

Notes on **BrainImage2Mesh**

A computational framework to predict the spreading of Alzheimer's disease

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This document is intended to clarify the usage of the processing pipeline BrainImage2Mesh presented in: A. Vazquez-Palomo, C. Betegón, J. Weickenmeier, E. Martínez-Pañeda. A computational framework to predict the spreading of Alzheimer's disease. *Engineering with Computers* 42, 78 (2026). Please cite the above paper if you are using this software.

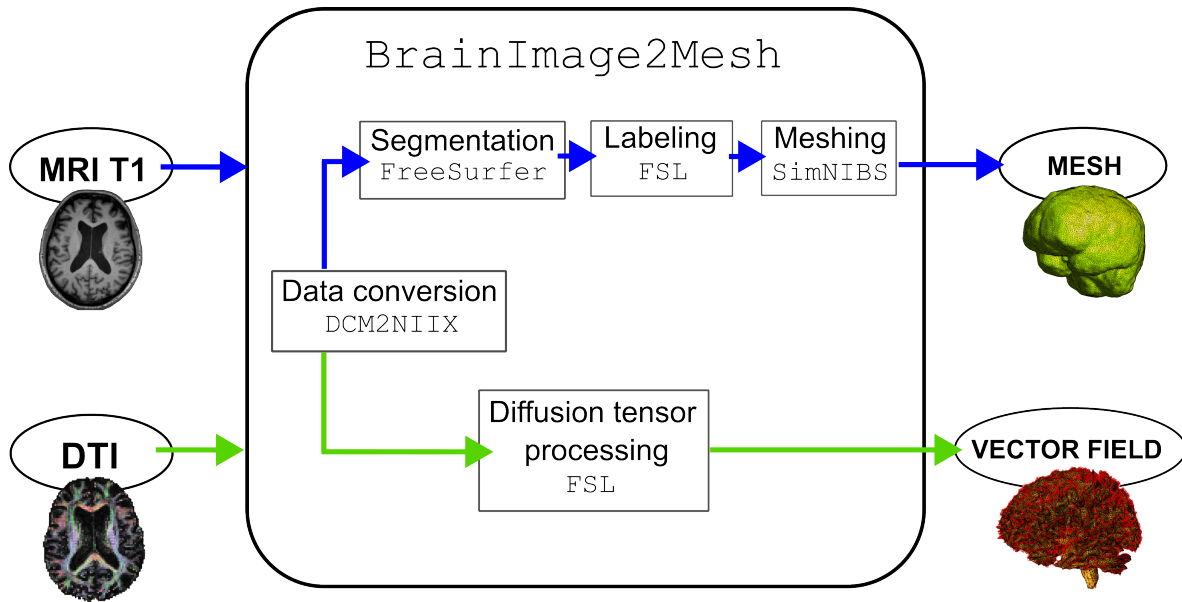


Figure 1: Schematic overview of the pipeline developed.

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1. Requirements

The pipeline has been developed and tested on a Linux environment (Ubuntu 22.04). The following tools should be installed and available in your `<base_path>`:

- FSL: The script was coded with the 5.0 version. Follow `SimNIBS` page instructions on how to set up FSL.
- `SimNIBS`: The script was coded with the 4.5.0 version.
- `dcm2niix`: The script was coded with the 1.0 version.

The following tools should be installed and available in your `/usr/local`:

- `FreeSurfer`: The script was coded with the 8.1.0 version. Remember to paste the `FreeSurfer` license file (`license.txt`) in the folder.

2. Permissions

Before running the script for the first time you may have to give it execution permission:

```
chmod +x ./process_subject_core.sh
```

3. Use

Run the script from a terminal with four positional arguments:

```
./BrainImage2Mesh.sh<subject_identifier><base_path><zip_T1><zip_DTI>
```

- `<subject_identifier>`: Desired identifier for the subject (e.g. `subject1`). A folder with this name will be created under `<base_path>`.
- `<base_path>`: Working directory where the subject folder will be created.
- `<zip_T1>`: path to the T1-weighted DICOM `.zip` file.
- `<zip_DTI>`: path to the DTI DICOM `.zip` file.

Example:

```
./brainimage2mesh.sh subject01 /home/user/study /home/user/dicoms/T1.zip /  
home/user/dicoms/DTI.zip
```

4. Output directory structure

The script creates a subject folder under <base_path> with the layout shown in 2.

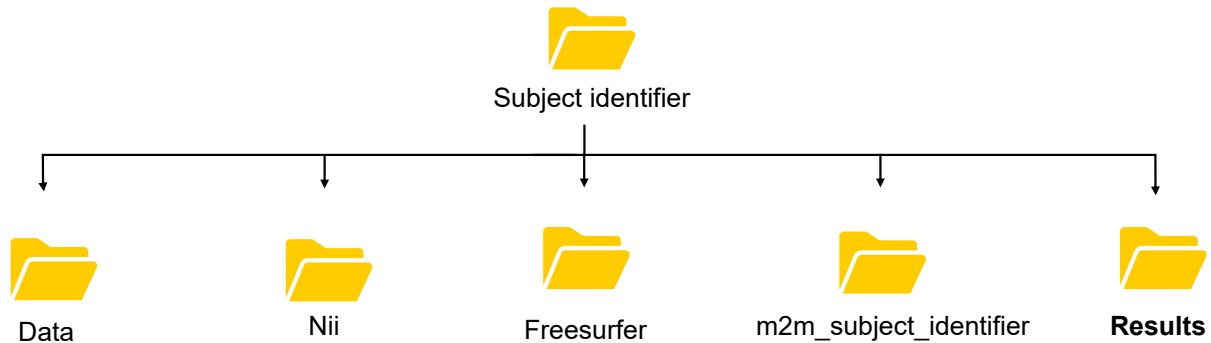


Figure 2: Output directory structure created by the pipeline.

Each top-level folder stores the output of a different processing stage:

- Data: unzipped DTI and T1 DICOM files.
- Nii: NIfTI versions of T1 and DTI.
- Freesurfer: FreeSurfer outputs.
- m2m_subject_identifier: SimNIBS head model, DWI and dMRI subfolders.
- Results: final deliverables.

The final deliverables placed in the results folder are:

- <subject>_mesh.bdf : volumetric labelled head mesh in Nastran bulk data format.
- vector_field.csv: per-element principal diffusion direction (unit vector) with its position, ready to be used as an anisotropy field in simulations.