Pre-Processing and 1-st Level Report

1. Pre-processing

Currently, I have 2 kinds of pre-processing, one with distortion correction (Xirui's data), one without (Josh's and Yizhou's data). This is because default fieldmap image we get does not reach SPM12's requirement. But in the 3rd pilot, we used another fieldmap sequence, so distortion correction is included since then. All pre-processings are finished by using SPM12, pipeline is:

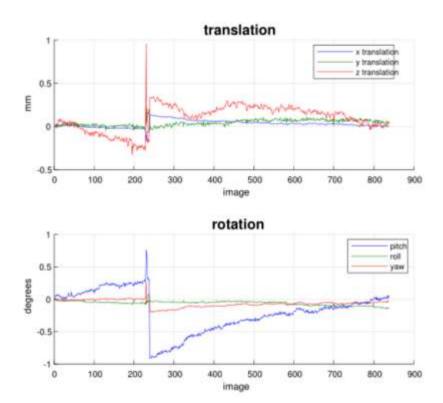
- (1) Realignment → slice timing → coregister → segmentation →
 normalization → smoothing in Josh's and Yihzou's data
- (2) Calculate VDM (for distortion correction) → realignment & unwarp → slice timing → coregister → segmentation → normalization → smoothing in Xirui's data

Detailed parameter setting can be found in each batch file.

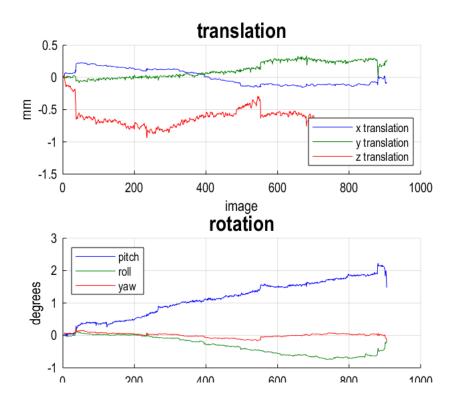
1) Motion parameters

The criterion I use here is translation < 2mm (voxel-wise), rotation < 2° . Yizhou's data have biggest head motion and rotation, with max value of more than 7 mm and 2° respectively. Josh's and Xirui's data are both good according to the criterion above, although max rotaion value in Josh's sms1 is a bit more than 2° .

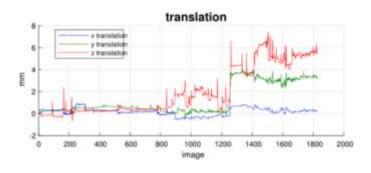
> Josh's Lili:

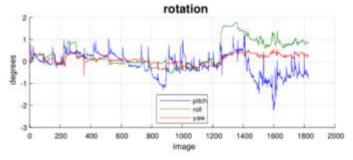


> Josh's sms1

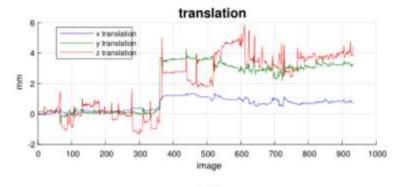


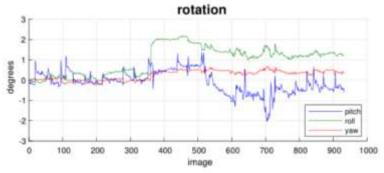
> Yizhou's sms2



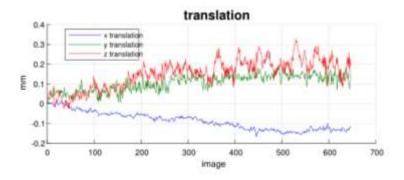


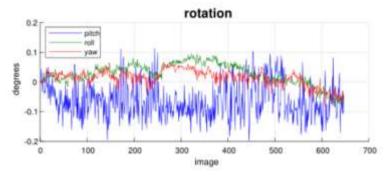
> Yizhou's sms3



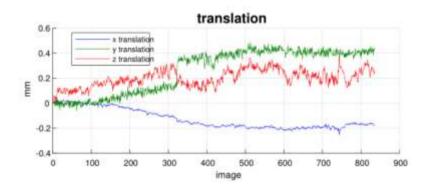


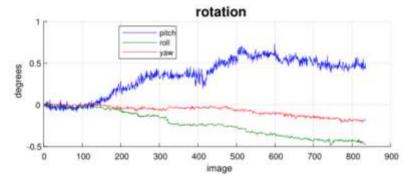
> Xirui's sms1





Xirui's sms3



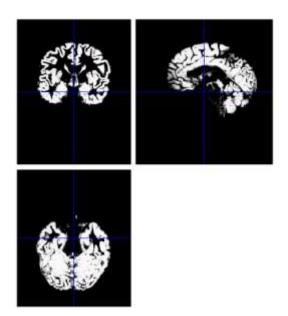


2) Brain extraction:

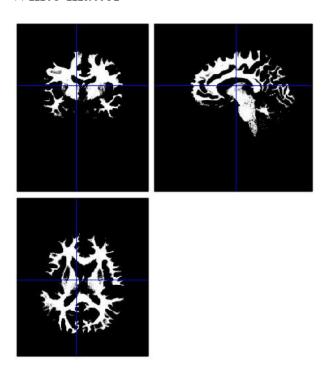
T1 sequence is constant within each sequence. Thus, here I only put brain extraction images within each subject rather than each sequence (sequences within one subject generate the same brain extraction). Unlike FSL, brain extraction in SPM is called segment, which extracts and divides brain into grey matter, white matter, CSF, bone, soft tissue and air/background according to SPM's default tissue probability map. Grey matter and white matter images are put to show brain extraction in SPM. Brain extraction is good across all subjects. Yizhou's data may look weird, but it is because his head was left-rotated during scanning.

➤ Josh's

1. Grey matter

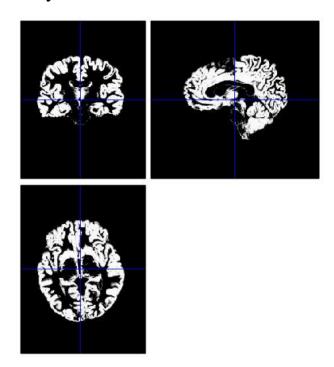


2. White matter

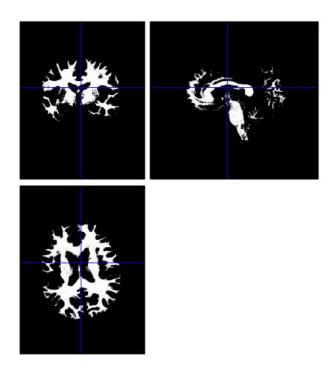


> Yizhou's

1. Grey matter

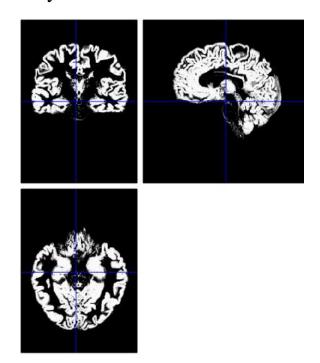


2. White matter

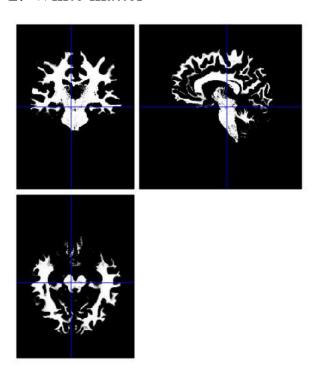


> Xirui's

1. Grey matter



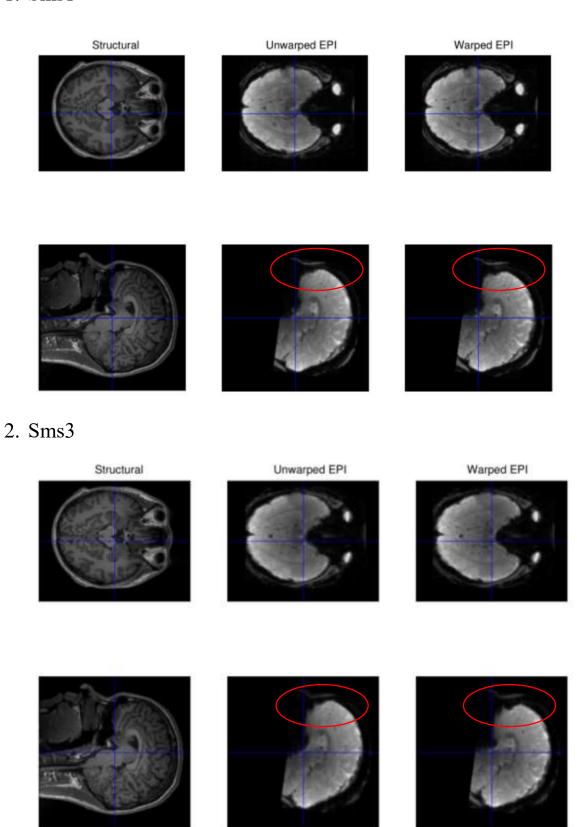
2. White matter



3) Distortion correction

Due to sequence issue, only Xirui's data finished this correction. After correction, both images are without warping. Here the white part above brain in each image is nose bone not warped part. However, like I said before, distortion correction is to correct EPI image to make its shape as close as structural image, while it can't deal with signal dropout. In sms1, we can see the unwarped EPI is corrected well (red circle part), but in sms3, it seems this correction did no good to EPI images. This also supports the problem in sms3 images might be signal loss.

1. Sms1



2. 1st-level analysis report.

In this version, I set conditions as fixation (duration is 1st ITI +fixation time), decision_now, decision_delay, confirmation, waiting (in short) and coins (in short). Then, I treat fixation as baseline activity to make contrast, e.g., decision – fixation to show specific activation of decision phase. So, total contrast will be:

- 1) Fixation
- 2) Decision (decision now+decision delay)
- 3) Decision now
- 4) Decision delay
- 5) Confirmation
- 6) Waiting (short)
- 7) Coin (short)
- 8) Decision Fixation (decision_now+decision_delay-fixation)
- 9) Decision now-Fixation
- 10) Decision_delay- Fixation
- 11) Confirmation–Fixation
- 12) Waiting-Fixation (short)
- 13) Coin–Fixation (short)

The top 7 contrasts are used as testing contrast to see if anything weird in EPI data. Contrast 8-14 are those for testing potential brain activities in each phase.

To save pages and also make it convenient for you to check. I am not going to put plot here, but will send my results mat files to you so that you can check them with SPM, and can also define new contrast as you want.