

Meeting's report for ELLEN WANG

Honour's student

08-11-2021

1. Meeting Agenda

- Follow up Jiyang meeting after Pierre asked for clarification on data.

2. Meeting Minutes from this week

- Do you align all the brains into a standard space?
 - The brain scans are acquired at different times in the same session in the modalities T1 and T2.
 - It starts with the acquisition of T1, and at different time points there's a chance that the participants will move their heads even slightly during these scans.
 - If we want to consider T1 and FLAIR together, we will need to align each individual's T1 and FLAIR scans and make sure they are aligned.
 - Different algorithms have different cost functions according to the intensity in the voxel. Calculate these cost functions, reach the minimum or maximum value then you can consider the two images together.
 - Setting one of them as a reference, the other one becomes a moving image.
 - T1 is higher resolution (so it's typically treated as reference), T2 and FLAIR images best align with T1. The default one is called the correlation ratio, not too sure how it's calculated.
 - Images are then aligned and then resliced. In this situation it is 1.5 by 1.5 by 3 (mm). For T1 images it is 1 by 1 by 1 resolution.
 - These two images are then rotated and mapped together, the voxel size is not the same, so then it's resliced so that FLAIR is also 1 by 1 by 1. All these things are already done in the images provided.
 - Note that each brain has a different shape, mapped to the same standard space.
 - Need to confirm that each individual brain is mapped to a standard space. Currently, each T1 and FLAIR image has been aligned in the same space. The images you have now are realigned, but between the subjects 1&2&3 etc they were not aligned. Jiyang doesn't think that we need to do that because we are considering the features within each individual brain.
 - Once you transform the brain into a standard space, it will include a non-linear transformation where raw information may be eliminated, so stick to the original image.
 - If I want this to happen, it's not a difficult transformation, it's just worrying that you might miss small additions/changes to the data.
 - Stick with the current data and maybe ask Melinda how she sliced the data.
 - Didn't use the brain images that didn't have lacunes in it.
- FILES DEFINITION:
 - ForAudrey.tar: not in standard space, saved in local machine, check the dimension of the images, if you want to consider location information you can still map all this information into the standard space back into the current one.
 - FLAIRinT1space_withLacunes_35.tar: FLAIR scan but after all the transformations it was transformed to be standardised in T1 space.

- Lacune_inT1space.tar: Lacune labelled in FLAIR images, did the transformation to make the FLAIR image in T1 space. This transformation was applied to the lacune labels so that the labels are also in T1 space. The labels in the T1 space.
- T1_withLacunes_35.tar: Just the original T1 space.
- T1softTiss_withLacunes_35.tar: Removed the skull and bones and water from the image. Soft tissue is classified as grey matter and white matter.
- T1softTissMask_withLacunes_35.tar: Mask of soft tissue, not a mask of the lacune.
- Lacune_T1space_JiyangCorrected20210920: replaces the lacune_T1space.tar with corrected masks.
- OTHERS:
 - Check the pre-processing steps of the MRI brain images.
 - Check the different volume and sizes of brains.
 - Are you only using the raw data?
 - How does Jiyang propose slicing the brain? Majority vote.
 - VIEWS: Axial: top-down, It's the z direction orientation. Go slice by slice where the resolutions are small. Don't miss information by taking slices in between.
 - Start with top to bottom view. Note the same lacune will show up from front to back and top to bottom though you may have different features for different views.
 - In one direction, you are considering the features from different orientations which may be similar in terms of identifying the lacunes. Different angle: if the lacune is a fluid you'll see it from all orientations.
 - TODO: Apply soft tissue mask to the first folder (FLAIR), extract the soft tissue in FLAIR space, now you have T1 and FLAIR. You have soft tissue in T1 and FLAIR after the mask was applied. Read the labels in to extract the intensity within the label. Then you can dilate the label to get the values around the lacune.
 - FEATURES: Get ratio of intensity and surrounding voxels (one of the features). Jiyang didn't binarize it (values other than 0 is 1), anything above 0 is 1. The actual values in MRI scan don't matter, some are very high values, it's the difference between them that is more important.
 - FEATURES: Need to get the ratio, don't use the raw values.
 - In terms of the scan: it's the right value and you need to NORMALISE before fitting your model as values from 100,000 to 700,000 is reasonable.
 - Calculating ratio for each subject is fine, but if you want to compare between subjects you need to standardise the normalisation.
 - TRAIN/TEST:
 - * Randomly select 70% for training and 30% for testing.
 - * If I have 35 brains all of them have lacunes, some have one some have two some have many. Randomly select 25 brains for training and 10 for testing.
 - * NOT all scans/slices have a lacune, and if that's the case put that into training. Predict the other 10 scans and each scan will have multiple slices.
 - * He's not sure how well the model will be trained with 25 scans, if it's not sufficient, ask Jiyang if more is needed. Have spreadsheet but not labelled data.
 - * Need to set a range in the images, some slices don't have values, you'll want to start with the 3-5 slices from the top to the bottom 3-5 slices and don't consider the empty values.
 - * Can try a mix of slices such as taking a random 70%, but not sure how many of those slices have lacunes (should be a very low percentage of slices with lacunes), make sure there's 25 lacunes in the training test.
 - * Could be something we try, not very in depth thought about this at the moment.

4. Planned work after this meeting

- Normalise brain values.
- Play around with data.