Introduction

This manual is edited to help researchers interested in reconstructing simultaneous multi-slice (SMS) inverse imaging (InI) data acquired from Siemens MRI scanner. We will specifically use the following software packages.

I.   FreeSurfer
     An open source software suite for processing and analyzing (human) brain MRI images. For more information, please check
     https://surfer.nmr.mgh.harvard.edu/

SMS-InI reconstruction basically involves the following steps:

- Convert raw data (meas_xxxxx_.dat format in Siemens) to Matlab (xxx.mat format).
- Co-register between the SoS image volume from the reference scan and the anatomical information reconstructed by FreeSurfer
- Reconstruct SMS-InI accelerated scan time point-by-time point

Environment setup

- **Login**
    1.   Open a SSH session
    2.   Login to server

    ```
    %ssh 140.119.165.24 -l username¹ -Y
    ```

- **Go to working directory and setup environment**

    3.   Goto your working directory²

    ```
    > cd /space/maki3/1/users/fhlin/ini_visual_var/
    subj15_082916/analysis
    ```

    4.   Prepare environment³

    ```
    >addpath('/space/maki/1/pubsw/packages/freesurfer/stable5_1
    _0/matlab/');
    >addpath('/space/home/fhlin/matlab/toolbox/fhlin_toolbox/')
    ;
    >source /space/maki/1/pubsw/bme-dev-env-dev.csh
    >
    >setenv SUBJECTS_DIR
    /space/maki3/1/users/fhlin/ini_visual_var/subjects
    ```

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¹ Here I use "username" as an example to login.

² In this analysis, I arranged all scripts and data for each subject at
`/space/maki3/1/users/fhlin/ini_visual_var/subj??_??????/analysi
s.` I used two digits to encode subjects and the 6 digits by the end of the folder's name
indicated the date of data collection. You can change this folder name and structure based
on your preference.

³ I arranged the FreeSurfer reconstructions for all subjects at
`/space/maki3/1/users/fhlin/ini_visual_var/subjects.` So, for example,
the FreeSurfer reconstruction folders/files for subject `subj15_082916` was at
`/space/maki3/1/users/fhlin/ini_visual_var/subjects/`
`subj15_082916.` You can change this folder name and structure based on your
preference.

Convert raw data to Matlab

- **Convert raw data from a Skyra scanner**
  The first step is to convert the raw data (`meas_XXXX_.dat` files) into a format that can be easily processed by Matlab. For data collected on a Skyra scanner using IDEA version VD13C (as of August 2016), you can try the following commands in Matlab:

  1. Edit the file `smsini_raw2mat.m`[4]
     Find the two lines highlighted in red. Replace them with first the folder where all the meas.dat files are (`path_dat_source`) and the second the folder where you want the converted data to be stored (`path_mat_destination`; in Matlab MAT format).

```
close all; clear all;
addpath('/autofs/space/maki6_001/users/eva/toolbox/tool_mb_
recon/');

path_dat_source={
'/media/usb/160829_SMSINI_subj1/160829_SMSINI_subj1/';
};
path_mat_destination='/space/maki3/1/users/fhlin/ini_visual
_var/subj15_082916/analysis';


......
```

  2.   Run `smsini_raw2mat.m` inside Matlab

```
> matlab —nojvm
```

  (*after Matlab starts*)

```
>> smsini_raw2mat;
```

  3.   By the end of running this script, you should have the following files:

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[4] Typically I use vi as the text editor. This is not the most user-friendly text editor but it is available on almost LINUX/UNIX/MAC. So it serves the purpose of minor text editing here. You can choose your preferred text editor to modify this script.

```
> ls
/space/maki3/1/users/fhlin/ini_visual_var/subj15_082916/ana
lysis

mb_run_1_ref.mat
mb_run_1_acc.mat
mb_run_2_ref.mat
mb_run_2_acc.mat
mb_run_3_ref.mat
mb_run_3_acc.mat
mb_run_4_ref.mat
mb_run_4_acc.mat
mb_run_5_ref.mat
mb_run_5_acc.mat
```

There will be one reference data file (xxx_ref.mat) and one SMS-InI data file (xxx_acc.mat) for each run. In this example, we have 5 runs of data collected and thus we got 5 reference data files and 2 SMS-InI data files.

- **Convert raw data from a Tim Trio scanner**
The SMS-InI sequence has also a VB version But details of converting data collected on Tim Trio has not been verified yet.

Prepare reference images for co-registration between SMS-InI and anatomical MRI

- **Prepare volumetric sum-of-square images**
  This step prepares the sum-of-square volumetric images from the reference scan. This will be needed for the following co-registration between SMS-InI and anatomical MRI after FreeSurfer reconstruction:

  1. Edit the file `smsini_make_ref.m`
     Find the lines highlighted in red. Replace them with all the reference images in Matlab format. In this example, we have converted 5 runs of SMS-InI data So we have 5 xxx_ref.mat files.

```
close all; clear all;

ref_mat={
'mb_run_1_ref.mat';
'mb_run_2_ref.mat';
'mb_run_3_ref.mat';
'mb_run_4_ref.mat';
'mb_run_5_ref.mat';
};


......
```

  4.   Run `smsini_make_ref.m` inside Matlab

```
> matlab —nojvm
```

(after Matlab starts)

```
>> smsini_make_ref;
```

  5.   By the end of running this script, you should have the following files:

```
> ls
/space/maki3/1/users/fhlin/ini_visual_var/subj15_082916/ana
lysis/*.mgh
```

```
mb_run_1_ref.mgh
mb_run_2_ref.mgh
mb_run_3_ref.mgh
mb_run_4_ref.mgh
mb_run_5_ref.mgh
```

There should be 5 volumetric images in .mgh format.

Co-register between the SoS image volume from the reference scan and the anatomical information reconstructed by FreeSurfer

We then need to register the SoS image volume from the reference scan to the anatomical brain reconstructed by FreeSurfer. Here you must have your FreeSurfer brain reconstructed first. The co-registration can be easily done by using `flirt` in the FSL package included in FreeSurfer.

```
fslregister --s subj15_082916 --mov ./mb_run_1_ref.mgh --reg ./register_01.dat --maxangle 70 --initxfm
```

You should have the FreeSurfer environment variable $SUBJETS_DIR setup correctly to include the target subject's reconstructed brain surfaces.

The output of this co-registration is a file named 'register_01.dat', which includes the image volume voxels size and 12 parameters for rigid-body transformation.

This script can be found at /space/maki3/1/users/fhlin/ini_visual_var/subj15_082916/analysis/register_01.script

Just simply run this script at the command line. If all environment setup is correct (with FreeSurfer environment and correct $SUBJECTS_DIR specified), it should run smoothly with an output file register_01.dat.

```
> cat register_01.dat

subj15_082916
5.000000
5.000000
0.150000
-9.999975e-01 7.351788e-04 2.199118e-03 -4.475670e+00
2.202192e-03 4.217683e-03 9.999883e-01 -1.628957e+01
7.258955e-04 9.999907e-01 -4.219353e-03 -1.014494e+01
0.000000e+00 0.000000e+00 0.000000e+00 1.000000e+00
round
```

Reconstruct SMS-InI accelerated scan time point-by-time point on to cortical surfaces

This step prepares the sum-of-square volumetric images from the reference scan. This will be needed for the following co-registration between SMS-InI and anatomical MRI after FreeSurfer reconstruction:

1. Edit the file `smsini_make_acc.m`

   Find the lines highlighted in red. Replace them with 1) SMS-InI data in matlab file (`acc_mat`), 2) converted reference file in mgh format (`acc_template`), 3) registration file (`file_register`), 4) the name of your subject (`subject`), and 5) the name of the 'target' subject (`target_subject`). Since we are morphing everyone's fMRI data on to a specified one to facilitate subsequent group analysis, you have to choose who is this target subject. In this example, I chose 'fsaverage', a standard average template subject in FreeSurfer, as the target subject.

```
close all; clear all;

acc_mat={
'mb_run_1_acc.mat';
'mb_run_2_acc.mat';
'mb_run_3_acc.mat';
'mb_run_4_acc.mat';
'mb_run_5_acc.mat';
};

acc_template={
'mb_run_1_ref.mgh';
'mb_run_2_ref.mgh';
'mb_run_3_ref.mgh';
'mb_run_4_ref.mgh';
'mb_run_5_ref.mgh';
};

file_register={
'register_01.dat';
'register_02.dat';
'register_03.dat';
'register_04.dat';
'register_05.dat';
};
```

```
TR=0.1; %second

flag_morph=1;
subject='subj15_082916';
target_subject='fsaverage';
```

......

   6.   Run `smsini_make_acc.m` inside Matlab

```
> matlab —nojvm
```

(*after Matlab starts*)

```
>> smsini_make_acc;
```

   7.   By the end of running this script, you should have the following files:

```
> ls
/space/maki3/1/users/fhlin/ini_visual_var/subj15_082916/ana
lysis/*.stc

subj15_082916_2_fsaverage_mb_run_1_acc-lh.stc
subj15_082916_2_fsaverage_mb_run_1_acc-rh.stc
subj15_082916_2_fsaverage_mb_run_2_acc-lh.stc
subj15_082916_2_fsaverage_mb_run_2_acc-rh.stc
subj15_082916_2_fsaverage_mb_run_3_acc-lh.stc
subj15_082916_2_fsaverage_mb_run_3_acc-rh.stc
subj15_082916_2_fsaverage_mb_run_4_acc-lh.stc
subj15_082916_2_fsaverage_mb_run_4_acc-rh.stc
subj15_082916_2_fsaverage_mb_run_5_acc-lh.stc
subj15_082916_2_fsaverage_mb_run_5_acc-rh.stc
```

   There should be 10 STC files, each of which presents a (# of cortical
   locations) x (# of time points) matrix on either left or right hemisphere.