Beginning:

- First, we need to prepare the anatomical data. Since we have 4 T1w images, we need to preprocess all T1w images and then generate an averaged anatomical T1w image according to those 4 images.
- To do this, two methods are possible: 1) using ANT and 2) using SPM-12
- All preprocessing methods in here are for glasslexical task but the same process would be applied for motor task which consists of two runs.

ANT averaging method:

```python
import os
import ants

# Define paths to the four T1-weighted images
# in this sample code it will only happens for the subject number one, you can run that for each of your subject
t1_images = [
    "D:\\sussex\\ids pro\\research group\\DATA\\raw data\\data\\ds000224_R1.0.2\\sub-MSC01\\ses-struct01\\anat\\sub-MSC01_ses-struct01_run-01_T1w.nii",
    "D:\\sussex\\ids pro\\research group\\DATA\\raw data\\data\\ds000224_R1.0.2\\sub-MSC01\\ses-struct01\\anat\\sub-MSC01_ses-struct01_run-02_T1w.nii",
    "D:\\sussex\\ids pro\\research group\\DATA\\raw data\\data\\ds000224_R1.0.2\\sub-MSC01\\ses-struct02\\anat\\sub-MSC01_ses-struct02_run-01_T1w.nii",
    "D:\\sussex\\ids pro\\research group\\DATA\\raw data\\data\\ds000224_R1.0.2\\sub-MSC01\\ses-struct02\\anat\\sub-MSC01_ses-struct02_run-02_T1w.nii"
]

# Load the first image as reference
ref_img = ants.image_read(t1_images[0])

# Initialize an empty list to store registered images
registered_imgs = [ref_img]

# Register all images to the reference
for img_path in t1_images[1:]:
    img = ants.image_read(img_path)
    # Supervisor should decide between "Rigid" , "Affine" , and "SyN" but "Affine" seems the best
    reg_img = ants.registration(fixed=ref_img, moving=img, type_of_transform='Affine')["warpedmovout"]
    registered_imgs.append(reg_img)

# Compute the average image
avg_t1 = sum(registered_imgs) / len(registered_imgs)

# Save the averaged image
output_path = "D:\\sussex\\ids pro\\research group\\DATA\\T1w_avg.nii.gz"
ants.image_write(avg_t1, output_path)

print(f"Averaged T1-weighted image saved at: {output_path}")
```

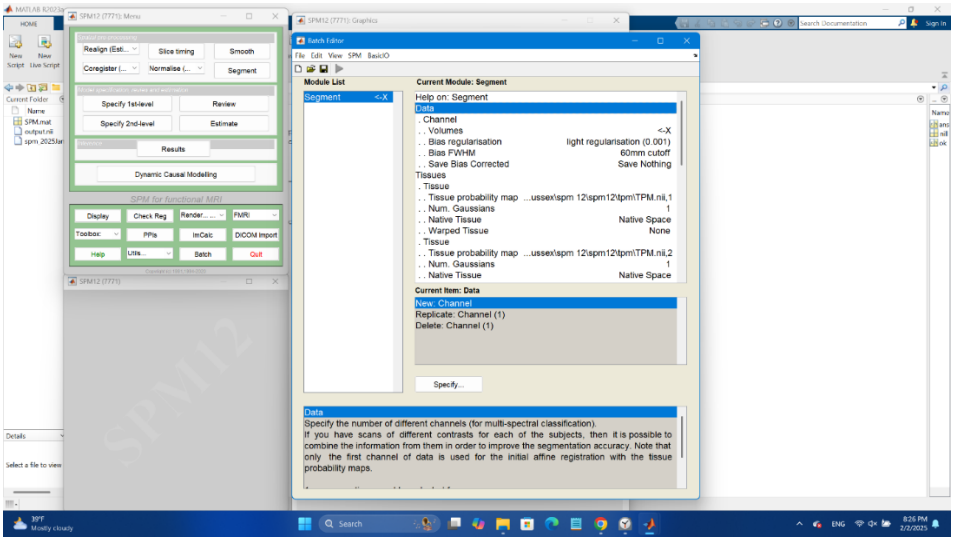
SPM-12 averaging method:

- four anatomical images need to be segmented to generate deformation fields. Then, using anatomical images and their deformation fields, these four images will be wrapped into MNI space.
- Then, 4 anatomical images will be smoothed using a 6 mm Gaussian kernel.
- The averaged anatomical image will be generated by averaging 4 normalized anatomical images (w prefixes) using the ImCalc option.

Anatomical segmentation:

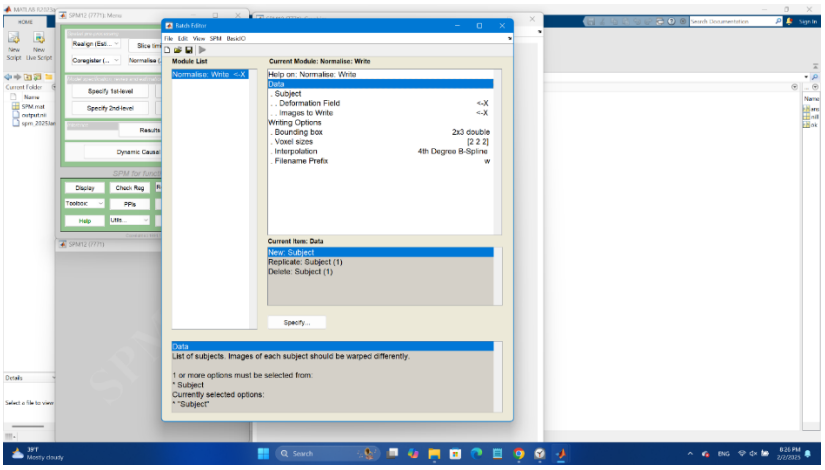
- The following image demonstrates the segmentation process. Images that need to be segmented should be added (e.g., in our case four anatomical images including 2 sessions and 2 runs in each session).
- The deformation field at the end of this batch folder should be set as “forward”.

- This will result in a file including “deformation fields” for all 4 images. These images have “y_” prefixes.



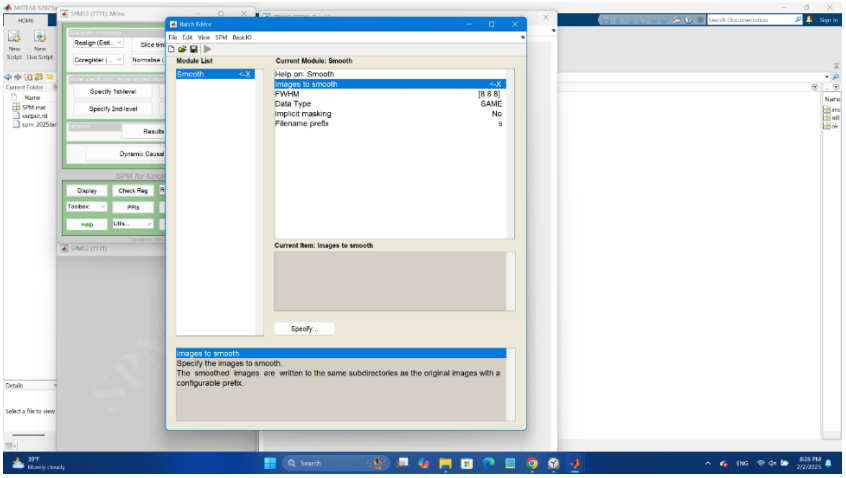
Anatomical normalization:

- Normalization batch will be used in this part for normalizing all 4 anatomical images in the same MNI space.
- Since the deformation field was set to forward in the previous step, only “write” will be selected for this step of normalization and not “estimate and write”.
- For each anatomical image, the image will be added in “images to write” and its corresponding deformation field (y_) will be added to the “deformation field” section.
- To do this for all 4 images, “replicate: subject” will be utilized while the same process is executing for the other three images.
- Files with “w” prefixes will be generated after normalization.



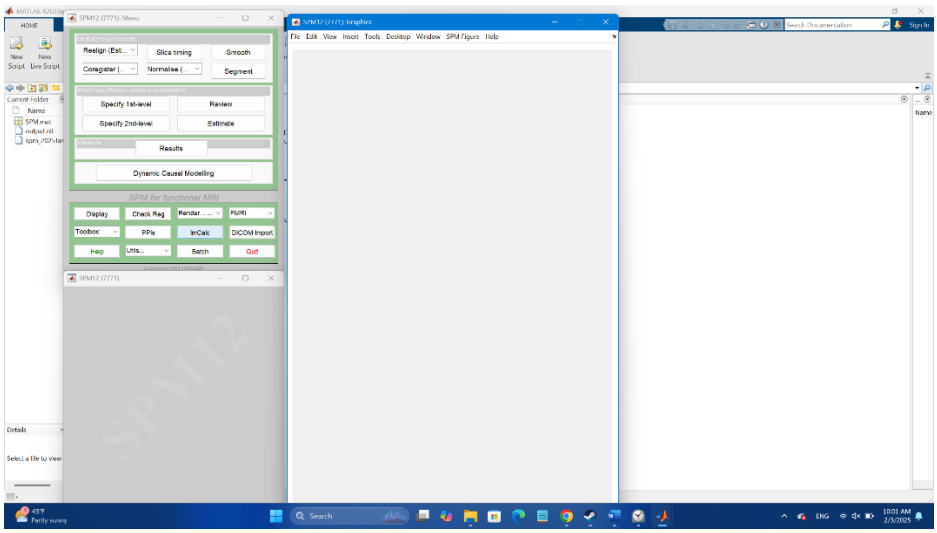
Anatomical smoothing:

- Finally, the smoothing batch will be used to generate smoothed images from 4 anatomical images.
- All images will be added together.
- Files with “s” prefixes will be generated after smoothing.

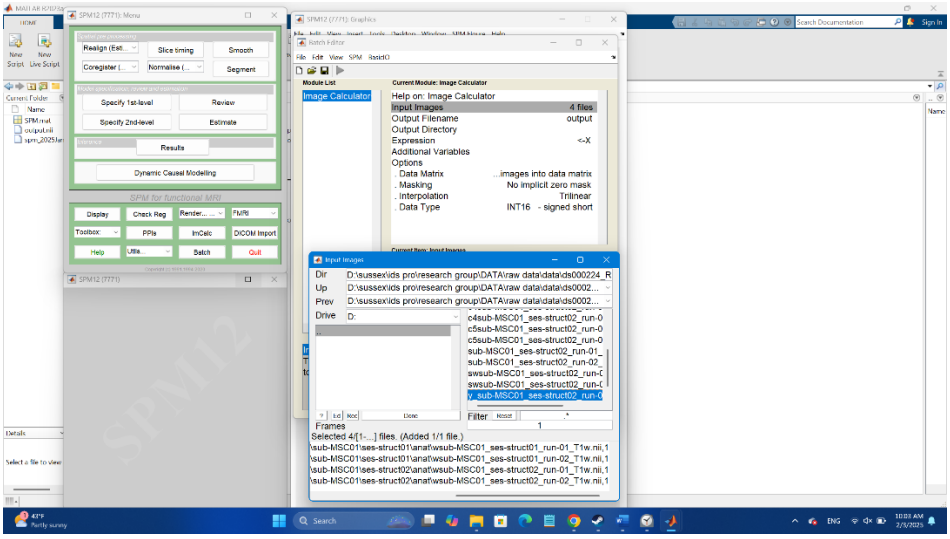


Anatomical averaging:

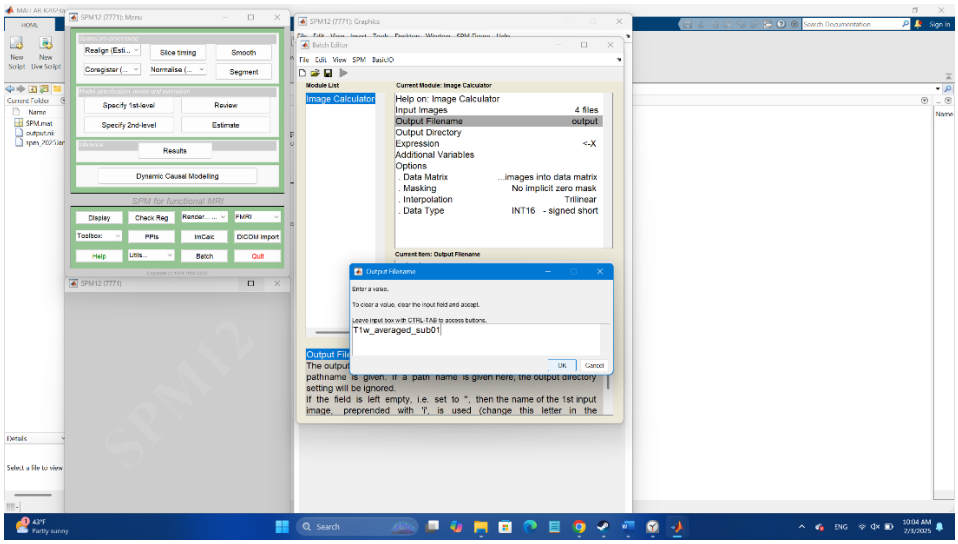
- ImClac batch folder will be selected, this batch will be used for averaging a number of images.



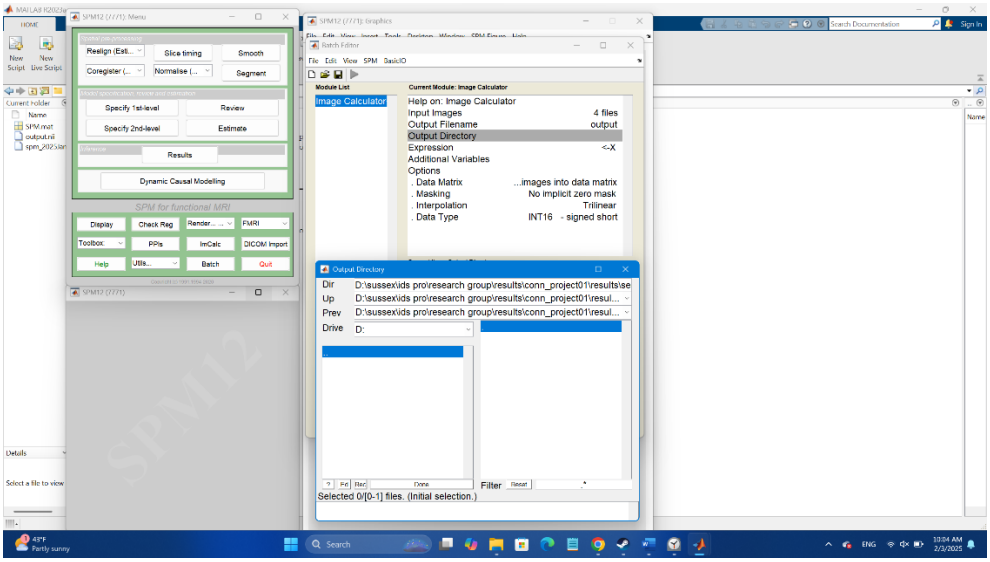
- In the input images, 4 normalized images will be selected including images with “w” prefixes from 2 sessions and their 2 runs (not adding images with “sw” prefixes, however, deciding the use of which image depends on your research-related factors and decision, in some cases “sw” images will be used).



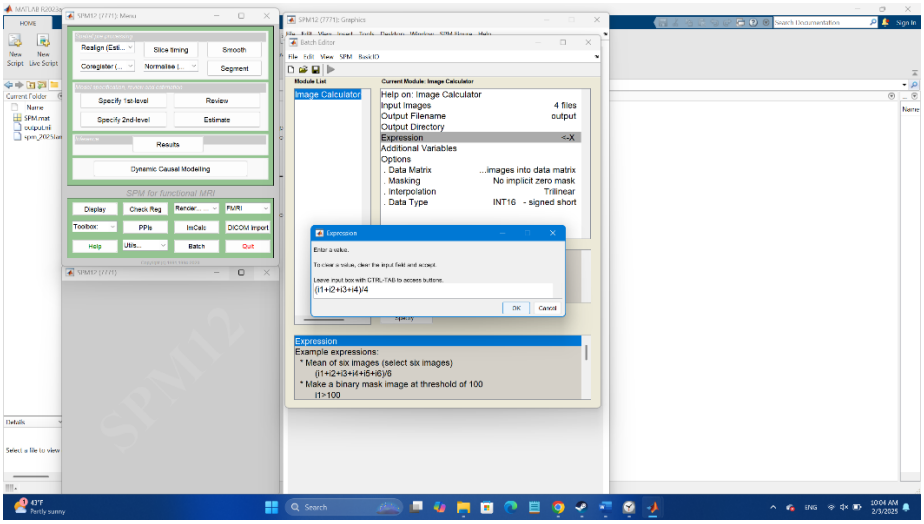
- The output file’s name will be selected (e.g., T1w_averaged_sub01)



- The output directory will be set in a path that you prefer.



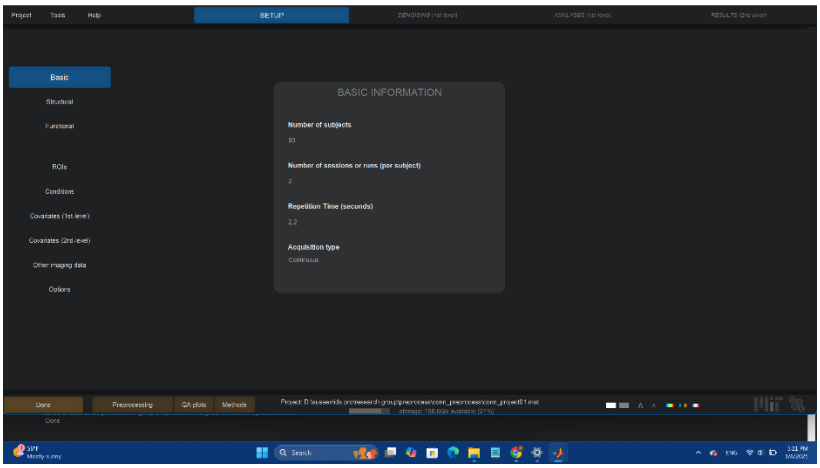
- In the expression section, you need to add the formula for your averaging. As is presented in the following image, since 4 images exist, the sum of all images was divided by the number of images.



CONN preprocessing pipeline:

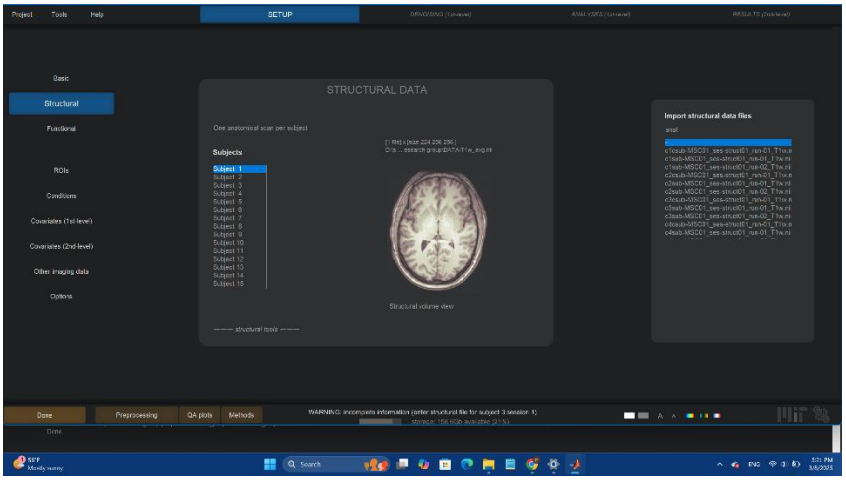
90 subjects, including 10 sessions for each 9 subjects (each subject's session would be treated as a single subject).

Since we have two runs for each glasslexical and motor, 2 sessions would be selected for each subject.

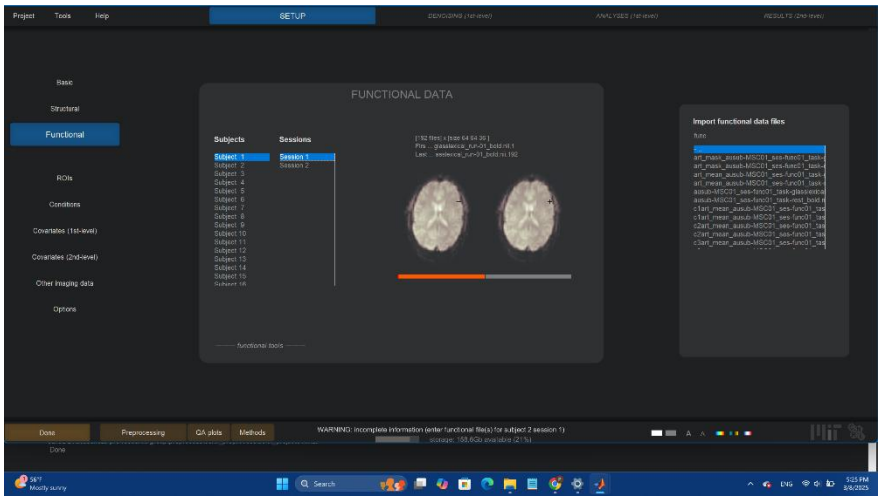


Averaged structural images for each subject would be imported.

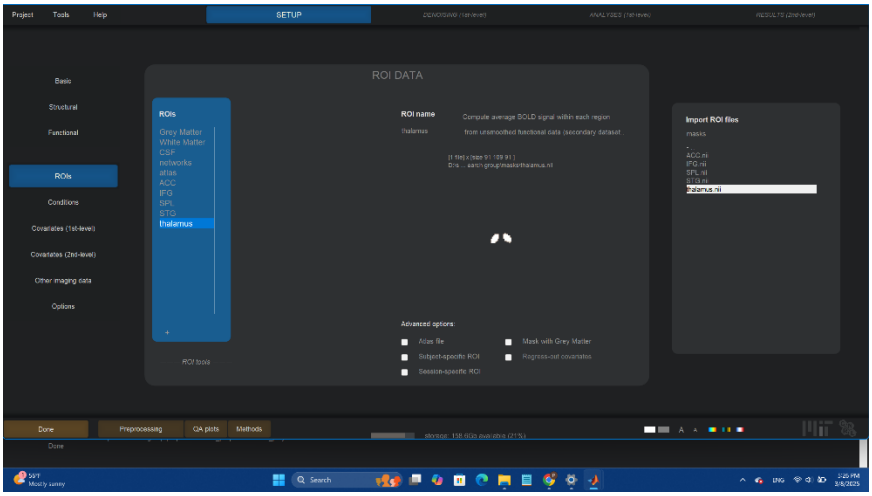
the averaged structural image is the same for every 10 images (e.g., 1-10,11-20,…)



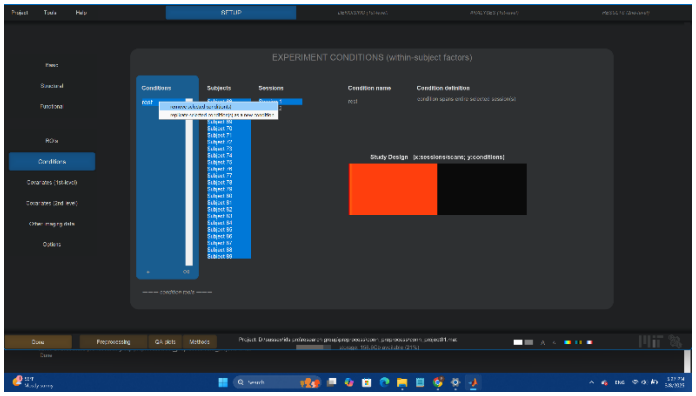
The first and second runs of the glasslexical functional image will be imported to the first and second sessions. (The same thing happens for the motor task.)

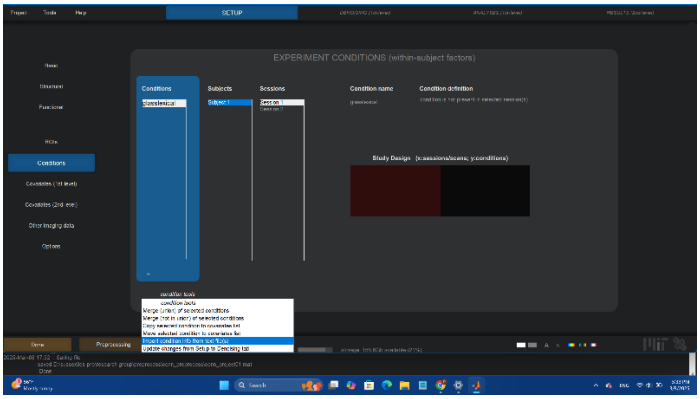


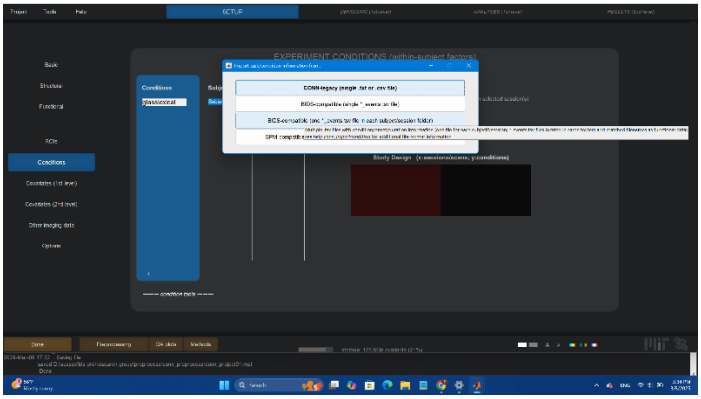
all masks will be imported in ROI section

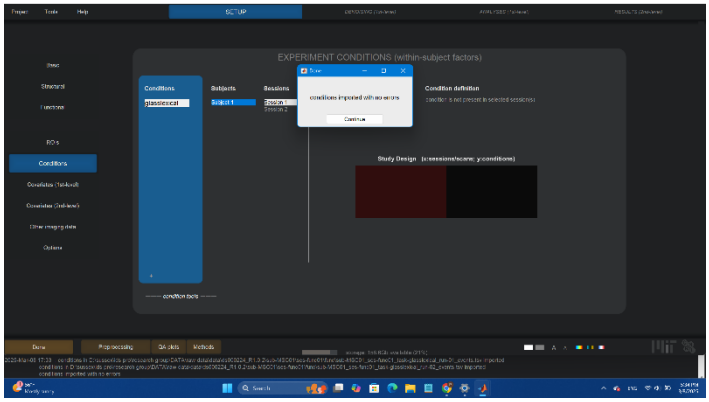


the existed condition will be deleted. The new condtion will be imported as following:

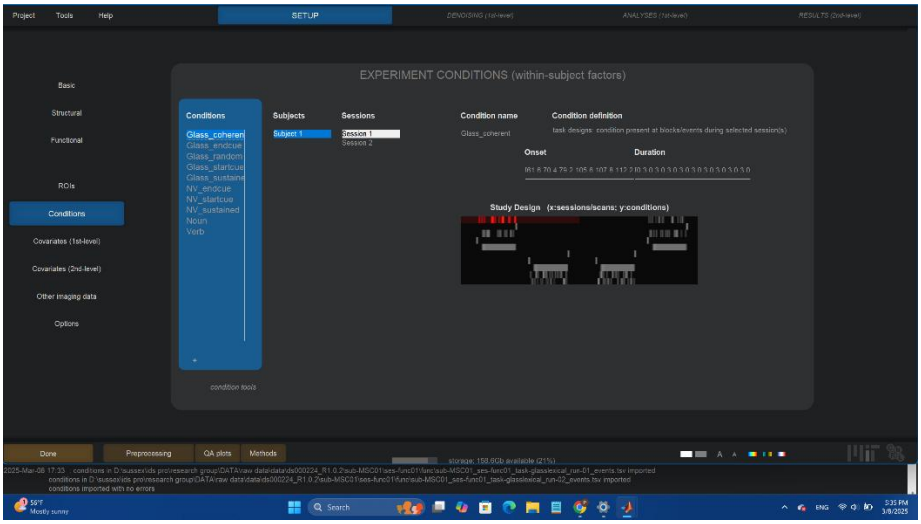




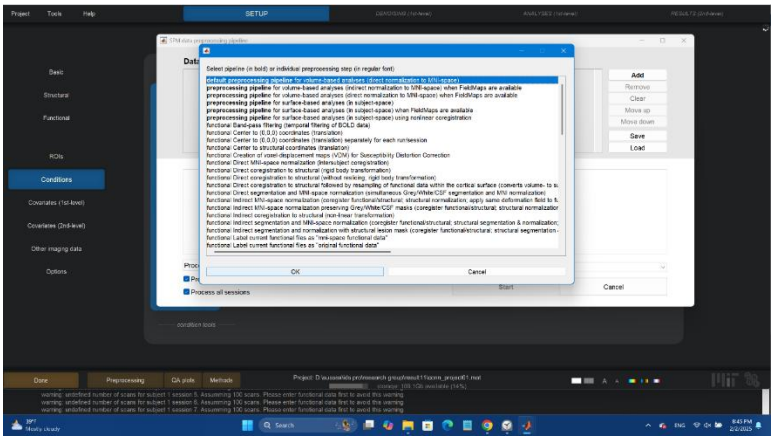




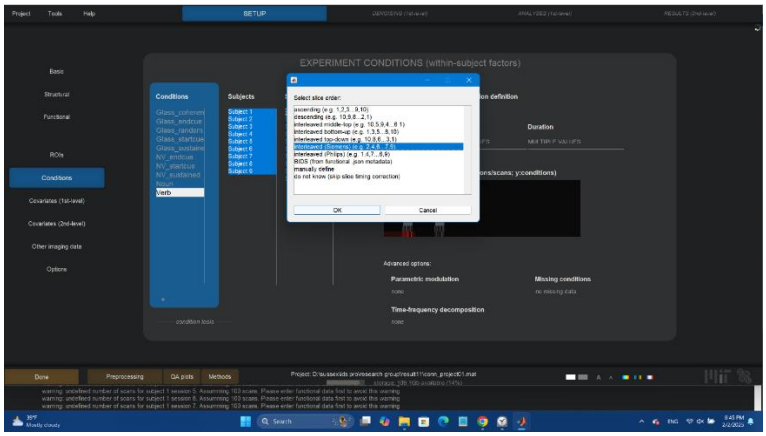
Which approach to follow? Having a whole condition named glasslexical or break this condition into its sections (e.g., noun, verb, and etc)



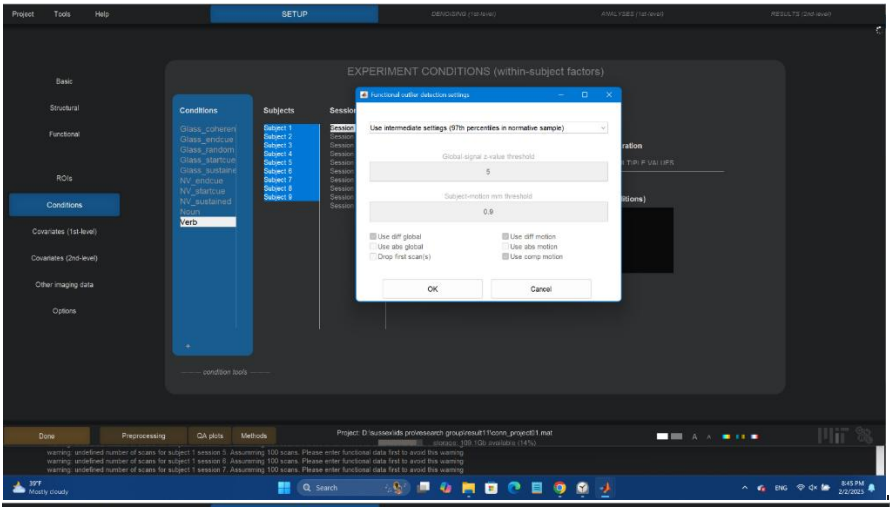
- The preprocessing will be selected from the toolbar located down the screen.

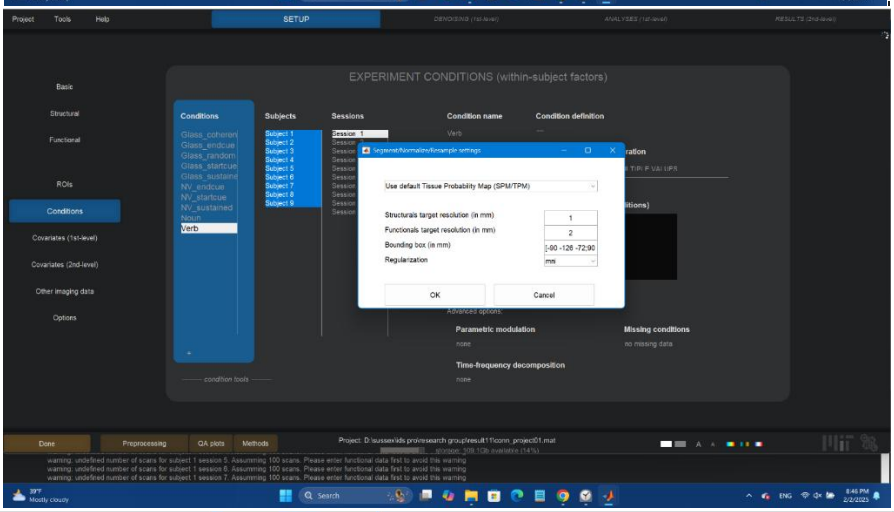


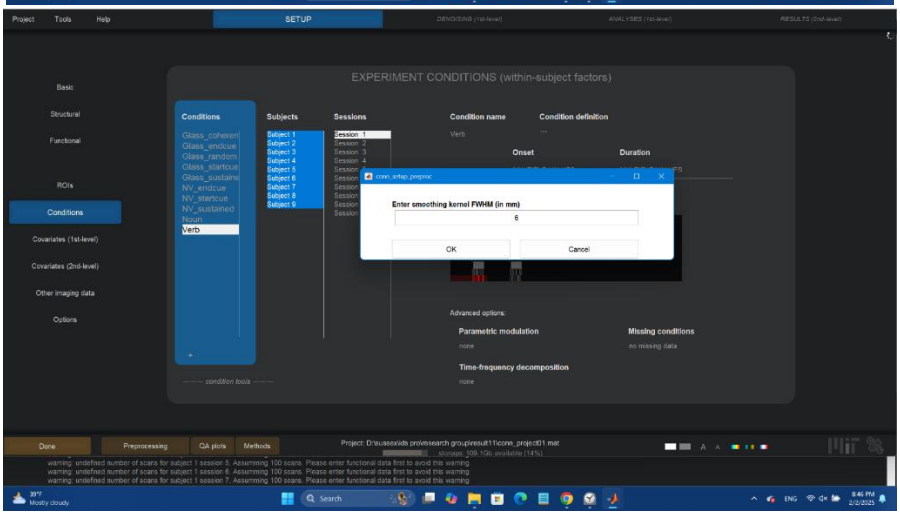
- According to the JSON file, interleaved (Simens) will be selected as slice order.



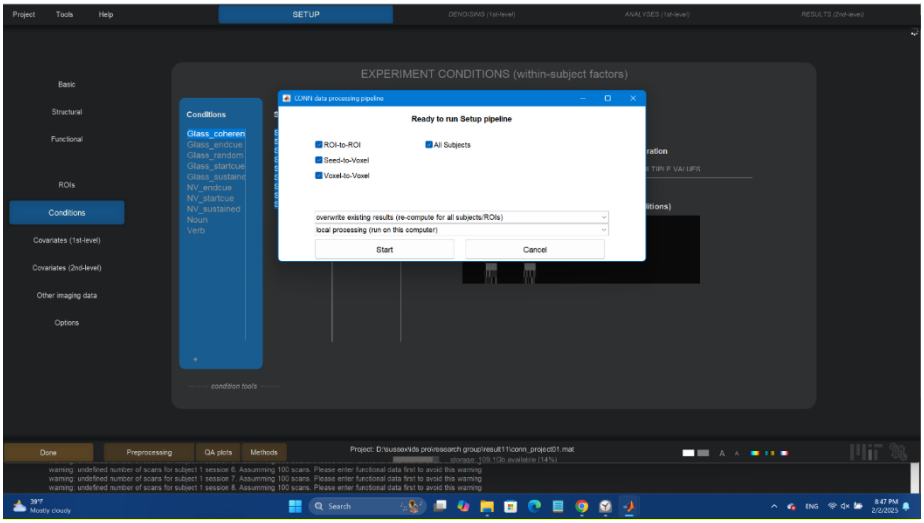
- All other parts would be set as default (only the Gaussian kernel will be set to 6mm)







- After preprocessing, the denoising part starts by clicking on Done.



- The denoising process will be shown. By clicking on “Done”, your data will be denoised and ready for the first-level analysis.