Using the *fsaverage* Anatomical Data as a Surrogate

This document outlines the steps to employ the *fsaverage* subject, which comes with the FreeSurfer software, as a surrogate if the MRI data of a subject are not available.

Note: Since the fsaverage subject is, as the name implies, an average based on the FreeSurfer surface-based morphing procedure, the locations of the MEG activity computed may be misleading. Furthermore, the *fsaverage* head size may not match your subject and the MEG/MRI coordinate alignment may thus not be accurate.

Another option is to use the data from another "real" subject with matching head size as surrogate anatomical data. The drawback of this approach is that the cortical surface reconstructions of individual subjects present all the details of the folding of the cortical mantle and, therefore, especially if a strict orientation constraint is used, the results may contain spatial details which would not appear if the true MRI data of the subject would be employed.

Step 1: Make a private copy of the *fsaverage* surface reconstruction

Copy the fsaverage reconstruction from $FREESURFER_HOME/subjects/fsaverage to $SUBJECTS_DIR/fsaverage, where $SUBJECTS_DIR is the directory containing the data of your subjcet.

Step 2: Copy the additional *fsaverage* data provided with MNE in place

Copy the fsaverage data from $MNE_ROOT/mne/setup/mne_analyze/fsaverage to $SUBJECTS_DIR/fsaverage/bem. These data include:

fsaverage-head.fif	The approximate head surface triangulation for fsaverage.
fsaverage_inner_skull-bem.fif	A single-compartment BEM for fsaverage. This surface would ultimately need some editing. There is an annoying bump on the top of the head, which may cause some distortion in the estimates near the vertex. However, this effect is probably minor.
fsaverage-fiducials.fif	The locations of the fiducial points (LPA, RPA, and nasion) in MRI coordinates, see Section 7.16.2 of the MNE Manual, version 2.6. If this file is present in a subject's bem directory, the fiducial locations are visualized as red spots in the viewer window of mne_analyze.
fsaverage-trans.fif	Contains a default MEG-MRI coordinate transformation suitable for fsaverage. For details of using the default transformation, see Section 7.5 of the MNE Manual. This transformation should not be used for computing the source estimates but is useful if contour map visualization is needed for subjects missing the

Note 1: The inner skull surface can be output in FreeSurfer format from fsaverage_inner_skull-bem.fif using the command:

    mne_list_bem --bem fsaverage_inner_skull-bem.fif --id 1 --surf --out inner_skull.surf

Note 2: The scalp surface can be output in FreeSurfer format from fsaverage-inner_skull-bem.fif using the command:

    mne_list_bem --bem fsaverage-head.fif --surf --out outer_skin.surf

Note 3: Because the outer skull surface is missing, *fsaverage* cannot be used for EEG modeling. I am happy to include the three-layer BEM for *fsaverage* to the MNE distribution if someone goes to the trouble of creating outer skull surface for *fsaverage*.

Step 3: Compute the BEM geometry data for the forward solution

This step creates the fsaverage_inner_skull-bem-sol.fif file which the BEM solution data dependent on the BEM surface geometry only:

> mne_prepare_bem_model --bem $SUBJECTS_DIR/fsaverage/bem/fsaverage-inner_skull-bem.fif

Step 4: Setup the source space

This command creates the standard source space with 5-mm spacing:

> mne_setup_source_space --subject fsaverage --spacing 5

Note: You can use any spacing value or the --ico option as usual.

Step 5: Setup the MRI (optional)

If you want to use the Neuromag mrilab tool for coordinate alignment, create the T1-neuromag and brain-neuromag directories with the command

> mne_setup_mri --subject fsaverage

Note: Steps 1 – 5 are needed only once. The remaining steps are needed for each subject/ measurement file you are going to use.

Step 6: Coordinate alignment

Load the fsaverage surfaces to mne_analyze and do the coordinate alignment as usual. If FreeSurfer environment is set up, you can look at the alignment in tkmedit conveniently through *View/Show MRI viewer...* It is recommended that you use the *Save...* option and save the coordinate alignment in the subject's MEG data directory rather than in $SUBJECTS_DIR/fsaverage/mri/T1-neuromag/sets using the *Save MRI set* choice because you can then use your private fsaverage reconstruction for multiple subjects. This is your only choice if you skipped Step 5.

Step 7: Compute the forward solution

This step computes the forward solution using the data of the *fsaverage* subject:

> mne_do_forward_solution --subject fsaverage --spacing 5 --meas <data file> --fwd <fwd file> --megonly

Again, any spacing option can be used, depending on the source space(s) you have created in Step 4.

Step 8: Compute the inverse operator

This step uses the forward solution from Step 7 and the noise covariance file which you have created as usual to calculate the inverse operator decomposition:

> mne_do_inverse_operator --senscov <noise covariance> --fwd <fwd solution> [other options]

Step 9: Analyze your data

Analyze your data as usual. Use the inverse operator you created in Step 8 and the anatomical data of fsaverage.