, fontsize_title=10, fun=None)
```

Plotting mep data and fitted curve together with uncertainties. If ``fun == None`, the optimal function is plotted.

Parameters

- **label** (*str*) – Plot title.
- **sigma** (*float*, *default:* 3) – Factor of standard deviations the uncertainty of the fit is plotted with.
- **plot_samples** (*bool*, *default:* True) – Plot sampling curves of the fit in the uncertainty interval.
- **show_plot** (*bool*, *default:* False) – Show or hide plot window (TRUE / FALSE).
- **fname_plot** (*str*, *default:* "") – Filename of plot showing fitted data (with .png extension).
- **ylim** (*list of float*, *optional*) –
(2) Min and max values of y-axis.
- **fontsize_axis** (*int*, *default:* 10) – Fontsize of axis numbers.
- **fontsize_legend** (*int*, *default:* 10) – Fontsize of Legend labels.
- **fontsize_label** (*int*, *default:* 10) – Fontsize of axis labels.
- **fontsize_title** (*int*, *default:* 10) – Fontsize of title.
- **fun** (*str*, *default:* None) – Which function to plot (None, sigmoid, exp, linear).

Returns

<File> – Plot of Mep data and fit (format: png).

Return type

.png file

```
run_fit_multistart(fun, x, y, p0, constraints=None, verbose=False, n_multistart=100)
```

Run multistart approach to fit data to function. `n_multistart` optimizations are performed based on random variations of the initial guess parameters `p0`. The fit with the lowest AIC (Akaike information criterion), i.e. best fit is returned as `gmodel` fit instance.

Parameters

- **fun** (*function*) – Function mep data has to be fitted with.
- **x** (*np.ndarray of float*) – (N_data) Independent variable the data is fitted on.
- **y** (*np.ndarray of float*) – (N_data) Dependent data the curve is fitted through.
- **p0** (*np.ndarray of float or list of float*) – Initial guess of parameter values.
- **constraints** (*dict*, *optional*) – Dictionary with parameter names as keys and [min, max] values as constraints.
- **verbose** (*bool*, *default:* False) – Show output messages.
- **n_multistart** (*int*, *default:* 100) – Number of repeated optimizations with different starting points to perform.

Returns

fit – Gmodel object instance of best parameter fit with lowest parameter variance.

Return type

object instance

`pynibs.expio.Mep.butter_lowpass(cutoff, fs, order=5)`

Setup Butter low-pass filter and return filter parameters.

Parameters

- **cutoff** (*float*) – Cutoff frequency in [Hz].
- **fs** (*float*) – Sampling frequency in [Hz].
- **order** (*int*, *default:* 5) – Filter order.

Returns

b, a – Numerator (b) and denominator (a) polynomials of the IIR filter.

Return type

`np.ndarray`, `np.ndarray`

`pynibs.expio.Mep.butter_lowpass_filter(data, cutoff, fs, order=5)`

Applies Butterworth lowpass filter.

Parameters

- **data** (*np.ndarray of float*) – (N_samples) Input of the digital filter.
- **cutoff** (*float*) – Cutoff frequency in [Hz].
- **fs** (*float*) – Sampling frequency in [Hz].
- **order** (*int*) – Filter order.

Returns

y – (N_samples) Output of the digital filter.

Return type

`np.ndarray`

`pynibs.expio.Mep.calc_p2p(sweep, tms_pulse_time=0.2, start_mep=20, end_mep=35, measurement_start_time=0, sampling_rate=4000, cutoff_freq=500, fn_plot=None)`

Calc peak-to-peak values of and mep sweep.

Parameters

- **sweep** (*np.ndarray of float*) – (Nx1) Input curve.
- **tms_pulse_time** (*float*, *default:* .2) – Onset time of TMS pulse trigger in [s].
- **start_mep** (*int*, *default:* 18) – Start of p2p search window after TMS pulse in [ms].
- **end_mep** (*int*, *default:* 35) – End of p2p search window after TMS pulse in [ms].
- **measurement_start_time** (*float*, *default:* 0) – Start time of the EMG measurement in [ms].
- **sampling_rate** (*int*, *default:* 2000) – Sampling rate in Hz.
- **cutoff_freq** (*int*, *default:* 500) – Desired cutoff frequency of the filter in Hz.
- **fn_plot** (*str*, *optional*) – Filename of sweep to plot (.png). If None, plot is omitted.

Returns

- **p2p** (*float*) – Peak-to-peak value of input curve.
- **sweep_filt** (*np.ndarray of float*) – Filtered input curve (Butter lowpass filter with specified cutoff_freq).
- **onset** (*float*) – MEP onset after tms_pulse_time.

`pynibs.expio.Mep.calc_p2p_old_exp0(sweep, start_mep=None, end_mep=None, tms_pulse_time=None, sampling_rate=None)`

Calc peak-to-peak values of an mep sweep. This version was probably used in the ancient times of experiment 0.

Parameters

- **sweep** (*np.ndarray of float*) – (Nx1) Input curve.
- **start_mep** (*None*) – Not used.
- **end_mep** (*None*) – Not used.
- **tms_pulse_time** (*None*) – Not used.
- **sampling_rate** (*None*) – Not used.

Returns

p2p – Peak-to-peak value of input curve.

Return type

float

`pynibs.expio.Mep.calc_p2p_old_exp1(sweep, start_mep=18, end_mep=35, tms_pulse_time=None, sampling_rate=2000)`

Calc peak-to-peak values of an mep sweep. This version was probably used for the first fits of experiment 1.

Parameters

- **sweep** (*np.ndarray of float*) – (Nx1) Input curve.
- **start_mep** (*float, default: 18*) – Starttime in [ms] after TMS for MEP search window.
- **end_mep** (*float, default: 35*) – Endtime in [ms] after TMS for MEP search window.
- **tms_pulse_time** (*None*) – Not used.
- **sampling_rate** (*int, default: 2000*) – Sampling rate in Hz.

Returns

p2p – Peak-to-peak value of input curve.

Return type

float

`pynibs.expio.Mep.dummy_fun(x, a)`

Dummy function for congruence factor calculation.

`pynibs.expio.Mep.exp(x, x0, r, y0)`

Parametrized exponential function.

$$y = y_0 + e^{r(x-x_0)}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **y0** (*float*) – Offset parameter.

Returns

y – Function value at x

Return type

np.ndarray of float [N_x]

`pynibs.expio.Mep.exp0(x, x0, r)`

Parametrized exponential function w/o offset.

$$y = e^{r(x-x_0)}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).

Returns

y – (N_x) Function value at x.

Return type

np.ndarray of float

`pynibs.expio.Mep.exp0_log(x, x0, r)`

Parametrized exponential function w/o offset.

$$y = e^{r(x-x_0)}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter.

Returns

y – (N_x) Function value at x.

Return type

np.ndarray of float

`pynibs.expio.Mep.exp_log(x, x0, r, y0)`

Parametrized exponential function (log).

$$y = y_0 + e^{r(x-x_0)}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **y0** (*float*) – y-offset parameter.

Returns

y – (N_x) Function value at x.

Return type

np.ndarray of float

`pynibs.expio.Mep.get_mep_elements(mep_fn, tms_pulse_time, drop_mep_idx=None, cfs_data_column=0, channels=None, time_format='delta', plot=False, start_mep=18, end_mep=35)`

Read EMG data from CED .cfs or .txt file and returns MEP amplitudes.

Parameters

- **mep_fn** (*string*) – path to .cfs-file or .txt file (Signal export).
- **tms_pulse_time** (*float*) – Time in [s] of TMS pulse as specified in signal.

- **drop_mep_idx** (*List of `int` or `None`, optional*) – Which MEPs to remove before matching.
- **cfs_data_column** (*`int` or `list of int`, `default: 0`*) – Column(s) of dataset in cfs file. +1 for .txt.
- **channels** (*`list of str`, optional*) – Channel names.
- **time_format** (*`str`, `default: "delta"`*) – Format of mep time stamps in `time_mep_lst` to return.
 - "delta" returns list of `datetime.timedelta` in seconds.
 - "hms" returns `datetime.datetime`(year, month, day, hour, minute, second, microsecond).
- **plot** (*`bool`, `default: False`*) – Plot MEPs.
- **start_mep** (*`float`, `default: 18`*) – Start of time frame after TMS pulse where p2p value is evaluated (in ms).
- **end_mep** (*`float`, `default: 35`*) – End of time frame after TMS pulse where p2p value is evaluated (in ms).

Returns

- **p2p_array** (*`np.ndarray of float`*) – (N_stim) Peak to peak values of N sweeps.
- **time_mep_lst** (*`list of datetime.timedelta`*) – MEP-timestamps
- **mep_raw_data** (*`np.ndarray of float`*) – (N_channel, N_stim, N_samples) Raw (unfiltered) MEP data.
- **mep_filt_data** (*`np.ndarray of float`*) – (N_channel, N_stim, N_samples) Filtered MEP data (Butterworth lowpass filter).
- **time** (*`np.ndarray of float`*) – (N_samples) Time axis corresponding to MEP data.
- **mep_onset_array** (*`np.ndarray of float`*) – (S_samples) MEP onset after TMS pulse.

`pynibs.expio.Mep.get_mep_sampling_rate(cfs_path)`

Returns sampling rate [Hz] for CED Signal EMG data in .cfs, .mat or .txt file.

The sampling rate is saved in the cfs header like this:

```
""Samplingrate" : 3999.999810,
```

Parameters

cfs_path

[str] Path to .cfs file or .txt file.

Returns

float

[sampling rate]

`pynibs.expio.Mep.get_mep_virtual_subject_DVS(x, x0=0.5, r=10, amp=1, sigma_x=0, sigma_y=0, y0=0.01, seed=None, rng=None)`

Creates random mep data using the 2 variability source model from Goetz et al. 2014 [1] together with a standard 3 parametric sigmoid function.

Parameters

- **x** (*`np.ndarray of float`*) – (n_x) Normalized stimulator intensities [0 ... 1].
- **x0** (*`float`, `default: 0.5`*) – Location of turning point sigmoidal function.
- **r** (*`float`, `default: 0.25`*) – Steepness of sigmoidal function.

- **amp** (*float*, *default*: 1.0) – Saturation amplitude of sigmoidal function.
- **sigma_x** (*float*, *default*: 0.1) – Standard deviation of additive x variability source.
- **sigma_y** (*float*, *default*: 0.1) – Standard deviation of additive y variability source.
- **y0** (*float*, *default*: 1e-2) – y-offset.
- **seed** (*int*, *optional*) – Seed to use.
- **rng** (*numpy._generator.Generator*, *optional*) – An already initialized random number generator that will be used instead of initializing a new one with seed.

Returns

mep – (n_x) Motor evoked potential values

Return type

np.ndarray of *float*

References

```
pynibs.expio.Mep.get_mep_virtual_subject_TVS(x, p1=-5.0818, p2=-2.4677, p3=3.6466, p4=0.42639,
                                             p5=1.6665, mu_y_add=8.283235329759169e-06,
                                             mu_y_mult=-0.9645334, mu_x_add=0.68827324,
                                             sigma_y_add=1.4739e-06, k=0.39316,
                                             sigma2_y_mult=0.022759, sigma2_x_add=0.023671,
                                             subject_variability=False, trial_variability=True)
```

Creates random mep data using the 3 variability source model from [1]. There are typos in the paper but the code seems to be correct. Originally from S. Goetz: <https://github.com/sgoetzduke/Statistical-MEP-Model>. Rewritten from MATLAB to Python by Konstantin Weise.

Parameters

- **x** (np.ndarray of *float*) – (n_x) Normalized stimulator intensities [0 ... 1].
- **p1** (*float*, *default*: -5.0818) – First parameter of sigmoidal hilltype function.
- **p2** (*float*, *default*: 4.5323) – Second parameter of sigmoidal hilltype function.
- **p3** (*float*, *default*: 3.6466) – Third parameter of sigmoidal hilltype function.
- **p4** (*float*, *default*: 0.42639) – Fourth parameter of sigmoidal hilltype function.
- **p5** (*float*, *default*: 1.6665) – Fifth parameter of sigmoidal hilltype function.
- **mu_y_add** (*float*, *default*: 10**(-5.0818)) – Mean value of additive y variability source.
- **mu_y_mult** (*float*, *default*: -0.9645334) – Mean value of multiplicative y variability source.
- **mu_x_add** (*float*, *default*: -0.68827324) – Mean value of additive x variability source.
- **sigma_y_add** (*float*, *default*: 1.4739*1e-6) – Standard deviation of additive y variability source.
- **k** (*float*, *default*: 0.39316) – Shape parameter of generalized extreme value distribution.
- **sigma2_y_mult** (*float*, *default*: 2.2759*1e-2) – Standard deviation of multiplicative y variability source.
- **sigma2_x_add** (*float*, *default*: 2.3671*1e-2) – Standard deviation of additive x variability source.

- **subject_variability** (*bool*, *default: False*) – Choose if shape parameters from IO curve are sampled from random distributions to model subject variability. This does not influence the trial-to-trial variability.
- **trial_variability** (*bool*, *default: True*) – Enable or disable trial-to-trial variability. Disabling it will result in ideal IO curves w/o noise.

Returns

mep – (n_x) Motor evoked potential values in mV.

Return type

np.ndarray of *float*

References

pynibs.expio.Mep.get_time_date(*cfs_paths*)

Get time and date of the start of the recording out of .cfs file.

Parameters

cfs_paths (*str*) – Path to .cfs mep file.

Returns

time_date – Date and time.

Return type

str

pynibs.expio.Mep.linear(*x, m, n*)

Parametrized linear function.

$$y = mx + n$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **m** (*float*) – Slope parameter.
- **n** (*float*) – Y-offset.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of *float*

pynibs.expio.Mep.linear_log(*x, m, n*)

Parametrized log linear function.

$$y = mx + n$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **m** (*float*) – Slope parameter (steepness).
- **n** (*float*) – Y-offset.

Returns

y – (N_x) Function value at x.

Return type

np.ndarray of *float*

`pynibs.expio.Mep.read_biosig_emg_data(fn_data, include_first_trigger=False, type='cfs')`

Reads EMG data from a biosig file.

Parameters

- **fn_data** (*str*) – Path to the biosig file.
- **include_first_trigger** (*bool*, *default: False*) – Whether to include the first trigger event in the data (default: False).
- **type** (*str*, *default: 'cfs'*) – Type of the biosig file.

Returns

- **emg_data** (*np.ndarray*) – (num_sweeps, num_channels, samples_per_sweep) EMG data with shape.
- **time_diff_list** (*list*) – Time differences between trigger events in seconds.
- **num_sweeps** (*int*) – Number of sweeps in the EMG data.
- **num_channels** (*int*) – Number of channels in the EMG data.
- **samples_per_sweep** (*int*) – Number of samples per sweep in the EMG data.
- **sampling_rate** (*int*) – Sampling rate of the EMG data.

`pynibs.expio.Mep.sigmoid(x, x0, r, amp)`

Parametrized sigmoid function.

$$y = \frac{amp}{1 + e^{-r(x-x_0)}}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **amp** (*float*) – Maximum value the sigmoid converges to.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of float

`pynibs.expio.Mep.sigmoid4(x, x0, r, amp, y0)`

Parametrized sigmoid function with 4 parameters.

$$y = y_0 + \frac{amp - y_0}{1 + e^{-r(x-x_0)}}$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) x-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **amp** (*float*) – Maximum value the sigmoid converges to.
- **y0** (*float*) – Offset value of the sigmoid.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of float

`pynibs.expio.Mep.sigmoid4_log(x, x0, r, amp, y0)`

Parametrized log transformed sigmoid function with 4 parameters.

$$y = \log \left(y_0 + \frac{amp - y_0}{1 + e^{-r(x-x_0)}} \right)$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **amp** (*float*) – Maximum value the sigmoid converges to (upper saturation).
- **y0** (*float*) – Y-offset value of the sigmoid.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of float

`pynibs.expio.Mep.sigmoid_log(x, x0, r, amp)`

Parametrized log transformed sigmoid function.

$$y = \log \left(\frac{amp}{1 + e^{-r(x-x_0)}} \right)$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) x-values the function is evaluated in.
- **x0** (*float*) – Horizontal shift along the abscissa.
- **r** (*float*) – Slope parameter (steepness).
- **amp** (*float*) – Maximum value the sigmoid converges to.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of float

pynibs.expio.brainsight module

Functions to import data from Rogue Research Brainsight neuronavigation systems

class `pynibs.expio.brainsight.BrainsightCSVParser`

Bases: *object*

Parser for Brainsight CSV files.

current_state

The current state of the parser.

Type

BrainsightCSVParser.State

header_file

The file header.

Type

str

header_data

The header data.

Type

list of str

data

The parsed data rows.

Type

list of list of str

check_state_transition(line)

Checks the state transition based on the given line.

parse_line(line)

Parses a line and updates the corresponding attributes.

class State

Bases: `object`

DATA = 3

DATA_HEADER = 2

FILE_HEADER = 0

FIN = 4

SKIPPING = 1

check_state_transition(line)

Checks the state transition based on the given line.

Parameters

line (*str*) – The line to check.

parse_line(line)

Parses a line and updates the corresponding attributes.

Parameters

line (*str*) – The line to parse.

`pynibs.expio.brainsight.create_merged_nnav_emg_file_brainsight(fn_brainsight_nnav_info, fn_emg_info, fn_out, p2p_window_start=18, p2p_window_end=35)`

Creates a merged file containing TMS coil positions and EMG data from Brainsight information.

Parameters

- **fn_brainsight_nnav_info** (*str*) – File path of the Brainsight nnav coil information.
- **fn_emg_info** (*str*) – File path of the EMG information.
- **fn_out** (*str*) – File path of the output merged file.
- **p2p_window_start** (*int*, *default:* 18) – Start of the time frame after TMS pulse where p2p value is evaluated (in ms).
- **p2p_window_end** (*int*, *default:* 35) – End of the time frame after TMS pulse where p2p value is evaluated (in ms).

```
pynibs.expio.brainsight.merge_exp_data_brainsight(subject, exp_idx, mesh_idx,
                                                  coil_outlier_corr_cond=False,
                                                  remove_coil_skin_distance_outlier=True,
                                                  coil_distance_corr=True, average_emg_data_from_same_condition=False,
                                                  verbose=False, plot=False, start_mep=18,
                                                  end_mep=35)
```

Merge the TMS coil positions and the mep data into an experiment.hdf5 file.

Parameters

- **subject** (*pynibs.Subject*) – Subject object.
- **exp_idx** (*str*) – Experiment ID.
- **mesh_idx** (*str*) – Mesh ID.
- **coil_outlier_corr_cond** (*bool*, *default: False*) – Correct outlier of coil position and orientation (+-2 mm, +-3 deg) in case of conditions.
- **remove_coil_skin_distance_outlier** (*bool*, *default: True*) – Remove outlier of coil position lying too far away from the skin surface (+- 5 mm).
- **coil_distance_corr** (*bool*, *default: True*) – Perform coil <-> head distance correction (coil is moved towards head surface until coil touches scalp).
- **average_emg_data_from_same_condition** (*bool*, *default: False*) – Flag indicating whether to average EMG data from the same condition. Only meaningful in conjunction with ‘coil_distance_correction’, which averages the coil position within a condition.
- **verbose** (*bool*, *default: False*) – Plot output messages.
- **plot** (*bool*, *default: False*) – Plot MEPs and p2p evaluation.
- **start_mep** (*float*, *default: 18*) – Start of time frame after TMS pulse where p2p value is evaluated (in ms).
- **end_mep** (*float*, *default: 35*) – End of time frame after TMS pulse where p2p value is evaluated (in ms).

```
pynibs.expio.brainsight.read_targets_brainsight(fn)
```

Reads target coil position and orientations from .txt file and returns it as 4 x 4 x N_targets numpy array.

Parameters

fn (*str*) – Filename of output file.

Returns

m_nnav – (4, 4, N_targets) Tensor containing the 4x4 matrices with coil orientation and position.

Return type

np.ndarray of *float*

```
pynibs.expio.brainsight.write_targets_brainsight(targets, fn_out, names=None, overwrite=True)
```

Writes coil position and orientations in .txt file for import into Brainsight.

Parameters

- **targets** (*np.ndarray of float*) –
- **(4** –
- **4** –
- **N_targets)** –
- **position.** (*Tensor containing the 4x4 matrices with coil orientation and*) –

- **fn_out** (*str*) – Filename of output file.
- **names** (*list of str, optional*) – Target names (if None they will be numbered by their order).
- **overwrite** (*bool, default: True*) – Overwrite existing .txt file.

Return type

<file> .txt file containing the targets for import into Brainsight

pynibs.expio.brainvis module

`pynibs.expio.brainvis.read_channel_names(fname)`

Reads the channel names from .vhdr (info) file, which is recorded during EEG.

Parameters

fname (*str*) – Filename of .vhdr info file.

Returns

channel_names – List containing the channel names.

Return type

list of str

`pynibs.expio.brainvis.read_sampling_frequency(fname)`

Reads the sampling frequency from .vhdr (info) file, which is recorded during EEG.

Parameters

fname (*str*) – Filename of .vhdr info file.

Returns

sampling_frequency – Sampling frequency.

Return type

float

pynibs.expio.cobot module

`pynibs.expio.cobot.merge_exp_data_cobot(subject, exp_idx, mesh_idx, coil_outlier_corr_cond=False, remove_coil_skin_distance_outlier=True, coil_distance_corr=True, verbose=False, plot=False)`

Merge the TMS coil positions and the mep data into an experiment.hdf5 file.

Parameters

- **subject** (`pynibs.subject.Subject`) – Subject object.
- **exp_idx** (*str*) – Experiment ID.
- **mesh_idx** (*str*) – Mesh ID.
- **coil_outlier_corr_cond** (*bool*) – Correct outlier of coil position and orientation (+-2 mm, +-3 deg) in case of conditions.
- **remove_coil_skin_distance_outlier** (*bool*) – Remove outlier of coil position lying too far away from the skin surface (+- 5 mm).
- **coil_distance_corr** (*bool*) – Perform coil <-> head distance correction (coil is moved towards head surface until coil touches scalp).
- **verbose** (*bool*) – Plot output messages.
- **plot** (*bool, optional, default: False*) – Plot MEPs and p2p evaluation.

pynibs.expio.exp module

`pynibs.expio.exp.add_sigmoidal_bestfit(mep, p0, constraints=None)`

Add best fitting sigmoidal function to instance (determined by multistart approach)

Parameters

- **mep** (*pynibs.expio.mep.Mep*) – Mep.
- **p0** (*float*) – Initial guess for the parameters of the sigmoidal function.
- **constraints** (*dict, optional*) – Dictionary with parameter names as keys and [min, max] values as constraints.

Returns

mep – Updated Mep object class instance with the following attributes.

Return type

object

Notes

Adds Attributes:

Mep.fun_sig

[function] Sigmoid function

Mep.popt_sig

[np.ndarray of float]

(3) Parameters of sigmoid function

`pynibs.expio.exp.calc_outlier(coords, dev_location, dev_radius, target=None, fn_out=None, verbose=True)`

Computes median coil position and angle, identifies outliers, plots neat figure. Returns a list of idx that are not outliers

Parameters

- **coords** (*np.ndarray*) – (4, 4, n_zaps)
- **dev_location** (*float*) – Max allowed location deviation.
- **dev_radius** (*float*) – Max allowed radius deviation.
- **target** (*np.ndarray, optional*) – (4, 4) matrix with target coordinates.
- **fn_out** (*string, optional*) – Output filename.
- **verbose** (*bool, default: True*) – Flag indicating verbosity.

Returns

list of int, list of int, list of int

Return type

idx_keep, idx_zero, idx_outlier

`pynibs.expio.exp.cfs2hdf5(fn_cfs, fn_hdf5=None)`

Converts EMG data included in .cfs file to .hdf5 format.

Parameters

- **fn_cfs** (*str*) – Filename of .cfs file.
- **fn_hdf5** (*str, optional*) – Filename of .hdf5 file (if not provided, a file with same name as fn_cfs will be created with .hdf5 extension).

Returns

<file> – File containing:

- EMG data in f[“emg”][:]
- Time axis in f[“time”][:]

Return type

.hdf5 File

```
pynibs.expio.exp.coil_distance_correction(exp=None, fn_exp=None, fn_exp_out=None,
                                          fn_geo_hdf5=None,
                                          remove_coil_skin_distance_outlier=False, fn_plot=None,
                                          min_dist=-5, max_dist=2)
```

Corrects the distance between the coil and the head assuming that the coil is touching the head surface during the experiments. This is done since the different coil tracker result in different coil head distances due to tracking inaccuracies. Also averages positions and orientations over the respective condition and writes both mean position and orientation for every condition in `fn_exp_out`.

Depending on if `exp` (dict containing lists) or `fn_exp` (csv file) is provided it returns the outlier corrected dict or writes a new <fn_exp_out>.csv file.

Parameters

- **exp** (*list of dict or dict of list, optional*) – List of dictionaries containing the experimental data.
- **fn_exp** (*str, optional*) – Filename (incl. path) of experimental .csv file.
- **fn_exp_out** (*str, optional*) – Filename (incl. path) of distance corrected experimental .csv file.
- **fn_geo_hdf5** (*str, optional*) – Filename (incl. path) of geometry mesh file (.hdf5).
- **remove_coil_skin_distance_outlier** (*bool, default: False*) – Remove coil positions, which are more than +- 2 mm located from the zero mean skin surface.
- **fn_plot** (*str, optional*) – Folder where plots will be saved in (fn_geo_hdf5 folder).
- **min_dist** (*int, default: -5*) – Ignored.
- **max_dist** (*int, default: 2*) – Ignored.

Returns

- <File> (.csv file) – experimental_dc.csv file with distance corrected coil positions.
- *or*
- **exp** (*dict*) – Dictionary containing the outlier corrected experimental data.

```
pynibs.expio.exp.coil_distance_correction_matsimnibs(matsimnibs, fn_mesh_hdf5, distance=0,
                                                    remove_coil_skin_distance_outlier=False)
```

Corrects the distance between the coil and the head assuming that the coil is located at a distance “d” with respect to the head surface during the experiments. This is done since the different coil tracker result in different coil head distances due to tracking inaccuracies.

Parameters

- **matsimnibs** (*np.ndarray of float*) – (4, 4) or (4, 4, n_mat) Tensor containing matsimnibs matrices.
- **fn_mesh_hdf5** (*str*) – .hdf5 file containing the head mesh.
- **distance** (*float or list of float, default: 0*) – Target distance in (mm) between coil and head due to hair layer. All coil positions are moved to this distance. If distance is list: `len(distance) == n_mat`.

- **remove_coil_skin_distance_outlier** (*bool*, *default: False*) – Remove coil positions, which are more than ± 6 mm located from the skin surface.

Returns

matsimnibs – (4, 4, n_mat) Tensor containing matsimnibs matrices with distance corrected coil positions.

Return type

np.ndarray of *float*

```
pynibs.expio.exp.coil_outlier_correction_cond(exp=None, fn_exp=None, fn_exp_out=None,  
                                              outlier_angle=5.0, outlier_loc=3.0)
```

Searches and removes outliers of coil orientation and location w.r.t. the average orientation and location from all zaps. It generates plots of the individual conditions showing the outliers in the folder of *fn_exp_out*. Depending on if *exp* (dict containing lists) or *fn_exp* (csv file) is provided it returns the outlier corrected dict or writes a new *<fn_exp_out>*.csv file. If *_exp_* is provided, all keys are kept.

Parameters

- **exp** (*list of dict*, *optional*) – List of dictionaries containing the experimental data.
- **fn_exp** (*str*, *optional*) – Filename (incl. path) of experimental .csv file.
- **fn_exp_out** (*str*, *optional*) – Filename (incl. path) of corrected experimental .csv file.
- **outlier_angle** (*float*, *default: 5.*) – Coil orientation outlier “cone” around axes in \pm deg. All zaps with coil orientations outside of this cone are removed.
- **outlier_loc** (*float*, *default: 3.*) – Coil position outlier “sphere” in \pm mm. All zaps with coil locations outside of this sphere are removed.

Returns

- **<File>** (*.csv file*) – experimental_oc.csv file with outlier corrected coil positions.
- **<Files>** (*.png files*) – Plot showing the coil orientations and locations (folder_of_fn_exp_out/COND_X_coil_position.png).
- *or*
- **exp** (*dict*) – Dictionary containing the outlier corrected experimental data.

```
pynibs.expio.exp.combine_nnav_ft(xml_paths, behavior_paths, im, coil_sn, nii_exp_path,  
                                nii_conform_path, patient_id, drop_trial_idx, nnav_system, cond,  
                                mesh_approach='headreco', temp_dir=None, plot=False)
```

Creates dictionary containing all experimental data.

Parameters

- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file if there is no coil1-file, use empty string
- **behavior_paths** (*list of str*) – Paths to .csv ft file
- **im** (*list of str*) – List of path to the instrument-marker-file or list of strings containing the instrument marker
- **coil_sn** (*str*) – Coil-serial-number
- **nii_exp_path** (*str*) – Path to the .nii file that was used in the experiment
- **nii_conform_path** (*str*) – Path to the conform*.nii file used to calculate the E-fields with SimNIBS
- **patient_id** (*str*) – Patient id
- **drop_trial_idx** (*List of int or None*) – Which fts to remove before matching.

- **temp_dir** (*str*, *default*: *None* (*fn_exp_mri_nii folder*)) – Directory to save temporary files (transformation .nii and .mat files)
- **nnav_system** (*str*) – Type of neuronavigation system (“Localite”, “Visor”)
- **cond** (*str*) – behavioral outcome
- **mesh_approach** (*str*, *default*: *"headreco"*) – Approach the mesh is generated with (“headreco” or “mri2mesh”)
- **plot** (*bool*, *default*: *False*) – Plot MEPs and p2p evaluation

Returns

dict_list – ‘number’ ‘condition’ ‘current’ ‘mep_raw_data’ ‘mep’ ‘mep_latency’ ‘mep_filt_data’ ‘mep_raw_data_time’ ‘time_tms’ ‘ts_tms’ ‘time_mep’ ‘date’ ‘coil_sn’ ‘patient_id’

Return type

list of dicts, one dict for each zap

```
pynibs.expio.exp.combine_nnav_mep(xml_paths, cfs_paths, im, coil_sn, nii_exp_path, nii_conform_path,
                                  patient_id, tms_pulse_time, drop_mep_idx, mep_onsets,
                                  nnav_system, mesh_approach='headreco', temp_dir=None,
                                  cfs_data_column=0, channels=None, plot=False, start_mep=18,
                                  end_mep=35)
```

Creates dictionary containing all experimental data.

Parameters

- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file; if there is no coil1-file, use empty string.
- **cfs_paths** (*list of str*) – Paths to .cfs mep file.
- **im** (*list of str*) – List of path to the instrument-marker-file or list of strings containing the instrument marker.
- **coil_sn** (*str*) – Coil-serial-number.
- **nii_exp_path** (*str*) – Path to the .nii file that was used in the experiment.
- **nii_conform_path** (*str*) – Path to the conform*.nii file used to calculate the E-fields with SimNIBS.
- **patient_id** (*str*) – Patient id.
- **tms_pulse_time** (*float*) – Time in [s] of TMS pulse as specified in signal.
- **drop_mep_idx** (*List of int or None*) – Which MEPs to remove before matching.
- **mep_onsets** (*List of int or None*) – If there are multiple .cfs per TMS Navigator sessions, onsets in [ms] of .cfs. E.g.: [0, 71186].
- **nnav_system** (*str*) – Type of neuronavigation system (“Localite”, “Visor”).
- **mesh_approach** (*str*, *default*: *"headreco"*) – Approach the mesh is generated with (“headreco” or “mri2mesh”).
- **temp_dir** (*str*, *default*: *None* (*fn_exp_mri_nii folder*)) – Directory to save temporary files (transformation .nii and .mat files) (*fn_exp_mri_nii folder*).
- **cfs_data_column** (*int or list of int*, *default*: *0*) – Column(s) of dataset in .cfs file.
- **channels** (*list of str*, *optional*) – Channel names.
- **plot** (*bool*, *default*: *False*) – Plot MEPs and p2p evaluation.
- **start_mep** (*float*, *default*: *18*) – Start of time frame after TMS pulse where p2p value is evaluated (in ms).

- **end_mep** (*float*, *default:* 35) – End of time frame after TMS pulse where p2p value is evaluated (in ms).

Returns

dict_lst – ‘number’ ‘condition’ ‘current’ ‘mep_raw_data’ ‘mep’ ‘mep_latency’ ‘mep_filt_data’ ‘mep_raw_data_time’ ‘time_tms’ ‘ts_tms’ ‘time_mep’ ‘date’ ‘coil_sn’ ‘patient_id’

Return type

list of dicts, one dict for each zap

`pynibs.expio.exp.combine_nnav_rt(xml_paths, behavior_paths, im, coil_sn, nii_exp_path, nii_conform_path, patient_id, drop_trial_idx, nnav_system, cond, mesh_approach='headreco', temp_dir=None, plot=False)`

Creates dictionary containing all experimental data.

Parameters

- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file if there is no coil1-file, use empty string.
- **behavior_paths** (*list of str*) – Paths to .cfs mep file.
- **im** (*list of str*) – List of path to the instrument-marker-file or list of strings containing the instrument marker.
- **coil_sn** (*str*) – Coil-serial-number.
- **nii_exp_path** (*str*) – Path to the .nii file that was used in the experiment.
- **nii_conform_path** (*str*) – Path to the conform*.nii file used to calculate the E-fields with SimNIBS.
- **patient_id** (*str*) – Patient id.
- **drop_trial_idx** (*List of int or None*) – Which MEPs to remove before matching.
- **nnav_system** (*str*) – Type of neuronavigation system (“Localite”, “Visor”).
- **cond** (*str*) – Condition name in data_path.
- **mesh_approach** (*str, default:* “headreco”) – Approach the mesh is generated with (“headreco” or “mri2mesh”).
- **temp_dir** (*str, optional*) – Directory to save temporary files (transformation .nii and .mat files) (fn_exp_mri_nii folder).
- **plot** (*bool, default:* False) – Plot MEPs and p2p evaluation.

Returns

dict_lst – ‘number’ ‘condition’ ‘current’ ‘mep_raw_data’ ‘mep’ ‘mep_latency’ ‘mep_filt_data’ ‘mep_raw_data_time’ ‘time_tms’ ‘ts_tms’ ‘time_mep’ ‘date’ ‘coil_sn’ ‘patient_id’

Return type

list of dicts, one dict for each zap

`pynibs.expio.exp.convert_csv_to_hdf5(fn_csv, fn_hdf5, overwrite_arr=True, verbose=False)`

Wrapper from experiment.csv to experiment.hdf5. Saves all relevant columns from the (old) experiment.csv file to an .hdf5 file.

```
fn_hdf5:/stim_data/
|--coil_sn
|--current
|--date
|--time_diff
|--time_mep
|--time_tms
|--ts_tms
|--coil0      # <- all coil0.** columns
|--coil1      # <- all coil1.** columns
|--coil_mean  # <- all coil_mean.** columns
```

All columns not found in experiment.csv are ignored (and a warning is thrown).

Parameters

- **fn_csv** (*str*) – experiment.csv filename.
- **fn_hdf5** (*str*) – experiment.hdf5 filename. File is created if not existing.
- **overwrite_arr** (*bool*, *default: True.*) – Overwrite existing arrays. Otherwise: fail.
- **verbose** (*bool*, *default: False*) – Flag indicating verbosity.

`pynibs.expio.exp.get_cnt_infos(fn_cnt)`

Read some meta information from .cnt file.

Parameters

fn_cnt (*str*) – Path to the .cnt file.

Returns

d – A dictionary containing the meta-information.

Return type

dict

`pynibs.expio.exp.get_coil_flip_m(source_system='simnibs', target_system=None)`

Returns a flimp matrix 4x4 to flip coil axis from one system to another.

Parameters

- **source_system** (*str*, *default: 'simnibs'*) – Atm only possible source: 'simnibs'.
- **target_system** (*str*, *optional*) – tmsnavigator, visor, brainsight.

Returns

flip_m – (4, 4) Flipped matrix.

Return type

np.ndarray

`pynibs.expio.exp.get_coil_sn_lst(fn_coil)`

Extract coil serial numbers from a list of coil paths.

Parameters

fn_coil (*list of list of str*) – List containing coil path information.

Returns

coil_sn_lst – A list of coil serial numbers extracted from the provided coil paths.

Return type

list of str

`pynibs.expio.exp.get_csv_matrix(dictionary)`

Process the given dictionary to create a 4x4 matrix for each coil specified.

Parameters

dictionary (*dict*) – The input dictionary containing the data.

Returns

The input dictionary updated with the newly created matrices and redundant keys removed.

Return type

dict

`pynibs.expio.exp.get_ft_data_from_csv(behavior_fn, cond, drop_trial_idx=None, startatzero=True)`

Reads trial data from csv file.

Parameters

- **behavior_fn** (*str*) – Filename with columns: ‘TMS_onset_time’, ‘p_p_amp’, ‘ct’. TMS_onset_time in 0.1 ms; p_p_amp in ms.
- **cond** (*str*) – behavioral output
- **drop_trial_idx** (*list of int, optional*) – ‘trialnum’ to remove.
- **startatzero** (*bool, default: True*) – Shift onset_time axis to zero.

Returns

- **ft** (*list of float*)
- **TMS_onsets** (*list of float*) – in [ms]
- **mean_isi** (*tuple of int*) – in [s]

`pynibs.expio.exp.get_intensity_e(e1, e2, target1, target2, radius1, radius2, headmesh, rmt=1, roi='midlayer_lh_rh', verbose=False)`

Computes the stimulator intensity adjustment factor based on the electric field.

Parameters

- **e1** (*str*) – .hdf5 e field with midlayer.
- **e2** (*str*) – .hdf5 e field with midlayer.
- **target1** (*np.ndarray (3,)*) – Coordinates of cortical site of MT.
- **target2** (*np.ndarray (3,)*) – Coordinates of cortical target site.
- **radius1** (*float*) – Electric field of field1 is averaged over elements inside this radius around target1.
- **radius2** (*float*) – Electric field of field2 is averaged over elements inside this radius around target2.
- **headmesh** (*str*) – .hdf5 headmesh.
- **rmt** (*float, default: 1*) – Resting motor threshold to be corrected.
- **roi** (*str, default: 'midlayer_lh_rh'*) – Name of roi. Expected to sit in mesh['/data/midlayer/roi_surface/'].
- **verbose** (*bool, default: False*) – Flag indicating verbosity.

Returns

rmt_e_corr – Adjusted stimulation intensity for target2.

Return type

float

`pynibs.expio.exp.get_intensity_e_old(mesh1, mesh2, target1, target2, radius1, radius2, rmt=1, verbose=False)`

Computes the stimulator intensity adjustment factor based on the electric field. Something weird is going on here - check simnibs coordinates of midlayer before usage.

Parameters

- **mesh1** (*str or simnibs.msh.mesh_io.Msh*) – Midlayer mesh containing results of the optimal coil position of MT in the midlayer (e.g.: `.../subject_overlays/00001.hd_fixed_TMS_1-0001_MagVenture_MCF_B65_REF_highres.ccd_scalar_central.msh`)
- **mesh2** (*str or simnibs.msh.mesh_io.Msh*) – Midlayer mesh containing results of the optimal coil position of the target in the midlayer (e.g.: `.../subject_overlays/00001.hd_fixed_TMS_1-0001_MagVenture_MCF_B65_REF_highres.ccd_scalar_central.msh`)
- **target1** (*np.ndarray*) – (3,) Coordinates of cortical site of MT.

- **target2** (*np.ndarray*) – (3,) Coordinates of cortical target site.
- **radius1** (*float*) – Electric field in target 1 is averaged over elements inside this radius.
- **radius2** (*float*) – Electric field in target 2 is averaged over elements inside this radius.
- **rmt** (*float*, *default:* 1) – Resting motor threshold, which will be corrected.
- **verbose** (*bool*, *default:* False) – Flag indicating verbosity.

Returns

rmt_e_corr – Adjusted stimulation intensity for target2.

Return type

float

`pynibs.expio.exp.get_intensity_stokes(mesh, target1, target2, spat_grad=3, rmt=0, scalp_tag=1005, roi=None, verbose=False)`

Computes the stimulator intensity adjustment factor according to Stokes et al. 2005 (doi:10.1152/jn.00067.2005). Adjustment is based on target-scalp distance differences: $adj = (Dist2 - Dist1) * spat_grad$

Parameters

- **mesh** (*str* or *simnibs.msh.mesh_io.Msh*) – Mesh of the head model.
- **target1** (*np.ndarray*) – (3,) Coordinates of cortical site of MT.
- **target2** (*np.ndarray*) – (3,) Coordinates of cortical target site.
- **spat_grad** (*float*, *default:* 3) – Spatial gradient.
- **rmt** (*float*, *default:* 0) – Resting motor threshold, which will be corrected.
- **scalp_tag** (*int*, *default:* 1005) – Tag in the mesh where the scalp is to be set.
- **roi** (*np.ndarray*, *optional*) – (3,N) Array of nodes to project targets onto.
- **verbose** (*bool*, *default:* False) – Print verbosity information.

Returns

rmt_stokes – Adjusted stimulation intensity for target2.

Return type

float

`pynibs.expio.exp.get_patient_id(xml_path)`

Read patient-ID.

Parameters

xml_path (*str*) – Path to coil0-file.

Returns

xml_pd.find('patientID').text – ID of patient.

Return type

str

`pynibs.expio.exp.get_trial_data_from_csv(behavior_fn, cond, drop_trial_idx=None, only_corr=True, startatzero=True)`

Reads trial data from csv file. Reaction time is in [0.1ms].

Parameters

- **behavior_fn** (*str*) – Filename with columns: 'trialtype', 'onset_time', 'rt'.
- **cond** (*str*) – Which condition to choose from .csv file.
- **drop_trial_idx** (*list of int*, *optional*) – 'trialnum' to remove.
- **only_corr** (*bool*, *default:* True) – Only return trials with correct responses.

- **startatzero** (*bool*, *default:* *True*) – Shift onset_time axis to zero.

Returns

- **rt** (*list of float*)
- **onsets** (*list of float*)
- **mean_isi** (*tuple of int*) – In [s]-

`pynibs.expio.exp.load_matsimnibs_txt(fn_matsimnibs)`

Loading matsimnibs matrices from .txt file.

Parameters

fn_matsimnibs (*str*) – Filename of .txt file the matsimnibs matrices are stored in.

Returns

matsimnibs – (4, 4) or (4, 4, n_mat) Tensor containing matsimnibs matrices.

Return type

np.ndarray of *float*

`pynibs.expio.exp.match_behave_and_triggermarker(mep_time_lst, xml_paths, bnd_factor=0.495, isi=None)`

Sort out timestamps of mep and tms files that do not match.

Parameters

- **mep_time_lst** (*list of datetime.timedelta*) – timedeltas of MEP recordings.
- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file; if there is no coil1-file, use empty string.
- **bnd_factor** (*float*, *default:* *0.99/2*) – Bound factor relative to interstimulus interval in which +- interval to match neuronavigation and mep data from their timestamps (0 means perfect matching, 0.5 means +- half interstimulus interval).
- **isi** (*float*, *optional*) – Interstimulus intervals. If not provided it's estimated from the first trial.

Returns

- **tms_index_lst** (*list of int*) – Indices of tms-timestamps that match.
- **mep_index_lst** (*list of int*) – Indices of mep-timestamps that match.
- **tms_time_lst** (*list of datetime*) – TMS timestamps.

`pynibs.expio.exp.nnav2simnibs(fn_exp_nii, fn_conform_nii, m_nnav, nnav_system, mesh_approach='headreco', fiducials=None, orientation='RAS', fsl_cmd=None, target='simnibs', temp_dir=None, rem_tmp=False, verbose=True)`

Transforming TMS coil positions from neuronavigation to simnibs space.

Parameters

- **fn_exp_nii** (*str*) – Filename of .nii file the experiments were conducted with.
- **fn_conform_nii** (*str*) – Filename of .nii file from SimNIBS mri2msh function, e.g. `'''.../fs_subjectID/subjectID_T1fs_conform.nii.gz'''`.
- **m_nnav** (*np.ndarray*) – (4, 4, N) Position matrices from neuronavigation.
- **nnav_system** (*str*) – Neuronavigation system:
 - "Localite" ... Localite neuronavigation system
 - "Visor" ... Visor neuronavigation system from ANT
 - "Brainsight" ... Brainsight neuronavigation system from Rouge Research

- **mesh_approach** (*str*, *default*: "headreco") – Approach the mesh is generated with ("headreco" or "mri2mesh").
- **fiducials** (*np.ndarray of float, optional*) – (3, 3) Fiducial points in ANT nifti space from file, e.g.:
`'''/data/pt_01756/probands/33791.b8/exp/1/33791.b8_recording/MRI/33791.b8_recording.mri'''`
 (x frontal-occipital, y right-left, z inferior-superior).
- **orientation** (*str*, *default*: 'RAS') – Orientation convention ('RAS' or 'LPS'), can be read from neuronavigation .xml file under `coordinateSpace="RAS"`.
- **fsl_cmd** (*str, optional*) – bash command to start FSL environment.
- **target** (*str*, *default*: 'simnibs') – Either transform to 'simnibs' or to 'nnav' space.
- **temp_dir** (*str, optional*) – Directory to save temporary files (transformation .nii and .mat files) (fn_exp_mri_nii folder).
- **rem_tmp** (*bool, default*: False) – Remove temporary files from registration.
- **verbose** (*bool, default*: True) – Print output.

Returns

m_simnibs – (4, 4, N) Transformed coil positions.

Return type

np.ndarray of float

`pynibs.expio.exp.outliers_mask(data, m=2.0)`

Generate a mask to identify outliers in a dataset using the Median Absolute Deviation (MAD) method.

Parameters

- **data** (*array-like*) – Input data for which outliers are to be detected.
- **m** (*float, default*: 2.0) – The threshold multiplier for identifying outliers.

Returns

mask – A boolean mask with the same shape as 'data' where True indicates outliers.

Return type

array-like

`pynibs.expio.exp.print_time(relation, tms_time, tms_time_index, mep_time, mep_time_index, time_bnd_l, time_bnd_h)`

Print timestamps that do not match.

Parameters

- **relation** (*str*) – 'bigger' or 'smaller'
- **tms_time** (*datetime.timedelta*) – TMS timestamps.
- **tms_time_index** (*int*) – Index of tms timestamp.
- **mep_time** (*datetime.timedelta*) – Mep timestamps.
- **mep_time_index** (*int*) – Index of mep timestamps.
- **time_bnd_l** (*datetime.timedelta*) – Lowest datetime timestamp for matching.
- **time_bnd_h** (*datetime.timedelta*) – Highest datetime timestamp for matching.

`pynibs.expio.exp.read_csv(csv_path)`

Read dictionary from .csv-file.

Parameters

csv_path (*str*) – Path to .csv-file.

Returns

dict_lst – Field name of the .csv-file as the key.

Return type

dict of list

`pynibs.expio.exp.read_exp_stimulations(fname_results_conditions, fname_simpos, filter_bad_trials=False, drop_idx=None)`

Reads results_conditions.csv and simPos.csv and returns data.

Parameters

- **fname_results_conditions** (*str*) – Filename of results_conditions.csv file.
- **fname_simpos** (*str*) – Filename of simPos.csv file.
- **filter_bad_trials** (*bool*, *default: False*) – If true, some filtering will be done to exclude erroneous data.
- **drop_idx** (*list*, *optional*) – Indices of trials to drop.

Returns

- **positions_all** (*list of np.ndarrays of float*) – (N_zaps, (4, 4)) List of position matrices of TMS coil, formatted in simnibs style.

$$\begin{bmatrix} | & | & | & | \\ x & y & z & pos \\ | & | & | & | \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

- **conditions** (*list of str*) – (N_zaps) Str labels of the condition corresponding to each zap.
- **position_list** (*list of float and str*) – (N_zaps x 55) List of data stored in results_conditions.csv (condition, MEP amplitude, locations of neuronavigation trackers).
- **mep_amp** (*np.array of float*) – (N_zaps) MEP amplitude in [V] corresponding to each zap.
- **intensities** (*np.ndarray of float*) – (N_zaps) Stimulator intensities corresponding to each zap.
- **fails_idx** (*np.ndarray*) – (N_fails_idx, 1) Which trials were dropped through filtering (only if filter_bad_trials).

`pynibs.expio.exp.save_matsimnibs_txt(fn_matsimnibs, matsimnibs)`

Saving matsimnibs matrices in .txt file.

Parameters

- **fn_matsimnibs** (*str*) – Filename of .txt file the matsimnibs matrices are stored in.
- **matsimnibs** (*np.ndarray of float*) – (4, 4) or (4, 4, n_mat) Tensor containing matsimnibs matrices.

Returns

<File> – Textfile containing the matsimnibs matrices.

Return type

.txt file

`pynibs.expio.exp.sort_by_condition(exp, conditions_selected=None)`

Sort experimental dictionary from experimental.csv into list by conditions.

Parameters

- **exp** (*dict or list of dict*) – Dictionary containing the experimental data information.

- **conditions_selected**(*str* or *list of str*, *optional*) – List of conditions returned by the function (in this order), the others are omitted, If None, all conditions are returned.

Returns

exp_cond – List of dictionaries containing the experimental data information sorted by condition.

Return type

list of dict

`pynibs.expio.exp.sort_data_by_condition(conditions, return_alph_sorted=True, conditions_selected=None, *data)`

Sorts data by condition and returns tuples of data with corresponding labels.

Parameters

- **conditions** (*list of str*) – (N_zaps) Str labels of the condition corresponding to each data.
- **return_alph_sorted** (*bool*, *default: True*) – Shall returns be in alphabetically or original order.
- **conditions_selected** (*list of str*, *optional*) – List of conditions returned by the function (in this order), the others are omitted.
- **data** (*tuple of data indexed by condition*) – (N_data, N_zaps, m) Data to sort.

Returns

- **cond_labels** (*list of str*) – (N_cond) Labels of conditions.
- **data_sorted** (*tuple of sorted data*) – (N_cond, N_data, N_zaps, m) Sorted data by condition.

`pynibs.expio.exp.splitext_niigz(fn)`

Splitting extension(s) from .nii or .nii.gz file.

Parameters

fn (*str*) – Filename of input image .nii or .nii.gz file.

Returns

- **path** (*str*) – Path and filename without extension(s).
- **ext** (*str*) – Extension, either .nii or .nii.gz.

`pynibs.expio.exp.square(x, a, b, c)`

Parametrized quadratic function.

$$y = ax^2 + bx + c$$

Parameters

- **x** (*np.ndarray of float*) – (N_x) X-values the function is evaluated in.
- **a** (*float*) – Slope parameter of x^2 .
- **b** (*float*) – Slope parameter of x .
- **c** (*float*) – Offset parameter.

Returns

y – (N_x) Function value at argument x.

Return type

np.ndarray of float

`pynibs.expio.exp.toRAS(fn_in, fn_out)`

Transforming MRI .nii image to RAS space.

Parameters

- **fn_in** (*str*) – Filename of input image .nii file.
- **fn_out** (*str*) – Filename of output image .nii file in RAS space.

Returns

<File> – .nii image in RAS space with filename fn_out.

Return type

.nii file

`pynibs.expio.exp.write_csv(csv_output_path, dict_lst)`

Write dictionary into .csv-file.

Parameters

- **csv_output_path** (*str*) – Path to output-file.
- **dict_lst** (*list of dict*) – Fields of the .csv-file.

`pynibs.expio.exp.write_triggermarker_stats(tm_array, idx_keep, idx_outlier, idx_zero, fn, **kwargs)`

Write some stats about the triggermarker analyses to a .csv. Use kwargs to add some more information, like subject id, experiment, conditions, etc.

Parameters

- **tm_array** (*np.ndarray*) – (N_zaps, 4, 4) The input array containing the triggermarker data.
- **idx_keep** (*list*) – List of indices to keep in the array for calculation.
- **idx_outlier** (*list*) – List of outlier indices in the array.
- **idx_zero** (*list*) – List of zero indices in the array.
- **fn** (*str*) – File name (including path) for the CSV file to be written.
- **kwargs** (*dict, optional*) – Additional information to be written to the CSV file. Example: subject=subject_id, experiment=experiment_name.

Example

pynibs.expio.localite module

Functions to import data from Localite TMS Navigator

`pynibs.expio.localite.arrays_similar(tm_matrix, tm_matrix_post, pos_rtol=0, pos_atol=3.6, ang_rtol=0.1, ang_atol=0.1)`

Compares angles and position for similarity.

Splitting the comparison into angles and position is advisable, as the absolute tolerance (atol) should be different for angles (degree) and position (millimeter) comparisons.

Parameters

- **tm_matrix** (*array-like*) – (4, 4) TMS Navigator trigger marker or instrument marker array.
- **tm_matrix_post** (*array-like*) – (4, 4) TMS Navigator trigger marker or instrument marker array.
- **pos_rtol** (*float, default: 0*) – Relative tolerance for position comparison.

- **pos_atol** (*float*, *default:* 3.6) – Absolute tolerance for position comparison in millimeters.
- **ang_rtol** (*float*, *default:* 0.1) – Relative tolerance for angle comparison in degrees.
- **ang_atol** (*float*, *default:* 0.1) – Absolute tolerance for angle comparison in degrees.

Returns

next_same – True if the position and angle differences between *tm_matrix* and *tm_matrix_post* are within the specified tolerances, False otherwise.

Return type

bool

`pynibs.expio.localite.get_instrument_marker(im_path)`

Wrapper function to read instrument-marker and conditions from Neuronavigator .xml-file.

This function allows you to read instrument-marker data from either a single file or a list of files. If a single file path is provided, the function reads the instrument-marker data from the specified file. If a list of file paths is provided, the function reads instrument-marker data from each file and selects the appropriate marker for each timestamp.

Parameters

im_path (*str* or *list of str*) – Path to the instrument-marker file(s) or a list of paths if multiple files are provided.

Returns

- **im_array** (*np.ndarray of float*) – A consolidated array of instrument-marker matrices with shape (N, 4, 4), where N is the number of instrument-marker matrices across all files.
- **marker_descriptions** (*list of str*) – Labels of the marker conditions.
- **marker_times** (*list of float*) – Onset times.

`pynibs.expio.localite.get_marker(im_path, markertype)`

Read instrument-marker and conditions from Neuronavigator .xml-file.

Parameters

- **im_path** (*str* or *list of str*) – Path to instrument-marker-file.
- **markertype** (*str*) – One of ['TriggerMarker', 'InstrumentMarker'].

Returns

- **im_array** (*np.ndarray of float*) – (M, 4, 4) Instrument marker matrices.
- **marker_descriptions** (*list of str*) – Labels of the marker conditions.
- **marker_times** (*list of float*) – Onset times.

`pynibs.expio.localite.get_single_marker_file(im_path, markertype)`

Read instrument-marker and conditions from Neuronavigator .xml-file.

Parameters

- **im_path** (*str* or *list of str*) – Path to instrument-marker-file.
- **markertype** (*str*) – One of ['TriggerMarker', 'InstrumentMarker'].

Returns

- **im_array** (*np.ndarray of float*) – (M, 4, 4) Instrument marker matrices.
- **marker_descriptions** (*list of str*) – Labels of the marker conditions.
- **marker_times** (*list of float*) – Onset times.

`pynibs.expio.localite.get_tms_elements(xml_paths, verbose=False)`

Read needed elements out of the tms-xml-file.

Parameters

- **xml_paths** (*list of str or str*) – Paths to coil0-file and optionally coil1-file. If there is no coil1-file, use empty string.
- **verbose** (*bool, default: False*) – Flag indicating verbosity.

Returns

- **coils_array** (*np.ndarray of float*) – (3, NX4, 4), Coil0, coil1 and mean-value of N 4x4 coil-arrays.
- **ts_tms_lst** (*list of int*) – [N] Timestamps of valid tms-measurements.
- **current_lst** (*list of int*) – [N] Measured currents.
- **idx_invalid** (*list of int*) – List of indices of invalid coil positions (w.r.t. all timestamps incl invalid).

`pynibs.expio.localite.marker_is_empty(arr)`

`pynibs.expio.localite.markers_are_empty(arr)`

`pynibs.expio.localite.match_instrument_marker_file(xml_paths, im_path)`

Assign right instrument marker condition to every triggermarker (get instrument marker out of file).

Parameters

- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file if there is no coil1-file, use empty string.
- **im_path** (*str*) – Path to instrument-marker-file.

Returns

- **coil_cond_lst** (*list of str*) – Right conditions.
- **drop_idx** (*list of int*) – Indices of trigger markers that were dropped.

`pynibs.expio.localite.match_instrument_marker_string(xml_paths, condition_order)`

Assign right instrument marker condition to every triggermarker (get instrument marker out of list of strings).

Parameters

- **xml_paths** (*list of str*) – Paths to coil0-file and optionally coil1-file if there is no coil1-file, use empty string.
- **condition_order** (*list of str*) – Conditions in the right order.

Returns

coil_cond_lst – Strings containing the right conditions. **drop_idx** : list of int
Indices of trigger markers that were dropped.

Return type

list of str

`pynibs.expio.localite.match_tm_to_im(tm_array, im_array, tms_time_arr, tms_cur_arr)`

Match triggermarker with instrumentmarker and get index of best fitting instrumentmarker.

Parameters

- **tm_array** (*np.ndarray of float*) – (N, 4, 4) Mean-value of Nx4x4 coil matrices.
- **im_array** (*np.ndarray of float*) – (M, 4, 4) Instrument-marker-matrices.
- **tms_time_arr** (*np.ndarray*) – Array of TMS times in seconds.

- **tms_cur_arr** (*np.ndarray*) – Array of TMS currents corresponding to ``tms_time_arr``.

Returns

- **im_index_lst** (*list of int*) – Indices of best fitting instrument markers.
- **drop_idx** (*list of int*) – Indices of trigger markers that were dropped.

```
pynibs.expio.localite.merge_exp_data_ft(subject, coil_outlier_corr_cond,
                                         remove_coil_skin_distance_outlier, coil_distance_corr,
                                         cond, exp_idx=0, mesh_idx=0, drop_trial_idx=None,
                                         verbose=False, plot=False)
```

Merge the TMS coil positions (TriggerMarker) and the mep data into an experiment.hdf5 file.

Parameters

- **subject** (*pynibs.subject.Subject*) – Subject object.
- **exp_idx** (*str*) – Experiment ID.
- **mesh_idx** (*str*) – Mesh ID.
- **coil_outlier_corr_cond** (*bool*) – Correct outlier of coil position and orientation (+-2 mm, +-3 deg) in case of conditions.
- **cond** (*string*) – Which behavioral measurement to analyse.
- **remove_coil_skin_distance_outlier** (*bool*) – Remove outlier of coil position lying too far away from the skin surface (+- 5 mm).
- **coil_distance_corr** (*bool*) – Perform coil <-> head distance correction (coil is moved towards head surface until coil touches scalp).
- **drop_trial_idx** (*List of int or None*) – Which MEPs to remove before matching.
- **verbose** (*bool*) – Plot output messages.
- **plot** (*bool, optional, default: False*) – Plot RTs and a running average over 10 trials.

```
pynibs.expio.localite.merge_exp_data_localite(subject, coil_outlier_corr_cond,
                                                remove_coil_skin_distance_outlier,
                                                coil_distance_corr, exp_idx=0, mesh_idx=0,
                                                drop_mep_idx=None, mep_onsets=None,
                                                cfs_data_column=None, channels=None,
                                                verbose=False, plot=False, start_mep=18,
                                                end_mep=35)
```

Merge the TMS coil positions (TriggerMarker) and the mep data into an experiment.hdf5 file.

Parameters

- **subject** (*pynibs.subject.Subject*) – Subject object.
- **coil_outlier_corr_cond** (*bool*) – Correct outlier of coil position and orientation (+-2 mm, +-3 deg) in case of conditions.
- **remove_coil_skin_distance_outlier** (*bool*) – Remove outlier of coil position lying too far away from the skin surface (+- 5 mm).
- **coil_distance_corr** (*bool*) – Perform coil <-> head distance correction (coil is moved towards head surface until coil touches scalp).
- **exp_idx** (*str, default: 0*) – Experiment ID.
- **mesh_idx** (*str, default: 0*) – Mesh ID.

- **drop_mep_idx** (*List of `int`, optional*) – Which MEPs to remove before matching.
- **mep_onsets** (*List of `int`, optional*) – If there are multiple .cfs per TMS Navigator sessions, onsets in [ms] of .cfs. E.g.: [0, 71186].
- **cfs_data_column** (*`int` or `list of int`, optional*) – Column(s) of dataset in .cfs file.
- **channels** (*`list of str`, optional*) – List of channel names.
- **verbose** (*`bool`, default: `false`*) – Flag to indicate verbosity.
- **plot** (*`bool`, default: `False`*) – Plot MEPs and p2p evaluation.
- **start_mep** (*`float`, default: 18*) – Start of time frame after TMS pulse where p2p value is evaluated (in ms).
- **end_mep** (*`float`, default: 35*) – End of time frame after TMS pulse where p2p value is evaluated (in ms).

```
pynibs.expio.localite.merge_exp_data_rt(subject, coil_outlier_corr_cond,
                                       remove_coil_skin_distance_outlier, coil_distance_corr,
                                       cond=None, exp_idx=0, mesh_idx=0, drop_trial_idx=None,
                                       verbose=False, plot=False)
```

Merge the TMS coil positions (TriggerMarker) and the mep data into an experiment.hdf5 file.

Parameters

- **subject** (*`pynibs.subject.Subject`*) – Subject object.
- **coil_outlier_corr_cond** (*`bool`*) – Correct outlier of coil position and orientation (+-2 mm, +-3 deg) in case of conditions.
- **remove_coil_skin_distance_outlier** (*`bool`*) – Remove outlier of coil position lying too far away from the skin surface (+- 5 mm).
- **coil_distance_corr** (*`bool`*) – Perform coil <-> head distance correction (coil is moved towards head surface until coil touches scalp).
- **cond** (*`string`, optional*) – Which condition to analyse.
- **exp_idx** (*`str`, default: 0*) – Experiment ID.
- **mesh_idx** (*`str`, default: 0*) – Mesh ID.
- **drop_trial_idx** (*`List of int`, optional*) – Which MEPs to remove before matching.
- **verbose** (*`bool`, default: `False`*) – Flag indicating verbosity.
- **plot** (*`bool`, default: `False`*) – Plot RTs and a running average over 10 trials.

```
pynibs.expio.localite.read_coil(xml_ma)
```

Read coil-data from xml element.

Parameters

xml_ma (*`xml-element`*) – Coil data.

Returns

coil – (4, 4) Coil elements.

Return type

`np.ndarray` of `float`

```
pynibs.expio.localite.read_triggermarker_localite(fn_xml)
```

Read instrument-marker and conditions from neuronavigator .xml-file.

Parameters

fn_xml (*str*) – Path to TriggerMarker.xml file (e.g. Subject_0/Sessions/Session_YYYYMMDDHHMMSS/TMSTrigger/TriggerMarkers_Coil1_YYYYMMDDHHMMSS

Returns**m_nnav**

[np.ndarray of float] (M, 4, 4) Neuronavigation coordinates of N stimuli (4x4 matrices).

didt

[np.ndarray of float]

(N) Rate of change of coil current in (A/us).

stim_int

[np.ndarray of float]

(N) Stimulator intensity in (%).

descr

[list of str]

(N) Labels of the instrument-marker-conditions.

rec_time

[list of str]

(N) Recording time in ms.

Return type

list of

pynibs.expio.visor module

Functions to import data from ANT Visor 2 / ANT EEG software go here

`pynibs.expio.visor.filter_emg(emg, fs)`

Filter EMG signals.

Parameters

- **emg** (*list of np.ndarray*) – (n_stimuli), Raw EMG data. Each list entry contains a np.ndarray of size [n_samples x n_channel]. Each channel is filtered in the same way.
- **fs** (*float*) – Sampling frequency.

Returns

emg_filt – (n_stimuli), Filtered EMG data.

Return type

list of np.ndarray

`pynibs.expio.visor.get_cnt_data(fn, channels='all', trigger_val='1', max_duration=10, fn_hdf5=None, path_hdf5=None, verbose=False, return_data=False)`

Reads ANT .cnt EMG/EEG data file and chunks timeseries into triggerN - triggerN+1.

It can directly write the zaps into hdf5 if argument is provided, starting with the first trigger and ending with get_sample_count()-1.

Parameters

- **fn** (*str*) – Path to the .cnt file.
- **channels** (*str, int, list of int, or list of str, default: 'all'*) – Which channel(s) to return. Can be channel number(s) or channel name(s).
- **trigger_val** (*str, default: '1'*) – Trigger value to read as zap trigger.

- **max_duration** (*int*, *default:* 10) – Maximum duration in [s] per chunk. Rest is dropped.
- **fn_hdf5** (*str*, *optional*) – If provided, the cnt data is written into an hdf5 file under “path_hdf5” as pandas dataframe with column name “qoi_name” and nothing is returned.
- **path_hdf5** (*str*, *default:* None) – If fn_hdf5, path within the HDF5 file where the data is saved (e.g. “/phys_data/raw/EEG”)
- **verbose** (*bool*, *default:* False) – Flag indicating verbosity.
- **return_data** (*bool*, *default:* False) – If true, the data is returned as list of numpy arrays.

Returns

data_lst – (samples,channels), List of EEG/EMG data. Only returned if “fn_hdf5” is not None.

Return type

list of np.ndarray, optional

`pynibs.expio.visor.get_instrument_marker(im_path, verbose=False)`

Return all instrument markers from visor .cnt file.

Coordinate system in raw ANT space (NLR) is defined as: - origin: intersection between line of ear fiducials and nasion - x-axis: origin -> nasion - y-axis: origin -> left ear - z-axis: origin -> superior

Parameters

- **im_path** (*str*) – Path to instrument-marker-file .cnt file.
- **verbose** (*bool*, *default:* False) – Flag indicating verbosity.

Returns

im_list – List containing stimulation parameters.

- coil_mean_raw: 4 x 4 numpy array
- StimulusID: int
- etc...

Return type

list of dict

Raises

AssertionError – If the .cnt file contains no instrument markers.

`pynibs.expio.visor.merge_exp_data_visor(subject, exp_id=0, mesh_idx=0, verbose=False, start_mep=18, end_mep=35)`

Merges all experimental data from visor experiment into one .hdf5 file.

Parameters

- **subject** (*pynibs.Subject*) – Subject object.
- **exp_id** (*int*, *default:* 0) – Experiment index.
- **mesh_idx** (*int*, *default:* 0) – Mesh index.
- **verbose** (*bool*, *default:* False) – Flag indicating verbosity.
- **start_mep** (*float*, *default:* 18) – Start of time frame after TMS pulse where p2p value is evaluated (in ms).
- **end_mep** (*float*, *default:* 35) – End of time frame after TMS pulse where p2p value is evaluated (in ms).

Returns

<File> – File containing the stimulation and physiological data as pandas dataframes:

- "stim_data": Stimulation parameters (e.g. coil positions, etc.)
- "phys_data/info/EMG": Information about EMG data recordings (e.g. sampling frequency, etc.)
- "phys_data/info/EEG": Information about EEG data recordings (e.g. sampling frequency, etc.)
- "phys_data/raw/EMG": Raw EMG data
- "phys_data/raw/EEG": Raw EEG data
- "phys_data/postproc/EMG": Post-processed EMG data (e.g. filtered, p2p, etc.)
- "phys_data/postproc/EEG": Post-processed EEG data (e.g. filtered, p2p, etc.)

Return type

.hdf5 file

`pynibs.expio.visor.read_nlr(fname)`

Reads NLR coordinates from *_recording.mri file.

Parameters

fname (*str*) – File path of the NLR recording MRI file.

Returns

fiducials – (3, 3) The rows contain the fiducial points in ANT NIFTI space (nasion, left ear, right ear). Each fiducial point is represented as [x, y, z] coordinates.

Return type

np.ndarray of float

pynibs.mesh package**Submodules****pynibs.mesh.mesh_struct module**

class `pynibs.mesh.mesh_struct.Mesh(mesh_name, subject_id, subject_folder)`

Bases: `object`

” Mesh class to initialize default attributes.

fill_defaults(*approach*)

Initializes attributes for a headreco mesh.

Parameters

approach (*str*) – ‘headreco’ ‘mri2mesh’ ‘charm’

print()

Print self information.

write_to_hdf5(*fn_hdf5, check_file_exist=False, verbose=False*)

Write this mesh’ attributes to .hdf5 file.

Parameters

- **fn_hdf5** (*str*) –
- **check_file_exist** (*bool*) – Check if provided filenames exist, warn if not.
- **verbose** (*bool*) – Print self information

```
class pynibs.mesh.mesh_struct.ROI(subject_id, roi_name, mesh_name)
```

Bases: `object`

” Region of interest class to initialize default attributes.

```
print()
```

Print self information.

```
write_to_hdf5(fn_hdf5, check_file_exist=False, verbose=False)
```

Write this mesh’ attributes to .hdf5 file.

Parameters

- **fn_hdf5** (*str*) –
- **check_file_exist** (*bool*) – Check if provided filenames exist, warn if not.
- **verbose** (*bool*) – Print self information

```
class pynibs.mesh.mesh_struct.TetrahedraLinear(points, triangles, triangles_regions, tetrahedra,  
                                              tetrahedra_regions)
```

Bases: `object`

Mesh, consisting of linear tetrahedra.

Parameters

- **points** (*array of float [N_points x 3]*) – Vertices of FE mesh
- **triangles** (*np.ndarray of int [N_tri x 3]*) – Connectivity of points forming triangles
- **triangles_regions** (*np.ndarray of int [N_tri x 1]*) – Region identifiers of triangles
- **tetrahedra** (*np.ndarray of int [N_tet x 4]*) – Connectivity of points forming tetrahedra
- **tetrahedra_regions** (*np.ndarray of int [N_tet x 1]*) – Region identifiers of tetrahedra

N_points

Number of vertices

Type

`int`

N_tet

Number of tetrahedra

Type

`int`

N_tri

Number of triangles

Type

`int`

N_region

Number of regions

Type

`int`

region

Region labels

Type

np.ndarray of int

tetrahedra_volume

Volumes of tetrahedra

Type

np.ndarray of float [N_tet x 1]

tetrahedra_center

Center of tetrahedra

Type

np.ndarray of float [N_tet x 1]

triangles_center

Center of triangles

Type

np.ndarray of float [N_tri x 1]

triangles_normal

Normal components of triangles pointing outwards

Type

np.ndarray of float [N_tri x 3]

calc_E(*grad_phi*, *omegaA*)

Calculate electric field with gradient of electric potential and omega-scaled magnetic vector potential A.

$$\mathbf{E} = -\nabla\varphi - \omega\mathbf{A}$$

Parameters

- **grad_phi** (np.ndarray of float [N_tet x 3]) – Gradient of Scalar DOF in tetrahedra center
- **omegaA** (np.ndarray of float [N_tet x 3]) – Magnetic vector potential in tetrahedra center (scaled with angular frequency omega)

Returns**E** – Electric field in tetrahedra center**Return type**

np.ndarray of float [N_tet x 3]

calc_E_normal_tangential_surface(*E*, *fname*)

Calculate normal and tangential component of electric field on given surfaces of mesh instance.

Parameters

- **E** (np.ndarray of float [N_tri x 3]) – Electric field data on surfaces
- **fname** (str) – Filename of the .txt file containing the tetrahedra indices, which are adjacent to the surface triangles generated by the method “calc_surface_adjacent_tetrahedra_idx_list(self, fname)”

Returns

- **En_pos** (np.ndarray of float [N_tri x 3]) – Normal component of electric field of top side (outside) of surface
- **En_neg** (np.ndarray of float [N_tri x 3]) – Normal component of electric field of bottom side (inside) of surface

- **n** (*np.ndarray of float [N_tri x 3]*) – Normal vector
- **Et** (*np.ndarray of float [N_tri x 3]*) – Tangential component of electric field lying in surface
- **t** (*np.ndarray of float [N_tri x 3]*) – Tangential vector

calc_E_on_GM_WM_surface(*E, roi*)

Determines the normal and tangential component of the induced electric field on a GM-WM surface using nearest neighbour principle.

Parameters

- **E** (*np.ndarray of float [N_tri x 3]*) – Induced electric field given in the tetrahedra centre of the mesh instance
- **roi** (*pynibs.roi.RegionOfInterestSurface*) – RegionOfInterestSurface object class instance

Returns

- **E_normal** (*np.ndarray of float [N_points x 3]*) – Normal vector of electric field on GM-WM surface
- **E_tangential** (*np.ndarray of float [N_points x 3]*) – Tangential vector of electric field on GM-WM surface

calc_E_on_GM_WM_surface3(*phi, dAdt, roi, verbose=True, mode='components'*)

Determines the normal and tangential component of the induced electric field on a GM-WM surface by recalculating phi and dA/dt in an epsilon environment around the GM/WM surface (upper and lower GM-WM surface).

Parameters

- **phi** (*np.ndarray of float*) – (N_nodes, 1) Scalar electric potential given in the nodes of the mesh.
- **dAdt** (*np.ndarray of float*) – (N_nodes, 3) Magnetic vector potential given in the nodes of the mesh.
- **roi** (*pynibs.mesh.mesh_struct.ORT*) – RegionOfInterestSurface object class instance.
- **verbose** (*bool*) – Print information to stdout.
- **mode** (*str*) – Select mode of output: - “components” : return x, y, and z component of tangential and normal components - “magnitude” : return magnitude of tangential and normal component (normal with sign for direction)

Returns

- **E_normal** (*np.ndarray of float*) – (N_nodes, 3) Normal vector of electric field on GM-WM surface.
- **E_tangential** (*np.ndarray of float*) – (N_nodes, 3) Tangential vector of electric field on GM-WM surface.

calc_E_on_GM_WM_surface_simnibs(*phi, dAdt, roi, subject, verbose=False, mesh_idx=0*)

Determines the normal and tangential component of the induced electric field on a GM-WM surface by recalculating phi and dA/dt in an epsilon environment around the GM/WM surface (upper and lower GM-WM surface) or by using the Simnibs interpolation function.

Parameters

- **phi** (*np.ndarray of float*) – (N_nodes, 1) Scalar electric potential given in the nodes of the mesh.
- **dAdt** (*np.ndarray of float*) – (N_nodes, 3) Magnetic vector potential given in the nodes of the mesh.

- **roi** (`pynibs.mesh.mesh_struct.ROI`) – RegionOfInterestSurface object class instance.
- **subject** (`pynibs.subject.Subject`) – Subject object loaded from .hdf5 file.
- **verbose** (*bool*) – Print information to stdout.
- **mesh_idx** (*int*) – Mesh index.

Returns

- **E_normal** (*np.ndarray of float*) – (N_points, 3) Normal vector of electric field on GM-WM surface.
- **E_tangential** (*np.ndarray of float*) – (N_points, 3) Tangential vector of electric field on GM-WM surface.

calc_E_on_GM_WM_surface_simnibs_KW(*phi, dAdt, roi, subject, verbose=False, mesh_idx=0*)

Determines the normal and tangential component of the induced electric field on a GM-WM surface by recalculating phi and dA/dt in an epsilon environment around the GM/WM surface (upper and lower GM-WM surface) or by using the Simnibs interpolation function.

Parameters

- **phi** (*np.ndarray of float*) – (N_nodes, 1) Scalar electric potential given in the nodes of the mesh.
- **dAdt** (*np.ndarray of float*) – (N_nodes, 1) Magnetic vector potential given in the nodes of the mesh.
- **roi** (`pynibs.mesh.mesh_struct.ROI`) – RegionOfInterestSurface object class instance.
- **subject** (`pynibs.subject.Subject`) – Subject object loaded from .hdf5 file.
- **verbose** (*bool*) – Print information to stdout.
- **mesh_idx** (*int*) – Mesh index.

Returns

- **E_normal** (*np.ndarray of float*) – (N_points, 3) Normal vector of electric field on GM-WM surface.
- **E_tangential** (*np.ndarray of float*) – (N_points, 3) Tangential vector of electric field on GM-WM surface.

calc_J(*E, sigma*)

Calculate current density J. The conductivity sigma is a list of np.arrays containing conductivities of regions (scalar and/or tensor).

$$\mathbf{J} = [\sigma]\mathbf{E}$$

Parameters

- **E** (*np.ndarray of float [N_tet x 3]*) – Electric field in tetrahedra center
- **sigma** (*list of np.ndarray of float [N_regions][3 x 3]*) – Conductivities of regions (scalar and/or tensor).

Returns

E – Electric field in tetrahedra center

Return type

np.ndarray of float [N_tet x 3]

calc_QOI_in_points(*qoi, points_out*)

Calculate QOI_out in points_out using the mesh instance and the quantity of interest (QOI).

Parameters

- **qoi** (*np.ndarray of float*) – Quantity of interest in nodes of tetrahedra mesh instance
- **points_out** (*np.ndarray of float*) – Point coordinates (x, y, z) where the qoi is going to be interpolated by linear basis functions

Returns

qoi_out – Quantity of interest in points_out

Return type

np.ndarray of float

calc_QOI_in_points_tet_idx(*qoi, points_out, tet_idx*)

Calculate QOI_out in points_out sitting in tet_idx using the mesh instance and the quantity of interest (QOI).

Parameters

- **qoi** (*np.ndarray of float*) – Quantity of interest in nodes of tetrahedra mesh instance
- **points_out** (*np.ndarray of float*) – Point coordinates (x, y, z) where the qoi is going to be interpolated by linear basis functions
- **tet_idx** (*np.ndarray of int*) – Element indices where the points_out are sitting

Returns

qoi_out – Quantity of interest in points_out

Return type

np.ndarray of float

calc_gradient(*phi*)

Calculate gradient of scalar DOF in tetrahedra center.

Parameters

phi (*np.ndarray of float [N_nodes]*) – Scalar DOF the gradient is calculated for

Returns

grad_phi – Gradient of Scalar DOF in tetrahedra center

Return type

np.ndarray of float [N_tet x 3]

calc_surface_adjacent_tetrahedra_idx_list(*fname*)

Determine the indices of the tetrahedra touching the surfaces and save the indices into a .txt file specified with fname.

Parameters

fname (*str*) – Filename of output .txt file

Returns

<File> – Element indices of the tetrahedra touching the surfaces (outer-most elements)

Return type

.txt file

data_elements2nodes(*data*)

Transforms an data in tetrahedra into the nodes after Zienkiewicz et al. (1992) [1]. Can only transform volume data, i.e. needs the data in the surrounding tetrahedra to average it to the nodes. Will not work well for discontinuous fields (like E, if several tissues are used).

Parameters

data (*np.ndarray [N_elements x N_data]*) – Data in tetrahedra

Returns

data_nodes – Data in nodes

Return type

np.ndarray [N_nodes x N_data]

Notes**data_nodes2elements(data)**

Interpolate data given in the nodes to the tetrahedra center.

Parameters**data** (np.ndarray [N_nodes x N_data]) – Data in nodes**Returns****data_elements** – Data in elements**Return type**

np.ndarray [N_elements x N_data]

get_faces(tetrahedra_indexes=None)

Creates a list of nodes in each face and a list of faces in each tetrahedra.

Parameters**tetrahedra_indexes** (np.ndarray) – Indices of the tetrahedra where the faces are to be determined (default: all tetrahedra)**Returns**

- **faces** (np.ndarray) – List of nodes in faces, in arbitrary order
- **th_faces** (np.ndarray) – List of faces in each tetrahedra, starts at 0, order=((0, 2, 1), (0, 1, 3), (0, 3, 2), (1, 2, 3))
- **face_adjacency_list** (np.ndarray) – List of tetrahedron adjacent to each face, filled with -1 if a face is in a single tetrahedron. Not in the normal element ordering, but only in the order the tetrahedra are presented

get_outside_faces(tetrahedra_indexes=None)

Creates a list of nodes in each face that are in the outer volume.

Parameters**tetrahedra_indices** (np.ndarray) – Indices of the tetrahedra where the outer volume is to be determined (default: all tetrahedra)**Returns****faces** – List of nodes in faces in arbitrary order**Return type**

np.ndarray

pynibs.mesh.transformations module**pynibs.mesh.transformations.cell_data_to_point_data(tris, data_tris, nodes, method='nearest')**

A wrapper for scipy.interpolate.griddata to interpolate cell data to node data.

Parameters

- **tris** (np.ndarray) – (n_tri, 3) element number list.
- **data_tris** (np.ndarray) – (n_tri x 3) data in tris.
- **nodes** (np.ndarray) – (n_nodes, 3) nodes coordinates.
- **method** (str, default: 'nearest') – Which method to use for interpolation. Default uses NearestNDInterpolator.

Returns

data_nodes – Data in nodes

Return type

np.ndarray

pynibs.mesh.transformations.**data_elements2nodes**(data, con, precise=False)

Transforms data in elements (triangles or tetrahedra) to nodes. Data can be list of multiple data arrays.

Parameters

- **data** (np.ndarray of float or list of np.ndarray) – (N_elements, N_data) Data given in the elements (multiple datasets who fit to con may be passed in a list).
- **con** (np.ndarray of int) – triangles: (N_elements, 3). tetrahedra: (N_elements, 4). Connectivity index list forming the elements.
- **precise** (bool, default: False) – Compute data transformation precisely but slow. Better for near-0 values..

Returns

out – (N_nodes, N_data) Data in nodes.

Return type

np.ndarray of float or list of np.ndarray

pynibs.mesh.transformations.**data_nodes2elements**(data, con)

Transforms data in nodes to elements (triangles or tetrahedra).

Parameters

- **data** (np.ndarray of float) – (N_nodes, N_data) Data given in the nodes.
- **con** (np.ndarray of int) – triangles: (N_elements, 3). tetrahedra: (N_elements, 4). Connectivity index list forming the elements.

Returns

out – (N_elements, N_data) Data given in the element scenters.

Return type

np.ndarray of float

pynibs.mesh.transformations.**map_data_to_surface**(datasets, points_datasets, con_datasets, fname_fsl_gm, fname_fsl_wm, fname_midlayer=None, delta=0.5, input_data_in_center=True, return_data_in_center=True, data_substitute=-1)

Maps data from ROI of fsl surface (wm, gm, or midlayer) to given Freesurfer brain surface (wm, gm, inflated).

Parameters

- **datasets** (np.ndarray of float [N_points x N_data] or list of np.ndarray) – Data in nodes or center of triangles in ROI (specify this in “data_in_center”)
- **points_datasets** (np.ndarray of float [N_points x 3] or list of np.ndarray) – Point coordinates (x,y,z) of ROI where data in datasets list is given, the points have to be a subset of the GM/WM surface (has to be provided for each dataset)
- **con_datasets** (np.ndarray of int [N_tri x 3] or list of np.ndarray) – Connectivity matrix of dataset points (has to be provided for each dataset)
- **fname_fsl_gm** (str or list of str or list of None) – Filename of pial surface fsl file(s) (one or two hemispheres) e.g. in mri2msh: .../fs_ID/surf/lh.pial
- **fname_fsl_wm** (str or list of str or list of None) – Filename of wm surface fsl file(s) (one or two hemispheres) e.g. in mri2msh: .../fs_ID/surf/lh.white

- **fname_midlayer** (*str* or *list of str*) – Filename of midlayer surface fsl file(s) (one or two hemispheres) e.g. in headreco: .../fs_ID/surf/lh.central
- **delta** (*float*) – Distance parameter where gm-wm surface was generated 0...1 (default: 0.5) 0 -> WM surface 1 -> GM surface
- **input_data_in_center** (*bool*) – Flag if data in datasets is given in triangle centers or in points (Default: True)
- **return_data_in_center** (*bool*) – Flag if data should be returned in nodes or in elements (Default: True)
- **data_substitute** (*float*) – Data substitute with this number for all points in the inflated brain, which do not belong to the given data set

Returns

data_mapped – Mapped data to target brain surface. In points or elements

Return type

np.ndarray of *float* [N_points_inf x N_data]

```
pynibs.mesh.transformations.midlayer_2_surf(midlayer_data, coords_target, coords_midlayer,
                                             midlayer_con=None, midlayer_data_in_nodes=False,
                                             max_dist=5, outside_roi_val=0, precise_map=True)
```

Convert midlayer data to whole-brain surface data, e.g. grey matter. Output is returned as data in nodes.

Parameters

- **midlayer_data** (np.ndarray of *float*) – (n_elm_midlayer,) or (n_nodes_midlayer,) the data in the midlayer.
- **coords_target** (np.ndarray of *float*) – (n_nodes_target, 3) Coordinates of the nodes of the target surface.
- **coords_midlayer** (np.ndarray of *float*) – (n_nodes_midlayer, 3) Coordinates of the nodes of the midlayer surface.
- **midlayer_con** (np.ndarray of *int*, optional) – (n_elm_midlayer, 3) Connectivity of the midlayer elements. Provide if data_in_points == True.
- **midlayer_data_in_nodes** (*bool*, default=False) – If midlayer data is provided in nodes, set to True and provide midlayer_con.
- **max_dist** (*float*, default=5) – Maximum distance between target and midlayer nodes to pull data from midlayer_data for.
- **outside_roi_val** (*float*, default=0) – Areas outside of max_dist are filled with outside_roi_val.
- **precise_map** (*bool*, default=True) – If elements to nodes mapping is done, perform this precise and slow or not.

Returns

data_target – (n_nodes_target, 1) The data in nodes of the target surface.

Return type

np.ndarray

```
pynibs.mesh.transformations.project_on_scalp(coords, mesh, scalp_tag=1005)
```

Find the node in the scalp closest to each coordinate

Parameters

- **coords** (nx3 np.ndarray) – Vectors to be transformed
- **mesh** (pynibs.TetrahedralLinear or simnibs.msh.mesh_io.Msh) – Mesh structure in simnibs or pynibs format
- **scalp_tag** (*int*, default: 1005) – Tag in the mesh where the scalp is to be set.

Returns

points_closest – (n, 3) coordinates projected scalp (closest skin points)

Return type

np.ndarray

pynibs.mesh.transformations.**project_on_scalp_hdf5**(*coords, mesh, scalp_tag=1005*)

Find the node in the scalp closest to each coordinate.

Parameters

- **coords** (*np.ndarray*) – (n, 3) Vectors to be transformed.
- **mesh** (*str* or *pynibs.TetrahedraLinear*) – Filename of mesh in .hdf5 format or Mesh structure.
- **scalp_tag** (*int*, *default: 1005*) – Tag in the mesh where the scalp is to be set.

Returns

points_closest – (n, 3) coordinates projected scalp (closest skin points).

Return type

np.ndarray

pynibs.mesh.transformations.**refine_surface**(*fn_surf, fn_surf_refined, center, radius, repair=True, remesh=True, verbose=True*)

Refines surface (.stl) in spherical ROI and saves as .stl file.

Parameters

- **fn_surf** (*str*) – Input filename (.stl).
- **fn_surf_refined** (*str*) – Output filename (.stl).
- **center** (*np.ndarray of float*) – (3) Center of spherical ROI (x,y,z).
- **radius** (*float*) – Radius of ROI.
- **repair** (*bool*, *default: True*) – Repair surface mesh to ensure that it is watertight and forms a volume.
- **remesh** (*bool*, *default: False*) – Perform remeshing with meshfix (also removes possibly overlapping facets and intersections).
- **verbose** (*bool*, *default: True*) – Print output messages.

Returns

<file>

Return type

.stl file

pynibs.mesh.utils module

pynibs.mesh.utils.**calc_distances**(*coords, mesh_fn, tissues=None*)

Calculates the distances between coords and tissue types.

Parameters

- **coords** (*list of list or list or np.ndarray*) – Coordinates (X, Y, Z) to compute depths for.
- **mesh_fn** (*str*) – pynibs.Mesh hdf5 filename.
- **tissues** (*list of int, optional*) – Which tissue types to compute depths for. If none, distances to all tissue types are computed.

Returns

distances – columns: coordr, tissue_type, distance

Return type

pd.DataFrame()

pynibs.mesh.utils.**calc_gradient_surface**(*phi, points, triangles*)

Calculate gradient of potential phi on surface (i.e. tangential component) given in vertices of a triangular mesh forming a 2D surface.

Parameters

- **phi** (*np.ndarray of float [N_points x 1]*) – Potential in nodes
- **points** (*np.ndarray of float [N_points x 3]*) – Coordinates of nodes (x,y,z)
- **triangles** (*np.ndarray of int32 [N_tri x 3]*) – Connectivity of triangular mesh

Returns

grad_phi – Gradient of potential phi on surface

Return type

np.ndarray of float [N_tri x 3]

pynibs.mesh.utils.**calc_tet_volume**(*points, abs=True*)

Calculate tetrahedra volumes.

Parameters

- **points** (*np.ndarray*) – shape: (n_tets,4,3)
- **abs** (*bool, default: true*) – Return magnitude

Returns

volume – shape: (n_tets)

Return type

np.ndarray

pynibs.mesh.utils.**calc_tetrahedra_volume_cross**(*P1, P2, P3, P4*)

Calculates volume of tetrahedra specified by the 4 points P1...P4 multiple tetrahedra can be defined by P1...P4 as 2-D np.ndarrays using the cross and vector dot product.

$$P1 = \begin{bmatrix} x_{tet_1} & y_{tet_1} & z_{tet_1} \\ x_{tet_2} & y_{tet_2} & z_{tet_2} \\ \dots & \dots & \dots \\ x_{tet_N} & y_{tet_N} & z_{tet_N} \end{bmatrix}$$

Parameters

- **P1** (*np.ndarray of float [N_tet x 3]*) – Coordinates of first point of tetrahedra
- **P2** (*np.ndarray of float [N_tet x 3]*) – Coordinates of second point of tetrahedra
- **P3** (*np.ndarray of float [N_tet x 3]*) – Coordinates of third point of tetrahedra
- **P4** (*np.ndarray of float [N_tet x 3]*) – Coordinates of fourth point of tetrahedra

Returns

tetrahedra_volume – Volumes of tetrahedra

Return type

np.ndarray of float [N_tet x 1]

`pynibs.mesh.utils.calc_tetrahedra_volume_det(P1, P2, P3, P4)`

Calculate volume of tetrahedron specified by 4 points P1...P4 multiple tetrahedra can be defined by P1...P4 as 2-D np.arrays using the determinant.

$$P1 = \begin{bmatrix} x_{tet_1} & y_{tet_1} & z_{tet_1} \\ x_{tet_2} & y_{tet_2} & z_{tet_2} \\ \dots & \dots & \dots \\ x_{tet_N} & y_{tet_N} & z_{tet_N} \end{bmatrix}$$

Parameters

- **P1** (*np.ndarray of float [N_tet x 3]*) – Coordinates of first point of tetrahedra
- **P2** (*np.ndarray of float [N_tet x 3]*) – Coordinates of second point of tetrahedra
- **P3** (*np.ndarray of float [N_tet x 3]*) – Coordinates of third point of tetrahedra
- **P4** (*np.ndarray of float [N_tet x 3]*) – Coordinates of fourth point of tetrahedra

Returns

tetrahedra_volume – Volumes of tetrahedra

Return type

np.ndarray of float [N_tet x 1]

`pynibs.mesh.utils.calc_tri_surface(points)`

Calculate triangle surface areas.

Parameters

points (*np.ndarray*) – (n_triangles,3,3)

Returns

triangle_area

Return type

np.ndarray

`pynibs.mesh.utils.check_islands_for_single_elm(source_elm, connectivity=None, adjacency=None, island_crit=1)`

This identifies islands in a mesh for a given element. An island is a set of elements, that is only connect via a single node to another set of elements. These islands usually crash the FEM solver and should be removed.

1. Find all elements connect to source_elm via one node (1-node-neighbor)
2. Start with source_elm and visit all 2-node-neighbors ('shared-edge')
3. Continue recursively with all 2-node-neighbors and visit their 2-node-neighbors
4. See if any 1-node-neighbors have not been visited with this strategy. If so, an island has been found

Parameters

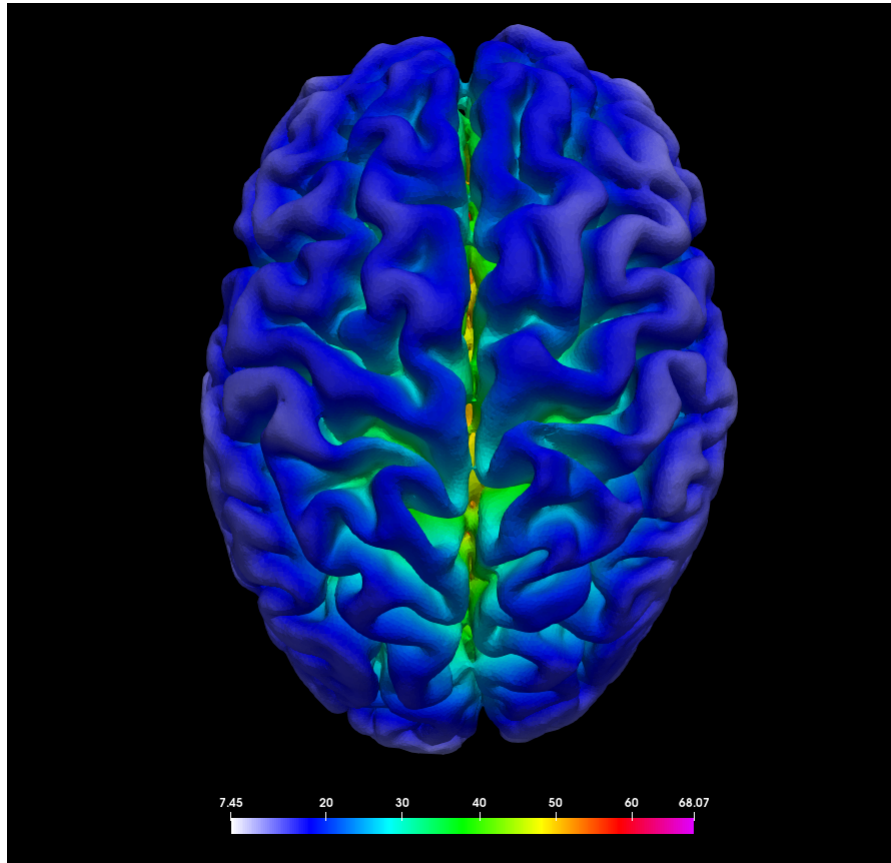
- **source_elm** (*int*) – The source element to check
- **connectivity** (*np.ndarray, optional*) – Connectivity ('node_number_list') starting with 0. Can be triangles or tetrahedra (n_elms, 3) or (n_elms, 4).
- **adjacency** (*np.ndpparray, optional*) – Adjacency matrix (n_elm, n_elm). Weights are supposed to be number of shared nodes. Computed from neighbors if not provided.
- **island_crit** (*int, default: 'any'*) – How many nodes to define islands? 'any' -> Elements connected via a single node or single edge are defined as an island. 'node' -> Elements connected via a single _node_ are defined as an island. 'edge' -> Elements connected via a single _edge_ are defined as an island.

Returns

- **n_visited** (*int*)
- **n_not_visited** (*int*)
- **neighbors_visited** (*dict*, which neighbors have been visited and which have not)

`pynibs.mesh.utils.cortical_depth(mesh_fn, geo_fn=None, write_xdmf=True, skin_surface_id=1005, verbose=False)`

Compute skin-cortex-distance (SCD) for surface and volume data in `mesh_fn`.



Cortical depth computed against skin surface.

Parameters

- **mesh_fn** (*str*) – *TetrahedralLinear* mesh file.
- **geo_fn** (*str*, *optional*) – *TetrahedralLinear* mesh file with geometric data. If provided, geometric information is read from here.
- **write_xdmf** (*bool*, *default:* `True`) – Write .xdmf or not.
- **skin_surface_id** (*int*, *default:* `1005`) – Which tissue type nr to compute distance against.
- **verbose** (*bool*, *default:* `False`) – Print some verbosity information.

Returns

- **<file>** (*.hdf5*) – `mesh_fn` or `geo_fn` with SCD information in `/data/tris/Cortex_dist` and `/data/tets/Cortex_dist`.
- **<file>** (*.xdmf*) – Only if `write_xdmf == True`.

`pynibs.mesh.utils.determine_e_midlayer(fn_e_results, fn_mesh_hdf5, subject, mesh_idx, roi_idx, n_cpu=4, midlayer_fun='simnibs', phi_scaling=1.0, verbose=False)`

Parallel version to determine the midlayer e-fields from a list of .hdf5 results files

Parameters

- **fn_e_results** (*list of str*) – List of results filenames (.hdf5 format)
- **fn_mesh_hdf5** (*str*) – Filename of corresponding mesh file
- **subject** (*pynibs.Subject*) – Subject object
- **mesh_idx** (*int*) – Mesh index
- **roi_idx** (*int*) – ROI index
- **n_cpu** (*int, default: 4*) – Number of parallel computations
- **midlayer_fun** (*str, default: "simnibs"*) – Method to determine the midlayer e-fields (“pynibs” or “simnibs”)
- **phi_scaling** (*float, default: 1.0*) – Scaling factor of scalar potential to change between “m” and “mm”

Returns

Adds midlayer e-field results to ROI

Return type

<File> .hdf5 file

```
pynibs.mesh.utils.determine_e_midlayer_workhorse(fn_e_results, subject, mesh_idx, midlayer_fun,
fn_mesh_hdf5, roi_idx, phi_scaling=1.0,
verbose=False)
```

phi_scaling: float

simnibs < 3.0 : 1000. simnibs >= 3.0 : 1. (Default)

```
pynibs.mesh.utils.find_element_idx_by_points(nodes, con, points)
```

Finds the tetrahedral element index of an arbitrary point in the FEM mesh.

Parameters

- **nodes** (*np.ndarray [N_nodes x 3]*) – Coordinates (x, y, z) of the nodes
- **con** (*np.ndarray [N_tet x 4]*) – Connectivity matrix
- **points** (*np.ndarray [N_points x 3]*) – Points for which the element indices are found.

Returns

ele_idx – Element indices of tetrahedra where corresponding ‘points’ are lying in

Return type

np.ndarray [N_points]

```
pynibs.mesh.utils.find_island_elms(connectivity=None, adjacency=None, verbose=False,
island_crit='edge', decision='cumulative')
```

Searches for islands in a mesh and returns element indices of the smallest island. Island is defines as a set of elements, which share a single node and/or single edge with the rest of the mesh.

Parameters

- **connectivity** (*np.ndarray, optional*) – Connectivity (‘node_number_list’) starting with 0. Can be triangles or tetrahedra (n_elms, 3) or (n_elms_4).
- **adjacency** (*np.ndparray, optional*) – Adjacency matrix (n_elm, n_elm). Weights are supposed to be number of shared nodes. Computed from neighbors if not provided.
- **island_crit** (*int, default: 'edge'*) – How many nodes to define islands? ‘node’ -> Elements connected via a single `_node_` are defined as an island. ‘edge’ -> Elements connected via a single `_edge_` are defined as an island.

- **decision** (*str*, *default: cumulative*) – ‘cumulative’ -> Return all element indices that are not visited any times ‘smallest’ -> Return smallest island.
- **verbose** (*bool*, *optional*) – Print some verbosity information. Default: False

Returns
island

Return type
list of island-elms

`pynibs.mesh.utils.find_islands(connectivity=None, adjacency=None, island_crit='any', verbose=False, largest=False)`

This identifies islands in a mesh. An island is a set of elements, that is only connect via a single node to another set of elements. These islands usually crash the FEM solver and should be removed.

For each element:

1. Find all elements connect to source_elm via one node (1-node-neighbor)
2. Start with source_elm and visit all 2-node-neighbors (‘shared-edge’)
3. Continue recursively with all 2-node-neighbors and visit their 2-node-neighbors
4. See if any 1-node-neighbors have not been visited with this strategy. If so, an island has been found

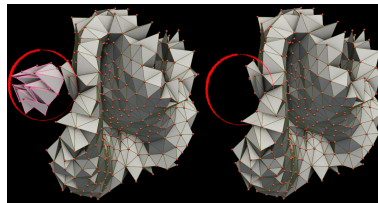


Fig. 1: Islands are groups of elements that are only connected via a single node/edge to another group.

Parameters

- **connectivity** (*np.ndarray*, *optional*) – Connectivity (‘node_number_list’) starting with 0. Can be triangles or tetrahedra (n_elms, 3) or (n_elms, 4).
- **adjacency** (*np.ndarray*, *optional*) – Adjacency matrix (n_elm, n_elm). Weights are supposed to be number of shared nodes. Computed from neighbors if not provided.
- **island_crit** (*int or str*, *default: 'any'*) – How many nodes to define islands? ‘any’ -> Elements connected via a single node or single edge are defined as an island. ‘node’ -> Elements connected via a single _node_ are defined as an island. ‘edge’ -> Elements connected via a single _edge_ are defined as an island.
- **largest** (*bool*, *default: False*) – Only return largest island, speeds up computation quite a bit if only one large, and many small islands exist.
- **verbose** (*bool*, *optional*) – Print some verbosity information. Default: False

Returns

- **elms_with_island** (*list*) – Elements with neighboring islands
- **counter_visited** (*np.ndarray*) – shape = (n_elms). How often as each element been visited.
- **counter_not_visited** (*np.ndarray*) – shape = (n_elms). How often as each element not been visited.

`pynibs.mesh.utils.find_nearest(array, value)`

Given an “array”, and given a “value”, returns an index `j` such that “value” is between `array[j]` and `array[j+1]`. “array” must be monotonic increasing. `j=-1` or `j=len(array)` is returned to indicate that “value” is out of range below and above respectively.

Parameters

- **array** (*np.ndarray of float*) – Monotonic increasing array.
- **value** (*float*) – Target value the nearest neighbor index in `array` is computed for.

Returns

idx – Index `j` such that “value” is between `array[j]` and `array[j+1]`.

Return type

int

`pynibs.mesh.utils.get_indices_discontinuous_data(data, con, neighbor=False, deviation_factor=2, min_val=None, not_fitted_elms=None, crit='median', neigh_style='point')`

Get element indices (and the best neighbor index), where the data is discontinuous

Parameters

- **data** (*np.ndarray of float [n_data]*) – Data array to analyze given in the element center
- **con** (*np.ndarray of float [n_data, 3 or 4]*) – Connectivity matrix
- **neighbor** (*bool, default: False*) – Return also the element index of the “best” neighbor (w.r.t. median of data)
- **deviation_factor** (*float*) – Allows data deviation from $1/\text{deviation_factor} < \text{data}[i]/\text{median} < \text{deviation_factor}$
- **min_val** (*float, optional*) – If given, only return elements which have a neighbor with data higher than `min_val`.
- **not_fitted_elms** (*np.ndarray*) – If given, these elements are not used as neighbors
- **crit** (*str, default: median*) – Criterium for best neighbor. Either median or max value
- **neigh_style** (*str, default: 'point'*) – Should neighbors share point or ‘edge’

Returns

- **idx_disc** (*list of int [n_disc]*) – Index list containing the indices of the discontinuous elements
- **idx_neighbor** (*list of int [n_disc]*) – Index list containing the indices of the “best” neighbors of the discontinuous elements

`pynibs.mesh.utils.get_sphere(mesh=None, mesh_fn=None, target=None, radius=None, roi_idx=None, roi=None, elmtype='tris', domain=None)`

Return element `idx` of elements within a certain distance to provided target. Element indices are 0-based (tris and tets start at 0, ‘pynibs’ style) Elements might be ‘tris’ (default) or ‘tets’

If `roi` object / `idx` and `mesh fn` is provided, the `roi` is expected to have midlayer information and the `roi` geometry is used.

Parameters

- **mesh** (*pynibs.mesh.mesh_struct.TetrahedraLinear, optional*) –
- **mesh_fn** (*str, optional*) – Filename to SimNIBS .msh or pyNIBS .hdf5 mesh file.
- **target** (*np.ndarray of float or list of float*) – (3,) X, Y, Z coordinates of target.

- **radius** (*float*) – Sphere radius in mm.
- **roi_idx** (*str* or *int*, *optional*) – ROI name.
- **elmtype** (*str*, *default*: 'tris') – Return triangles or tetrahedra in sphere around target. One of ('tris', 'tets').

Returns

elems_in_sphere – (n_elements): Indices of elements found in ROI

Return type

np.ndarray

pynibs.mesh.utils.**in_hull**(*points*, *hull*)

Test if points in *points* are in *hull*. *points* should be a [N x K] coordinates of N points in K dimensions. *hull* is either a scipy.spatial.Delaunay object or the [M x K] array of the coordinates of M points in K dimensions for which Delaunay triangulation will be computed.

Parameters

- **points** (np.ndarray) – (N_points x 3) Set of floating point data to test whether they are lying inside the hull or not.
- **hull** (scipy.spatial.Delaunay or np.ndarray) – (M x K) Surface data.

Returns

inside – TRUE: point inside the hull FALSE: point outside the hull

Return type

np.ndarray of bool

pynibs.mesh.utils.**sample_sphere**(*n_points*, *r*)

Creates n_points evenly spread in a sphere of radius r.

Parameters

- **n_points** (*int*) – Number of points to be spread, must be odd.
- **r** (*float*) – Radius of sphere.

Returns

points – (N x 3), Evenly spread points in a unit sphere.

Return type

np.ndarray of float

pynibs.mesh.utils.**tets_in_sphere**(*mesh*, *target*, *radius*, *roi*, *domain=None*)

Worker function for get_sphere()

Returns element idx of elements within a certain distance to provided target. If roi object / idx and mesh fn is provided, the roi is expected to have midlayer information and the roi geometry is used.

If radius is None or 0, the nearest element is returned.

Parameters

- **mesh** (pynibs.TetrahedraLinear, *optional*) –
- **target** (np.ndarray of float, *optional*) – (3,) X, Y, Z coordinates of target
- **radius** (*float*, *optional*) – Sphere radius in mm
- **roi** (pynibs.mesh.ROI, *optional*) – Region of interest

Returns

tets_in_sphere – (n_tets): Indices of elements found in ROI

Return type

np.ndarray

`pynibs.mesh.utils.tris_in_sphere(mesh, target, radius, roi)`

Worker function for `get_sphere()`.

Returns triangle idx of elements within a certain distance to provided target. If roi object / idx and mesh fn is provided, the roi is expected to have midlayer information and the roi geometry is used.

If radius is None or 0, the nearest element is returned.

Parameters

- **mesh** (`pynibs.mesh.TetrahedraLinear`, optional) –
- **target** (`np.ndarray` of `float` or `list` of `float`) – (3,) X, Y, Z coordinates of target
- **radius** (`float`) – Sphere radius in mm
- **roi** (`pynibs.mesh.mesh_struct.ROI`, optional) – ROI

Returns

tris_in_sphere – (n_triangles): Indices of elements found in sphere

Return type

`np.ndarray`

pynibs.models package

pynibs.neuron package

Submodules

pynibs.neuron.neuron_regression module

`pynibs.neuron.neuron_regression.calc_e_effective(e, layerid, theta, gradient=None, neuronmodel='sensitivity_weighting', mep=None, waveform='biphasic', e_thresh_subject=70)`

Determines the effective electric field using a neuron mean field model. Transforms the electric field by subtracting the threshold map (in V/m) from the original electric field. The remaining field is the effective electric field (`e_eff`), generating the stimulation effect, i.e. behavioural effects start at `e_eff > 0` because lower fields were not able to stimulate neurons.

Parameters

- **e** (`np.ndarray`) – Electric field (matrix) [N_stim x N_ele]
- **layerid** (`str`) – Choose from the neocortical layers (e.g. “L1”, “L23”, “L4”, “L5”, “L6”)
- **theta** (`np.ndarray`) – Theta angle (matrix) [N_stim x N_ele] of electric field with respect to surface normal
- **gradient** (`np.ndarray`, optional, default: `None`) – Electric field gradient (matrix) [N_stim x N_ele] between layer 1 and layer 6. Optional, the neuron mean field model is more accurate when provided.
- **neuronmodel** (`str`, optional, default: `"threshold"`) – Select neuron model to modify the electric field values - “sensitivity_weighting”: normalize threshold map and divide raw e-field by it. - “threshold_subtract”: subtract mean threshold from electric field - “threshold_binary”: assign e-field a binary value to predict MEPs (False -> below threshold, True, above threshold) - “IOcurve”: subtract value read from precomputed neuron IO curve from electric field

- **mep** (*np.array of float [N_stim], optional, default: None*) – MEP data (required in case of “IOcurve” approach (neuronmodel))
- **waveform** (*str, optional, default: biphasic*) – Waveform of TMS pulse: - “monophasic” - “biphasic”
- **e_thresh_subject** (*float, optional, default: 70*) – Subject specific stimulation threshold in V/m. Typically between 60 ... 80 V/m.

Returns

e_eff – Effective electric field (matrix) [N_stim x N_ele] the regression analysis can be performed with.

Return type

np.ndarray

pynibs.neuron.neuron_regression.**calc_e_threshold**(*layerid, theta, gradient=None, mep=None, neuronmodel='sensitivity_weighting', waveform='biphasic', e_thresh_subject=70*)

Determine sensitivity map of electric field

Parameters

- **layerid** (*str*) – Choose from the neocortical layers (e.g. “L1”, “L23”, “L4”, “L5”, “L6”). The respective threshold model will be loaded.
- **theta** (*np.ndarray*) – Theta angle (matrix) [N_stim x N_ele] of electric field with respect to surface normal. in degrees [0 .. 180]
- **gradient** (*np.ndarray, optional, default: None*) – Electric field gradient (matrix) [N_stim x N_ele] between layer 1 and layer 6. Optional, the neuron mean field model is more accurate when provided. Percent [-100 .. 100]
- **mep** (*np.array of float [N_stim], optional, default: None*) – MEP data (required in case of “IOcurve” approach (neuronmodel))
- **neuronmodel** (*str, optional, default: "threshold"*) – Select neuron model to modify the electric field values - “sensitivity_weighting”: normalize threshold map and divide raw e-field by it. - “threshold_subtract”: subtract mean threshold from electric field - “threshold_binary”: assign e-field a binary value to predict MEPs (False -> below threshold, True, above threshold) - “IOcurve”: subtract value read from precomputed neuron IO curve from electric field
- **waveform** (*str, optional, default: biphasic*) – Waveform of TMS pulse: - “monophasic” - “biphasic”
- **e_thresh_subject** (*float, optional, default: 70*) – Subject specific stimulation threshold in V/m. Typically between 60 ... 80 V/m.

Returns

e_sens – Electric field sensitivity maps [N_stim x N_ele]

Return type

np.ndarray

pynibs.neuron.neuron_regression.**load_cell_model**(*fn_csv*)

Load interpolation points of the mean field model from the specified CSV file.

Parameters

fn_csv (*str*) – Fully qualified path to the CSV containing the interpolation points of the mean field model.

Returns

- - *scipy.interpolate.LinearNDInterpolator*
- - *interpolation points 'theta'*

- - *interpolation points 'gradient'*

`pynibs.neuron.neuron_regression.workhorse_interp(idx_list, interp, params)`

Single core workhorse to interpolate data.

Parameters

- **idx_list** (*np.array or list of float [n_interpolations]*) – Indices in params array where the interpolation has to be performed (subset of all indices in params array)
- **interp** (*scipy.interpolate instance*) – Interpolator instance
- **params** (*np.array of float [N_interpolations x N_params]*) – Array containing the parameters the function is evaluated (total array with all parameters)

Returns

res – Interpolation results (subset `params[idx_list, :]`)

Return type

`np.array of float [n_interpolations]`

pynibs.neuron.util module

`pynibs.neuron.util.DI_wave(t, intensity, t0=5, dt=1.4, width=0.25)`

Determines cortical DI waves from TMS

Parameters

- **t** (*ndarray of float [n_t]*) – Time axis in ms
- **intensity** (*float*) – Stimulator intensity w.r.t resting motor threshold (typical range: [0 ... 2])
- **t0** (*float*) – offset time
- **dt** (*float*) – Spacing of waves in ms
- **width** (*float*) – Width of waves

Returns

y – DI waves

Return type

`ndarray of float [n_t]`

pynibs.pckg package

Subpackages

pynibs.pckg.libeeep package

Submodules

pynibs.pckg.libeeep.pyeeep module

`pynibs.pckg.libeeep.pyeeep.add_channel()`

add channel to channel info handle

`pynibs.pckg.libeeep.pyeeep.add_samples()`

add samples

`pynibs.pckg.libeep.pyeep.close()`
close handle

`pynibs.pckg.libeep.pyeep.close_channel_info()`
close channel info handle

`pynibs.pckg.libeep.pyeep.create_channel_info()`
create channel info handle

`pynibs.pckg.libeep.pyeep.get_channel_count()`
get channel count

`pynibs.pckg.libeep.pyeep.get_channel_label()`
get channel label

`pynibs.pckg.libeep.pyeep.get_channel_reference()`
get channel reference

`pynibs.pckg.libeep.pyeep.get_channel_unit()`
get channel unit

`pynibs.pckg.libeep.pyeep.get_sample_count()`
get sample count

`pynibs.pckg.libeep.pyeep.get_sample_frequency()`
get sample frequency

`pynibs.pckg.libeep.pyeep.get_samples()`
get samples

`pynibs.pckg.libeep.pyeep.get_trigger()`
get samples

`pynibs.pckg.libeep.pyeep.get_trigger_count()`
get trigger count

`pynibs.pckg.libeep.pyeep.get_version()`
get libeep version

`pynibs.pckg.libeep.pyeep.read()`
open libeep file for reading

`pynibs.pckg.libeep.pyeep.write_cnt()`
open libeep cnt file for writing

pynibs.regression package

This holds methods for the TMS-based cortical localization approach as published in [1]

References

Submodules

pynibs.regression.regression module

class `pynibs.regression.regression.Element`(*x*, *y*, *ele_id*, *fun*=<function sigmoid4>, *score_type*='R2', *select_signed_data*=False, *constants*=None, ***kwargs*)

Bases: `object`

Fit Element object class

calc_score()

Determine goodness-of-fit score.

run_fit(*max_nfev=1000*)

Perform data fit with lmfit.

run_select_signed_data()

Selects positive or negative data by performing an initial linear fit by comparing the resulting p-values, slopes and R2 values. Either positive or negative data (w.r.t. x-axis) yielding a fit with a p-value < 0.05, a positive slope and the higher R2 value is used and the remaining data with the other sign is omitted from the analysis

set_constants(*value*)

Sets constants in self.constants and gmodel instance

set_init_vals(*value*)

Sets initial values in self.init_vals and gmodel instance

set_limits(*value*)

Sets limits in self.limits and gmodel instance

Parameters

value (*dict*) – Parameters (keys) to set in self as limits.

set_random_init_vals()

Set random initial values

setup_model()

Setup model parameters (limits, initial values, etc. ...)

`pynibs.regression.regression.fit_elms(elm_idx_list, e_matrix, mep, zap_idx=None, fun=<function sigmoid4>, init_vals=None, limits=None, log_scale=False, constants=None, max_nfev=None, bad_elm_idx=None, score_type='R2', verbose=False)`

Workhorse for Mass-univariate nonlinear regressions on raw MEP_{AMP} ~ E. That is, for each element in *elm_idx_list*, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise r2 score is returned.

Parameters

- **elm_idx_list** (*list of int or np.ndarray*) – List containing the element indices the fit is performed for
- **e_matrix** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field matrix
- **mep** (*np.ndarray of float [n_zaps]*) – Motor evoked potentials for every stimulation
- **zap_idx** (*np.ndarray [n_zaps]*, *default: None*) – Indices of zaps the congruence factor is calculated with (default: all)
- **fun** (*str*) – A function name of `pynibs.exp.Mep` (`exp0`, `sigmoid`)
- **init_vals** (*np.ndarray of dict*) – Dictionary containing the initial values for each element as `np.ndarray [len(elm_idx_list)]`. The keys are the free parameters of *fun*, e.g. “x0”, “amp”, etc
- **limits** (*pd.DataFrame*) – Dictionary containing the limits of each parameter for each element e.g.: `limits[“x0”][elm_idx] = [min, max]`
- **log_scale** (*bool*, *default: False*) – Log-transform data before fit (necessary for functions defined in the log domain)
- **constants** (*dict of <string>:<num>*, *default: None*) – key:value pair of model parameters not to optimize.

- **max_nfev** (*int*, *default: None*) – Max fits, passed to `model.fit()` as `max_nfev=max_nfev*len(x)`.
- **bad_elm_idx** (*np.ndarray*) – Indices of elements not to fit, with indices corresponding to indices (not values) of `elm_idx_list`
- **score_type** (*str*, *default: "R2"*) – Goodness of fit measure; Choose SR for non-linear fits and R2 or SR for linear fits: * "R2": R2 score (Model variance / Total variance) [0, 1] for linear models; 0: bad fit; 1: perfect fit * "SR": Relative standard error of regression (1 - Error 2-norm / Data 2-norm) [-inf, 1]; 1: perfect fit
- **verbose** (*bool*, *default: False*) – Print verbosity information

Returns

- **r2** (*np.ndarray of float [n_roi, 1]*) – R2 for each element in `elm_idx_list`
- **best_values** (*np.ndarray of object*) – Fit parameters returned from the optimizer

`pynibs.regression.regression.get_bad_elms(x, y, method='lstsq', verbose=False)`

This does an element-wise fast linear regression fit to identify bad elements. Bad is defined here as a negative slope.

x

[*np.ndarray of float [n_zaps x n_ele]*] Electric field matrix

y

[*np.ndarray of float [n_zaps]*] Motor evoked potentials for every stimulation

method

[*str*, *default: "lstsq"*] Which method to use. (`numpy.linalg.lstsq`, (`scipy.stats.linregress`, or `pinv`

verbose

[*bool*, *default: False*] Print verbosity information

Returns

idx – Indices of bad elements

Return type

np.ndarray

`pynibs.regression.regression.get_model_init_values(fun, elm_idx_list, e_matrix, mep, mask_e_field=None, rem_empty_hints=True)`

Calc appropriate init, limit, and max values for models fits depending on the data. If negative and positive x-data is present in case of e.g. normal component values are set according to the side (positive or negative) where more values are present. When more positive x-axis values are present, negative x-axis values will be ignored. When more negative x-axis values are present, the absolute values will be taken and the positive values are ignored.

Only parameters for sigmoid* are optimized.

Parameters

- **fun** (*pyfempp.exp.Mep*) – IO curve function object
- **elm_idx_list** (*np.ndarray of int*) – Array containing the element indices the fit is performed for
- **e_matrix** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field matrix
- **mep** (*np.ndarray of float [n_zaps]*) – Motor evoked potentials for every stimulation
- **mask_e_field** (*np.ndarray of bool [n_zaps x n_ele]*, *default: None*) – Mask indicating for which e-field (and mep) values the fit is performed for. Changes for normal component in each element because of the sign and p-values. If None, all data is used in each element.

- **rem_empty_hints** (*bool*, *default: True*) – Remove any non-filled param hints from limits dict.

Returns

- **log_scale** (*bool*) – Log scale
- **limits** (*dict of list [n elm_index_list]*) – Element-wise limit values for function fitting.
- **init_vals** (*dict of list [n elm_index_list]*) – Element-wise init values for function fitting.
- **max_vals_refit** (*dict of list [n elm_index_list]*) – Element-wise perturbation range for refitting function.

`pynibs.regression.regression.init(l, zap_lists, res_fn)`

Pool init function to use with `regression_nl_hdf5_single_core_write`

Parameters

- **l** (*multiprocessing.Lock()*) –
- **zap_lists** (*list of list of int*) – Which zaps to compute.
- **res_fn** (*str*) – .hdf5 fn

`pynibs.regression.regression.logistic_regression()`

Some ideas on how to improve regression approach

1. De-log data

Data range has to be transformed to a reasonable range. For a full sigmoid, -10:10 looks ok

```
sig <- function(z) {  
  return( 1 / (1 + exp(-z)))  
}
```

```
desig <- function(x) {  
  return(- log((1/x) - 1))  
}
```

This might be a reasonable fast approach, but the parameter range has to be estimated. Maybe remove some outliers?

2. fit logistic regression to raw data `scipy.optimize` provides `fit_curve()`, which does OLS-ish fitting to a given function <https://stackoverflow.com/questions/54376900/fit-sigmoid-curve-in-python>

I expect this to be rather slow.

3. Use the `sklearn logistic_regression` classifier and access raw fit data The `logistic_regression` is implemented as a classifier, maybe it's possible to use its regression fit results. Implementation should be pretty fast.

`pynibs.regression.regression.nl_hdf5(elm_idx_list=None, fn_reg_hdf5=None, qoi_path_hdf5=None, e_matrix=None, mep=None, fun=<function sigmoid4>, zap_idx=None, n_cpu=4, con=None, n_refit=50, return_fits=False, score_type='R2', verbose=False, pool=None, refit_discontinuities=True)`

Mass-univariate nonlinear regressions on raw MEP_{AMP} ~ E. That is, for each element in `elm_idx_list`, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise r2 score is returned. The function reads the precomputed array of E-MEP data from an .hdf5 file.

Parameters

- **elm_idx_list** (*np.ndarray of int*) – List containing the element indices the fit is performed for
- **fn_reg_hdf5** (*str*) – Filename (incl. path) containing the precomputed E-MEP dataframes
- **qoi_path_hdf5** (*Union[str, list[str]]*) – Path in .hdf5 file to dataset of electric field qoi e.g.: ["E", "E_norm", "E_tan"]

- **e_matrix** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field matrix
- **mep** (*np.ndarray of float [n_zaps]*) – Motor evoked potentials for every stimulation
- **zap_idx** (*np.array [n_zaps], default: None*) – Indices of zaps the congruence factor is calculated with (default: all)
- **fun** (*pynibs.exp.Mep function*) – A function of pynibs.exp.Mep (exp0, sigmoid)
- **n_cpu** (*int*) – Number of threads
- **con** (*np.ndarray of float [n_roi, 3 or 4], default: None*) – Connectivity matrix of ROI (needed in case of refit because of discontinuity check)
- **n_refit** (*int, default: 50*) – Maximum number of refits of zero elements. No refit is applied in case of n_refit = 0.
- **return_fits** (*bool, default: False*) – Return fit objects containing the parameter estimates
- **score_type** (*str, default: "R2"*) – Error measure of fit: * "R2": R2 score (Model variance / Total variance); linear fits: [0, 1], 1 ... perfect fit * "SR": Relative standard error of regression (1 - Error 2-norm / Data 2-norm); [-Inf, 1], 1 ... perfect fit
- **verbose** (*bool, default: False*) – Plot output messages
- **pool** (*multiprocessing.Pool()*) – pool instance to use.
- **refit_discontinuities** (*bool, default: True*) – Run refit for discontinuous elements at the end

Returns

r2 – R2 for each element in elm_idx_list

Return type

np.ndarray of float [n_roi, n_qoi]

```
pynibs.regression.regression.nl_hdf5_single_core(zap_idx, elm_idx_list, fn_reg_hdf5=None,
                                                qoi_path_hdf5=None, e_matrix=None,
                                                mep=None, fun=<function sigmoid4>,
                                                con=None, n_refit=50, return_fits=False,
                                                constants=None, verbose=False, seed=None,
                                                rem_bad_elms=True,
                                                return_e_field_stats=True)
```

Mass-univariate nonlinear regressions on raw MEP_{AMP} ~ E. That is, for each element in elm_idx_list, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise r2 score is returned. The function reads the precomputed array of E-MEP data from an .hdf5 file.

Parameters

- **elm_idx_list** (*np.ndarray of int*) – List containing the element indices the fit is performed for
- **fn_reg_hdf5** (*str*) – Filename (incl. path) containing the precomputed E-MEP dataframes
- **qoi_path_hdf5** (*str or list of str*) – Path in .hdf5 file to dataset of electric field qoi e.g.: ["E", "E_norm", "E_tan"]
- **e_matrix** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field matrix
- **mep** (*np.ndarray of float [n_zaps]*) – Motor evoked potentials for every stimulation
- **zap_idx** (*np.array [n_zaps], default: None*) – Indices of zaps the congruence factor is calculated with (default: all)

- **fun** (*function object*) – A function of `pynibs.exp.Mep` (`exp0`, `sigmoid`)
- **con** (*np.ndarray of float [n_roi, 3 or 4], default: None*) – Connectivity matrix of ROI (needed in case of refit because of discontinuity check)
- **n_refit** (*int, default: 50*) – Maximum number of refits of zero elements. No refit is applied in case of `n_refit = 0`.
- **return_fits** (*bool, default: False*) – Return fit objects containing the parameter estimates
- **constants** (*dict of <string>:<num>, default: None*) – key:value pair of model parameters not to optimize.
- **verbose** (*bool, default: False*) – Plot output messages
- **seed** (*int, default: None*) – Seed to use.
- **rem_bad_elms** (*bool, default: True*) – Remove elements based on a fast linear regression slope estimation
- **return_e_field_stats** (*bool, default: True*) – Return some stats on the efield variance

Returns

r2 – R2 for each element in `elm_idx_list`

Return type

`np.ndarray of float [n_roi, n_qoi]`

```
pynibs.regression.regression.nl_hdf5_single_core_write(i, elm_idx_list, fn_reg_hdf5=None,
                                                       qoi_path_hdf5=None, e_matrix=None,
                                                       mep=None, fun=<function sigmoid4>,
                                                       con=None, n_refit=50,
                                                       return_fits=False, constants=None,
                                                       verbose=False, seed=None,
                                                       stepdown=False, score_type='R2',
                                                       return_progress=False, geo=None)
```

```
pynibs.regression.regression.regress_data(e_matrix, mep, elm_idx_list=None, element_list=None,
                                           fun=<function sigmoid4>, n_cpu=4, con=None,
                                           n_refit=50, zap_idx=None, return_fits=False,
                                           score_type='R2', verbose=False, pool=None,
                                           refit_discontinuities=True, select_signed_data=False,
                                           mp_context='fork', **kwargs)
```

Mass-univariate nonlinear regressions on raw MEP_{AMP} ~ E. That is, for each element in `elm_idx_list`, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise R2 score is returned. The function reads the precomputed array of E-MEP data from an `.hdf5` file.

Parameters

- **e_matrix** (*np.ndarray of float*) – (n_zaps, n_ele) Electric field matrix
- **mep** (*np.ndarray of float*) – (n_zaps,) Motor evoked potential for each stimulation
- **elm_idx_list** (*np.ndarray of int or list of int*) – (n_zaps,) List containing the element indices the fit is performed for
- **element_list** (*list of Element object instances, optional*) – [n_ele] `pynibs.Element` objects ot skip initialization here.
- **fun** (*pynibs.exp.Mep, default: pynibs.sigmoid4*) – A `pynibs.exp.Mep` function (`exp0`, `sigmoid`, `sigmoid4`, ...)
- **n_cpu** (*int*) – Number of threads, if `n_cpu=1` no parallel pool will be opened and all calculations are done in serial

- **con** (*np.ndarray of float, optional*) – (*n_ele*, 3 or 4) Connectivity matrix of ROI. Needed in case of refit for discontinuity checks
- **n_refit** (*int, default: 50*) – Maximum number of refits of zero elements. No refit is applied in case of *n_refit* = 0.
- **zap_idx** (*np.ndarray of int or list of int, optional*) – Which e/mep pairs to use.
- **return_fits** (*bool, optional*) – Return fit objects containing the parameter estimates
- **score_type** (*str, default: "R2"*) – Error measure of fit: * "R2": R2 score (Model variance / Total variance); linear fits: [0, 1], 1 ... perfect fit * "SR": Relative standard error of regression (1 - Error 2-norm / Data 2-norm); [-Inf, 1], 1 ... perfect fit * "rho": Spearman correlation coefficient [-1, 1]; finds any monotonous correlation (0 means no correlation)
- **verbose** (*bool, default: False*) – Plot output messages
- **pool** (*multiprocessing.Pool()*) – pool instance to use
- **refit_discontinuities** (*bool, default: True*) – Refit discontinuous elements. If True, provide *_con_*
- **mp_context** (*str, default: "fork"*) – Controls the method the sub-processes of the multiprocessing pool (in case of *n_cpu* > 1) are launched. * *fork*: (only supported by Unix) mp processes diverge from the main process,

the entire stack, variables and other resources are copied over. From the docs: "The child process, when it begins, is effectively identical to the parent process. All resources of the parent are inherited by the child process. Note that safely forking a multithreaded process is problematic."
- *spawn*: (supported by Window and Unix) mp processes are launched in an entirely new Python interpreter as separate processes. Variables are copied other resources are freshly instantiated. From the docs: "In particular, unnecessary file descriptors and handles from the parent process will not be inherited. Starting a process using this method is rather slow compared to using *fork* or *forkserver*."
- ****kwargs** – Passed on to *pynibs.Element()* to set fit parameters.

Returns

- **score** (*np.ndarray of float (n_roi, n_qoi)*) – Score for each element.
- **best_values** (*list of dict (n_ele)*) – List of parameter fits, only return if *return_fits=True*.

pynibs.regression.regression.ridge_from_hdf5(*elm_idx_list*, *fn_reg_hdf5*, *qoi_path_hdf5*, *zap_idx=None*)

Mass-univariate ridge regressions on raw MEP_{AMP} ~ E. That is, for each element in *elm_idx_list*, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise *sklearn.metrics.regression.r2_score* is returned. The function reads the precomputed array of E-MEP data from an .hdf5 file. Always uses all cores of a machine!

elm_idx_list

[list of int] List containing the element indices the fit is performed for

fn_hdf5

[str] Filename (incl. path) containing the precomputed E-MEP dataframes

qoi_path_hdf5

[str] Path in .hdf5 file to dataset of electric field qoi

zap_idx

[np.ndarray [n_zaps], default: None] Indices of zaps the congruence factor is calculated with (default: all)

Returns

r2 – R^2 for each element in elm_idx_list

Return type

np.ndarray of float [n_roi, n_datasets]

`pynibs.regression.regression.sing_elm_fitted(elm_idx_list, mep_lst, mep_params, e, alpha=1000, n_samples=100)`

Mass-univariate ridge regressions on fitted MEP_{AMP} ~ E. That is, for each element in elm_idx_list, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise sklearn.metrics.regression.r2_score is returned.

elm_idx_list: np.ndarray [chunksizes]

List of element indices, the congruence factor is computed for

mep_lst: list of Mep object instances [n_cond]

List of fitted Mep object instances for all conditions (see exp.py for more information of Mep class)

mep_params: np.ndarray of float [n_mep_params_total]

List of all mep parameters of curve fits used to calculate the MEP (accumulated into one array) (e.g.: [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...])

e: np.ndarray of float with e.shape == (n_elm, n_cond, n_qoi)

array of the electric field to compute the r2 factor for, e.g. (e_mag, e_norm, e_tan)

n_samples

[int, default=100] Number of data points to generate discrete mep and e curves

Returns

r2 – R^2 for each element in elm_idx_list

Return type

np.ndarray of float [n_roi, n_datasets]

`pynibs.regression.regression.sing_elm_raw(elm_idx_list, mep_lst, mep_params, e, alpha=1000)`

Mass-univariate ridge regressions on raw MEP_{AMP} ~ E. That is, for each element in elm_idx_list, it's E (mag | norm | tan) for each zap regressed on the raw MEP amplitude. An element wise sklearn.metrics.regression.r2_score is returned.

elm_idx_list: np.ndarray [chunksizes]

List of element indices, the congruence factor is computed for

mep: list of Mep object instances [n_cond]

List of fitted Mep object instances for all conditions (see exp.py for more information of Mep class)

mep_params: np.ndarray of float [n_mep_params_total]

List of all mep parameters of curve fits used to calculate the MEP (accumulated into one array) (e.g.: [mep_#1_para_#1, mep_#1_para_#2, mep_#1_para_#3, mep_#2_para_#1, mep_#2_para_#1, ...])

e: np.ndarray of float with e.shape == (n_elm, n_cond, n_qoi)

array of the electric field to compute the r2 factor for, e.g. (e_mag, e_norm, e_tan)

Returns

r2 – R^2 for each element in elm_idx_list

Return type

np.ndarray of float [n_roi, n_datasets]

`pynibs.regression.regression.single_fit(x, y, fun)`

Performs a single fit and returns fit object.

Parameters

- **x** (*ndarray of float*) – x-values.
- **y** (*ndarray of float*) – y-values.
- **fun** (*function*) – Function for fitting.

Returns

fit – Fit object.

Return type

gmodel fit object

`pynibs.regression.regression.stepdown_approach(zap_idx, elm_idx_list, fn_reg_hdf5=None, qoi_path_hdf5=None, e_matrix=None, mep=None, fun=<function sigmoid4>, con=None, n_refit=50, return_fits=False, constants=None, verbose=False, seed=None, rem_bad_elms=True, return_e_field_stats=True, score_type='R2', return_progress=False, smooth_data=True, geo=None)`

Mass-univariate nonlinear regressions on raw MEP_{AMP} ~ E in a stepdown manner to speed up computation.

Initially, one set of fits is done for the complete dataset. Afterwards, the best 1% of the elements are used as initial fitting parameters for their neighboring elements. Then, neighboring elements are fitted accordingly and iteratively. Finally, discontinuous elements are refitted until a smooth map is found or n_refit is hit.

Can be sped up with rem_bad_elms that computes a fast linear fit to identify elements with a negative slope.

The function reads the precomputed array of E-MEP data from an .hdf5 file.

Parameters

- **elm_idx_list** (*np.ndarray of int*) – List containing the element indices the fit is performed for
- **fn_reg_hdf5** (*str*) – Filename (incl. path) containing the precomputed E-MEP dataframes
- **qoi_path_hdf5** (*str or list of str*) – Path in .hdf5 file to dataset of electric field qoi e.g.: ["E", "E_norm", "E_tan"]
- **e_matrix** (*np.ndarray of float [n_zaps x n_ele] | [n_zapid x n_ele]*) – Electric field matrix
- **mep** (*np.ndarray of float [n_zaps]*) – Motor evoked potentials for every stimulation
- **zap_idx** (*np.array [n_zaps], default: None*) – Indices of zaps the congruence factor is calculated with (default: all)
- **fun** (*function object*) – A function of pynibs.exp.Mep (exp0, sigmoid)
- **con** (*np.ndarray of float [n_elm_roi, 3 or 4], default: None*) – Connectivity matrix of ROI (needed in case of refit because of discontinuity check)
- **n_refit** (*int, default: 50*) – Maximum number of refits of zero elements. No refit is applied in case of n_refit = 0.
- **return_fits** (*bool, default: False*) – Return fit objects containing the parameter estimates
- **constants** (*dict of <string>:<num>, default: None*) – key:value pair of model parameters not to optimize.

- **verbose** (*bool*, *default*: *False*) – Plot output messages
- **seed** (*int*, *default*: *None*) – Seed to use.
- **rem_bad_elms** (*bool*, *default*: *True*) – Remove elements based on a fast linear regression slope estimation
- **return_e_field_stats** (*bool*, *default*: *True*) – Return some stats on the efield variance
- **score_type** (*str*, *default*: *"R2"*) – Error measure of fit: * *"R2"*: R2 score (Model variance / Total variance); linear fits: [0, 1], 1 ... perfect fit * *"SR"*: Relative standard error of regression (1 - Error 2-norm / Data 2-norm); [-Inf, 1], 1 ... perfect fit * *"rho"*: Spearman correlation coefficient [-1, 1]; finds any monotonous correlation (0 means no correlation)
- **return_progress** (*bool*, *default*: *False*) – Return c maps for all steps to allow visualization over e-fitting over timesteps.
- **smooth_data** (*bool*, *default*: *False*) – Smooth c-map as final step.
- **geo** (*object*, *optional*) – Geometriy data.

Returns

r2

[np.ndarray of float [n_roi, n_qoi]] R2 for each element in elm_idx_list

best_values: list of dict, optional

fit information

stats

[dict, optional]

'mc': float, optional

Mutual coherence for e fields

'sv_rat'

[float, optional] SVD singular value ratio

progress : cmaps for each step

Return type

dict

```
pynibs.regression.regression.workhorse_element_init(ele_id, e_matrix, mep, fun, score_type,  
                                                    select_signed_data, constants, **kwargs)
```

Workhorse to initialize Elements.

```
pynibs.regression.regression.workhorse_element_run_fit(element, max_nfev=10)
```

Workhorse to run single Element fit. If status is False, the element will not be fitted.

```
pynibs.regression.regression.write_regression_hdf5(fn_exp_hdf5, fn_reg_hdf5, qoi_path_hdf5,  
                                                  qoi_phys, e_results_folder, qoi_e, roi_idx,  
                                                  conds_exclude)
```

Reads the stimulation intensities from the experiment.hdf5 file. Reads the qoi from the experiment.hdf5 file. Reads the electric fields from the electric field folder. Weights the electric field voxel wise with the respective intensities and writes an .hdf5 file containing the preprocessed data (pandas dataframe).

fn_exp_hdf5: str

Filename of the experiment.hdf5 file

fn_reg_hdf5: str

Filename of output regression.hdf5 file

qoi_path_hdf5: str

Path in experiment.hdf5 file pointing to the pandas dataframe containing the qoi (e.g.: "phys_data/postproc/EMG")

qoi: str

Name of QOI the congruence factor is calculated with (e.g.: “p2p”)

fn_e_results: str

Folder containing the electric fields (e.g.: “/data/pt_01756/probands/13061.30/results/electric_field/1”)

qoi_e: str or list of str

Quantities of the electric field used to calculate the congruence factor (e.g. [“E”, “E_norm”, “E_tan”])

Has to be included in e.hdf5 -> e.g.: “data/midlayer/roi_surface/1/E”

roi_idx: int

ROI index

conds_exclude: str or list of str

Conditions to exclude

Returns

<File> – File containing the intensity (current) scaled E-fields of the conditions in the ROI.

Saved in datasets with the same name as qoi_e [“E”, “E_norm”, “E_tan”]

Return type

.hdf5 file

pynibs.regression.score_types module**pynibs.util package****Submodules****pynibs.util.quality_measures module**

`pynibs.util.quality_measures.c_map_comparison(c1, c2, t1, t2, nodes, tris)`

Compares two c-maps in terms of NRMSD and calculates the geodesic distance between the hotspots.

Parameters

- **c1** (*np.ndarray of float [n_ele]*) – First c-map
- **c2** (*np.ndarray of float [n_ele]*) – Second c-map (reference)
- **t1** (*np.ndarray of float [3]*) – Coordinates of the hotspot in the first c-map
- **t2** (*np.ndarray of float [3]*) – Coordinates of the hotspot in the second c-map
- **nodes** (*np.ndarray of float [n_nodes x 3]*) – Node coordinates
- **tris** (*np.ndarray of float [n_tris x 3]*) – Connectivity of ROI elements

Returns

- **nrmsd** (*float*) – Normalized root-mean-square deviation between the two c-maps in (%)
- **gdist** (*float*) – Geodesic distance between the two hotspots in (mm)

`pynibs.util.quality_measures.calc_tms_motion_params(coil_positions, reference=None)`

Computes motion parameters for a set of `coil_positions`, i.e., coil shifts in [mm] in RAS coordinate system and rotations (pitch, roll, yaw) in [°]. Motion is computed w.r.t. the first (‘absolute’) and to the previous (‘relative’) stimulation.

Position shifts are quantified with respect to the subject/nifti-specific RAS coordinate system. Rotational changes are quantified with respect to the coil axes as follows: - pitch: rotation around left/right axis of coil - roll: rotation around coil handle axis - yaw: rotation around axis from center of coil towards head

Motion parameters for first coil position are set to 0.

Parameters

- **coil_positions** (*np.ndarray* of *float*) – (4, 4, n_pulses).
- **reference** (*np.ndarray* of *float*, *optional*) – (4, 4) Reference coil placement. If None (default), the first placement from **coil_positions** is used.

Returns

- **pos_diff_abs** (*np.ndarray*) – (3, n_pulses) Absolute position differences (R, A, S).
- **euler_rots_abs** (*np.ndarray*) – (3, n_pulses) Absolute rotation angles in euler angles (alpha, beta, gamma).
- **pos_diff_rel** (*np.ndarray*) – (3, n_pulses) Relative position differences (R, A, S).
- **euler_rots_rel** (*np.ndarray*) – (3, n_pulses) Relative rotation angles in euler angles (alpha, beta, gamma).

`pynibs.util.quality_measures.compute_pcd(delta_pos, delta_rot, skin_cortex_distance=20)`

Computes $\Delta_{Pulsewise} \Delta_{Coil} \Delta_{Displacements}$ (PCD) based on 3 position parameters (**delta_pos**) and 3 rotation parameters (**delta_rot**). The coil rotations (in euler angles) are transformed into a positional change projected on the cortex based on **skin_cortex_distance** as a proxy for the (local) change of the stimulation.

delta_pos and **delta_rot** are expected to quantify motion w.r.t. the target coil position/rotation, for example the absolute deltas to the first stimulation.

Example

```
# get TriggerMarkers from a Localite session
mats = pynibs.read_triggermarker_localite(tm_fn)[0]

# calculate absolute and relative coil displacements
delta_pos_abs, delta_rot_abs, delta_pos_rel, delta_rot_rel = pynibs.calc_tms_motion_params(mats)

# Compute PCD
pcd, delta_pos, delta_rot = pynibs.compute_pcd(delta_pos_abs, delta_rot_abs)

# plot movement
axes = pynibs.plot_tms_motion_parameter(pos_diff_rel, euler_rots_rel, pcd)
matplotlib.pyplot.show()
```

Parameters

- **delta_pos** (*np.ndarray*) – (3, n_pulses) Absolute position differences (R, A, S).
- **delta_rot** (*np.ndarray*) – (3, n_pulses) Absolute rotation angles in euler angles (alpha, beta, gamma).
- **skin_cortex_distance** (*int*, *default: 20*) – Cortical depth of target to adjust coil rotations for.

Returns

- **pcd** (*np.ndarray*) – Pulsewise coil displacements.
- **delta_pos** (*np.ndarray*) – (n_pulses,) $\sum(\text{abs}(\text{delta_pos}))$ per pulse.
- **delta_rot** (*np.ndarray*) – (n_pulses,) $\sum(\text{abs}(\text{delta_rot projected by skin_cortex_distance}))$ per pulse.

`pynibs.util.quality_measures.euclidean_dist(nodes, tris, source, source_is_node=True)`

Returns **euclidean_dist** distance of all nodes to source node (tria).

This is just a wrapper for the **gdist** package.

Example

```
with h5py.File(fn, 'r') as f:
    tris = f['mesh/elm/triangle_number_list'][:]
    nodes = f['mesh/nodes/node_coord'][:]
    nodes_dist_euc, tris_dist_euc = euclidean_dist(nodes, tris, 3017)

pynibs.write_data_hdf5(data_fn,
                      data=[tris_dist_euc, nodes_dist_euc],
                      data_names=["tris_dist_euc", "nodes_dist_euc", ])
pynibs.write_xdmf(data_fn, hdf5_geo_fn=fn)
```

Parameters

- **nodes** (`np.ndarray(n_nodes, 3)`) –
- **tris** (`np.ndarray(n_tris, 3)`) –
- **source** (`np.ndarray(int)` or `int`) – geodesic distances of all nodes to this will be computed
- **source_is_node** (`bool`) – Is source a node idx or a tr idx

Returns

- **nodes_dist** (`np.ndarray(n_nodes,)`)
- **tris_dist** (`np.ndarray(n_tris,)`)

`pynibs.util.quality_measures.geodesic_dist(nodes, tris, source, source_is_node=True)`

Returns geodesic distance of all nodes to source node (or tri).

This is just a wrapper for the `gdist` package.

Example

```
with h5py.File(fn, 'r') as f:
    tris = f['mesh/elm/triangle_number_list'][:]
    nodes = f['mesh/nodes/node_coord'][:]
    nodes_dist_ged, tris_dist_ged = geodesic_dist(nodes, tris, 3017)

pynibs.write_data_hdf5(data_fn,
                      data=[tris_dist_ged, nodes_dist_ged],
                      data_names=["tris_dist_ged", "nodes_dist_ged"])
pynibs.write_xdmf(data_fn, hdf5_geo_fn=fn)
```

Parameters

- **nodes** (`np.ndarray(n_nodes, 3)`) –
- **tris** (`np.ndarray(n_tris, 3)`) –
- **source** (`np.ndarray(int)` or `int`) – Geodesic distances of all nodes (or tri) to this will be computed
- **source_is_node** (`bool`) – Is source a node idx or a tr idx

Returns

- **nodes_dist** (`np.ndarray(n_nodes,)`)
- **tris_dist** (`np.ndarray(n_tris,)`)

`pynibs.util.quality_measures.nrmsd(array, array_ref, error_norm='relative', x_axis=False)`

Determine the normalized root-mean-square deviation between input data and reference data.

$$\text{nrmsd} = \text{np.sqrt}(1.0 / \text{n_points} * \text{np.sum}((\text{data} - \text{data_ref}) ** 2)) / (\text{max}(\text{array_ref}) - \text{min}(\text{array_ref}))$$

Parameters

- **array** (`np.ndarray`) – input data [(x), y0, y1, y2 ...].
- **array_ref** (`np.ndarray`) – reference data [(x_ref), y0_ref, y1_ref, y2_ref ...]. if `array_ref` is 1D, all sizes have to match.

- **error_norm** (*str*, *optional*, *default="relative"*) – Decide if error is determined “relative” or “absolute”.
- **x_axis** (*bool*, *default: False*) – If True, the first column of array and array_ref is interpreted as the x-axis, where the data points are evaluated. If False, the data points are assumed to be at the same location.

Returns

normalized_rms – ([array.shape[1]]) Normalized root-mean-square deviation between the columns of array and array_ref.

Return type

np.ndarray of *float*

pynibs.util.quality_measures.**nrmse**(array, array_ref, x_axis=False)

Determine the normalized root-mean-square deviation between input data and reference data.

```
nrmse = np.linalg.norm(array - array_ref) / np.linalg.norm(array_ref)
```

Parameters

- **array** (*np.ndarray*) – input data [(x), y0, y1, y2 ...].
- **array_ref** (*np.ndarray*) – reference data [(x_ref), y0_ref, y1_ref, y2_ref ...]. if array_ref is 1D, all sizes have to match.
- **error_norm** (*str*, *optional*, *default="relative"*) – Decide if error is determined “relative” or “absolute”.
- **x_axis** (*bool*, *default: False*) – If True, the first column of array and array_ref is interpreted as the x-axis, where the data points are evaluated. If False, the data points are assumed to be at the same location.

Returns

nrmse – ([array.shape[1]]) Normalized root-mean-square deviation between the columns of array and array_ref.

Return type

np.ndarray of *float*

pynibs.util.quality_measures.**plot_tms_motion_parameter**(pos_diff, euler_rots, pcd=None, fname=None)

Plots TMS coil motion parameters.

Parameters

- **pos_diff** (*np.ndarray*) – (3, n_pulses) Position differences (R, A, S).
- **euler_rots** (*np.ndarray*) – (3, n_pulses) Rotation angles in euler angles (alpha, beta, gamma).
- **pcd** (*np.ndarray*, *optional*) – (n_pulses,) pulsewise coil displacements.
- **fname** (*str*, *optional*) – Filename to save plot.

Returns

axes – Figure axes.

Return type

matplotlib.pyplot.axes

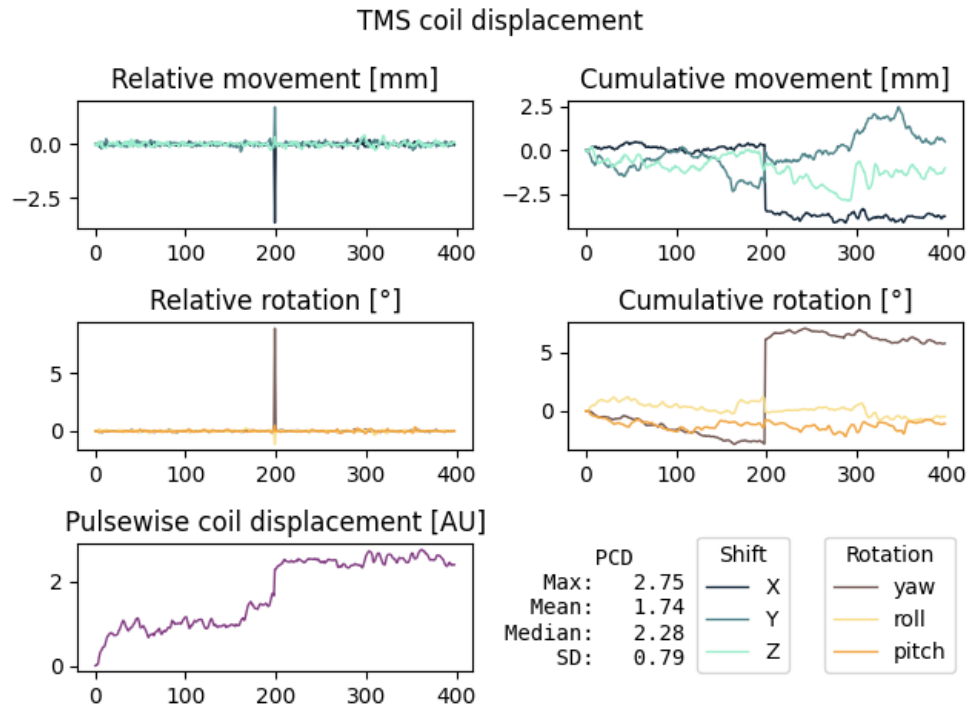


Fig. 2: Pulsewise Coil Displacement (PCD) is a compound metric to quantify TMS coil movements. Data for a double (space) cTBS400 protocol is shown (with a break after 200 bursts).

pynibs.util.rotations module

`pynibs.util.rotations.bases2rotmat(v1, v2)`

Computes rotation matrix to rotate basis 1 (v1) to another basis (v2)

Parameters

- **v1** (`np.ndarray`) – (3, 3) original basis
- **v2** (`np.ndarray`) – (3, 3) rotated basis

Returns

rot_mat – (3, 3) rotation matrix to go from v1 to v2

Return type

`np.ndarray`

`pynibs.util.rotations.euler_angles_to_rotation_matrix(theta)`

Determines the rotation matrix from the three Euler angles $\theta = [\text{Psi}, \text{Theta}, \text{Phi}]$ (in rad), which rotate the coordinate system in the order z, y', x''.

Parameters

theta (`np.ndarray [3]`) – Euler angles in rad

Returns

r – Rotation matrix (z, y', x'')

Return type

`np.ndarray [3 x 3]`

`pynibs.util.rotations.normalize_rot(rot)`

Normalize rotation matrix.

Parameters

rot (`np.ndarray of float [3 x 3]`) – Rotation matrix

Returns

rot_norm – Normalized rotation matrix

Return type

np.ndarray of float [3 x 3]

pynibs.util.rotations.**quat_rotation_angle**(q)

Computes the rotation angle from the quaternion in rad.

Parameters

q (np.ndarray of float) – Quaternion, either only the imaginary part (length=3) [qx, qy, qz] or the full quaternion (length=4) [qw, qx, qy, qz]

Returns

alpha – Rotation angle of quaternion in rad

Return type

float

pynibs.util.rotations.**quat_to_rot**(q)

Computes the rotation matrix from quaternions.

Parameters

q (np.ndarray of float) – Quaternion, either only the imaginary part (length=3) or the full quaternion (length=4)

Returns

rot – (3 x 3) Rotation matrix, containing the x, y, z axis in the columns

Return type

np.ndarray of float

pynibs.util.rotations.**quaternion_conjugate**(q)

<https://stackoverflow.com/questions/15425313/inverse-quaternion>

Parameters

q –

Returns

Return type

pynibs.util.rotations.**quaternion_diff**(q1, q2)

<https://math.stackexchange.com/questions/2581668/> error-measure-between-two-rotations-when-one-matrix-might-not-be-a-valid-rotatio

Parameters

- **q1** –
- **q2** –

Returns

Return type

pynibs.util.rotations.**quaternion_inverse**(q)

<https://stackoverflow.com/questions/15425313/inverse-quaternion>

Parameters

q –

Returns

Return type

`pynibs.util.rotations.rootate_matsimnibs_euler(axis, angle, matsimnibs, metric='rad')`

Rotates a matsimnibs matrix around axis by angle

Parameters

- **axis** (*str*) – One of ('x','y','z').
- **angle** (*float*) – Angle to rotate system around axis.
- **matsimnibs** (*np.ndarray*) – (4, 4) SimNIBS matsimnibs coil orientation and position matrix.
- **metric** (*str*, *default*: 'rad') – One of ('rad', 'deg'). If deg, angle is transformed to radians.

Returns

rotated_matsimnibs – (4, 4) Rotated system.

Return type

np.ndarray

`pynibs.util.rotations.rot_to_quat(rot)`

Computes the quaternions from rotation matrix. (see e.g. <http://www.euclideanspace.com/maths/geometry/rotations/conversions/matrixToQuaternion/>)

Parameters

rot (*np.ndarray of float*) – (3 x 3) Rotation matrix, containing the x, y, z axis in the columns

Returns

q – Quaternion, full (length=4)

Return type

np.ndarray of float

`pynibs.util.rotations.rotation_matrix_to_euler_angles(r)`

Calculates the euler angles theta = [Psi, Theta, Phi] (in rad) from the rotation matrix R which, rotate the coordinate system in the order z, y', x". (<https://www.learnopencv.com/rotation-matrix-to-euler-angles/>)

Parameters

r (*np.array [3 x 3]*) – Rotation matrix (z, y', x")

Returns

theta – Euler angles in rad

Return type

np.array [3]

pynibs.util.simnibs module

`pynibs.util.simnibs.calc_e_in_midlayer_roi(e, roi, mesh=None, qoi=None, layer_gm_wm_info=None)`

This is to be called by Simnibs as postprocessing function per FEM solve.

Parameters

- **e** (*np.ndarray or tuple*) – E to interpolate. Used to be (v, dAdt).
- **roi** (*pynibs.roi.RegionOfInterestSurface*) –
- **mesh** (*simnibs.msh.Mesh*) –
- **qoi** (*list of str*) – List of identifiers of the to-be calculated quantities of interest.
- **layer_gm_wm_info** (*dict[str, dict[str, np.ndarray]]*) – For each layer defined in the mesh (outer dict key: layer_id), provide pre-computed geometrical information as a dictionary (outer dict value):

- key: `gm_nodes`, For each layer node, the corresponding point on the GM surface.
- key: `wm_nodes`, For each layer node, the corresponding point on the WM surface.
- key: `gm_center_distance`, The distance between the layer nodes and the corresponding points on the GM.
- key: `wm_center_distance`, The distance between the layer nodes and the corresponding points on the WM.

Returns

`(roi.n_tris, 4)` – `(len(roi.layers)x(roi.layers[idx].surface.n_tris,4))` : `np.vstack((e_mag, e_norm, e_tan, e_angle)).transpose()`

Return type

`np.vstack((e_mag, e_norm, e_tan, e_angle)).transpose()` for the midlayer

`pynibs.util.simmibs.check_mesh(mesh, verbose=False)`

Check a `simmibs.Mesh` for degenerated elements:

- zero surface triangles
- zero volume tetrahedra
- negative volume tetrahedra

Parameters

- **mesh** (*str* or *simmibs.Mesh*) –
- **verbose** (*bool*, *default*: *False*) – Print some verbosity messages.

Returns

- **zero_tris** (*np.ndarray*) – Element indices for zero surface tris (0-indexed)
- **zero_tets** (*np.ndarray*) – Element indices for zero volume tets (0-indexed)
- **neg_tets** (*np.ndarray*) – Element indices for negative volume tets (0-indexed)

`pynibs.util.simmibs.e_field_angle_theta(surface, mesh)`

Compute angle between local the E-field vector and surface vector at the ROI nodes.

Parameters

- **surface** (*simmibs.Msh*) – The surface object representing the ROI.
- **mesh** (*simmibs.Msh*) – The (volumetric) head mesh.

Returns

theta – The angle between local the E-field vector and surface vector for each surface element of the ROI.

Return type

`simmibs.mesh.mesh_io.ElementData`

`pynibs.util.simmibs.e_field_gradient_between_wm_gm(roi_surf, mesh, gm_nodes, wm_nodes, gm_center_distance, wm_center_distance)`

Compute local the E-field gradient at the ROI nodes between the gray and white matter boundary surfaces. Adapted from `neuronibs/cortical_layer.py/add_e_field_gradient_between_wm_gm_field`

Parameters

- **roi_surf** (*simmibs.Msh*) – The surface object representing the ROI.
- **mesh** (*simmibs.Msh*) – SimNIBS headmesh.
- **gm_nodes** (*np.ndarray*, `(3, len(roi_surf.nodes))`) – For each node of ‘roi_surf’ (representing, e.g., a cortical layer) the corresponding point on the gray matter surface. -> as returned by ‘precompute_geo_info_for_layer_field_interpolation’

- **wm_nodes** (*np.ndarray*, (3, *len(roi_surf.nodes)*)) – For each node of ‘roi_surf’ (representing, e.g., a cortical layer) the corresponding point on the white matter surface. -> as returned by ‘precompute_geo_info_for_layer_field_interpolation’
- **gm_center_distance** (*np.ndarray*, (3, *len(roi_surf.nodes)*)) – The distance between the layer nodes and their corresponding point on the gray matter surface. -> as returned by ‘precompute_geo_info_for_layer_field_interpolation’
- **wm_center_distance** (*np.ndarray*, (3, *len(roi_surf.nodes)*)) – The distance between the layer nodes and their corresponding point on the white matter surface. -> as returned by ‘precompute_geo_info_for_layer_field_interpolation’

Returns

e_field_gradient_per_mm – The E-field gradient from the GM to the WM surface normalized to 1 mm with respect to the gray matter thickness. per ROI node

Return type

`simnibs.mesh.mesh_io.ElementData`

`pynibs.util.simnibs.fix_mesh(mesh, verbose=False)`

Fixes `simnibs.Mesh` by removing any zero surface tris and zero volume tets and by fixing negative volume tets.

Parameters

- **mesh** (*str* or *simnibs.Mesh*) – Filename of mesh or mesh object.
- **verbose** (*bool*, *default: False*) – Print some verbosity messages.

Returns

fixed_mesh

Return type

`simnibs.Mesh`

`pynibs.util.simnibs.get_opt_mat(folder, roi=0)`

Load optimal coil position/orientation matsimnibs from SimNIBS online FEM.

`pynibs.util.simnibs.get_skin_cortex_distance(mesh, coords, radius=5)`

Computes the skin-cortex distance (SCD).

Parameters

- **mesh** (*str* or *simnibs.Mesh*) – Mesh object or .msh filename.
- **coords** (*np.ndarray*) – [3,] x,y,z coordinates to compute skin-cortex-distance for.
- **radius** (*float*, *default: 5*) – Spherical radius around coords to include points in for SCD computation.

Returns

- **SCD** (*np.ndarray of float*) – Skin-cortex distance.
- **elm_in_roi** (*np.ndarray of int*) – Element numbers from `mesh.elm.elm_number` that where used to calculate PCD for.

`pynibs.util.simnibs.precompute_geo_info_for_layer_field_interpolation(simnibs_mesh, roi)`

Precomputes geometric properties of the corresponding GM and WM nodes in the ‘simnibs_mesh’ of each node of each layer in ‘roi’.

- The corresponding point on the GM and WM surface to each vertex of te ROI surface are determined (by raycasting and nearest neighbour search as fallback) (interpolation will take place between these nodes)
- The nodes are moved inside the gray matter by 20 % of their total distance from the GM/WM boundary to the midlayer.

- The distance of the relocated GM and WM nodes to the ROI nodes is determined (required to computed the gradient per mm).

Parameters

- **simnibs_mesh** (*simnibs.Mesh*) – The head model volume mesh.
- **roi** (*pynibs.roi.RegionOfInterestSurface*) – The ROI object containing the layers.

Returns

layer_gm_wm_info – For each layer defined in the mesh (outer dict key: *layer_id*), provide pre-computed geometrical information as a dictionary (outer dict value):

- key: *gm_nodes* For each layer node, the corresponding point on the GM surface.
- key: *wm_nodes* For each layer node, the corresponding point on the WM surface.
- key: *gm_center_distance* The distance between the layer nodes and the corresponding points on the GM.
- key: *wm_center_distance* The distance between the layer nodes and the corresponding points on the WM.

Return type

`dict[str, dict[str, np.ndarray]]`

`pynibs.util.simnibs.read_coil_geo(fn_coil_geo)`

Reads a coil .geo file.

Parameters

fn_coil_geo (*str*) – Filename of .geo file created from SimNIBS containing the dipole information

Returns

- **dipole_pos** (*np.ndarray of float*) – (n_dip, 3) Dipole positions (*x*, *y*, *z*).
- **dipole_mag** (*np.ndarray of float*) – (n_dip, 1) Dipole magnitude.

`pynibs.util.simnibs.smooth_mesh(mesh, output_fn, smooth=0.8, approach='taubin', skin_only_output=False, smooth_tissue='skin')`

Smooths the skin compartment of a simnibs mesh. Uses one of three trimesh.smoothing approaches. Because tetrahedra and triangle share the same nodes, this also smooths the volume domain.

Parameters

- **mesh** (*str* or *simnibs.Mesh*) –
- **output_fn** (*str*) –
- **smooth** (*float*, *default:* 0.8) – Smoothing aggressiveness. [0, ..., 1].
- **approach** (*str*, *default:* 'taubin') – Which smoothing approach to use. One of ('taubin', 'laplacian', 'humphrey').
- **smooth_tissue** (*str* or *list of int*, *default:* 'skin') – Which tissue type to smooth. E.g. 'gm' or [2, 1002].
- **skin_only_output** (*bool*, *default:* True) – If true, a skin only mesh is written out instead of the full mesh.

Returns

- **<file>** (*The smoothed mesh.*)

- `.. figure:: ../doc/images/smooth_mesh.png --scale: 50 % :alt: Original and smoothed surfaces and volumes.`

Left: original, spiky mesh. Right: smoothed mesh.

pynibs.util.util module

`pynibs.util.util.add_center(var)`

Adds center to argument list.

Parameters

var (*list of float [2]*) – List containing two values [f1,f2]

Returns

out – List containing the average value in the middle [f1, mean(f1,f2), f2]

Return type

list of float [3]

`pynibs.util.util.bash(command)`

Executes bash command and returns output message in stdout (uses os.popen).

Parameters

command (*str*) – Bash command

Returns

- **output** (*str*) – Output from stdout
- **error** (*str*) – Error message from stdout

`pynibs.util.util.bash_call(command)`

Executes bash command and returns output message in stdout (uses subprocess.Popen).

Parameters

command (*str*) – bash command

`pynibs.util.util.calc_n_network_combs(n_e, n_c, n_i)`

Determine number of combinations if all conditions may be replaced between N_i elements (mixed interaction)

Parameters

- **n_e** (*int*) – Number of elements in the ROI
- **n_c** (*int*) – Number of conditions (I/O curves)
- **n_i** (*int*) – Number of maximum interactions

Returns

n_comb – Number of combinations

Return type

int

`pynibs.util.util.compute_chunks(seq, num)`

Splits up a sequence `_seq_` into `_num_` chunks of similar size. If `len(seq) < num`, `(num-len(seq))` empty chunks are returned so that `len(out) == num`

Parameters

- **seq** (*list of something [N_ele]*) – List containing data or indices, which is divided into chunks
- **num** (*int*) – Number of chunks to generate

Returns

out – num sub-lists of seq with each of a similar number of elements (or empty).

Return type

list of num sublists

`pynibs.util.util.cross_product(A, B)`

Evaluates the cross product between the vector pairs in a and b using pure Python.

Parameters

- **A** (*np.ndarray of float 2 x [N x 3]*) –
- **B** (*np.ndarray of float 2 x [N x 3]*) – Input vectors, the cross product is evaluated between

Returns

c – Cross product between vector pairs in a and b

Return type

np.ndarray of float [N x 3]

`pynibs.util.util.cross_product_einsum2(a, b)`

Evaluates the cross product between the vector pairs in a and b using the double Einstein sum.

Parameters

- **a** (*np.ndarray of float 2 x [N x 3]*) –
- **b** (*np.ndarray of float 2 x [N x 3]*) – Input vectors, the cross product is evaluated between

Returns

c – Cross product between vector pairs in a and b

Return type

np.ndarray of float [N x 3]

`pynibs.util.util.differential_evolution(fobj, bounds, mut=0.8, crossp=0.7, popsize=20, its=1000, **kwargs)`

Differential evolution optimization algorithm

Parameters

- **fobj** (*function object*) – Function to optimize
- **bounds** (*dict*) – Dictionary containing the bounds of the free variables to optimize
- **mut** (*float*) – Mutation factor
- **crossp** (*float*) – Cross population factor
- **popsize** (*int*) – Population size
- **its** (*int*) – Number of iterations
- **kwargs** (*dict*) – Arguments passed to fobj (constants etc...)

Returns

- **best** (*dict*) – Dictionary containing the best values
- **fitness** (*float*) – Fitness value of best solution

`pynibs.util.util.generalized_extreme_value_distribution(x, mu, sigma, k)`

Generalized extreme value distribution

Parameters

- **x** (*ndarray of float [n_x]*) – Events
- **mu** (*float*) – Mean value
- **sigma** (*float*) – Standard deviation

- **k** (*float*) – Shape parameter

Returns

y – Probability density of events

Return type

ndarray of *float* [n_x]

`pynibs.util.util.get_cartesian_product(array_list)`

Generate a cartesian product of input arrays (all combinations).

`cartesian_product = get_cartesian_product(array_list)`

Parameters

array_list (*list of 1D ndarray of float*) – Arrays to compute the cartesian product with

Returns

cartesian_product – Array containing the cartesian products (all combinations of input vectors) (M, len(arrays))

Return type

ndarray of *float*

Examples

```
>>> import pygpc
>>> out = pygpc.get_cartesian_product([[1, 2, 3], [4, 5], [6, 7]])
>>> out
```

`pynibs.util.util.intersection_vec_plan(ray_dir, ray_origin, plane_n, plane_p, eps=1e-06)`

Computes intersection between vector ('ray') and plane.

Parameters

- **ray_dir** (*np.ndarray*) – (3,) (Rotated) vector direction.
- **ray_origin** (*np.ndarray*) – (3,) Any point on the ray.
- **plane_n** (*np.ndarray*) – (3,) Plane normal.
- **plane_p** (*np.ndarray*) – (3,) Any point on the plane.
- **eps** (*float*, *default=1e-6*) – Resolution.

Returns

inters – (3,) Intersection location. (np.inf, np.inf, np.inf) if no intersection.

Return type

np.ndarray

`pynibs.util.util.invert(trans)`

Invert rotation matrix.

Parameters

trans (*np.ndarray of float [3 x 3]*) – Rotation matrix

Returns

rot_inv – Inverse rotation matrix

Return type

np.ndarray of float [3 x 3]

`pynibs.util.util.likelihood_posterior(x, y, fun, bounds=None, verbose=True, normalized_params=False, **params)`

Determines the likelihood of the data following the function “fun” assuming a two variability source of the data pairs (x, y) using the posterior distribution.

Parameters

- **x** (*ndarray of float [n_points]*) – x data
- **y** (*ndarray of float [n_points]*) – y data
- **fun** (*function*) – Function to fit the data to (e.g. sigmoid)
- **bounds** (*dict, default: None*) – Dictionary containing the bounds of “sigma_x” and “sigma_y” and the free parameters of fun
- **verbose** (*bool, default: True*) – Print function output after every calculation
- **normalized_params** (*bool, default: False*) – Are the parameters passed in normalized space between [0, 1]? If so, bounds are used to denormalize them before calculation
- ****params** (*dict*) – Free parameters to optimize. Contains “sigma_x”, “sigma_y”, and the free parameters of fun

Returns

l – Negative likelihood

Return type

float

`pynibs.util.util.list2dict(l)`

Transform list of dicts with same keys to dict of list

Parameters

l (*list of dict*) – List containing dictionaries with same keys

Returns

d – Dictionary containing the entries in a list

Return type

dict of lists

`pynibs.util.util.load_muaps(fn_muaps, fs=1000000.0, fs_downsample=100000.0)`

`pynibs.util.util.mutual_coherence(array)`

Calculate the mutual coherence of a matrix A. It can also be referred as the cosine of the smallest angle between two columns.

`mutual_coherence = mutual_coherence(array)`

Parameters

array (*ndarray of float*) – Input matrix

Returns

mutual_coherence – Mutual coherence

Return type

float

`pynibs.util.util.norm_percentile(data, percentile)`

Normalizes data to a given percentile.

Parameters

- **data** (*np.ndarray [n_data,]*) – Dataset to normalize
- **percentile** (*float*) – Percentile of normalization value [0 ... 100]

Returns

data_norm – Normalized dataset

Return type

np.ndarray [n_data,]

`pynibs.util.util.rd(array, array_ref)`

Determine the relative difference between input data and reference data.

Parameters

- **array** (*np.ndarray*) – input data [(x), y0, y1, y2 ...]
- **array_ref** (*np.ndarray*) – reference data [(x_ref), y0_ref, y1_ref, y2_ref ...] if array_ref is 1D, all sizes have to match

Returns

rd – Relative difference between the columns of array and array_ref

Return type

ndarray of *float* [array.shape[1]]

`pynibs.util.util.recursive_len(item)`

Determine len of list of lists (recursively).

Parameters

item (*list of list*) – List of list

Returns

len – Total length of list of lists

Return type

int

`pynibs.util.util.sigmoid_log_p(x, p)`

`pynibs.util.util.tal2mni(coords, direction='tal2mni', style='nonlinear')`

Transform Talairach coordinates into (SPM) MNI space and vice versa.

This is taken from <https://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach> and <http://gibms.mc.ntu.edu.tw/bmlab/tools/data-analysis-codes/mni2tal-m/>

Parameters

- **coords** (*np.ndarray or list*) – x,y,z coordinates
- **direction** (*str, default: 'tal2mni'*) – Transformation direction. One of ('tal2mni', 'mni2tal')
- **style** (*str, default: 'nonlinear'*) – Transformation style. One of ('linear', 'non-linear')

Returns

coords_trans

Return type

np.ndarray

`pynibs.util.util.unique_rows(a)`

Returns the unique rows of *np.array(a)*.

Parameters

a (*np.ndarray of float [m x n]*) – Array to search for double row entries

Returns

a_unique – array a with only unique rows

Return type

np.array [k x n]

pynibs.visualization package

Submodules

pynibs.visualization.plot_2D module

```
pynibs.visualization.plot_2D.plot_io_curve(mep_data, local_mag_e, title='I/O curve',  
                                           y_axis_label='EMG p2p-amplitude,  $\mu V$ ',  
                                           x_axis_label='mag(E), V/m, scaled', fit_fun=None,  
                                           screenshot_fn=None, interactive=False)
```

Plot scattered data of MEP-mag(E) pairs (\Rightarrow I/O curve). Optionally the fit of the provided fit function can be overlaid.

Parameters

- **mep_data** (*np.ndarray[[float](#)]*, [*n_stims*]) – The acquired MEPs for each stimulation.
- **local_mag_e** (*np.ndarray[[float](#)]*, [*n_stims*]) – The local electric field magnitude at the ROI element the I/O curve should be plotted from.
- **title** (*str*, *optional*) – The title of the plot; default: “I/O curve”
- **y_axis_label** (*str*, *optional*) – The title of the y-axis; default: “EMG p2p-amplitude, μV ”
- **x_axis_label** (*str*, *optional*) – The title of the x-axis; default: “mag(E), V/m, scaled”
- **fit_fun** (*Callable*, *optional*) – If provided, the fit of the I/O curve with the provided function will be computed and displayed. Currently supported: `pynibs.sigmoid4`, `pynibs.sigmoid4_log`, `pynibs.linear`
- **screenshot_fn** (*str*, *optional*) – If provided, output the plotted image to that file location.
- **interactive** (*bool*) – If True, spawn plot in blocking window.

Return type

True if successful, False otherwise.

pynibs.visualization.render_3D module

```
pynibs.visualization.render_3D.render_coil_positions(coil_conf_set_1_positions,  
                                                    coil_conf_set_1_orientations,  
                                                    coil_conf_set_2_positions=None,  
                                                    coil_conf_set_2_orientations=None,  
                                                    fn_mesh=None, surf_type='skin',  
                                                    viewport_dim=(1280, 720),  
                                                    camera_polar_coords=(-175, 66, 110),  
                                                    screenshot_fn=None, interactive=False)
```

Plots coil positions (and their orientation) in space, optionally also display a second set of coil positions, optionally also display a surface (e.g. gray matter or skin)

```
pynibs.visualization.render_3D.render_data_on_surface(points, tris, data, viewport_dim=(1280,  
                                                                                   720), camera_polar_coords=(-175, 66,  
                                                                                   110), title=None, data_name='Data',  
                                                                                   colormap='jet', screenshot_fn=None,  
                                                                                   interactive=False)
```

Plots data on surface: - If the number of data points equals the number of vertices in the mesh, the data will

be displayed as point data. - If the number of data points equals the number of triangles in the mesh, the data will be displayed as cell data.

Parameters

- **points** (`np.darray[float]`, [*n_points* x 3]) – Points (vertices) of surface mesh.
- **tris** (`np.array[float]`, [*n_tris* x 3]) – Connectivity list of triangles.
- **data** (`np.array[float]`, [*n_tris*]) – Data in triangular center
- **viewport_dim** (`Tuple[int, int]`) – Size of the viewport. Default: (1280, 720)
- **camera_polar_coords** (`Tuple[float, float, float]`) – The coordinate of the camera around the object in polar coordinates: (azimuthal angle, polar angle, radius)
- **title** (`str`) – Title of the rendering window.
- **data_name** (`str`) – Name of the visualized data set.
- **colormap** (`str`) – Identifier of the desired color map. Available colormaps are: ‘Accent’, ‘Blues’, ‘BrBG’, ‘BuGn’, ‘BuPu’, ‘CMRmap’, ‘Dark2’, ‘GnBu’, ‘Greens’, ‘Greys’, ‘OrRd’, ‘Oranges’, ‘PRGn’, ‘Paired’, ‘Pastel1’, ‘Pastel2’, ‘PiYG’, ‘PuBu’, ‘PuBuGn’, ‘PuOr’, ‘PuRd’, ‘Purples’, ‘RdBu’, ‘RdGy’, ‘RdPu’, ‘RdYlBu’, ‘RdYlGn’, ‘Reds’, ‘Set1’, ‘Set2’, ‘Set3’, ‘Spectral’, ‘Vega10’, ‘Vega20’, ‘Vega20b’, ‘Vega20c’, ‘Wistia’, ‘YlGn’, ‘YlGnBu’, ‘YlOrBr’, ‘YlOrRd’, ‘afmhot’, ‘autumn’, ‘binary’, ‘black-white’, ‘blue-red’, ‘bone’, ‘brg’, ‘bwr’, ‘cool’, ‘coolwarm’, ‘copper’, ‘cubehelix’, ‘file’, ‘flag’, ‘gist_earth’, ‘gist_gray’, ‘gist_heat’, ‘gist_ncar’, ‘gist_rainbow’, ‘gist_stern’, ‘gist_yarg’, ‘gnuplot’, ‘gnuplot2’, ‘gray’, ‘hot’, ‘hsv’, ‘inferno’, ‘jet’, ‘magma’, ‘nipy_spectral’, ‘ocean’, ‘pink’, ‘plasma’, ‘prism’, ‘rainbow’, ‘seismic’, ‘spectral’, ‘spring’, ‘summer’, ‘terrain’, ‘viridis’, ‘winter’
- **screenshot_fn** (`str / None`) – If provided a screenshot will be saved to that path.
- **interactive** (`bool`) – If true, a blocking window will be spawned.

Return type

True if successful, False in case of a fatal error.

1.1.2 Submodules

1.1.3 pynibs.coil module

All functions to operate on TMS coils go here, for example to create `.xdmf` files to visualize coil positions.

`pynibs.coil.calc_coil_position_pdf(fn_rescon=None, fn_simpos=None, fn_exp=None, orientation='quaternions', folder_pdfplots=None)`

Determines the probability density functions of the transformed coil position (*x*, *y*, *z*) and quaternions of the coil orientations (*x*, *y*, *z*)

Parameters

- **fn_rescon** (`str`) – Filename of the results file from TMS experiments (results_conditions.csv)
- **fn_simpos** (`str`) – Filename of the positions and orientation from TMS experiments (simPos.csv)
- **fn_exp** (`str`) – Filename of experimental.csv file from experiments
- **orientation** (`str`) – Type of orientation estimation: ‘quaternions’ or ‘euler’
- **folder_pdfplots** (`str`) – Folder, where the plots of the fitted pdfs are saved (omitted if not provided)

Returns

- **pdf_paras_location** (*list of list of np.ndarray*) –
[n_conditions] Pdf parameters (limits and shape) of the coil position for x', y', and z' for each:
 - beta_paras ... [p, q, a, b] (2 shape parameters and limits)
 - moments ... [data_mean, data_std, beta_mean, beta_std]
 - p_value ... p-value of the Kolmogorov Smirnov test
 - uni_paras ... [a, b] (limits)
- **pdf_paras_orientation_euler** (*list of np.ndarray*) –
[n_conditions] Pdf parameters (limits and shape) of the coil orientation Psi, Theta, and Phi for each:
 - beta_paras ... [p, q, a, b] (2 shape parameters and limits)
 - moments ... [data_mean, data_std, beta_mean, beta_std]
 - p_value ... p-value of the Kolmogorov Smirnov test
 - uni_paras ... [a, b] (limits)
- **OP_mean** (*List of [3 x 4] np.ndarray*) – [n_conditions] List of mean coil position and orientation for different conditions (global coordinate system)

$$\begin{bmatrix} | & | & | & | \\ ori_x & ori_y & ori_z & pos \\ | & | & | & | \end{bmatrix}$$

- **OP_zeromean** (*list of [3 x 4 x n_con_each] np.ndarray [n_conditions]*) – List over conditions containing zero-mean coil orientations and positions
- **V** (*list of [3 x 3] np.ndarrays [n_conditions]*) – Transformation matrix of coil positions from global coordinate system to transformed coordinate system
- **P_transform** (*list of np.ndarray [n_conditions]*) – List over conditions containing transformed coil positions [x', y', z'] of all stimulations (zero-mean, rotated by SVD)
- **quaternions** (*list of np.ndarray [n_conditions]*) – List over conditions containing imaginary part of quaternions [x'', y'', z''] of all stimulations

pynibs.coil.calc_coil_transformation_matrix(LOC_mean, ORI_mean, LOC_var, ORI_var, V)

Calculate the modified coil transformation matrix needed for SimNIBS based on location and orientation variations observed in the framework of uncertainty analysis

Parameters

- **LOC_mean** (*np.ndarray of float*) – (3), Mean location of TMS coil
- **ORI_mean** (*np.ndarray of float*) – (3 x 3) Mean orientations of TMS coil

$$\begin{bmatrix} | & | & | \\ x & y & z \\ | & | & | \end{bmatrix}$$

- **LOC_var** (*np.ndarray of float*) –
(3) Location variation in normalized space (dx', dy', dz'), i.e. zero mean and projected on principal axes
- **ORI_var** (*np.ndarray of float*) –
(3) Orientation variation expressed in Euler angles [alpha, beta, gamma] in deg
- **V** (*np.ndarray of float*) – (3x3) V-matrix containing the eigenvectors from ___, V = numpy.linalg.svd

Returns

- **mat** (*np.ndarray of float*)
- (4, 4) Transformation matrix containing 3 axis and 1 location vector –

$$\begin{bmatrix} | & | & | & | \\ x & y & z & pos \\ | & | & | & | \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

`pynibs.coil.check_coil_position(points, hull)`

Check if magnetic dipoles are lying inside head region

Parameters

- **points** (*np.ndarray of float*) – (N_points, 3) Coordinates (x,y,z) of magnetic dipoles
- **hull** (*Delaunay object or np.ndarray of float*) – (N_surface_points, 3) Head surface data

Returns

valid – Validity of coil position: TRUE: valid FALSE: invalid

Return type

bool

`pynibs.coil.create_stimsite_from_exp_hdf5(fn_exp, fn_hdf, datanames=None, data=None, overwrite=False)`

This takes an experiment.hdf5 file and creates an .hdf5 + .xdmf tuple for all coil positions for visualization.

Parameters

- **fn_exp** (*str*) – Path to experiment.hdf5
- **fn_hdf** (*str*) – Filename for the resulting .hdf5 file. The .xdmf is saved with the same basename. Folder should already exist.
- **datanames** (*str or list of str, optional*) – Dataset names for data
- **data** (*np.ndarray, optional*) – Dataset array with shape = (len(poslist.pos), len(datanames())).
- **overwrite** (*bool, default: False*) – Overwrite existing files.

`pynibs.coil.create_stimsite_from_list(fn_hdf, poslist, datanames=None, data=None, overwrite=False)`

This takes a list of matsimnibs-style coil position and orientations and creates an .hdf5 + .xdmf tuple for all positions.

Centers and coil orientations are written to disk, with optional data for each coil configuration.

Parameters

- **fn_hdf** (*str*) – Filename for the .hdf5 file. The .xdmf is saved with the same basename. Folder should already exist.
- **poslist** (*list of np.ndarray*) – (4,4) Positions.
- **datanames** (*str or list of str, optional*) – Dataset names for data.
- **data** (*np.ndarray, optional*) – Dataset array with shape = (len(poslist.pos), len(datanames())).
- **overwrite** (*bool, default: False*) – Overwrite existing files.

```
pynibs.coil.create_stimsite_from_matsimnibs(fn_hdf, matsimnibs, datanames=None, data=None,
                                           overwrite=False)
```

This takes a matsimnibs array and creates an .hdf5 + .xdmf tuple for all coil positions for visualization.

Centers and coil orientations are written disk.

Parameters

- **fn_hdf** (*str*) – Filename for the .hdf5 file. The .xdmf is saved with the same basename. Folder should already exist.
- **matsimnibs** (*np.ndarray*) – (4, 4, n_pos) Matsimnibs matrices containing the coil orientation (x,y,z) and position (p)

$$\begin{bmatrix} | & | & | & | \\ x & y & z & p \\ | & | & | & | \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

- **datanames** (*str* or *list of str*, *optional*) – Dataset names for data.
- **data** (*np.ndarray*, *optional*) – (len(poslist.pos), len(datanames)).
- **overwrite** (*bool*, *default: False*) – Overwrite existing files.

```
pynibs.coil.create_stimsite_from_tmslist(fn_hdf, poslist, datanames=None, data=None,
                                         overwrite=False)
```

This takes a :py:class:simnibs.sim_struct.TMSLIST from simnibs and creates an .hdf5 + .xdmf tuple for all positions.

Centers and coil orientations are written to disk, with optional data for each coil configuration.

Parameters

- **fn_hdf** (*str*) – Filename for the .hdf5 file. The .xdmf is saved with the same basename. Folder should already exist.
- **poslist** (*simnibs.sim_struct.TMSLIST*) – poslist.pos[*].matsimnibs have to be set.
- **datanames** (*str* or *list of str*, *optional*) – Dataset names for data.
- **data** (*np.ndarray*, *optional*) – Dataset array with shape = (len(poslist.pos), len(datanames())).
- **overwrite** (*bool*, *default: False*) – Overwrite existing files

```
pynibs.coil.create_stimsite_hdf5(fn_exp, fn_hdf, conditions_selected=None, sep='_',
                                merge_sites=False, fix_angles=False, data_dict=None,
                                conditions_ignored=None)
```

Reads results_conditions and creates an hdf5/xdmf pair with condition-wise centers of stimulation sites and coil directions as data.

Parameters

- **fn_exp** (*str*) – Path to results.csv.
- **fn_hdf** (*str*) – Path where to write file. Gets overridden if already existing.
- **conditions_selected** (*str* or *list of str*, *optional*) – List of conditions returned by the function, the others are omitted. If None, all conditions are returned.
- **sep** (*str*, *default: "_"*) – Separator between condition label and angle (e.g. M1_0, or M1-0).
- **merge_sites** (*bool*) – If true, only one coil center per site is generated.
- **fix_angles** (*bool*) – rename 22.5 -> 0, 0 -> -45, 67.5 -> 90, 90 -> 135.

- **data_dict** (*dict of np.ndarray of float [n_stimsites] (optional), default: None*) – Dictionary containing data corresponding to the stimulation sites (keys).
- **conditions_ignored** (*str or list of str, optional*) – Conditions, which are not going to be included in the plot.

Returns

<Files> – Contains information about condition-wise stimulation sites and coil directions (fn_hdf)

Return type

hdf5/xdmf file pair

Example

```
pynibs.create_stimsite_hdf5('/exp/1/experiment_corrected.csv',
                           '/stimsite', True, True)
```

`pynibs.coil.get_coil_dipole_pos(coil_fn, matsimnibs)`

Apply transformation to coil dipoles and return position.

Parameters

- **coil_fn** (*str*) – Filename of coil .ccd file.
- **matsimnibs** (*np.ndarray of float*) – Transformation matrix.

Returns

dipoles_pos – (N, 3) Cartesian coordinates (x, y, z) of coil magnetic dipoles.

Return type

np.ndarray

`pynibs.coil.get_invalid_coil_parameters(param_dict, coil_position_mean, svd_v, del_obj, fn_coil, fn_hdf5_coilpos=None)`

Finds gpc parameter combinations, which place coil dipoles inside subjects head. Only endpoints (and midpoints) of the parameter ranges are examined.

`get_invalid_coil_parameters(param_dict, pos_mean, v, del_obj, fn_coil, fn_hdf5_coilpos=None)`

Parameters

- **param_dict** (*dict*) – Dictionary containing dictionary with 'limits' and 'pdfshape'. keys: 'x', 'y', 'z', 'psi', 'theta', 'phi'.
- **coil_position_mean** (*np.ndarray*) – (3, 4) Mean coil positions and orientations.
- **svd_v** (*np.ndarray*) – (3, 3) SVD matrix V.
- **del_obj** (*scipy.spatial.Delaunay*) – Skin surface.
- **fn_coil** (*str*) – Filename of coil .ccd file.
- **fn_hdf5_coilpos** (*str*) – Filename of .hdf5 file to save coil_pos in (incl. path and .hdf5 extension).

Returns

fail_params – Index and combination of failed parameter.

Return type

list of int

`pynibs.coil.random_walk_coil(start_mat, n_steps, fn_mesh_hdf5, angles_dev=3, distance_low=1, distance_high=4, angles_metric='deg', coil_pos_fn=None)`

Computes random walk coil positions/orientations for a SimNIBS matsimnibs coil pos/ori.

Parameters

- **start_mat** (*np.ndarray*) – (4, 4) SimNIBS matsimnibs.
- **n_steps** (*int*) – Number of steps to walk.
- **fn_mesh_hdf5** (*str*) – .hdf5 mesh filename, used to compute skin-coil distances.
- **angles_dev** (*float* or *list of float*, *default:* 3) – Angles deviation, ``np.random.normal(scale=angles_dev)``. If list, angles_dev = [alpha, beta, theta].
- **distance_low** (*float*, *default:* 1) – Minimum skin-coil distance.
- **distance_high** (*float*, *default:* 4) – Maximum skin-coil distance.
- **angles_metric** (*str*, *default:* 'deg') – One of ('deg', 'rad').
- **coil_pos_fn** (*str*, *optional*) – If provided, .hdf5/.xdmf tuple is written with coil positions/orientations.

Returns

- **walked_coils** (*np.ndarray*) – (4, 4, n_steps + 1) coil positions / orientations.
- **<file>** (*.hdf5/.xdmf file tuple with n_steps + 1 coil positions/orientations.*)

`pynibs.coil.sort_opt_coil_positions(fn_coil_pos_opt, fn_coil_pos, fn_out_hdf5=None, root_path='/0/0/', verbose=False, print_output=False)`

Sorts coil positions according to Traveling Salesman problem

Parameters

- **fn_coil_pos_opt** (*str*) – Name of .hdf5 file containing the optimal coil position indices
- **fn_coil_pos** (*str*) – Name of .hdf5 file containing the matsimnibs matrices of all coil positions
- **fn_out_hdf5** (*str*) – Name of output .hdf5 file (will be saved in the same format as fn_coil_pos_opt)
- **verbose** (*bool*, *default:* False) – Print output messages
- **print_output** (*bool* or *str*, *default:* False) – Print output image as .png file showing optimal path

Return type

<file> .hdf5 file containing the sorted optimal coil position indices

`pynibs.coil.test_coil_position_gpc(parameters)`

Testing valid coil positions for gPC analysis

`pynibs.coil.write_coil_pos_hdf5(fn_hdf, centers, m0, m1, m2, datanames=None, data=None, overwrite=False)`

Creates a .hdf5 + .xdmf file tuple for all coil positions. Coil centers and coil orientations are saved, and - optionally - data for each position if data and datanames are provided.

Parameters

- **fn_hdf** (*str*) – Filename for the .hdf5 file. The .xdmf is saved with the same basename. Folder should already exist.
- **centers** (*np.ndarray of float*) – (n_pos, 3) Coil positions.
- **m0** (*np.ndarray of float*) – (n_pos, 3) Coil orientation x-axis (looking at the active (patient) side of the coil pointing to the right).
- **m1** (*np.ndarray of float*) – (n_pos, 3) Coil orientation y-axis (looking at the active side of the coil pointing up away from the handle).
- **m2** (*np.ndarray of float*) – (n_pos, 3) Coil orientation z-axis (looking at the active (patient) side of the coil pointing to the patient).

- **datanames** (*str* or *list of str*, *optional*) – (n_data) Dataset names for data
- **data** (*np.ndarray*, *optional*) – (n_pos, n_data) Dataset array with (len(poslist.pos), len(datanames())).
- **overwrite** (*bool*, *default: False*) – Overwrite existing files.

1.1.4 pynibs.freesurfer module

This holds methods to interact with FreeSurfer ([1]), for example to translate FreeSurfer files into Paraview readable .vtk files.

References

```
pynibs.freesurfer.data_sub2avg(fn_subject_obj, fn_average_obj, hemisphere, fn_in_hdf5_data,
                               data_hdf5_path, data_label, fn_out_hdf5_geo, fn_out_hdf5_data,
                               mesh_idx=0, roi_idx=0, subject_data_in_center=True,
                               data_substitute=-1, verbose=True, replace=True, reg_fn='sphere.reg')
```

Maps the data from the subject space to the average template. If the data is given only in an ROI, the data is mapped to the whole brain surface.

Parameters

- **fn_subject_obj** (*str*) – Filename of subject object .hdf5 file (incl. path), e.g. .../probands/subjectID/subjectID.hdf5
- **fn_average_obj** (*str*) – Filename of average template object .pkl file (incl. path), e.g. .../probands/avg_template/avg_template.hdf5.
- **hemisphere** (*str*) – Define hemisphere to work on ('lh' or 'rh' for left or right hemisphere, respectively).
- **fn_in_hdf5_data** (*str*) – Filename of .hdf5 data input file containing the subject data.
- **data_hdf5_path** (*str*) – Path in .hdf5 data file where data is stored (e.g. '/data/tris/').
- **data_label** (*str* or *list of str*) – Label of datasets contained in hdf5 input file to map.
- **fn_out_hdf5_geo** (*str*) – Filename of .hdf5 geo output file containing the geometry information.
- **fn_out_hdf5_data** (*str*) – Filename of .hdf5 data output file containing the mapped data.
- **mesh_idx** (*int*) – Index of mesh used in the simulations.
- **roi_idx** (*int*) – Index of region of interest used in the simulations.
- **subject_data_in_center** (*bool*, *default: True*) – Specify if the data is given in the center of the triangles or in the nodes.
- **data_substitute** (*float*) – Data substitute with this number for all points outside the ROI mask
- **verbose** (*bool*) – Verbose output (Default: True)
- **replace** (*bool*) – Replace output files (Default: True)
- **reg_fn** (*str*) – Sphere.reg fn

Returns

<Files> – Geometry and corresponding data files to plot with Paraview:

- `fn_out_hdf5_geo.hdf5`: geometry file containing the geometry information of the average template
- `fn_out_hdf5_data.hdf5`: geometry file containing the data

Return type

.hdf5 files

`pynibs.freesurfer.freesurfer2vtk(in_fns, out_folder, hem='lh', surf='pial', prefix=None, fs_subject='fsaverage', fs_subjects_dir=None)`

Transform multiple FreeSurfer .mgh files into one .vtk file. This can be read with Paraview and others.

Parameters

- `in_fns` (*list of str or str*) – Input filenames.
- `out_folder` (*str*) – Output folder.
- `hem` (*str, default: 'lh'*) – Which hemisphere: 'lh' or 'rh'.
- `surf` (*str, default: 'pial'*) – Which FreeSurfer surface: 'pial', 'inflated', ...
- `prefix` (*str, optional*) – Prefix to add to each filename.
- `fs_subject` (*str, default: 'fsaverage'*) – FreeSurfer subject.
- `fs_subjects_dir` (*str, optional*) – FreeSurfer subjects directory. If not provided, read from environment.

Returns

<File> – One .vtk file with data as overlays from all .mgh files provided

Return type

out_folder/{prefix}_{hem}_{surf}.vtk

`pynibs.freesurfer.make_average_subject(subjects, subject_dir, average_dir, fn_reg='sphere.reg')`

Generates the average template from a list of subjects using the FreeSurfer average.

Parameters

- `subjects` (*list of str*) – Paths of subjects directories, where the FreeSurfer files are located, e.g. for `simnibs mri2mesh` .../fs_SUBJECT_ID.
- `subject_dir` (*str*) – Temporary subject directory of FreeSurfer (symlinks of subjects will be generated in there and average template will be temporarily stored before it is copied to `average_dir`).
- `average_dir` (*str*) – path to directory where average template will be stored, e.g. `probands/avg_template_15/mesh/0/fs_avg_template_15`.
- `fn_reg` (*str, default: 'sphere.reg' --> ?h.sphere.reg*) – Filename suffix of FreeSurfer registration file containing registration information to template.

Returns

<Files> – Average template in `average_dir` and registered curvature files, `?h.sphere.reg` in `subjects/surf` folders.

Return type

.tif and .reg files

`pynibs.freesurfer.make_group_average(subjects=None, subject_dir=None, average=None, hemi='lh', template='mytemplate', steps=3, n_cpu=2, average_dir=None)`

Creates a group average from scratch, based on one subject. This prevents for example the `fsaverage` problems of large elements at M1, etc. This is an implementation of [2] ‘Creating a registration template from scratch (GW)’.

References

Parameters

- **subjects** (*list of str*) – List of FreeSurfer subjects names.
- **subject_dir** (*str*) – Temporary subject directory of FreeSurfer (symlinks of subjects will be generated in there and average template will be temporarily stored before it is copied to `average_dir`).
- **average** (*str*, default: `subjects[0]`) – Which subject to base new average template on.
- **hemi** (*str*, default: `'lh'`) – Which hemisphere: `lh` or `rh`.
Deprecated since version 0.0.1: Don't use any more.
- **template** (*str*, default: `'mytemplate'`) – Basename of new template.
- **steps** (*int*, default: `2`) – Number of iterations.
- **n_cpu** (*int*, default: `4`) – How many cores for multithreading.
- **average_dir** (*str*) – Path to directory where average template will be stored, e.g. `proband/avg_template_15/mesh/0/fs_avg_template_15`.

Returns

- **<File>** (*.tif file*) – `SUBJECT_DIR/TEMPLATE*.tif`, `TEMPLATE0.tif` based on `AVERAGE`, rest on all subjects.
- **<File>** (*.myreg file*) – `SUBJECT_DIR/SUBJECT*/surf/HEMI.sphere.myreg*`.
- **<File>** (*.tif file*) – Subject wise sphere registration based on `TEMPLATE*.tif`.

`pynibs.freesurfer.read_curv_data(fname_curv, fname_inf, raw=False)`

Read curvature data provided by FreeSurfer with optional normalization.

Parameters

- **fname_curv** (*str*) – Filename of the FreeSurfer curvature file (e.g. `?h.curv`), contains curvature data in nodes can be found in `mri2mesh` proband folder: `proband_ID/fs_ID/surf/?h.curv`.
- **fname_inf** (*str*) – Filename of inflated brain surface (e.g. `?h.inflated`), contains points and connectivity data of surface can be found in `mri2mesh` proband folder: `proband_ID/fs_ID/surf/?h.inflated`.
- **raw** (*bool*) – If raw-data is returned or if the data is normalized to `-1` for neg. and `+1` for pos. curvature.

Returns

curv – Curvature data in element centers.

Return type

`np.ndarray` of `float` or `int`

1.1.5 pynibs.hdf5_io module

`pynibs.hdf5_io.create_fibre_geo_hdf5(fn_fibres_hdf5, overwrite=True)`

Reformats geometrical fibre data and adds a /plot subfolder containing geometrical fibre data including connectivity

Parameters

- **fn_fibres_hdf5** (*str*) – Path to fibre.hdf5 file containing the original fibre data
- **overwrite** (*bool*) – Overwrites existing /plot subfolder in .hdf5 file

`pynibs.hdf5_io.create_fibre_xdmf(fn_fibre_geo_hdf5, fn_fibre_data_hdf5=None, overwrite=True, fibre_points_path='fibre_points', fibre_con_path='fibre_con', fibre_data_path='')`

Creates .xdmf file to plot fibres in Paraview

Parameters

- **fn_fibre_geo_hdf5** (*str*) – Path to fibre_geo.hdf5 file containing the geometry (in /plot subfolder created with create_fibre_geo_hdf5())
- **fn_fibre_data_hdf5** (*str* (*optional*) *default: None*) – Path to fibre_data.hdf5 file containing the data to plot (in parent folder)
- **fibre_points_path** (*str* (*optional*) *default: fibre_points*) – Path to fibre point array in .hdf5 file
- **fibre_con_path** (*str* (*optional*) *default: fibre_con*) – Path to fibre connectivity array in .hdf5 file
- **fibre_data_path** (*str* (*optional*) *default: ""*) – Path to parent data folder in data.hdf5 file (Default: no parent folder)

Returns

<File>

Return type

.xdmf file for Paraview

`pynibs.hdf5_io.create_position_path_xdmf(sorted_fn, coil_pos_fn, output_xdmf, stim_intens=None, coil_sorted='/0/0/coil_seq')`

Creates one .xdmf file that allows paraview plottings of coil position paths.

Paraview can be used to visualize the order of realized stimulation positions.

Parameters

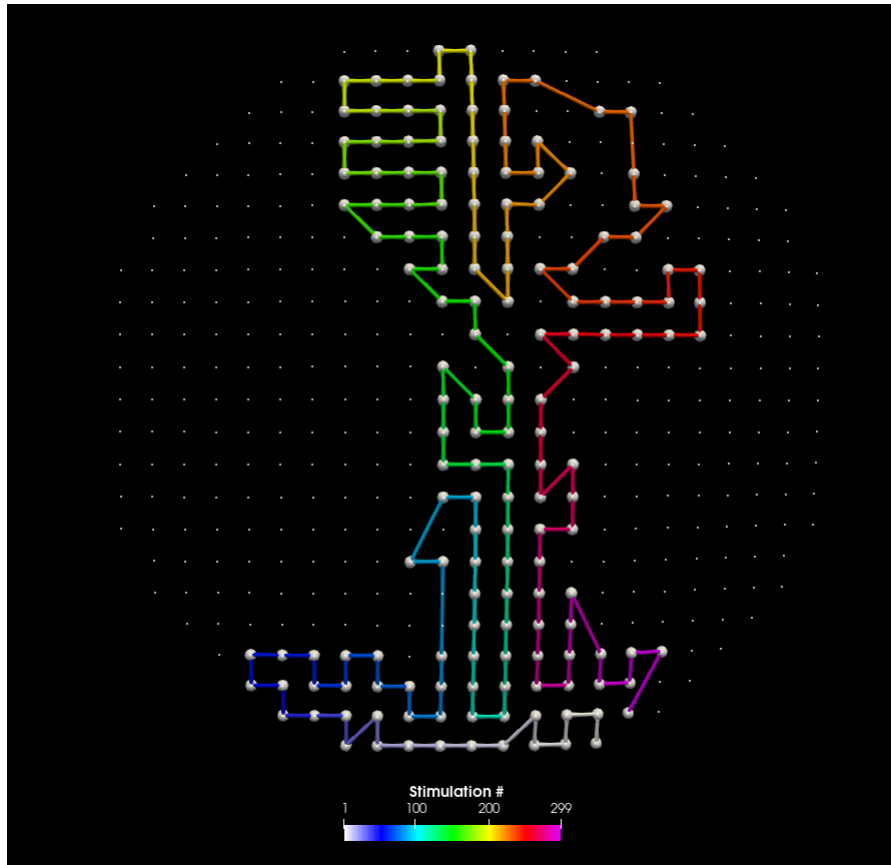
- **sorted_fn** (*str*) – .hdf5 filename with position indices, values, intensities from `pynibs.sort_opt_coil_positions()`.
- **coil_pos_fn** (*str*) – .hdf5 filename with original set of coil positions. Indices from sorted_fn are mapped to this. Either '/matsimnibs' or 'm1' and 'm2' datasets.
- **output_xdmf** (*str*) –
- **stim_intens** (*int*, *optional*) – Intensities are multiplied by this factor.
- **coil_sorted** (*str*) – Path to coil positions in sorted_fn

Returns

`output_xdmf`

Return type

<file>



```
pynibs.hdf5_io.data_superimpose(fn_in_hdf5_data, fn_in_geo_hdf5, fn_out_hdf5_data,
                                data_hdf5_path='/data/tris/', data_substitute=-1, normalize=False)
```

Overlaying data stored in .hdf5 files except in regions where data_substitute is found. These points are omitted in the analysis and will be replaced by data_substitute instead.

Parameters

- **fn_in_hdf5_data** (*list of str*) – Filenames of .hdf5 data files with common geometry, e.g. generated by `pynibs.data_sub2avg(...)`.
- **fn_in_geo_hdf5** (*str*) – Geometry .hdf5 file, which corresponds to the .hdf5 data files.
- **fn_out_hdf5_data** (*str*) – Filename of .hdf5 data output file containing the superimposed data.
- **data_hdf5_path** (*str*) – Path in .hdf5 data file where data is stored (e.g. `'/data/tris/'`).
- **data_substitute** (*float or np.NaN, default: -1*) – Data substitute with this number for all points in the inflated brain, which do not belong to the given data set.
- **normalize** (*bool or str, default: False*) – Decide if individual datasets are normalized w.r.t. their maximum values before they are superimposed.
 - `'global'`: global normalization w.r.t. maximum value over all datasets and subjects
 - `'dataset'`: dataset wise normalization w.r.t. maximum of each dataset individually (over subjects)
 - `'subject'`: subject wise normalization (over datasets)

Returns

<File> – Overlaid data.

Return type

.hdf5 file

`pynibs.hdf5_io.hdf_2_ascii(hdf5_fn)`

Prints out structure of given .hdf5 file.

Parameters

hdf5_fn (*str*) – Filename of .hdf5 file.

Returns

h5 – Structure of .hdf5 file

Return type

items

`pynibs.hdf5_io.load_mesh_hdf5(fname)`

Loading mesh from .hdf5 file and setting up *TetrahedraLinear* class.

Parameters

fname (*str*) – Name of .hdf5 file (incl. path)

Returns

obj – *TetrahedraLinear* object

Return type

pynibs.mesh.mesh_struct.TetrahedraLinear

Example

.hdf5 file format and contained groups. The content of .hdf5 files can be shown using the tool HDFView (<https://support.hdfgroup.org/products/java/hdfview/>)

mesh		
I---/elm		
I I--/elm_number	[1,2,3,...,N_ele]	Running index over all elements starting at 1, triangles and tetrahedra
I I--/elm_type	[2,2,...,4,4]	Element type: 2 triangles, 4 tetrahedra
I I--/node_number_list	[1,5,6,0;...;1,4,8,9]	Connectivity of triangles [X, X, X, 0] and tetrahedra [X, X, X, X]
I I--/tag1	[1001,1001, ..., 4,4,4]	Surface (100X) and domain (X) indices with 1000 offset for surfaces
I I--/tag2	[1, 1, ..., 4,4,4]	Surface (X) and domain (X) indices w/o offset
I		
I---/nodes		
I I--/node_coord	[1.254, 1.762, 1.875;...]	Node coordinates in (mm)
I I--/node_number	[1,2,3,...,N_nodes]	Running index over all points starting at 1
I I--/units	["mm"]	.value is unit of geometry
I		
I---/fields		
I I--/E/value	[E_x_1, E_y_1, E_z_1;...]	Electric field in all elms, triangles and tetrahedra
I I--/J/value	[J_x_1, J_y_1, J_z_1;...]	Current density in all elms, triangles and tetrahedra
I I--/normE/value	[normE_1,..., normE_N_ele]	Magnitude of electric field in all elements, triangles and tetrahedra
I I--/normJ/value	[normJ_1,..., normJ_N_ele]	Magnitude of current density in all elements, triangles and tetrahedra
/data		
I---/potential	[phi_1, ..., phi_N_nodes]	Scalar electric potential in nodes (size N_nodes)
I---/dAdt	[A_x_1, A_y_1, A_z_1,...]	Magnetic vector potential (size 3xN_nodes)

`pynibs.hdf5_io.load_mesh_msh(fname)`

Loading mesh from .msh file and return *TetrahedraLinear* object.

Parameters

fname (*str*) – .msh filename (incl. path)

Returns

obj

Return type

pynibs.mesh.mesh_struct.TetrahedraLinear

`pynibs.hdf5_io.msh2hdf5(fn_msh=None, skip_roi=False, skip_layer=True, include_data=False, approach='mri2mesh', subject=None, mesh_idx=None)`

Transforms mesh from .msh to .hdf5 format. Mesh is read from subject object or from fn_msh.

Parameters

- **fn_msh** (*str*, *optional*) – Filename of .msh file.
- **skip_roi** (*bool*, *default: False*) – Skip generating ROI in .hdf5
- **skip_layer** (*bool*, *default: True*) – Don't create gm layers.
- **include_data** (*bool*, *default: False*) – Also convert data in .msh file to .hdf5 file
- **subject** (*pynibs.Subject*, *optional*) – Subject information, ust be set to use skip_roi=False..
- **mesh_idx** (*int or list of int or str or list of str*, *optional*) – Mesh index, the conversion from .msh to .hdf5 is conducted for.
- **approach** (*str*) – Approach the headmodel was created with (“mri2mesh” or “head-reco”).

Deprecated since version 0.0.1: Not supported any more.

Returns

<File> – .hdf5 file with mesh information

Return type

.hdf5 file

`pynibs.hdf5_io.print_attrs(name, obj)`

Helper function for `hdf_2_ascii()`. To be called from `h5py.Group.visititems()`

Parameters

- **name** (*str*) – Name of structural element
- **obj** (*object*) – Structural element

Returns

<Print>

Return type

Structure of .hdf5 file

`pynibs.hdf5_io.read_arr_from_hdf5(fn_hdf5, folder)`

Reads array from and .hdf5 files and returns as list: Strings are returned as *np.bytes_ to str* and ‘None’ to None

Parameters

- **fn_hdf5** (*str*) – Filename of .hdf5 file
- **folder** (*str*) – Folder inside .hdf5 file to read

Returns

data_from_hdf5 – List containing data from .hdf5 file

Return type

list

`pynibs.hdf5_io.read_data_hdf5(fname)`

Reads phi and dA/dt data from .hdf5 file (phi and dAdt are given in the nodes).

Parameters

fname (*str*) – Filename of .hdf5 data file

Returns

- **phi** (*np.ndarray of float [N_nodes]*) – Electric potential in the nodes of the mesh
- **da_dt** (*np.ndarray of float [N_nodesx3]*) – Magnetic vector potential in the nodes of the mesh

`pynibs.hdf5_io.read_dict_from_hdf5(fn_hdf5, folder)`

Read all arrays from from hdf5 file and return them as dict

Parameters

- **fn_hdf5** (*str*) – Filename of .hdf5 file
- **folder** (*str*) – Folder inside .hdf5 file to read

Returns

d – Dictionary from .hdf5 file folder

Return type

dict

`pynibs.hdf5_io.simmibs_results_msh2hdf5(fn_msh, fn_hdf5, S, pos_tms_idx, pos_local_idx, subject, mesh_idx, mode_xdmf='r+', n_cpu=4, verbose=False, overwrite=False, mid2roi=False)`

Converts simnibs .msh results file(s) to .hdf5 / .xdmf tuple.

Parameters

- **fn_msh** (*str list of str*) – Filenames (incl. path) of .msh results files from SimNIBS.
- **fn_hdf5** (*str or list of str*) – Filenames (incl. path) of .hdf5 results files.
- **S** (*Simnibs Session object*) – Simnibs Session object the simulations are conducted with.
- **pos_tms_idx** (*list of int*) – Index of the simulation w.r.t. to the simnibs TMSList (inside Session object S) For every coil a separate TMSList exists, which contains multiple coil positions.
- **pos_local_idx** (*list of int*) – Index of the simulation w.r.t. to the simnibs POSlist in the TMSList (inside Session object S) For every coil a separate TMSList exists, which contains multiple coil positions.
- **subject** (*pynibs.subject.Subject*) – Subject object.
- **mesh_idx** (*int or str*) – Mesh id.
- **mode_xdmf** (*str, default: "r+"*) – Mode to open hdf5_geo file to write xdmf. If hdf5_geo is already separated in tets and tris etc., the file is not changed, use “r” to avoid IOErrors in case of parallel computing.
- **n_cpu** (*int*) – Number of processes.
- **verbose** (*bool, default: False*) – Print output messages.
- **overwrite** (*bool, default: False*) – Overwrite .hdf5 file if existing.
- **mid2roi** (*bool or string, default: False*) – If the mesh contains ROIs and the e-field was calculated in the midlayer using simnibs (`S.map_to_surf = True`), the midlayer results will be mapped from the simnibs midlayer to the ROIs (takes some time for large ROIs).

Returns

<File> – .hdf5 file containing the results. An .xdmf file is also created to link the results with the mesh .hdf5 file of the subject

Return type

.hdf5 file

`pynibs.hdf5_io.simmibs_results_msh2hdf5_workhorse(fn_msh, fn_hdf5, S, pos_tms_idx, pos_local_idx, subject, mesh_idx, mode_xdmf='r+', verbose=False, overwrite=False, mid2roi=False)`

Converts simnibs .msh results file to .hdf5 (including midlayer data if desired)

Parameters

- **fn_msh** (*list of str*) – Filenames (incl. path) of .msh results files from simnibs
- **fn_hdf5** (*str or list of str*) – Filenames (incl. path) of .hdf5 results files
- **S** (*Simnibs Session object*) – Simnibs Session object the simulations are conducted with
- **pos_tms_idx** (*list of int*) – Index of the simulation w.r.t. to the simnibs TMSList (inside Session object S) For every coil a separate TMSList exists, which contains multiple coil positions.
- **pos_local_idx** (*list of int*) – Index of the simulation w.r.t. to the simnibs POSList in the TMSList (inside Session object S) For every coil a separate TMSList exists, which contains multiple coil positions.
- **subject** (*Subject object*) – Subject object loaded from .pkl file
- **mesh_idx** (*int*) – Mesh index
- **mode_xdmf** (*str, default: "r+"*) – Mode to open hdf5_geo file to write xdmf. If hdf5_geo is already separated in tets and tris etc, the file is not changed, use "r" to avoid IOErrors in case of parallel computing.
- **verbose** (*bool, default: False*) – Print output messages
- **overwrite** (*bool, default: False*) – Overwrite .hdf5 file if existing
- **mid2roi** (*bool, list of string, or string, default: False*) – If the mesh contains ROIs and the e-field was calculated in the midlayer using simnibs (*S.map_to_surf = True*), the midlayer results will be mapped from the simnibs midlayer to the ROIs (takes some time for large ROIs)

Returns

<File> – .hdf5 file containing the results. An .xdmf file is also created to link the results with the mesh .hdf5 file of the subject

Return type

.hdf5 file

`pynibs.hdf5_io.split_hdf5(hdf5_in_fn, hdf5_geo_out_fn="", hdf5_data_out_fn=None)`

Splits one hdf5 into one with spatial data and one with statistical data. If coil data is present in `hdf5_in`, it is saved in `hdf5Data_out`. If new spatial data is added to file (curve, inflated, whatever), add this to the `geogroups` variable.

Parameters

- **hdf5_in_fn** (*str*) – Filename of .hdf5 input file
- **hdf5_geo_out_fn** (*str*) – Filename of .hdf5 .geo output file
- **hdf5_data_out_fn** (*str*) – Filename of .hdf5 .data output file (if none, remove data from `hdf5_in`)

Returns

- <File> (*.hdf5 file*) – `hdf5Geo_out_fn` (spatial data)
- <File> (*.hdf5 file*) – `hdf5Data_out_fn` (data)

`pynibs.hdf5_io.write_arr_to_hdf5(fn_hdf5, arr_name, data, overwrite_arr=True, verbose=False, check_file_exist=False)`

Takes an array and adds it to an hdf5 file

If data is list of dict, `write_dict_to_hdf5()` is called for each dict with adapted hdf5-folder name Otherwise, data is casted to `np.ndarray` and dtype of unicode data casted to ' |S'.

Parameters

- **fn_hdf5** (*str*) – Filename of .hdf5 file
- **arr_name** (*str*) – Complete path in .hdf5 file with array name
- **data** (*ndarray*, *list* or *dict*) – Data to write
- **overwrite_arr** (*bool*, *default:* *True*) – Overwrite existing array
- **verbose** (*bool*, *default:* *False*) – Print information

`pynibs.hdf5_io.write_coil_sequence_xdmf(coil_pos_fn, data, vec1, vec2, vec3, output_xdmf)`

`pynibs.hdf5_io.write_data_hdf5(out_fn, data, data_names, hdf5_path='/data', mode='a')`

Creates a .hdf5 file with data.

Parameters

- **out_fn** (*str*) – Filename of output .hdf5 file containing the geometry information
- **data** (*np.ndarray* or *list* of *nparrays* of *float*) – Data to save in hdf5 data file
- **data_names** (*str* or *list* of *str*) – Labels of data
- **hdf5_path** (*str*) – Folder in .hdf5 geometry file, where the data is saved in (Default: /data)
- **mode** (*str*, *default:* "a") – Mode: "a" append, "w" write (overwrite)

Returns

<File> – File containing the stored data

Return type

.hdf5 file

Example

File structure of .hdf5 data file

data		
---/data_names[0]	[data[0]]	First dataset
---/
---/data_names[N-1]	[data[N-1]]	Last dataset

`pynibs.hdf5_io.write_data_hdf5_surf(data, data_names, data_hdf_fn_out, geo_hdf_fn, replace=False, replace_array_in_file=True)`

Saves surface data to .hdf5 data file and generates corresponding .xdmf file linking both. The directory of data_hdf_fn_out and geo_hdf_fn should be the same, as only basenames of files are stored in the .xdmf file.

Parameters

- **data** (*np.ndarray* or *list*) – (N_points_ROI, N_components) Data to map on surfaces.
- **data_names** (*str* or *list*) – Names for datasets.
- **data_hdf_fn_out** (*str*) – Filename of .hdf5 data file.
- **geo_hdf_fn** (*str*) – Filename of .hdf5 geo file containing the geometry information (has to exist).
- **replace** (*bool*, *default:* *False*) – Replace existing .hdf5 and .xdmf file completely.
- **replace_array_in_file** (*bool*, *default:* *True*) – Replace existing array in file.

Returns

- <File> (*.hdf5 file*) – data_hdf_fn_out.hdf5 containing data

- **<File>** (*.xdmf file*) – data_hdf_fn_out.xdmf containing information about .hdf5 file structure for Paraview

Example

File structure of .hdf5 data file

```
/data
|---/tris
|   |---dataset_0   [dataset_0]   (size: N_dataset_0 x M_dataset_0)
|   |--- ...
|   |---dataset_K   [dataset_K]   (size: N_dataset_K x M_dataset_K)
```

`pynibs.hdf5_io.write_data_hdf5_vol(data, data_names, data_hdf_fn_out, geo_hdf_fn, replace=False, replace_array_in_file=True)`

Saves surface data to .hdf5 data file and generates corresponding .xdmf file linking both. The directory of data_hdf_fn_out and geo_hdf_fn should be the same, as only basenames of files are stored in the .xdmf file.

Parameters

- **data** (*np.ndarray* or *list*) – (N_points_ROI, N_components) Data to map on surfaces.
- **data_names** (*str* or *list*) – Names for datasets.
- **data_hdf_fn_out** (*str*) – Filename of .hdf5 data file.
- **geo_hdf_fn** (*str*) – Filename of .hdf5 geo file containing the geometry information (has to exist).
- **replace** (*bool*, *default: False*) – Replace existing .hdf5 and .xdmf file completely.
- **replace_array_in_file** (*bool*, *default: True*) – Replace existing array in file.

Returns

- **<File>** (*.hdf5 file*) – data_hdf_fn_out.hdf5 containing data
- **<File>** (*.xdmf file*) – data_hdf_fn_out.xdmf containing information about .hdf5 file structure for Paraview

Example

File structure of .hdf5 data file

```
/data
|---/tris
|   |---dataset_0   [dataset_0]   (size: N_dataset_0 x M_dataset_0)
|   |--- ...
|   |---dataset_K   [dataset_K]   (size: N_dataset_K x M_dataset_K)
```

`pynibs.hdf5_io.write_dict_to_hdf5(fn_hdf5, data, folder, check_file_exist=False, verbose=False)`

Takes dict (from subject.py) and passes its keys to write_arr_to_hdf5()

```
fn_hdf5: folder/
|---key1
|---key2
|...
```

Parameters

- **fn_hdf5** (*str*) –
- **data** (*dict* or *pynibs.Mesh*) –
- **folder** (*str*) –
- **verbose** (*bool*) –
- **check_file_exist** (*bool*) –

`pynibs.hdf5_io.write_geo_hdf5(out_fn, msh, roi_dict=None, hdf5_path='/mesh')`

Creates a .hdf5 file with geometry data from mesh including region of interest(s).

Parameters

- **out_fn** (*str*) – Output hdf5 filename for mesh' geometry information.
- **msh** (`pynibs.mesh.mesh_struct.TetrahedraLinear`) – Mesh to write to file.
- **roi_dict** (dict of (*RegionOfInterestSurface* or *RegionOfInterestVolume*)) – Region of interest (surface and/or volume) information.
- **hdf5_path** (*str*, *default:* `'/mesh'`) – Path in output file to store geometry information.

Returns

<File> – File containing the geometry information

Return type

.hdf5 file

Example

File structure of .hdf5 geometry file

```
mesh
I---/elm
I I--/elm_number      [1,2,3,...,N_ele]      Running index over all elements starting at 1
                                   (triangles and tetrahedra)
I I--/elm_type        [2,2,2,...,4,4]      Element type: 2 triangles, 4 tetrahedra
I I--/tag1            [1001,1001, ..., 4,4,4] Surface (100X) and domain (X) indices with 1000
                                   offset for surfaces
I I--/tag2            [ 1, 1, ..., 4,4,4]   Surface (X) and domain (X) indices w/o offset
I I--/triangle_number_list [1,5,6;...;1,4,8] Connectivity of triangles [X, X, X]
I I--/tri_tissue_type  [1,1, ..., 3,3,3]     Surface indices to differentiate between surfaces
I I--/tetrahedra_number_list [1,5,6,7;...;1,4,8,12] Connectivity of tetrahedra [X, X, X, X]
I I--/tet_tissue_type  [1,1, ..., 3,3,3]     Volume indices to differentiate between volumes
I I--/node_number_list [1,5,6,0;...;1,4,8,9] Connectivity of triangles [X, X, X, 0] and
                                   tetrahedra [X, X, X, X]
I
I---/nodes
I I--/node_coord      [1.254, 1.762, 1.875;...] Node coordinates in (mm)
I I--/node_number     [1,2,3,...,N_nodes]      Running index over all points starting at 1
I I--/units            ['mm']                  .value is unit of geometry

roi_surface
I---/0
I I--/node_coord_up   [1.254, 1.762, 1.875;...] Coordinates of upper surface points
I I--/node_coord_mid  [1.254, 1.762, 1.875;...] Coordinates of middle surface points
I I--/node_coord_low  [1.254, 1.762, 1.875;...] Coordinates of lower surface points
I I--/tri_center_coord_up [1.254, 1.762, 1.875;...] Coordinates of upper triangle centers
I I--/tri_center_coord_mid [1.254, 1.762, 1.875;...] Coordinates of middle triangle centers
I I--/tri_center_coord_low [1.254, 1.762, 1.875;...] Coordinates of lower triangle centers
I I--/node_number_list [1,5,6,0;...;1,4,8,9] Connectivity of triangles [X, X, X]
I I--/delta            0.5                   Distance parameter between GM and WM surface
I I--/tet_idx_tri_center_up [183, 913, 56, ...] Tetrahedra indices where triangle center of
                                   upper surface are lying in
I I--/tet_idx_tri_center_mid [185, 911, 58, ...] Tetrahedra indices where triangle center of
                                   middle surface are lying in
I I--/tet_idx_tri_center_low [191, 912, 59, ...] Tetrahedra indices where triangle center of
                                   lower surface are lying in
I I--/tet_idx_node_coord_mid [12, 15, 43, ...] Tetrahedra indices where the node_coords_mid
                                   are lying in
I I--/gm_surf_fname    .../surf/lh.pial       Filename of GM surface from segmentation
I I--/wm_surf_fname    .../surf/lh.white      Filename of WM surface from segmentation
I I--/layer            3                     Number of layers
I I--/fn_mask          .../simnibs/mask.mgh   Filename of region of interest mask
I I--/X_ROI            [-10, 15]             X limits of region of interest box
I I--/Y_ROI            [-10, 15]             Y limits of region of interest box
I I--/Z_ROI            [-10, 15]             Z limits of region of interest box
I
I---/1
I I ...

roi_volume
I---/0
I I--/node_coord      [1.254, 1.762, 1.875;...] Coordinates (x,y,z) of ROI nodes
I I--/tet_node_number_list [1,5,6,7;...;1,4,8,9] Connectivity matrix of ROI tetrahedra
I I--/tri_node_number_list [1,5,6;...;1,4,8] Connectivity matrix of ROI triangles
I I--/tet_idx_node_coord [183, 913, 56, ...] Tetrahedra indices where ROI nodes are
I I--/tet_idx_tetrahedra_center [12, 15, 43, ...] Tetrahedra indices where center points of
                                   ROI tetrahedra are
I I--/tet_idx_triangle_center [12, 15, 43, ...] Tetrahedra indices where center points of
                                   ROI triangles are
I
I---/1
I I ...
```

`pynibs.hdf5_io.write_geo_hdf5_surf(out_fn, points, con, replace=False, hdf5_path='/mesh')`

Creates a .hdf5 file with geometry data from midlayer.

Parameters

- **out_fn** (*str*) – Filename of output .hdf5 file containing the geometry information.
- **points** (*np.ndarray*) – (N_points, 3) Coordinates of nodes (x,y,z).
- **con** (*np.ndarray*) – (N_tri, 3) Connectivity list of triangles.
- **replace** (*bool*) – Replace .hdf5 geometry file (True / False).
- **hdf5_path** (*str*, *default: '/mesh'*) – Folder in .hdf5 geometry file, where the geometry information is saved in.

Returns

<File> – File containing the geometry information.

Return type

.hdf5 file

Example

File structure of .hdf5 geometry file:

```
mesh
|---/elm
| |---/triangle_number_list [1,5,6;... ;1,4,8] Connectivity of triangles [X, X, X]
| |---/tri_tissue_type [1,1, ..., 3,3,3] Surface indices to differentiate between surfaces
|
|---/nodes
| |---/node_coord [1.2, 1.7, 1.8; ...] Node coordinates in (mm)
```

`pynibs.hdf5_io.write_geo_hdf5_vol(out_fn, points, con, replace=False, hdf5_path='/mesh')`

Creates a .hdf5 file with geometry data from midlayer.

Parameters

- **out_fn** (*str*) – Filename of output .hdf5 file containing the geometry information.
- **points** (*np.ndarray*) – (N_points, 3) Coordinates of nodes (x,y,z).
- **con** (*np.ndarray*) – (N_tri, 3) Connectivity list of triangles.
- **replace** (*bool*) – Replace .hdf5 geometry file (True / False).
- **hdf5_path** (*str*, *default: '/mesh'*) – Folder in .hdf5 geometry file, where the geometry information is saved in.

Returns

<File> – File containing the geometry information.

Return type

.hdf5 file

Example

File structure of .hdf5 geometry file:

```
mesh
|---/elm
| |---/triangle_number_list [1,5,6;... ;1,4,8] Connectivity of triangles [X, X, X]
| |---/tri_tissue_type [1,1, ..., 3,3,3] Surface indices to differentiate between surfaces
|
|---/nodes
| |---/node_coord [1.2, 1.7, 1.8; ...] Node coordinates in (mm)
```

`pynibs.hdf5_io.write_temporal_xdmf(hdf5_fn, data_folder='c', coil_center_folder=None, coil_ori_0_folder=None, coil_ori_1_folder=None, coil_ori_2_folder=None, coil_current_folder=None, hdf5_geo_fn=None, overwrite_xdmf=False, verbose=False)`

Creates .xdmf markup file for given ROI hdf5 data file with 4D data. This was written to be able to visualize data from the permutation analysis of the regression approach. It expects an .hdf5 with a data group with (many) subarrays. The N subarrays name should be named from 0 to N-1. Each subarray has shape (N_elems, 1).

Not tested for whole brain.

```
hdf5:/data_folder/0
/1
/2
/3
/4
...
```

Parameters

- **hdf5_fn** (*str*) – Filename of hdf5 file containing the data.
- **data_folder** (*str*) – Path within hdf5 to group of dataframes.
- **hdf5_geo_fn** (*str*, *optional*) – Filename of hdf5 file containing the geometry.
- **overwrite_xdmf** (*bool*) – Overwrite existing .xdmf file if present.
- **coil_center_folder** (*str*) –
- **coil_ori_0_folder** (*str*) –
- **coil_ori_1_folder** (*str*) –
- **coil_ori_2_folder** (*str*) –
- **coil_current_folder** (*str*) –
- **verbose** (*bool*) – Print output or not.

Returns

<File> – hdf5_fn[-4].xdmf

Return type

.xdmf file

```
pynibs.hdf5_io.write_xdmf(hdf5_fn, hdf5_geo_fn=None, overwrite_xdmf=False, overwrite_array=False,
                           verbose=False, mode='r+')
```

Creates .xdmf markup file for given hdf5 file, mainly for paraview visualization. Checks if triangles and tetrahedra already exists as distinct arrays in hdf5_fn. If not, these are added to the .hdf5 file and rebased to 0 (from 1). If only hdf5_fn is provided, spatial information has to be present as arrays for tris and tets in this dataset.

Parameters

- **hdf5_fn** (*str*) – Filename of hdf5 file containing the data
- **hdf5_geo_fn** (*str*, *optional*) – Filename of hdf5 file containing the geometry
- **overwrite_xdmf** (*bool*, *default: False*) – Overwrite existing xdmf file if present.
- **overwrite_array** (*bool*, *default: False*) – Overwrite existing arrays if present
- **verbose** (*bool*) – Print output.
- **mode** (*str*, *default: "r+"*) – Mode to open hdf5_geo file. If hdf5_geo is already separated in tets and tris etc., nothing has to be written, use “r” to avoid IOErrors in case of parallel computing.

Returns

- **fn_xml** (*str*) – Filename of the created .xml file
- <File> (*.xdmf file*) – hdf5_fn[-4].xdmf (only data if hdf5Geo_fn provided)
- <File> (*.hdf5 file*) – hdf5_fn changed if necessary
- <File> (*.hdf5 file*) – hdf5geo_fn containing spatial data

1.1.6 pynibs.muap module

`pynibs.muap.calc_mep_wilson(firing_rate_in, t, Qvmax=900, Qmmax=300, q=8, Tmin=14, N=100, M0=42, lam=0.002, tau0=0.006)`

Determine motor evoked potential from incoming firing rate

Parameters

- **firing_rate_in** (ndarray of float [n_t]) – Input firing rate from alpha motor neurons
- **t** (ndarray of float [n_t]) – Time axis in s
- **Qvmax** (float, optional, default: 900) – Max of incoming firing rate [1/s]
- **Qmmax** (float, optional, default: 300) – Max of MU firing rate [1/s]
- **q** (float, optional, default: 8) – Min firing rate of MU [1/s]
- **Tmin** (float, optional, default: 14) – Min MU threshold [1/s]
- **N** (float, optional, default: 100) – Number of MU
- **M0** (float, optional, default: 42) – Scaling constant of MU amplitude [mV/s]
- **lam** (float, optional, default: 0.002) – MUAP timescale of first order Hermite Rodriguez function [s]
- **tau0** (float, optional, default: 0.006) – Standard shift of MUAP to ensure causality [s]

Returns

mep – Motor evoked potential at surface electrode

Return type

ndarray of float [n_t]

`pynibs.muap.compute_signal(signal_matrix, sensor_matrix)`

Determine average signal from one single muscle fibre on all point electrodes

Parameters

- **signal_matrix** (ndarray of float [n_time x n_fibre]) – Signal matrix containing the action potential values for each time step in the rows
- **sensor_matrix** (ndarray of float [n_fibre x n_ele]) – Sensor matrix containing the inverse distances weighted with the anisotropy of muscle tissue

Returns

signal – Average signal detected all point electrodes

Return type

ndarray of float [n_time]

`pynibs.muap.create_electrode(l_x, l_z, n_x, n_z)`

Creates electrode coordinates

Parameters

- **l_x** (float) – X-extension of electrode in mm
- **l_z** (float) – Z-extension of electrode in mm
- **n_x** (int) – Number of point electrode in x-direction
- **n_z** (int) – Number of point electrodes in z-direction

Returns

electrode_coords – Coordinates of point electrodes (x, y, z)

Return typendarray of `float` [`n_ele` x 3]`pynibs.muap.create_muscle_coords(l_x, l_y, n_x, n_y, h)`

Create x and y coordinates of muscle fibres in muscle

Parameters

- `l_x` (`float`) – X-extension of muscle in mm
- `l_y` (`float`) – Y-extension of muscle in mm
- `n_x` (`int`) – Number of muscle fibres in x-direction
- `n_y` (`int`) – Number of muscle fibres in y-direction
- `h` (`float`) – Offset of muscle from electrode plane in mm

Returns`muscle_coords` – Coordinates of muscle fibres in x-y plane (x, y, z)**Return type**ndarray of `float` [`n_muscle` x 3]`pynibs.muap.create_muscle_fibre(x0, y0, L, n_fibre)`

Creates muscle fibre coordinates (in z-direction)

Parameters

- `x0` (`float`) – X-location of muscle fibre
- `y0` (`float`) – Y-location of muscle fibre
- `L` (`float`) – Length of muscle fibre
- `n_fibre` (`float`) – Number of discrete fibre elements

Returns`fibre_coords` – Coordinates of muscle fibre in z-direction (x, y, z)**Return type**ndarray of `float` [`n_fibre` x 3]`pynibs.muap.create_sensor_matrix(electrode_coords, fibre_coords, sigma_r=1, sigma_z=1)`

Create sensor matrix containing the inverse distances from the point electrodes to the fibre elements weighted by the anisotropy factor of the muscle tissue.

Parameters

- `electrode_coords` (ndarray of `float` [`n_ele` x 3]) – Coordinates of point electrodes (x, y, z)
- `fibre_coords` (ndarray of `float` [`n_fibre` x 3]) – Coordinates of muscle fibre in z-direction (x, y, z)
- `sigma_r` (`float`, optional, default: 1) – Radial conductivity of muscle
- `sigma_z` (`float`, optional, default: 1) – Axial conductivity of muscle along fibre

Returns`sensor_matrix` – Sensor matrix containing the inverse distances weighted with the anisotropy of muscle tissue**Return type**ndarray of `float` [`n_fibre` x `n_ele`]

`pynibs.muap.create_signal_matrix(T, dt, fibre_coords, z_e, v)`

Create signal matrix containing the travelling action potential on the fibre

Parameters

- **T** (*float*) – Total time
- **dt** (*float*) – Time step
- **fibre_coords** (*ndarray of float [n_fibre x 3]*) – Coordinates of muscle fibre in z-direction (x, y, z)
- **z_e** (*float*) – Location of action potential generation
- **v** (*float*) – Velocity of action potential

Returns

signal_matrix – Signal matrix containing the action potential values for each time step in the rows

Return type

ndarray of float [n_time x n_fibre]

`pynibs.muap.dipole_potential(z, loc, response)`

Returns dipole potential at given coordinates z (interpolates given dipole potential)

`pynibs.muap.hermite_rodriguez_1st(t, tau0=0, tau=0, lam=0.002)`

First order Hermite Rodriguez function to model surface MUAPs

Parameters

- **t** (*ndarray of float [n_t]*) – Time axis in s
- **tau0** (*float, optional, default: 0*) – initial shift to ensure causality in s
- **tau** (*float, optional, default: 0*) – shift (firing time) in s
- **lam** (*float, optional, default: 2*) – Timescale in s

Returns

y – Surface MUAP

Return type

ndarray of float [n_t]

`pynibs.muap.sfap(z, sigma_i=1.01, d=5.4999999999999995e-05, alpha=0.5)`

Single fibre propagating transmembrane current (second spatial derivative of transmembrane potential).

S. D. Nandedkar and E. V. Stalberg, “Simulation of single muscle fiber action potentials” Med. Biol. Eng. Comput., vol. 21, pp. 158–165, Mar. 1983.

J. Duchene and J.-Y. Hogrel, “A model of EMG generation,” IEEE Trans. Biomed. Eng., vol. 47, no. 2, pp. 192–200, Feb. 2000

Hamilton-Wright, A., & Stashuk, D. W. (2005). Physiologically based simulation of clinical EMG signals. IEEE Transactions on biomedical engineering, 52(2), 171-183.

Parameters

- **t** (*ndarray of float [n_t]*) – Time in (ms)
- **sigma_i** (*float, optional, default: 1.01*) – Intracellular conductivity in (S/m)
- **d** (*float, optional, default: 55*1e-6*) – Diameter of muscle fibre in (m)
- **v** (*float, optional, default: 1*) – Conduction velocity in (m/s)
- **alpha** (*float, optional, default: 0.5*) – Scaling factor to adjust length of AP

Returns

i – Transmembrane current of muscle fibre

Return type

ndarray of `float` [n_t]

`pynibs.muap.sfap_dip(z)`

`pynibs.muap.weight_signal_matrix(signal_matrix, fn_imp, t, z)`

Weight signal matrix with impulse response from single dipole at every location

1.1.7 pynibs.opt module

`pynibs.opt.calc_opt_gain_map(e_matrix_ref, e_matrix_opt, points, con, fn_out=None, threshold=0.75)`

Calculates the gain map between a reference e_matrix (e.g. from random sampling) and an optimized sequence of electric fields for mapping.

Parameters

- **e_matrix_ref** (`np.ndarray of float [n_ref, n_ele_roi]`) – Electric field matrix of reference simulations. E-fields in ROI are in the rows. (n_ref does not have to match n_opt)
- **e_matrix_opt** (`np.ndarray of float [n_opt, n_ele_roi]`) – Electric field matrix of optimal simulations. E-fields in ROI are in the rows. (n_ref does not have to match n_opt)
- **points** (`np.ndarray of float [n_points_roi, 3]`) – Node coordinates of the ROI.
- **con** (`np.ndarray of float [n_ele_roi, 3]`) – Connectivity matrix of ROI surface.
- **fn_out** (`str, optional, default: None`) – Filename of .hdf5 and .xdmf file for plots with paraview. (Without file extension)
- **threshold** (`float, optional, default: 0.75`) – Threshold of correlation the focality is quantified by area.

Returns

- **focality_ref** (`np.ndarray of float [n_ele_roi, 3]`) – Focality measure (area) of PSF in each element > threshold for reference case.
- **focality_opt** (`np.ndarray of float [n_ele_roi, 3]`) – Focality measure (area) of PSF in each element > threshold for optimal case.
- **focality_dif** (`np.ndarray of float [n_ele_roi, 3]`) – Difference between focality_opt and focality_ref quantifying absolute gain in mm². Values < 0 : Optimal solution has smaller PSF than reference if hotspot would be in this element. Values > 0 : Optimal solution has larger PSF than reference if hotspot would be in this element.
- **<file>** (`.hdf5 and .xdmf`) – Geo and data files for visualization in paraview.

`pynibs.opt.get_det_fim(x, fun, p, fim_matrix)`

Updates the Fisher Information Matrix and returns the negative determinant based on the sample x. It is a score how much information the additional sample yields.

Parameters

- **fun** (`function object`) – Function object defined in interval [0, 1].
- **x** (`float`) – Single sample location (interval [0, 1]).
- **p** (`dict`) – Dictionary containing the parameter estimates. The keys are the parameter names of fun.

- **fim_matrix** (*np.ndarray of float*) – (n_params, n_params) Fisher Information Matrix.

Returns

det – Determinant of the Fisher Information Matrix after adding sample x.

Return type

float

`pynibs.opt.get_fim_sample(fun, x, p)`

Get Fisher Information Matrix of one single sample.

Parameters

- **fun** (*function object*) – Function object the fisher information matrix is calculated for. The sample is passed as the first argument.
- **x** (*float*) – Sample passed to function.
- **p** (*dict*) – Dictionary containing the parameter estimates. The keys are the parameter names of fun.

Returns

fim_matrix – (n_params, n_params) Fisher information matrix.

Return type

np.ndarray of float

`pynibs.opt.get_optimal_coil_positions(e_matrix, criterion, n_stim, ele_idx_1=None, ele_idx_2=None, fn_out_hdf5=None, n_cpu=4, zap_idx_opt=None, regression_cmap=None, regression_fit_parameters=None, metrics_weights=None, overwrite=True, verbose=True, fn_coilpos_hdf5=None, start_zap_idx=-1, fim_fit_fun=None, fim_p2p_amps=None, fim_didt_list=None, fim_rmt_mso=None, fim_mso_didt_conversion_factor=1.43, fim_visited_positions_e_mat=None, fim_regression_n_refit=10, fim_debug_screenshot_dir_fn=None, fim_roi_pts=None, fim_roi_tris=None, fim_use_gpu=False)`

Determine set of optimal coil positions for TMS regression analysis.

Parameters

- **e_matrix** (*np.ndarray of float*) – (n_stim, n_ele) Matrix containing the electric field values in the ROI.
- **criterion** (*str*) – Optimization criterion: * “mc_cols”: Minimization of mutual coherence between columns * “mc_rows”: Minimization of mutual coherence between rows * “svd”: Minimization of condition number * “dist”: Equal distant sampling * “dist_svd”: Minimization of condition number and equidistant sampling * “dist_mc_cols”: Minimization of mutual coherence between columns and equidistant sampling * “dist_mc_rows”: Minimization of mutual coherence between rows and equidistant sampling * “coverage”: Maximizes the electric field coverage * “variability”: Maximizes variability between elements
- **n_stim** (*int*) – Maximum number of stimulations.
- **ele_idx_1** (*np.ndarray of int, optional*) – Element indices the first optimization goal is performed for. If None, all elements are considered.
- **ele_idx_2** (*np.ndarray of int, optional*) – Element indices the first optimization goal is performed for. If None, all elements are considered.
- **n_cpu** (*int*) – Number of threads.

- **fn_out_hdf5** (*str*, *optional*) – Returns the list of optimal zap indices if `fn_out_hdf5` is `None`, otherwise, save the results in `.hdf5` file. Filename of output `.hdf5` file where the zap index lists are saved in subfolder “zap_index_lists”
 - “zap_index_lists/0”: [213]
 - “zap_index_lists/1”: [213, 5]
 - etc
- **zap_idx_opt** (*list of int*, *optional*) – List of already selected optimal coil positions (those are ignored in the optimization and will not be picked again).
- **fim_fit_fun** (*function object*) – Function object defined in interval [0, 1] (only needed for fim optimization).
- **regression_fit_parameters** (*dict [n_ele]*, *optional*, *optional*) – The parameter estimates that should be used for the FIM optimization (whole ROI). The keys are the parameter names of `fun` (only needed for fim and dist optimization).
- **regression_cmap** (*np.ndarray of float [n_ele]*, *optional*, *optional*) – Congruence factor in each ROI element. Used to weight fim and dist optimization (only needed for fim and dist optimization).
- **metrics_weights** (*list of float [2]*, *default: [0.5, 0.5]*) – Weights of optimization criteria in case of multiple goal functions (`e_all_coil_pos.g.` `fim_svd`). Higher weight means higher importance for the respective criteria. By default both optimization criteria are weighted equally [0.5, 0.5].
- **overwrite** (*bool*, *default: True*) – Overwrite existing solutions or read existing `hdf5` file and continue optimization.
- **verbose** (*bool*, *default: True*) – Print output messages.
- **fn_coilpos_hdf5** (*str*) – File containing the corresponding coil positions and orientations (centers, `m0`, `m1`, `m2`).
- **start_zap_idx** (*int*, *default: 0*) – First zap index to start greedy search.
- **fim_didt_list** (*np.ndarray[float]*, (*len(zap_idx_opt)*)) – List of realized `dI/dt` of each of the already stimulated coil configurations in ‘zap_idx_opt’. Not required for any other metric than FIM.
- **fim_rmt_mso** (*int*) – Resting motor threshold used as the lower boundary of the FIM optimal e-field scaling. Unit in %MSO Not required for any other metric than FIM.
- **fim_mso_didt_conversion_factor** (*float*, *default: 1.43*) – Factor to convert between realized current (`dI/dt`) and percentage of maximum stimulator output (%MSO). Defaults to 1.43 describing the factor of a Magventure Pro with an MCF-B65 coil. Not required for any other metric than FIM.
- **fim_visited_positions_e_mat** (*np.ndarray[float]*, (*len(zap_idx_opt)*, *n_ele*), *optional*) – The efield matrix computed using the actually approached coil configurations. This is intended to make the FIM method even more precise by taking into account slight deviations in the approached coil configuration instead of relying on the static pre-computed coil configurations. Not required for any other metric than FIM.
- **fim_p2p_amps** (*np.ndarray[float]*, (*len(zap_idx_opt)*)) – EMG peak to peak amplitudes associated with the already collected (optimal) coil positions. Not required for any other metric than FIM.
- **fim_didt_list** – Realized current (`didt`) in TMS coil (as returned by the stimulator). of the already collected (optimal) coil positions. Not required for any other metric than FIM.
- **fim_regression_n_refit** (*float*) – Number of refits used in the $\text{mag}(E) \propto p2p$ regression during FIM optimization. Not required for any other metric than FIM.

- **fim_debug_screenshot_dir_fn** (*str*) – String representation of the fully qualified path to a directory where a 3D rendering of the the FIM optimal coil positions, ie coil positions that can reach the FIM optimal e-field strength at the current target hotspot given the MSO bounds [fim_rmt_mso, 100], should be saved. Not required for any other metric than FIM.
- **fim_roi_pts** (*np.ndarray, (n_points x 3)*) – Points (vertices) of ROI surface mesh (where the congruence scores should be computed on). Not required for any other metric than FIM.
- **fim_roi_tris** (*np.ndarray, (n_tris x 3)*) – Connectivity list of the 'fim_roi_points'. Not required for any other metric than FIM.
- **fim_use_gpu** (*bool*) – True: Use cupy and CUDA acceleration for the computation of the correlation matrix. False: Use Python multiprocessing for the computation of the correlation matrix. Not required for any other metric than FIM.

Returns

- **zap_idx_e_opt** (*list of int*) – (n_stim) Optimal zap indices.
- *<File> .hdf5 file* – Output file containing the zap index lists.

`pynibs.opt.get_optimal_sample_fim(fun, p, x=None)`

Determines optimal location of next sample by maximizing the determinant of the Fisher Information Matrix.

Parameters

- **fun** (*function object*) – Function object (interval [0, 1]).
- **x** (*np.ndarray of float, optional*) – Previous sample locations (interval [0, 1]).
- **p** (*dict*) – Dictionary containing the parameter estimates. The keys are the parameter names of fun.

Returns

x_opt – Optimal location of next sample (interval [0, 1]).

Return type

float

`pynibs.opt.init_fim_matrix(fun, x, p)`

Initializes the Fisher Information Matrix based on the samples given in x.

Parameters

- **fun** (*function object*) – Function object defined in interval [0, 1].
- **x** (*np.ndarray of float*) – Initial sample locations (interval [0, 1]).
- **p** (*dict*) – Dictionary containing the parameter estimates. The keys are the parameter names of fun.

Returns

fim_matrix – Fisher Information Matrix.

Return type

np.ndarray of float [n_params x n_params]

`pynibs.opt.online_optimization(fn_subject_hdf5, fn_roi_ss_indices_hdf5, fn_out_hdf5, fn_stimsites_hdf5, e_matrix, mep, mesh_idx, roi_idx, n_zaps_init=3, criterion_init='mc_rows', criterion='coverage', n_cpu=4, threshold=0.8, weights=None, eps0=0.01, eps0_dist=1, exponent=5, perc=99, n_refit=0, fun=<function sigmoid>, verbose=True)`

Performs virtual online optimization to determine the congruence factor. After an initial set of coil positions, the algorithm iteratively optimizes the next coil position based on the virtually measured MEP data.

Parameters

- **fn_subject_hdf5** (*str*) – Filename of subject .hdf5 file.
- **fn_roi_ss_indices_hdf5** (*str*) – Filename of .hdf5 file containing the element indices of the subsampled ROI in `f["roi_indices"]`.
- **e_matrix** (*np.ndarray of float*) – (*n_zaps*, *n_ele*) Electric field matrix.
- **mep** (*np.ndarray of float*) – (*n_zaps*) Motor evoked potentials for every stimulation.
- **fn_out_hdf5** (*str*) – Filename of .hdf5 output file containing the coil positions and the congruence factor maps for every iteration.
- **fn_stimsites_hdf5** (*str*) – Filename of the .hdf5 file containing the stimulation sites in “centers”, “m0”, “m1”, “m2”.
- **mesh_idx** (*int*) – Mesh index.
- **roi_idx** (*int*) – ROI index.
- **n_zaps_init** (*int*, *default:* 3) – Number of initial samples optimized using optimization criterion specified in `criterion_init`.
- **criterion_init** (*str*, *default:* “mc_rows”) – Optimization criterion for which the initial samples are optimized (e.g. “mc_rows”, “svd”, ...).
- **criterion** (*str*, *default:* “coverage”) – Optimization criterion for which the online optimization is performed (e.g. “coverage”, “mc_rows”, “svd”, ...).
- **n_cpu** (*int*, *optional*, *default:* 4) – Number of CPU cores to use.
- **threshold** (*float*, *default:* 0.1) – Threshold between [0 ... 1] of the maximal congruence factor. Elements where $c > \text{threshold} * \max(c)$ are included in the online optimization to select the next optimal coil position.
- **weights** (*list of float [2]*, *default:* [0.5, 0.5]) – Weights of optimization criteria in case of multiple goal functions (e.g. `fim_svd`). Higher weight means higher importance for the respective criteria. By default, both optimization criteria are weighted equally [0.5, 0.5].
- **eps0** (*float*, *default:* 0.01) – First error threshold to terminate the online optimization. The normalized root mean square deviation is calculated between the current and the previous solution. If the error is lower than `eps0` for 3 times in a row, the online optimization terminates and returns the results.
- **eps0_dist** (*float*, *default:* 1) – Second error threshold to terminate the online optimization. The geodesic distance in mm of the hotspot is calculated between the current and the previous solution. If the error is lower than `eps0_dist` for 3 times in a row, the online optimization terminates and returns the results.
- **exponent** (*float*, *default:* 5) – Exponent the congruence factor map is scaled $c^{**\text{exponent}}$.
- **perc** (*float*, *default:* 99) – Percentile the congruence factor map is normalized (between 0 and 100).
- **n_refit** (*int*, *default:* 0) – Number of refit iterations. No refit is applied if `n_refit=0`.
- **fun** (*function object*, *default:* `pynibs.linear`) – Function to use to determine the congruence factor (e.g. `pynibs.linear`, `pynibs.sigmoid`, ...).
- **verbose** (*bool*, *default:* True) – Plot output messages.

Returns

Results output file containing the coil positions and the congruence factor maps for every iteration.

Return type

<file> .hdf5 file

`pynibs.opt.rowvec_diff(candidate_coil_idcs, selected_coil_idcs, efields_diff_mat)`

Given a difference matrix (e.g. of row vectors/coil configurations) this function returns the coil configuration out of all available configurations exhibiting the highest minimum difference to the already selected configurations.

Parameters

- **candidate_coil_idcs** – `np.ndarray[int]` List of indices of coil configurations that are still available to pick for the optimized sequence.
- **selected_coil_idcs** – `np.ndarray[int]` List of indices of coil configurations that have already been selected for the optimized sequence.
- **efields_diff_mat** – `np.ndarray[float]`, `[n_coil, n_coil]` Difference matrix, where each cell denotes the magnitude of the difference vector between two coil configurations (determined by `row_idx, col_idx`).

Returns

coil_idx – index of coil configuration with maximal minimal difference to the set of already selected coil configurations.

Return type`int``pynibs.opt.workhors_rowvec_diff_prepare(idx_list, array, ele_idx_1)`

Computes the part of the difference matrix of row-vectors specified by the row indices in `idx_list`. Assumption: ‘`idx_list`’ must be sorted and valid within ‘`array`’.

Parameters

- **idx_list** – `typing.List[int]` List of row indices whose difference should be determined.
- **array** – `numpy.typing.ArrayLike` `[n_coil x n_ele]` E-field matrix of all possible coil positions.
- **ele_idx_1** – `numpy.typing.ArrayLike` `[n_ele]` Indices of the ROI elements that should be considered for optimization.

Returns

`numpy.typing.ArrayLike` `[array.shape[0] x array.shape[0]] = [n_rows x n_rows]` The difference matrix with the length of the difference vectors between pairs of row vectors specified by `idx_list`. All other (not calculated) pairs of row vectors have a score of 0 in this matrix.

`pynibs.opt.workhorse_coil_wise_corr(idx_list, array, ele_idx_1)`**Parameters**

- **idx_list** –
- **array** –
- **ele_idx_1** –

Returns`pynibs.opt.workhorse_coverage(idx_list, array, x, y, ele_idx_1)`

Determine coverage score (likelihood) for given zap indices in `idx_list`

Parameters

- **idx_list** (*list of lists* `[n_combs][n_zaps]`) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float* `[n_zaps x n_ele]`) – Electric field for different coil positions and elements.

- **x** (*np.ndarray of float [200 x n_ele]*) – x-values of coverage distributions, defined in interval [0, 1] (element wise normalized electric field).
- **y** (*np.ndarray of float [200 x n_ele]*) – y-values of coverage distributions (element wise probability of already included e-fields).
- **ele_idx_1** (*np.ndarray of float [n_roi]*) – Element indices for which the coverage optimization is performed for.

Returns

res – Coverage score (likelihood) for given electric field combinations. Lower values indicate that the new zap fills a gap which was not covered before.

Return type

np.ndarray of float [n_combs]

`pynibs.opt.workhorse_coverage_prepare(idx_list, array, zap_idx)`

Prepares coverage calculation. Determines coverage distributions for elements in `idx_list` given the zaps in `zap_idx`

Parameters

- **idx_list** (*list [n_ele]*) – Index lists of elements.
- **array** (*ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **zap_idx** (*ndarray of int*) – Included zaps in coverage distribution.

Returns

- **x** (*ndarray of float [200 x n_ele]*) – x-values of coverage distributions, defined in interval [0, 1] (element wise normalized electric field).
- **y** (*ndarray of float [200 x n_ele]*) – y-values of coverage distributions (element wise probability of already included e-fields).

`pynibs.opt.workhorse_dist(idx_list, array, ele_idx_1)`

Determines distance score for given zap indices in `idx_list`.

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float [n_ele]*) – Element indices for which the optimization is performed.

Returns

res – Distance based score. Lower values indicate more equidistant sampling (better)

Return type

np.ndarray of float [n_combs]

`pynibs.opt.workhorse_dist_mc(idx_list, array, ele_idx_1, ele_idx_2, mode='cols')`

Determines distance score and mutual coherence for given zap indices in `idx_list`. If `c_max_idx` is given, the distance based score is calculated only for this element. The condition number however is optimized for all elements in array.

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.

- **mode** (*str*, *default*: "cols") – Set if the mutual coherence is calculated w.r.t. columns or rows ("cols", "rows").
- **ele_idx_1** (*np.ndarray of float [n_ele]*) – Element indices for which the dist optimization is performed for.
- **ele_idx_2** (*np.ndarray of float [n_ele]*) – Element indices for which the mc optimization is performed for.

Returns

- **res_dist** (*np.ndarray of float [n_combs]*) – Distance based score. Lower values indicate more equidistant sampling (better).
- **res_mc** (*np.ndarray of float [n_combs]*) – Mutual coherence. Lower values indicate more orthogonal e-field combinations (better).

`pynibs.opt.workhorse_dist_svd(idx_list, array, ele_idx_1, ele_idx_2)`

Determines distance score and condition number for given zap indices in `idx_list`. If `c_max_idx` is given, the distance based score is calculated only for this element. The condition number however is optimized for all elements in `array`

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float [n_ele]*) – Element indices for which the dist optimization is performed for.
- **ele_idx_2** (*np.ndarray of float [n_ele]*) – Element indices for which the svd optimization is performed for.

Returns

- **res_dist** (*np.ndarray of float [n_combs]*) – Distance based score. Lower values indicate more equidistant sampling (better).
- **res_svd** (*np.ndarray of float [n_combs]*) – Condition number. Lower values indicate more orthogonal e-field combinations (better).

`pynibs.opt.workhorse_fim(idx_list, array, ele_idx_1, e_opt, c=None)`

Determine difference between e-fields and optimal e-field determined using the Fisher Information Matrix.

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float [n_roi]*) – Element indices for which the fim optimization is performed for.
- **e_opt** (*np.ndarray of float [n_roi]*) – Optimal electric field value(s) (target) determined by FIM method.
- **c** (*np.ndarray of float [n_ele], optional*) – Congruence factor map normalized to 1 (whole ROI) used to weight the difference between the optimal e-field and the candidate e-field. If None, no weighting is applied.

Returns

res – Difference between e-fields and optimal e-field.

Return type

np.ndarray of float [n_combs]

pynibs.opt.workhorse_fim_mc(idx_list, array, ele_idx_1, ele_idx_2, e_opt, c=None, mode='rows')

Determine difference between e-fields and optimal e-field determined using the Fisher Information Matrix and mutual coherence.

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float [n_roi_1]*) – Element indices for which the fim optimization is performed for.
- **ele_idx_2** (*np.ndarray of float [n_roi_2]*) – Element indices for which the mc optimization is performed for.
- **e_opt** (*float*) – Optimal electric field value (target) determined by FIM method.
- **c** (*np.ndarray of float [n_ele], optional*) – Congruence factor map normalized to 1 (whole ROI) used to weight the difference between the optimal e-field and the candidate e-field. If None, no weighting is applied.

Returns

- **res_fim** (*np.ndarray of float [n_combs]*) – Difference between e-fields and optimal e-field.
- **res_mc** (*np.ndarray of float [n_combs]*) – Mutual coherence. Lower values indicate more orthogonal e-field combinations (better)

pynibs.opt.workhorse_fim_svd(idx_list, array, ele_idx_1, ele_idx_2, e_opt, c=None)

Determine difference between e-fields and optimal e-field determined using the Fisher Information Matrix and condition number.

Parameters

- **idx_list** (*list of lists [n_combs][n_zaps]*) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float [n_zaps x n_ele]*) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float [n_roi_1]*) – Element indices for which the fim optimization is performed for.
- **ele_idx_2** (*np.ndarray of float [n_roi_2]*) – Element indices for which the svd optimization is performed for.
- **e_opt** (*float*) – Optimal electric field value (target) determined by FIM method.
- **c** (*np.ndarray of float [n_ele], optional*) – Congruence factor map normalized to 1 (whole ROI) used to weight the difference between the optimal e-field and the candidate e-field. If None, no weighting is applied.

Returns

- **res_fim** (*np.ndarray of float [n_combs]*) – Difference between e-fields and optimal e-field.
- **res_svd** (*np.ndarray of float [n_combs]*) – Condition number. Lower values indicate more orthogonal e-field combinations (better)

`pynibs.opt.workhorse_mc(idx_list, array, ele_idx_1, mode='cols')`

Determines mutual coherence for given zap indices in `idx_list`.

Parameters

- **idx_list** (*list of lists* `[n_combs][n_zaps]`) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float* `[n_zaps x n_ele]`) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float* `[n_ele]`) – Element indices for which the optimization is performed.
- **mode** (*str, default: "cols"*) – Set if the mutual coherence is calculated w.r.t. columns or rows (“cols”, “rows”).

Returns

res – Mutual coherence. Lower values indicate more orthogonal e-field combinations (better).

Return type

`np.ndarray of float [n_combs]`

`pynibs.opt.workhorse_roi_elmt_wise_corr(idx_list, array, ele_idx_1, decorrelate_hotspot_only=False, backend=<module 'numpy' from '/home/docs/checkouts/readthedocs.org/user_builds/pynibs/envs/latest/lib/python3.10/site-packages/numpy/__init__.py'>)`

Correlation :param `idx_list`: List of realized efields + 1 achievable e-field. Indices are for array. :type `idx_list`: list of int :param `array`: All e-fields. :type `array`: `np.ndarray` :param `ele_idx_1`: All element indices to compute corcoeff for. :type `ele_idx_1`: list of int :param `decorrelate_hotspot_only`: :param `backend`:

`pynibs.opt.workhorse_smooth(idx_list, array, ele_idx_1)`

`pynibs.opt.workhorse_svd(idx_list, array, ele_idx_1)`

Determines condition number for given zap indices in `idx_list`.

Parameters

- **idx_list** (*list of lists* `[n_combs][n_zaps]`) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float* `[n_zaps x n_ele]`) – Electric field for different coil positions and elements.
- **ele_idx_1** (*np.ndarray of float* `[n_ele]`) – Element indices for which the optimization is performed.

Returns

res – Condition number. Lower values indicate more orthogonal e-field combinations (better).

Return type

`np.ndarray of float [n_combs]`

`pynibs.opt.workhorse_var(idx_list, array, ele_idx_1)`

`pynibs.opt.workhorse_variability(idx_list, array, ele_idx_1)`

Determines variability score for given zap indices in `idx_list`.

Parameters

- **idx_list** (*list of lists* `[n_combs][n_zaps]`) – Index lists of zaps containing different possible combinations. Usually only the last index changes.
- **array** (*np.ndarray of float* `[n_zaps x n_ele]`) – Electric field for different coil positions and elements.

- **ele_idx_1** (*np.ndarray of float [n_ele]*) – Element indices for which the optimization is performed.

Returns

res – Condition number. Lower values indicate more orthogonal e-field combinations (better).

Return type

np.ndarray of float [n_combs]

1.1.8 pynibs.para module

pynibs.para.ResetSession()

Resets Paraview session (needed if multiple plots are generated successively)

pynibs.para.b2rcw(cmin_input, cmax_input)

BLUEWHITERED Blue, white, and red color map. This function is designed to generate a blue to red colormap. The color of the colorbar is from blue to white and then to red, corresponding to the data values from negative to zero to positive, respectively. The color white always corresponds to value zero. The brightness of blue and red will change according to your setting, so that the brightness of the color corresponded to the color of his opposite number. e.g. b2rcw(-3,6) is from light blue to deep red e.g. b2rcw(-3,3) is from deep blue to deep red

Parameters

- **cmin_input** (*float*) – Minimum value of data
- **cmax_input** (*float*) – Maximum value of data

Returns

newmap

Return type

nparray of float [N_RGB x 3]

pynibs.para.create_plot_settings_dict(plotfunction_type)

Creates a dictionary with default plotsettings.

Parameters

plotfunction_type (*str*) – Plot function the dictionary is generated for:

- 'surface_vector_plot'
- 'surface_vector_plot_vtu'
- 'volume_plot'
- 'volume_plot_vtu'

Returns

- **ps** (*dict*) – Dictionary containing the plotsettings:
- **axes** (*bool*) – Show orientation axes.
- **background_color** (*nparray*) – (1m 3) Set background color of exported image RGB (0...1).
- **calculator** (*str*) – Format string with placeholder of the calculator expression the quantity to plot is modified with, e.g.: "{ }^5".
- **clip_coords** (*nparray of float*) – (N_clips, 3) Coordinates of clip surface origins (x,y,z).
- **clip_normals** (*nparray of float*) – (N_clips, 3) Surface normals of clip surfaces pointing in the direction where the volume is kept for clip_type = ['clip' ...] (x,y,z).
- **clip_type** (*list of str*) – Type of clipping:

- 'clip': cut geometry but keep volume behind
- 'slice': cut geometry and keep only the slice
- **coil_dipole_scaling** (*list [1 x 2]*) – Specify the scaling type of the dipoles (2 entries):
coil_dipole_scaling[0]:
 - 'uniform': uniform scaling, i.e. all dipoles have the same size
 - 'scaled': size scaled according to dipole magnitude
 coil_dipole_scaling[1]:
 - scalar scale parameter of dipole size
- **coil_dipole_color** (*str or list*) – Color of the dipoles; either str to specify colormap (e.g. 'jet') or list of RGB values [1 x 3] (0...1)
- **coil_axes** (*bool, default: True*) – Plot coil axes visualizing the principle direction and orientation of the coil.
- **colorbar_label** (*str*) – Label of plotted data close to colorbar.
- **colorbar_position** (*list of float*) – (1, 2) Position of colorbar (lower left corner) 0...1 [x_pos, y_pos].
- **colorbar_orientation** (*str*) – Orientation of colorbar ('Vertical', 'Horizontal').
- **colorbar_aspectratio** (*int*) – Aspectratio of colorbar (higher values make it thicker).
- **colorbar_titlefontsize** (*float*) – Fontsize of colorbar title.
- **colorbar_labelfontsize** (*float*) – Fontsize of colorbar labels (numbers).
- **colorbar_labelformat** (*str*) – Format of colorbar labels (e.g.: '%e-#6.3g').
- **colorbar_numberoflabels** (*int*) – maximum number of colorbar labels.
- **colorbar_labelcolor** (*list of float*) – (1, 3) Color of colorbar labels in RGB (0...1).
- **colormap** (*str or nparray*) – If nparray [1 x 4*N]: custom colormap providing data and corresponding RGB values

$$\begin{bmatrix} data_1 & R_1 & G_1 & B_1 \\ data_2 & R_2 & G_2 & B_2 \\ \dots & \dots & \dots & \dots \\ data_N & R_N & G_N & B_N \end{bmatrix}$$

if str: colormap of plotted data chosen from included presets:

- 'Cool to Warm',
- 'Cool to Warm (Extended)',
- 'Blue to Red Rainbow',
- 'X Ray',
- 'Grayscale',
- 'jet',
- 'hsv',
- 'erdc_iceFire_L',
- 'Plasma (matplotlib)',
- 'Viridis (matplotlib)',
- 'gray_Matlab',
- 'Spectral_lowBlue',

- 'BuRd'
- 'Rainbow Blended White'
- 'b2rcw'
- **colormap_categories** (*bool*) – Use categorized (discrete) colormap.
- **datarange** (*list*) – (1, 2) Minimum and Maximum of plotted datarange [MIN, MAX] (default: automatic).
- **domain_IDs** (*int or list of int*) – Domain IDs surface plot: Index of surface where the data is plotted on (Default: 0) volume plot: Specify the domains IDs to show in plot (default: all) Attention! Has to be included in the dataset under the name 'tissue'! e.g. for SimNIBS:
 - 1 -> white matter (WM)
 - 2 -> grey matter (GM)
 - 3 -> cerebrospinal fluid (CSF)
 - 4 -> skull
 - 5 -> skin
- **domain_label** (*str*) – Label of the dataset which contains the domain IDs (default: 'tissue_type').
- **edges** (*BOOL*) – Show edges of mesh.
- **fname_in** (*str or list of str*) – Filenames of input files, 2 possibilities:
 - .xmdf-file: filename of .xmdf (needs the corresponding .hdf5 file(s) in the same folder)
 - .hdf5-file(s): filename(s) of .hdf5 file(s) containing the data and the geometry. The data can be provided in the first hdf5 file and the geometry can be provided in the second file. However, both can be also provided in a single hdf5 file.
- **fname_png** (*str*) – Name of output .png file (incl. path).
- **fname_vtu_volume** (*str*) – Name of .vtu volume file containing volume data (incl. path).
- **fname_vtu_surface** (*str*) – Name of .vtu surface file containing surface data (incl. path) (to distinguish tissues).
- **fname_vtu_coil** (*str*) – Name of coil .vtu file (incl. path) (optional).
- **info** (*str*) – Information about the plot the settings are belonging to.
- **interpolate** (*bool*) – Interpolate data for visual smoothness.
- **NanColor** (*list of float*) –
 - (3) RGB color values for “Not a Number” values (range 0 ... 1).
- **opacitymap** (*np.ndarray*) – Points defining the piecewise linear opacity transfer function (transparency) (default: no transparency) connecting data values with opacity (alpha) values ranging from 0 (max. transparency) to 1 (no transparency).

$$\begin{bmatrix} data_1 & opac_1 & 0.5 & 0 \\ data_2 & opac_2 & 0.5 & 0 \\ \dots & \dots & \dots & \dots \\ data_N & opac_N & 0.5 & 0 \end{bmatrix}$$
- **plot_function** (*str*) – Function the plot is generated with:
 - 'surface_vector_plot'
 - 'surface_vector_plot_vtu'

- 'volume_plot'
- 'volume_plot_vtu'
- **png_resolution** (*float*) – Resolution parameter of output image (1...5)
- **quantity** (*str*) – Label of magnitude dataset to plot
- **surface_color** (*nparray [1 x 3]*) – Color of brain surface in RGB (0...1) for better visibility of tissue borders
- **surface_smoothing** (*bool*) – Smooth the plotted surface (True/False)
- **show_coil** (*bool, default: True*) – show coil if present in dataset as block termed 'coil'
- **vcolor** (*nparray of float [N_vecs x 3]*) – Array containing the RGB values between 0...1 of the vector groups in dataset to plot
- **vector_mode** (*dict*) – dict key determines the type how many vectors are shown:
 - 'All Points'
 - 'Every Nth Point'
 - 'Uniform Spatial Distribution'
 dict value (int) is the corresponding number of vectors
 - 'All Points' (not set)
 - 'Every Nth Point' (every Nth vector is shown in the grid)
 - 'Uniform Spatial Distribution' (not set)
- **view** (*list*) – Camera position and angle [[3 x CameraPosition], [3 x CameraFocalPoint], [3 x CameraViewUp], 1 x CameraParallelScale]
- **viewsize** (*nparray [1 x 2]*) – Set size of exported image in pixel [width x height] will be extra scaled by parameter png_resolution
- **vlables** (*list of str*) – Labels of vector datasets to plot (other present datasets are ignored)
- **vscales** (*list of float*) – Scale parameters of vector groups to plot
- **vscale_mode** (*list of str [N_vecs x 1]*) – List containing the type of vector scaling:
 - 'off': all vectors are normalized
 - 'vector': vectors are scaled according to their magnitude

`pynibs.para.crop_data_hdf5_to_datarange(ps)`

Crops the data (quantity) in .hdf5 data file to datarange and overwrites the original .hdf5 data file pointed by the .xmdf file.

Parameters

ps (*dict*) – Plot settings dictionary created with `create_plotsettings_dict(plot_function)`

Returns

- **fn_hdf5** (*str*) – Filename (incl. path) of data .hdf5 file (read from .xmdf file)
- **<File>** (*.hdf5 file*) – *_backup.hdf5 backup file of original .hdf5 data file
- **<File>** (*.hdf5 file*) – Cropped data

`pynibs.para.crop_image(fname_image, fname_image_cropped)`

Remove surrounding empty space around an image. This implementation assumes that the surrounding space has the same colour as the top leftmost pixel.

Parameters

fname_image (*str*) – Filename of image to be cropped

Returns

<File> – Cropped image file saved as “fname_image_cropped”

Return type

.png file

`pynibs.para.surface_vector_plot(ps)`

Generate plot with Paraview from data in .hdf5 file(s).

Parameters

ps (*dict*) – Plot settings dict initialized with create_plot_settings_dict(plotfunction_type='surface_vector_plot')

Returns

<File> – Generated plot

Return type

.png file

`pynibs.para.surface_vector_plot_vtu(ps)`

Generate plot with Paraview from data in .vtu file.

Parameters

ps (*dict*) – Plot settings dict initialized with create_plot_settings_dict(plotfunction_type='surface_vector_plot_vtu')

Returns

<File> – Generated plot

Return type

.png file

`pynibs.para.volume_plot(ps)`

Generate plot with Paraview from data in .hdf5 file.

Parameters

ps (*dict*) – Plot settings dict initialized with create_plot_settings_dict(plotfunction_type='volume_plot')

Returns

<File> – Generated plot

Return type

.png file

`pynibs.para.volume_plot_vtu(ps)`

Generate plot with Paraview from data in .vtu file.

Parameters

ps (*dict*) – Plot settings dict initialized with create_plot_settings_dict(plotfunction_type='volume_plot_vtu')

Returns

<File> – Generated plot

Return type

.png file

`pynibs.para.write_vtu(fname, data_labels, points, connectivity, idx_start, data)`

Writes data in tetrahedra centers into .vtu file, which can be loaded with Paraview.

Parameters

- **fname** (*str*) – Name of .vtu file (incl. path)
- **data_labels** (*list with N_data str*) – Label of each dataset
- **points** (*array of float [N_points x 3]*) – Coordinates of vertices

- **connectivity** (array of *int* [*N_tet* x 4]) – Connectivity of points forming tetrahedra
- **idx_start** (*int*) – Smallest index in connectivity matrix, defines offset w.r.t Python indexing, which starts at '0'
- ***data** (array(s) [*N_tet* x *N_comp(N_data)*]) – Arrays containing data in tetrahedra center multiple components per dataset possible e.g. [Ex, Ey, Ez]

Returns

<File> – Geometry and data information

Return type

.vtu file

pynibs.para.**write_vtu_coilpos**(*fname_geo*, *fname_vtu*)

Read dipole data of coil (position and magnitude of each dipole) from geo file and store it as vtu file.

Parameters

- **fname_geo** (*str*) – .geo file from SimNIBS.
- **fname_vtu** (*str*) – .vtu output file. Nodes and nodedata.

Returns

<File> – Magnetic dipoles of the TMS coil

Return type

.vtu file

pynibs.para.**write_vtu_mult**(*fname*, *data_labels*, *points*, *triangles*, *tetrahedras*, *idx_start*, **data*)

Writes data in triangles and tetrahedra centers into .vtu file, which can be loaded with Paraview.

Parameters

- **fname** (*str*) – Name of .vtu file (incl. path)
- **data_labels** (list of *str* [*N_data*]) – Label of each dataset
- **points** (nparray of *float* [*N_points* x 3]) – Coordinates of vertices
- **triangles** (nparray of *int* [*N_tri* x 3]) – Connectivity of points forming triangles
- **tetrahedras** (nparray of *int* [*N_tri* x 4]) – Connectivity of points forming tetrahedra *idx_start*: int smallest index in connectivity matrix, defines offset w.r.t python indexing, which starts at '0'
- ***data** (nparray(s) [*N_tet* x *N_comp(N_data)*]) – Arrays containing data in tetrahedra center multiple components per dataset possible e.g. [Ex, Ey, Ez]

Returns

<File> – Geometry and data information

Return type

.vtu file

1.1.9 pynibs.roi module

class pynibs.roi.CorticalLayer(*create_key, id, volumetric_mesh=None, roi=None, depth=None, path=None, surface=None*)

Bases: `object`

class Settings

Bases: `object`

GRID_POINTS_PER_MM = 1.5

NUM_TRIANGLE_SMOOTHING_STEPS = 30

ROI_SIZE_OFFSET = 5

TAG_GRAY_MATTER_SURF = 1002

TAG_GRAY_MATTER_VOL = 2

TAG_WHITE_MATTER_SURF = 1001

TAG_WHITE_MATTER_VOL = 1

classmethod create_in_bbox(*id, bbox, depth, volmesh*)

Factory method for constructing a CorticalLayer-object within a region-of-interest and a specified cortical depth.

Parameters

- **id** (`str`) – Identifier of the layer.
- **bbox** (`List[float]`) – List of bounding values around the ROI box: [x_min, x_max, y_min, y_max, z_min, z_max].
- **depth** (`float`) – Normalized distance of the layer from gray matter surface. Provide values in the open interval (0,1)
- **volmesh** (`simnibs.Msh`) – The tetrahedral volume mesh, in which the layer should be generated.

classmethod create_in_roi(*id, roi, depth, volmesh*)

Factory method for constructing a CorticalLayer-object within a region-of-interest and a specified cortical depth.

Parameters

- **id** (`str`) – Identifier of the layer.
- **roi** (`RegionOfInterestSurface instance`) – RegionOfInterestSurface
- **depth** (`float`) – Normalized distance of the layer from gray matter surface. Provide values in the open interval (0,1)
- **volmesh** (`simnibs.Msh`) – The tetrahedral volume mesh, in which the layer should be generated.

static crop_mesh_with_box(*mesh, roi, keep_elements=False*)

Returns the cropped mesh with all points that are inside the region of interest

Parameters

- **keep_elements** (`bool`, `default = False`) – If True, keeps elements with at least one point in roi, else removes them.
- **mesh** (`simnibs.Msh`) – The mesh that is supposed to be cropped.
- **roi** (`List[float]`) – The bounding box of the region of interest which the mesh should be cropped to. [x-min, x-max, y-min, y-max, z-min, z-max]

Returns

mesh_cropped – The cropped mesh.

Return type

`simnibs.Msh`

static `crop_mesh_with_surface(mesh, roi, keep_elements=False, radius=3)`

Returns the cropped mesh with all points that are close to the surface of interest

Parameters

- **keep_elements** (*bool*, *default* = *False*) – If True, keeps elements with at least one point in roi, else removes them.
- **mesh** (*simnibs.Msh*) – The mesh that is supposed to be cropped.
- **roi** (*RegionOfInterestSurface* *instance*) – *RegionOfInterestSurface*
- **radius** (*float*, *default* = *3*) – Search radius of mesh elements around ROI nodes

Returns

mesh_cropped – The cropped mesh.

Return type

`simnibs.Msh`

generate_layer(depth, roi)

Create the geometry of the layer at the specified depth using marching cubes.

Parameters

- **depth** (*float*) – The depth below the GM surface at which the layer should be generated; in [0,1].
- **roi** (*RegionOfInterestSurface* *instance*) – *RegionOfInterestSurface*

get_evenly_spaced_element_subset(elements_per_square_mm)

Subsample the surface representation of the ayer.

Parameters

elements_per_square_mm (*float*) – Number of triangles per mm² in the layer.

Returns

selected elements – List of indices of selected elements as a result of the subsampling.

Return type

`typing.List[int]`

get_smoothed_normals()

Computed the smoothed normals of the surface representation of this layer.

Note: For the later stages, we don't want a smoothed surface, but smooth normals in order to maintain the location of the cells, but orient them more smoothly. Therefore, we use smoothed normals, e.g. for the computation of the theta angle, but do not smooth the entire layer surface.

Returns

normals – The tetrahedral volume mesh, in which the layer should be generated.

Return type

`np.ndarray`

classmethod `init_from_file(id, fn)`

Factory method for constructing a *CorticalLayer*-object from a file.

Parameters

- **id** (*str*) – Identifier of the layer.
- **fn** (*str*) – File path to a region of interest surfe (e.g. midlayer).

classmethod `init_from_surface(id, surf)`

Factory method for constructing a CorticalLayer-object from a Simnibs-surface object.

Parameters

- **id** (*str*) – Identifier of the layer.
- **surf** (*simnibs.Msh*) – The surface representation of an already existing layer (e.g. midlayer).

remove_unconnected_surfaces()

Remove elements small unconnected element-clusters from this layer.

static `roi_bbox_from_points(points, offset=0)`

Find the minimal bounding box around the provided points.

Parameters

- **points** (*simnibs.Msh*) – The tetrahedral volume mesh, in which the layer should be generated.
- **offset** (*float*) – Normalized distance of the layer from gray matter surface. Provide values in the open interval (0,1)

Returns

bounding_box – List of bounding values around the provided points: [x_min, x_max, y_min, y_max, z_min, z_max].

Return type

List[float]

save(fn)

Save the current surface representation of this CorticalLayer instance at the specified location.

Parameters

fn (*str*) – Target file name of the surface-file of this layer.

class `pynibs.roi.RegionOfInterestSurface`

Bases: *object*

Region of interest (surface).

node_coord_up

(N_points, 3) Coordinates (x,y,z) of upper surface nodes

Type

np.ndarray

node_coord_mid

(N_points, 3) Coordinates (x,y,z) of middle surface nodes

Type

np.ndarray

node_coord_low

(N_points, 3) Coordinates (x,y,z) of lower surface nodes

Type

np.ndarray

node_number_list

(N_points, 3) Connectivity matrix of triangles

Type

np.ndarray

delta

Distance parameter between WM and GM (0 -> WM, 1 -> GM)

Type

float

tet_idx_tri_center_up

Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the upper surface are lying in

Type

np.ndarray [N_points]

tet_idx_tri_center_mid

Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the middle surface are lying in

Type

np.ndarray [N_points]

tet_idx_tri_center_low

Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the lower surface are lying in

Type

np.ndarray [N_points]

tet_idx_node_coord_mid

(N_tri,) Tetrahedra indices of TetrahedraLinear object instance where the nodes of the middle surface are lying in

Type

np.ndarray

tri_center_coord_up

(N_tri, 3) Coordinates of roi triangle center of upper surface

Type

np.ndarray

tri_center_coord_mid

(N_tri, 3) Coordinates of roi triangle center of middle surface

Type

np.ndarray

tri_center_coord_low

(N_tri, 3) Coordinates of roi triangle center of lower surface

Type

np.ndarray

fn_mask

Filename for surface mask in subject space. .mgh file or freesurfer surface file.

Type

string

fn_mask_avg

Filename for .mgh mask in fsaverage space. Absolute path or relative to mesh folder.

Type

string

fn_mask_nii

Filename for .nii or .nii.gz mask. Absolute path or relative to mesh folder.

Type

string

X_ROI

Region of interest [Xmin, Xmax], whole X range if empty [0,0] or None (left - right)

Type

list of float

Y_ROI

Region of interest [Ymin, Ymax], whole Y range if empty [0,0] or None (anterior - posterior)

Type

list of float

Z_ROI

Region of interest [Zmin, Zmax], whole Z range if empty [0,0] or None (inferior - superior)

Type

list of float

template

‘MNI’, ‘fsaverage’, ‘subject’

Type

str

center

Center coordinates for spherical ROI in self.template space

Type

list of float

radius

Radius in [mm] for spherical ROI

Type

float

gm_surf_fname

Filename(s) of GM surface generated by freesurfer (lh and/or rh) (e.g. in mri2msh: .../fs_ID/surf/lh.pial)

Type

str or list of str

wm_surf_fname

Filename(s) of WM surface generated by freesurfer (lh and/or rh) (e.g. in mri2msh: .../fs_ID/surf/lh.white)

Type

str or list of str

layer

Define the number of layers:

- 1: one layer
- 3: additionally upper and lower layers are generated around the central midlayer

Type

int

decimate(*fraction=0.075*)

Subsample ROI surface based on a decimation factor and return element indices. (no Freesurfer surfaces associated with the ROI surface required)

Parameters

fraction (*float*, *default:* .075) – Multiplied by the total number of ROI elements determines (approximately) the number of remaining ROI elements after decimation.

Returns

ele_idx – [approx. *fraction* * *n_ele*] Element indices of the subsampled surface; sorted.

Return type

np.ndarray of *float*

determine_element_idx_in_msh(*msh*)

Determines tetrahedra indices of *msh* where the triangle center points of upper, middle and lower surface and the nodes of middle surface are lying in.

Parameters

msh (*pynibs.mesh.mesh_struct.TetrahedraLinear*) – TetrahedraLinear object.

Returns

- **RegionOfInterestSurface.tet_idx_tri_center_up** (*np.ndarray*) – (*N_points*) Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the upper surface are lying in.
- **RegionOfInterestSurface.tet_idx_tri_center_mid** (*np.ndarray*) – (*N_points*) Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the middle surface are lying in.
- **RegionOfInterestSurface.tet_idx_tri_center_low** (*np.ndarray*) – (*N_points*) Tetrahedra indices of TetrahedraLinear object instance where the center points of the triangles of the lower surface are lying in.
- **RegionOfInterestSurface.tet_idx_node_coord_mid** (*np.ndarray*) – (*N_tri*) Tetrahedra indices of TetrahedraLinear object instance where the nodes of the middle surface are lying in.

generate_cortical_laminae(*head_model_mesh*, *bbox=None*, *laminae=(0.06, 0.4, 0.55, 0.65, 0.85)*, *layer_ids=('L1', 'L23', 'L4', 'L5', 'L6')*)

Create the cortical layering with the provided laminar depths.

Defaults to the standard depths of the laminae in the neo-cortex from layer I to VI from “Simulation of transcranial magnetic stimulation in head model with morphologically-realistic cortical neurons”, Aberra et al., <https://doi.org/10.1016/j.brs.2019.10.002>

Parameters

- **head_model_mesh** (*simnibs.Msh*) – The head model volume mesh. Inside the GM compartment of this mesh, the layering will be generated.
- **bbox** (*np.ndarray*, *optional*) – Bounding coordinates of the region of interest. Optional, if the mid-layer surface is already existing (and can thus be used to determine the bounding coordinates).
- **laminae** (*Dict[str, float]* | *Tuple*) – List of depths of the individual to-be created laminae.

make_GM_WM_surface(*gm_surf_fname=None*, *wm_surf_fname=None*, *midlayer_surf_fname=None*, *mesh_folder=None*, *delta=0.5*, *x_roi=None*, *y_roi=None*, *z_roi=None*, *layer=1*, *fn_mask=None*, *refine=False*)

Generating a surface between WM and GM in a distance of delta 0...1 for ROI, given by Freesurfer mask or coordinates.

Parameters

- **gm_surf_fname** (*str* or *list of str*) – Filename(s) of GM FreeSurfer surface(s) (lh and/or rh). Either relative to mesh_folder (fs_ID/surf/lh.pial) or absolute (/full/path/to/lh.pial)
- **wm_surf_fname** (*str* or *list of str*) – Filename(s) of WM FreeSurfer surface(s) (lh and/or rh) Either relative to mesh_folder (fs_ID/surf/lh.white) or absolute (/full/path/to/lh.white)
- **midlayer_surf_fname** (*str* or *list of str*) – Filename(s) of midlayer surface (lh and/or rh) Either relative to mesh_folder (fs_ID/surf/lh.central) or absolute (/full/path/to/lh.central)
- **mesh_folder** (*str*) – Root folder of mesh, Needed if paths above are given relative, or refine=True
- **m2m_mat_fname** (*[defunct]*) – Filename of mri2msh transformation matrix (e.g. in mri2msh: .../m2m_ProbandID/MNI2conform_6DOF.mat)
- **delta** (*float*) – Distance parameter where surface is generated 0...1 (default: 0.5)
 - 0 -> WM surface
 - 1 -> GM surface
- **x_roi** (*list of float*) – Region of interest [Xmin, Xmax], whole X range if empty [0,0] or None (left - right)
- **y_roi** (*list of float*) – Region of interest [Ymin, Ymax], whole Y range if empty [0,0] or None (anterior - posterior)
- **z_roi** (*list of float*) – Region of interest [Zmin, Zmax], whole Z range if empty [0,0] or None (inferior - superior)
- **layer** (*int*) – Define the number of layers:
 - 1: one layer
 - 3: additionally upper and lower layers are generated around the central midlayer
- **fn_mask** (*str*) – Filename for FreeSurfer .mgk mask.
- **refine** (*bool, optional, default: False*) – Refine ROI by splitting elements

Returns

- **node_coord_up** (*np.ndarray of float [N_roi_points x 3]*) – Node coordinates (x, y, z) of upper epsilon layer of ROI surface
- **node_coord_mid** (*np.ndarray of float [N_roi_points x 3]*) – Node coordinates (x, y, z) of ROI surface
- **node_coord_low** (*np.ndarray of float [N_roi_points x 3]*) – Node coordinates (x, y, z) of lower epsilon layer of ROI surface
- **node_number_list** (*np.ndarray of int [N_roi_tri x 3]*) – Connectivity matrix of intermediate surface layer triangles
- **delta** (*float*) – Distance parameter where surface is generated 0...1 (default: 0.5)
 - 0 -> WM surface
 - 1 -> GM surface
- **tri_center_coord_up** (*np.ndarray of float [N_roi_tri x 3]*) – Coordinates (x, y, z) of triangle center of upper epsilon layer of ROI surface
- **tri_center_coord_mid** (*np.ndarray of float [N_roi_tri x 3]*) – Coordinates (x, y, z) of triangle center of ROI surface

- **tri_center_coord_low** (*np.ndarray of float [N_roi_tri x 3]*) – Coordinates (x, y, z) of triangle center of lower epsilon layer of ROI surface
- **fn_mask** (*str*) – Filename for freesurfer mask. If given, this is used instead of *_ROIs
- **X_ROI** (*list of float*) – Region of interest [Xmin, Xmax], whole X range if empty [0,0] or None (left - right)
- **Y_ROI** (*list of float*) – Region of interest [Ymin, Ymax], whole Y range if empty [0,0] or None (anterior - posterior)
- **Z_ROI** (*list of float*) – Region of interest [Zmin, Zmax], whole Z range if empty [0,0] or None (inferior - superior)

Example

```
make_GH_WM_surface(self, gm_surf_fname, wm_surf_fname, delta, X_ROI, Y_ROI, Z_ROI)
make_GH_WM_surface(self, gm_surf_fname, wm_surf_fname, delta, mask_fn, layer=3)
```

project_on_midlayer(*target, verbose=False*)

Project a coordinate on the nearest midlayer node

Parameters

- **target** (*np.ndarray*) – Coordinate to project as (3,) array
- **verbose** (*bool*) – Print some verbosity information. Default: False

Returns

target_proj – Node coordinate of nearest midlayer node.

Return type

np.ndarray

subsample(*dist=10, fn_sphere=None*)

Subsample ROI surface based on a spacing and return element indices (Freesurfer surfaces associated with the ROI surface required)

Parameters

- **dist** (*float*) – Distance in mm the subsampled points lie apart.
- **fn_sphere** (*str*) – Name of ?.sphere file (freesurfer).

Returns

ele_idx – (n_ele) Element indices of the subsampled surface.

Return type

ndarray of float

class pynibs.roi.RegionOfInterestVolume

Bases: *object*

Region of interest (volume) class

node_coord

Coordinates (x,y,z) of ROI tetrahedra nodes.

Type

np.ndarray [N_points x 3]

tet_node_number_list

Connectivity matrix of ROI tetrahedra.

Type

np.ndarray [N_tet_roi x 3]

tri_node_number_list

Connectivity matrix of ROI tetrahedra.

Type

np.ndarray [N_tri_roi x 3]

tet_idx_node_coord

Tetrahedra indices of TetrahedraLinear object instance where the ROI nodes are lying in.

Type

np.ndarray [N_points]

tet_idx_tetrahedra_center

(N_tet_roi) Tetrahedra indices of TetrahedraLinear object instance where the center points of the ROI tetrahedra are lying in.

Type

np.ndarray

tet_idx_triangle_center

(N_tri_roi) Tetrahedra indices of TetrahedraLinear object instance where the center points of the ROI triangle are lying in. If the ROI is directly generated from the msh instance using “make_roi_volume_from_msh”, these indices are the triangle indices of the head mesh since the ROI mesh and the head mesh are overlapping. If the ROI mesh is not the same as the head mesh, the triangle center of the ROI mesh are always lying in a tetrahedra of the head mesh (these indices are given in this case).

Type

np.ndarray

make_roi_volume_from_msh(*msh*, *volume_type*='box', *x_roi*=None, *y_roi*=None, *z_roi*=None)

Generate region of interest (volume) and extract nodes, triangles and tetrahedra from msh instance.

Parameters

- **msh** (`pynibs.mesh.mesh_struct.TetrahedraLinear`) – Mesh object instance of type TetrahedraLinear
- **volume_type** (*str*) – Type of ROI ('box' or 'sphere')
- **x_roi** (*list of float*) –
 - type = 'box': [Xmin, Xmax] (in mm), whole X range if empty [0,0] or None (left - right)
 - type = 'sphere': origin [x,y,z]
- **y_roi** (*list of float*) –
 - type = 'box': [Ymin, Ymax] (in mm), whole Y range if empty [0,0] or None (anterior - posterior)
 - type = 'sphere': radius (in mm)
- **z_roi** (*list of float*) –
 - type = 'box': [Zmin, Zmax] (in mm), whole Z range if empty [0,0] or None (inferior - superior)
 - type = 'sphere': None

Returns

- **RegionOfInterestVolume.node_coord** (*np.ndarray [N_points x 3]*) – Coordinates (x,y,z) of ROI tetrahedra nodes
- **RegionOfInterestVolume.tet_node_number_list** (*np.ndarray [N_tet_roi x 3]*) – Connectivity matrix of ROI tetrahedra

- **RegionOfInterestVolume.tri_node_number_list** (*np.ndarray [N_tri_roi x 3]*) – Connectivity matrix of ROI tetrahedra
- **RegionOfInterestVolume.tet_idx_node_coord** (*np.ndarray [N_points]*) – Tetrahedra indices of TetrahedraLinear object instance where the ROI nodes are lying in
- **RegionOfInterestVolume.tet_idx_tetrahedra_center** (*np.ndarray [N_tet_roi]*) – Tetrahedra indices of TetrahedraLinear object instance where the center points of the ROI tetrahedra are lying in
- **RegionOfInterestVolume.tet_idx_triangle_center** (*np.ndarray [N_tri_roi]*) – Tetrahedra indices of TetrahedraLinear object instance where the center points of the ROI triangle are lying in. If the ROI is directly generated from the msh instance using “make_roi_volume_from_msh”, these indices are the triangle indices of the head mesh since the ROI mesh and the head mesh are overlapping. If the ROI mesh is not the same as the head mesh, the triangle center of the ROI mesh are always lying in a tetrahedra of the head mesh (these indices are given in this case)

`pynibs.roi.clean_roi(img, vox_thres=0.5, fn_out=None)`

Remove values < vox thres from image.

Parameters

- **img** (*str or nibabel.nifti1.Nifti1Image*) –
- **vox_thres** (*float, optional*) –
- **fn_out** (*str*) –

Returns

- **img_thres** (*nibabel.nifti1.Nifti1Image*)
- **img_thres** (<file>) – If fn_out is specified, thresholded image is saved here

`pynibs.roi.create_refine_spherical_roi(center, radius, final_tissues_nii, out_fn, target_size=0.5, outside_size=None, outside_factor=3, out_spher_fn=None, tissue_types=None, verbose=False)`

Create a spherical roi nifti for simnibs 4 refinement. Only tissue types according to _tissue_types will be refined.

Use the resulting output file as input for –sizing_field in SimNIBS-4/simnibs/cli/meshmesh.py

Parameters

- **center** (*list of float*) – Center of spherical ROI in mm
- **radius** (*float*) – Radius of spherical ROI in mm
- **final_tissues_nii** (*string or nib.nifti1.Nifti1Image*) – final_tissues.nii.gz to create roi for.
- **out_fn** (*str*) – Final output filename
- **target_size** (*float, default = 0.5*) – Target element size of refined areas in mm (?)
- **outside_size** (*float, default = None*) – Element size outside of target size.
- **outside_factor** (*float, default = None*) – Distance factor to define the ‘outside’ area: outsidefactor * radius -> outside
- **out_spher_fn** (*str, optional*) – Output filename of original, raw spherical ROI
- **tissue_types** (*list of float, default = [1, 2, 3]*) – Which tissue types to refine. Defaults to WM, GM, CSF
- **verbose** (*bool, optional, default=False*) – Print additional information

`pynibs.roi.determine_element_idx_in_mesh(fname, msh, points, compute_baricentric=False)`

Finds the tetrahedron that contains each of the described points using a stochastic walk algorithm. Implemented from Devillers et al. (2002) [1]

Parameters

- **msh** (`pynibs.mesh.mesh_struct.TetrahedraLinear`) –
- **fname** (`str` or `None`) – Filename of saved .txt file containing the element indices (no data is saved when `fname=None` or `fname=""`)
- **points** (`np.ndarray (N, 3)` or `list of np.ndarray`) – List of points to be queried
- **compute_baricentric** (`bool`) – Whether or not to compute baricentric coordinates of the points

Returns

- **th_with_points** (`np.ndarray`) – List with the tetrahedron that contains each point. If the point is outside the mesh, the value will be -1
- **baricentric** (`np.ndarray [n, 4]` (if `compute_baricentric == True`)) – Baricentric coordinates of point. If the point is outside, a list of zeros

Notes

`pynibs.roi.elem_workhorse(chunk, points_out, P1_all, P2_all, P3_all, P4_all, N_points_total, N_CPU)`

Parameters

- **chunk** (`np.ndarray`) – Indices of points the CPU thread is computing the element indices for
- **points_out** (`np.ndarray of float`) – (N_points, 3) Coordinates of points, the tetrahedra indices are computed for
- **P1_all** (`np.ndarray of float`) –
- **(N_tet** –
- **tetrahedra** (3) *Coordinates of first point of* –
- **P2_all** (`np.ndarray of float`) – (N_tet, 3) Coordinates of second point of tetrahedra
- **P3_all** (`np.ndarray of float`) – (N_tet, 3) Coordinates of third point of tetrahedra
- **P4_all** (`np.ndarray of float`) – (N_tet, 3) Coordinates of fourth point of tetrahedra
- **N_points_total** (`int`) – Total number of points
- **N_CPU** (`int`) – Number of CPU cores to use

Returns

tet_idx_local

Return type

`np.ndarray of int (N_points,)`

`pynibs.roi.get_mask(areas, fn_annot, fn_inflated_fs, fn_out)`

Determine freesurfer average mask .overlay file, which is needed to generate subject specific ROIs.

Parameters

- **areas** (`list of str`) – Brodmann areas (e.g. ['Brodmann.6', 'Brodmann.4', 'Brodmann.3', 'Brodmann.1'])

- **fn_annot** (*str*) – Annotation file of freesurfer (e.g. 'FREESURFER_DIR/fsaverage/label/lh.PALS_B12_Brodmann.annot')
- **fn_inflated_fs** (*str*) – Inflated surface of freesurfer average (e.g. 'FREESURFER_DIR/fsaverage/surf/lh.inflated')
- **fn_out** (*str*) – Filename of .overlay file of freesurfer mask

Returns

<File> – fn_out.overlay file of freesurfer mask

Return type

.overlay file

`pynibs.roi.get_sphere_in_nii(center, radius, nii=None, out_fn=None, thresh_by_nii=True, val_in=1, val_out=0, outside_val=0, outside_radius=inf)`

Computes a spherical ROI for a given Nifti image (defaults to SimNIBS MNI T1 tissue). The ROI area is defined in nifti coordinates. By default, everything inside the ROI is set to 1, areas outside = 0. The ROI is further thresholded by the nifti. A nib.Nifti image is returned and optionally saved.

Parameters

- **center** (*array-like*) – X, Y, Z coordinates in nifti space
- **radius** (*float*) – radius of sphere
- **nii** (*string or nib.nifti1.Nifti1Image, optional*) – The nifti image to work with.
- **out_fn** (*string, optional*) – If provided, sphere ROI image is saved here
- **outside_val** (*float, default = None*) – Value outside of outside_radius.
- **outside_radius** (*float, default = None*) – Distance factor to define the 'outside' area: outsidefactor * radius -> outside
- **thresh_by_nii** (*bool, optional*) – Mask sphere by nii != 0
- **val_in** (*float, optional*) – Value within ROI
- **val_out** (*float, optional*) – Value outside ROI

Returns

- **sphere_img** (*nib.nifti1.Nifti1Image*)
- **sphere_img** (<file>, *optional*)

Raises

ValueError – If the final ROI is empty.

`pynibs.roi.load_roi_surface_obj_from_hdf5(fname)`

Loading and initializing RegionOfInterestSurface object/s from .hdf5 mesh file.

Parameters

fname (*str*) – Filename (incl. path) of .hdf5 mesh file, e.g. from subject.fn_mesh_hdf5

Returns

RegionOfInterestSurface – RegionOfInterestSurface

Return type

pynibs.roi.RegionOfInterestSurface or list of *pynibs.roi.RegionOfInterestSurface*

`pynibs.roi.make_GM_WM_surface(gm_surf_fname, wm_surf_fname, mesh_folder, midlayer_surf_fname=None, delta=0.5, x_roi=None, y_roi=None, z_roi=None, layer=1, fn_mask=None, refine=False)`

Generating a surface between WM and GM in a distance of delta 0...1 for ROI, given by freesurfer mask or coordinates.

Parameters

- **gm_surf_fname** (*str* or *list of str*) – Filename(s) of GM surface generated by freesurfer (lh and/or rh) (e.g. in mri2msh: fs_ID/surf/lh.pial)
- **wm_surf_fname** (*str* or *list of str*) – Filename(s) of WM surface generated by freesurfer (lh and/or rh) (e.g. in mri2msh: fs_ID/surf/lh.white)
- **mesh_folder** (*str*) – Path of mesh (parent directory)
- **midlayer_surf_fname** (*str* or *list of str*) – filename(s) of midlayer surface generated by headreco (lh and/or rh) (e.g. in headreco: fs_ID/surf/lh.central) (after conversion)
- **m2m_mat_fname** (*[defunct]*) – Filename of mri2msh transformation matrix (e.g. in mri2msh: m2m_ProbandID/MNI2conform_6DOF.mat)
- **delta** (*float*) – Distance parameter where surface is generated 0...1 (default: 0.5)
 - 0 -> WM surface
 - 1 -> GM surface
- **x_roi** (*list of float* or *None*) – Region of interest [Xmin, Xmax], whole X range if empty [0,0] or None (left - right)
- **y_roi** (*list of float* or *None*) – Region of interest [Ymin, Ymax], whole Y range if empty [0,0] or None (anterior - posterior)
- **z_roi** (*list of float* or *None*) – Region of interest [Zmin, Zmax], whole Z range if empty [0,0] or None (inferior - superior)
- **layer** (*int*) – Define the number of layers:
 - 1: one layer
 - 3: additionally upper and lower layers are generated around the central midlayer
- **fn_mask** (*string* or *None*) – Filename for freesurfer mask. If given, this is used instead of *_ROIs
- **refine** (*bool*, *optional*, *default: False*) – Refine ROI by splitting elements

Returns

- *if layer == 3*
- **surface_points_upper** (*np.ndarray of float*) – (N_points, 3) Coordinates (x, y, z) of surface + epsilon (in GM surface direction)
- **surface_points_middle** (*np.ndarray of float*) – (N_points, 3) Coordinates (x, y, z) of surface
- **surface_points_lower** (*np.ndarray of float*) – (N_points, 3) Coordinates (x, y, z) of surface - epsilon (in WM surface direction)
- **connectivity** (*np.ndarray of int*) – (N_tri x 3) Connectivity of triangles (indexation starts at 0!)
- *else*
- **surface_points_middle** (*np.ndarray of float*) – (N_points, 3) Coordinates (x, y, z) of surface
- **connectivity** (*np.ndarray of int*) – (N_tri x 3) Connectivity of triangles (indexation starts at 0!)

Example

```
make_GM_WM_surface(self, gm_surf_fname, wm_surf_fname, delta, X_ROI, Y_ROI, Z_ROI)
make_GM_WM_surface(self, gm_surf_fname, wm_surf_fname, delta, mask_fn, layer=3)
```

`pynibs.roi.nii2msh(mesh, m2m_dir, nii, out_folder, hem, out_fsaverage=False, roi_name='ROI')`

Transform a nifti ROI image to subject space .mgh file.

Parameters

- **mesh** (*simnibs.Mesh* or *str*) –
- **m2m_dir** (*str*) –
- **nii** (*nibabel.nifti1.Nifti1Image* or *str*) –
- **out_folder** (*str*) –
- **hem** (*str*) – ‘lh’ or ‘rh’
- **out_fsaverage** (*bool*) –
- **roi_name** (*str*) – How to name the ROI

Returns

roi – f”{out_folder}/{hem}.mesh.central.{roi_name}”

Return type

file

1.1.10 pynibs.subject module

class `pynibs.subject.Subject(subject_id, subject_folder)`

Bases: `object`

Subject containing subject specific information, like mesh, roi, uncertainties, plot settings.

self.id

Subject id from MPI database

Type

str

Notes

Initialization

Parameters

id

[*str*] Subject id

fn_mesh

[*str*] .msh or .hdf5 file containing the mesh information

Subject.seg, **segmentation information dictionary**

fn_lh_wm

[*str*] Filename of left hemisphere white matter surface

fn_rh_wm

[*str*] Filename of right hemisphere white matter surface

fn_lh_gm

[*str*] Filename of left hemisphere grey matter surface

fn_rh_gm

[str] Filename of right hemisphere grey matter surface

fn_lh_curv

[str] Filename of left hemisphere curvature data on grey matter surface

fn_rh_curv

[str] Filename of right hemisphere curvature data on grey matter surface

Subject.mri, mri information dictionary

fn_mri_T1

[str] Filename of T1 image

fn_mri_T2

[str] Filename of T2 image

fn_mri_DTI

[str] Filename of DTI dataset

fn_mri_DTI_bvec

[str] Filename of DTI bvec file

fn_mri_DTI_bval

[str] Filename of DTI bval file

fn_mri_conform

[str] Filename of conform T1 image resulting from SimNIBS mri2mesh function

Subject.ps, plot settings dictionary

see plot functions in para.py for more details

Subject.exp, experiment dictionary

info

[str] General information about the experiment

date

[str] Date of experiment (e.g. 01/01/2018)

fn_tms_nav

[str] Path to TMS navigator folder

fn_data

[str] Path to data folder or files

fn_exp_csv

[str] Filename of experimental data .csv file containing the merged experimental data information

fn_coil

[str] Filename of .ccd or .nii file of coil used in the experiment (contains ID)

fn_mri_nii

[str] Filename of MRI .nii file used during the experiment

cond

[str or list of str] Conditions in the experiment in the recorded order (e.g. ['PA-45', 'PP-00'])

experimenter

[str] Name of experimenter who conducted the experiment

incidents

[str] Description of special events occurred during the experiment

Subject.mesh, mesh dictionary

info

[str] Information about the mesh (e.g. discretization etc)

fn_mesh_msh

[str] Filename of the .msh file containing the FEM mesh

fn_mesh_hdf5

[str] Filename of the .hdf5 file containing the FEM mesh

seg_idx

[int] Index indicating to which segmentation dictionary the mesh belongs

Subject.roi region of interest dictionary**type**

[str] Specify type of ROI ('surface', 'volume')

info

[str] Info about the region of interest, e.g. "M1 midlayer from freesurfer mask xyz"

region

[list of str or float] Filename for freesurfer mask or [[X_min, X_max], [Y_min, Y_max], [Z_min, Z_max]]

delta

[float] Distance parameter between WM and GM (0 -> WM, 1 -> GM) (for surfaces only)

add_experiment_info(*exp_dict*)

Adding information about a particular experiment.

Parameters

exp_dict (*dict of dict or list of dict*) – Dictionary containing information about the experiment

Notes**Adds Attributes****exp**

[list of dict] Dictionary containing information about the experiment

add_mesh_info(*mesh_dict*)

Adding filename information of the mesh to the subject object (multiple filenames possible).

Parameters

mesh_dict (*dict or list of dict*) – Dictionary containing the mesh information

Notes**Adds Attributes****Subject.mesh**

[list of dict] Dictionaries containing the mesh information

add_mri_info(*mri_dict*)

Adding MRI information to the subject object (multiple MRIs possible).

Parameters

mri_dict (*dict or list of dict*) – Dictionary containing the MRI information of the subject

Notes

Adds Attributes

Subject.mri

[list of dict] Dictionary containing the MRI information of the subject

add_plotsettings(*ps_dict*)

Adding ROI information to the subject object (multiple ROIs possible).

Parameters

ps_dict (*dict* or *list of dict*) – Dictionary containing plot settings of the subject

Notes

Adds Attributes

Subject.ps

[list of dict] Dictionary containing plot settings of the subject

add_roi_info(*roi_dict*)

Adding ROI (surface) information of the mesh with mesh_index to the subject object (multiple ROIs possible).

Parameters

roi_dict (*dict of dict* or *list of dict*) – Dictionary containing the ROI information of the mesh with mesh_index [mesh_idx][roi_idx]

Notes

Adds Attributes

Subject.mesh[mesh_index].roi

[list of dict] Dictionaries containing ROI information

pynibs.subject.check_file_and_format(*fname*)

Checking existence of file and transforming to list if necessary.

Parameters

fname (*str* or *list of str*) – Filename(s) to check

Returns

fname – Checked filename(s) as list

Return type

list of str

pynibs.subject.fill_from_dict(*obj, d*)

Set all attributes from d in obj.

Parameters

- **obj** (*pynibs.Mesh* or *pynibs.ROI*) –
- **d** (*dict*) –

Returns

obj

Return type

pynibs.Mesh or *pynibs.ROI*

`pynibs.subject.load_subject(fname, filetype=None)`

Wrapper for pkl and hdf5 subject loader

Parameters

- **fname** (*str*) – `endwith('.pkl')` | `endwith('.hdf5')`
- **filetype** (*str*) – Explicitly set file version.

Returns

subject

Return type

pynibs.subject.Subject

`pynibs.subject.load_subject_hdf5(fname)`

Loading subject information from .hdf5 file and returning subject object.

Parameters

fname (*str*) – Filename with .hdf5 extension (incl. path)

Returns

subject – Loaded Subject object

Return type

pynibs.subject.Subject

`pynibs.subject.load_subject_pkl(fname)`

Loading subject object from .pkl file.

Parameters

fname (*str*) – Filename with .pkl extension

Returns

subject – Loaded Subject object

Return type

pynibs.subject.Subject

`pynibs.subject.save_subject(subject_id, subject_folder, fname, mri_dict=None, mesh_dict=None, roi_dict=None, exp_dict=None, ps_dict=None, **kwargs)`

Saves subject information in .pkl or .hdf5 format (preferred)

Parameters

- **subject_id** (*str*) – ID of subject
- **subject_folder** (*str*) – Subject folder
- **fname** (*str*) – Filename with .hdf5 or .pkl extension (incl. path)
- **mri_dict** (*list of dict, optional, default: None*) – MRI info
- **mesh_dict** (*list of dict, optional, default: None*) – Mesh info
- **roi_dict** (*list of list of dict, optional, default: None*) – Mesh info
- **exp_dict** (*list of dict, optional, default: None*) – Experiment info
- **ps_dict** (*list of dict, optional, default: None*) – Plot-settings info
- **kwargs** (*str or np.array*) – Additional information saved in the parent folder of the .hdf5 file

Returns

<File> – Subject information

Return type

.hdf5 file

```
pynibs.subject.save_subject_hdf5(subject_id, subject_folder, fname, mri_dict=None, mesh_dict=None,
                                roi_dict=None, exp_dict=None, ps_dict=None, overwrite=True,
                                check_file_exist=False, verbose=False, **kwargs)
```

Saving subject information in hdf5 file.

Parameters

- **subject_id** (*str*) – ID of subject
- **subject_folder** (*str*) – Subject folder
- **fname** (*str*) – Filename with .hdf5 extension (incl. path)
- **mri_dict** (*list of dict, optional, default: None*) – MRI info
- **mesh_dict** (*list of dict, optional, default: None*) – Mesh info
- **roi_dict** (*list of list of dict, optional, default: None*) – Mesh info
- **exp_dict** (*list of dict or dict of dict, optional, default: None*) – Experiment info
- **ps_dict** (*list of dict, optional, default: None*) – Plot-settings info
- **overwrite** (*bool*) – Overwrites existing .hdf5 file
- **check_file_exist** (*bool*) – Hide warnings.
- **verbose** (*bool*) – Print information about meshes and ROIs.
- **kwargs** (*str or np.ndarray*) – Additional information saved in the parent folder of the .hdf5 file

Returns

<File> – Subject information

Return type

.hdf5 file

```
pynibs.subject.save_subject_pkl(sobj, fname)
```

Saving subject object as pickle file.

Parameters

- **sobj** (*object*) – Subject object to save
- **fname** (*str*) – Filename with .pkl extension

Returns

<File> – Subject object instance

Return type

.pkl file

1.1.11 pynibs.tensor_scaling module

```
pynibs.tensor_scaling.ellipse_eccentricity(a, b)
```

Calculates the eccentricity of an 2D ellipse with the semi axis a and b. An eccentricity of 0 corresponds to a sphere and an eccentricity of 1 means complete eccentric (line) with full restriction to the other axis

Parameters

- **a** (*float*) – First semi axis parameter
- **b** (*float*) – Second semi axis parameter

Returns

e – Eccentricity (0...1)

Return type

float

pynibs.tensor_scaling.rescale_lambda_centerized(*D*, *s*, *tsc=False*)

Rescales the eigenvalues of the matrix *D* according to their eccentricity. The scale factor is between 0...1 a scale factor of 0.5 would not alter the eigenvalues of the matrix *D*. A scale factor of 0 would unify all eigenvalues to one value such that it corresponds to a isotropic sphere. A scale factor of 1 alters the eigenvalues in such a way that the resulting ellipsoid is fully eccentric and anisotropic.

Parameters

- **D** (nparray of float) – (3, 3) Diffusion tensor.
- **s** (float) – Scale parameter [0 (iso) ... 0.5 (unaltered)... 1 (aniso)].
- **tsc** (bool) – Tensor singularity correction.

Returns

Ds – (3, 3) Scaled diffusion tensor.

Return type

np.ndarray of float

pynibs.tensor_scaling.rescale_lambda_centerized_workhorse(*D*, *s*, *tsc=False*)

Rescales the eigenvalues of the matrix *D* according to their eccentricity. The scale factor is between 0...1 a scale factor of 0.5 would not alter the eigenvalues of the matrix *D*. A scale factor of 0 would unify all eigenvalues to one value such that it corresponds to a isotropic sphere. A scale factor of 1 alters the eigenvalues in such a way that the resulting ellipsoid is fully eccentric and anisotropic

Parameters

- **D** (ndarray of float) – (n, 9) Diffusion tensor.
- **s** (float) – Scale parameter [0 (iso) ... 0.5 (unaltered)... 1 (aniso)].
- **tsc** (bool) – Tensor singularity correction.

Returns

Ds – (3, 3) Scaled diffusion tensor

Return type

list of nparray of float

1.1.12 pynibs.tms_pulse module

pynibs.tms_pulse.biphasic_pulse(*t*, *R=0.0338*, *L=1.55e-05*, *C=0.0001936*, *alpha=1089.8*, *f=2900*)

Returns normalized single biphasic pulse waveform of electric field (first derivative of coil current)

Parameters

- **t** (ndarray of float [n_t]) – Time array in seconds
- **R** (float, optional, default: 0.0338 Ohm) – Resistance of coil in (Ohm)
- **L** (float, optional, default: 15.5*1e-6 H) – Inductance of coil in (H)
- **C** (float, optional, default: 193.6*1e-6) – Capacitance of coil in (F)
- **alpha** (float, optional, default: 1089.8 1/s) – Damping coefficient in (1/s)
- **f** (float, optional, default: 2900 Hz) – Frequency in (Hz)

Returns

e – Normalized electric field time course (can be scaled with electric field)

Return type

ndarray of float [n_t]

- [genindex](#)
- [modindex](#)
- [search](#)

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