May 26, 2018 Version 2

MELD Protocol 5 - Post-processing Pipeline V.2

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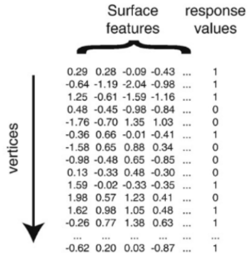

Surface features					response values
0.29	0.28	-0.09	-0.43	...	1
-0.64	-1.19	-2.04	-0.98	...	1
1.25	-0.61	-1.59	-1.16	...	1
0.48	-0.45	-0.98	-0.84	...	0
-1.76	-0.70	1.35	1.03	...	0
-0.36	0.66	-0.01	-0.41	...	1
-1.58	0.65	0.88	0.34	...	0
-0.98	-0.48	0.65	-0.85	...	0
0.13	-0.33	0.48	-0.30	...	0
1.59	-0.02	-0.33	-0.35	...	1
1.98	0.57	1.23	0.41	...	0
1.62	0.98	1.05	0.48	...	1
-0.26	0.77	1.38	0.63	...	1
...	...	...	...	...	...
-0.62	0.20	0.03	-0.87	...	1

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Protocol status: Working
We use this protocol and it's working

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Protocol Integer ID: 12462

Abstract

The MELD Project is an international collaboration aiming to create open-access, robust and generalisable tools for FCD detection. To this end, we will train a neural network classifier on MRI features from FCD patients from multiple centres worldwide.

Protocol 5 provides instructions for post-processing FreeSurfer reconstructions to create final feature matrices.

Guidelines

If you have any questions or run into problems, please feel free to contact the MELD project: (meld.study@gmail.com)

Safety warnings

PLEASE DO NOT SHARE ANY IDENTIFIABLE DATA

Data sharing only occurs at the level of anonymised demographics information and anonymised data matrices. These are in a template space that cannot be traced back to an individual.

Before start

These steps require FreeSurfer and Python

FreeSurfer

Instructions for installing Freesurfer are included in MELD Protocol 2

NB: FreeSurfer and its utilities need to be in your path or this script will not run properly. You can type tksurfer on the command line to make sure it is available.

Before you want to work with FreeSurfer, you must make sure three things have happened:

1. The variableFREESURFER_HOME is set (so your computer knows where FreeSurfer is installed):

```
setenv FREESURFER_HOME <freesurfer_installation_directory>/freesurfer
```

1. The FreeSurfer set up script must be sourced (so FreeSurfer knows the location of everything it needs):

```
source $FREESURFER_HOME/SetUpFreeSurfer.csh
```

1. FreeSurfer has been pointed to a directory of subjects to work on:

```
setenv SUBJECTS_DIR <path>/meld/output
```

Set up FreeSurfer environment

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Installing anaconda and environment

2 This step is necessary if you did not install anaconda in Protocol 4

https://conda.io/docs/user-guide/install/macos.html

To install anaconda for a mac:
1) download the 'anaconda python 2.7' version installer from here: https://www.anaconda.com/download/ (make sure it's the mac version being downloaded)
2) Double click the .pkg file to install
3) follow the prompts on the installer screen.

To install anaconda on a linux:
1) Download the 'anaconda python 2.7' version installer from here: https://www.anaconda.com/download/ (make sure it's the linux version being downloaded)

2) In your terminal window, run:

```
bash Anaconda-latest-Linux-x86_64.sh
```

3) follow the prompts on the installer screen

To create the anaconda environment, with all of the necessary python packages, run the following:

```
cd <path>/meld/scripts
conda env create -f meld_env.yaml
```

Finally add the scripts directory to your PYTHONPATH by running the following

```
open ~/.bashrc
```

This will open your bash profile

add the following line

```
export PYTHONPATH='${PYTHONPATH}:<path>/meld/scripts'
```

Remember to replace <path> with the correct path according to your file system.

Running the pipeline

3 All the necessary scripts are called by a single master script “meld_pipeline.sh”.

To run:

```
cd <path>/meld/scripts
source activate meld_env
bash meld_pipeline.sh <INSERT_SUBJECTS_DIRECTORY> <SITE_CODE>
```

At GOSH this would be:

```
bash meld_pipeline.sh <path>/meld/ H1
```

This should run the script through all patients and controls, creating a large feature matrix in the MELD subjects directory called:

SUBJECTS_DIR/MELD_SITE_CODE_featurematrix.txt

e.g. MELD_H1_featurematrix.txt

Once started, it should take ~2 hours per subject.

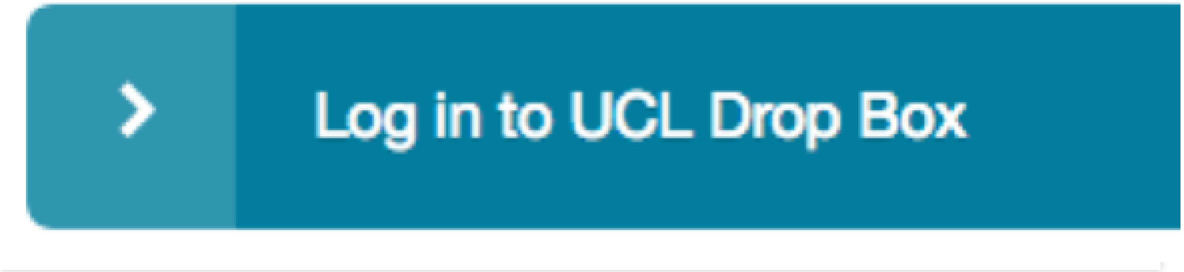
The slow step is the creation of xhemi. If you need to rerun this script, this will not need to be redone and the script should run much more quickly!

Send anonymised data to Sophie Adler

4 Send the anonymised data: MELD_site_code_participants.csv and MELD_site_code_featurematrix.txt to Sophie Adler at UCL

Go to
http://www.ucl.ac.uk/isd/services/comms-collaborate/dropbox

Click



5 Enter the following details:

From:
Enter your Name, Organization and Email address

To:
Name: Sophie Adler
Email address: sophie.adler.13@ucl.ac.uk

6 **Upload the following files:**
List_subjects.txt
MELD_site_code_control_featurematrix.hdf5
MELD_site_code_patient_featurematrix.hdf5
MELD_site_code_participants.xls
outliers.log

Please note – due to the file sizes, it may take a while to upload!

Sophie Adler will confirm receipt of any files.

REMINDER: ONLY SEND ANONYMISED DATA OVER UCL DROPBOX