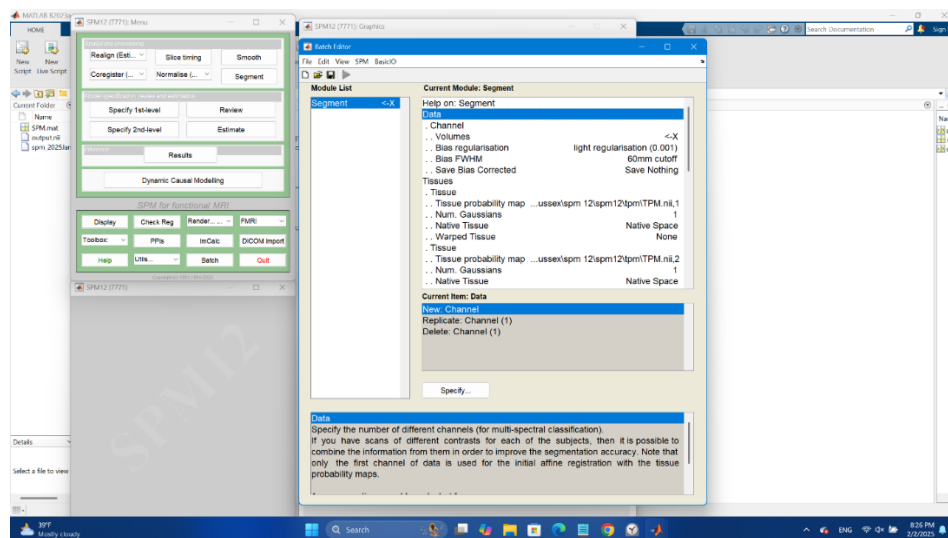


## Beginning:

- 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, 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.

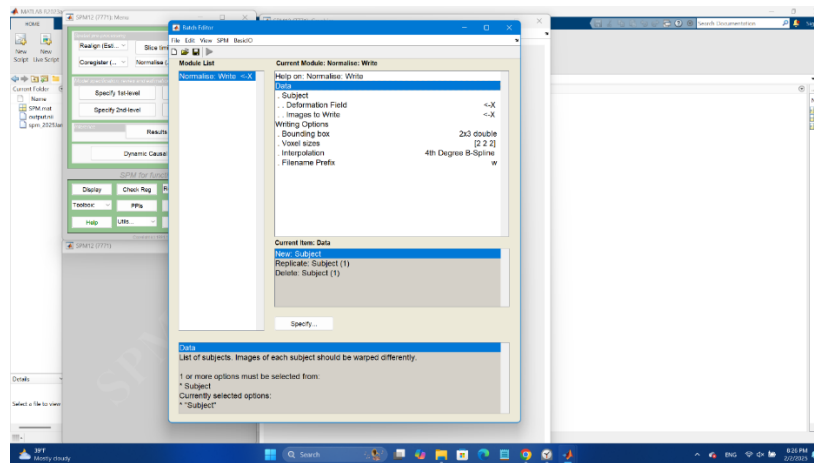
## Anatomical segmentation:

- 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.



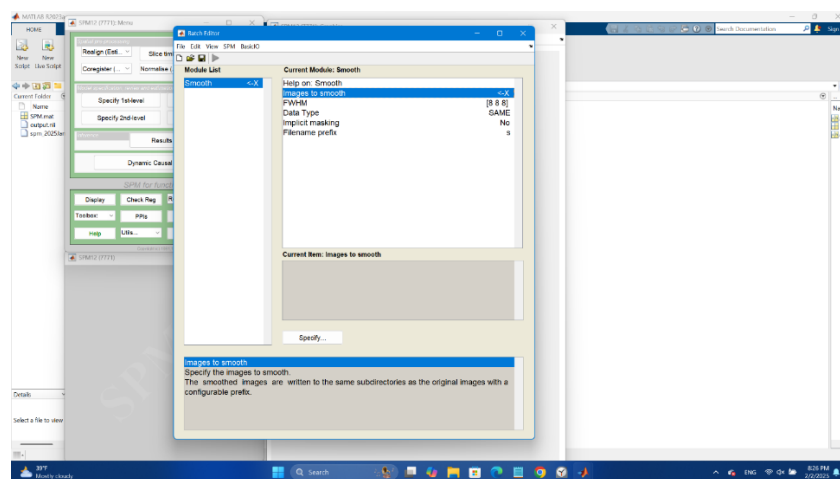
## Anatomical normalization:

- 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.



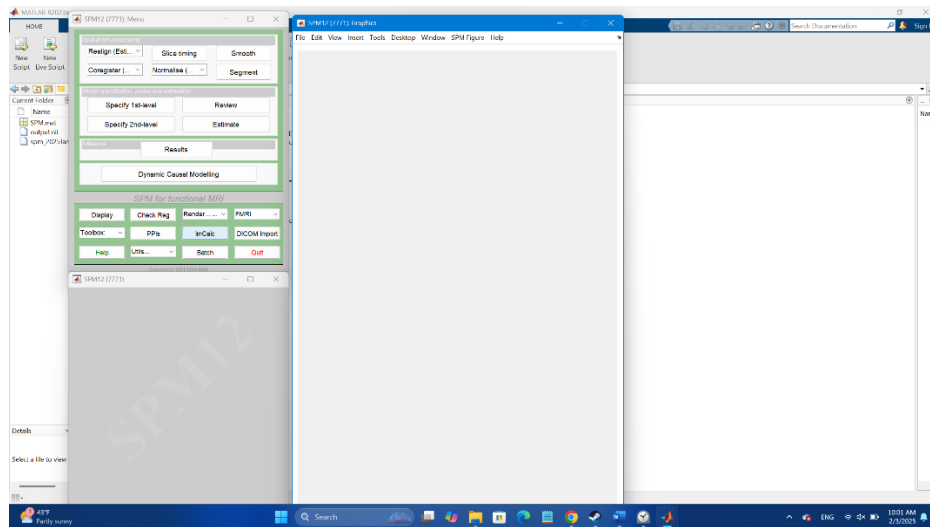
## Anatomical smoothing:

- 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.

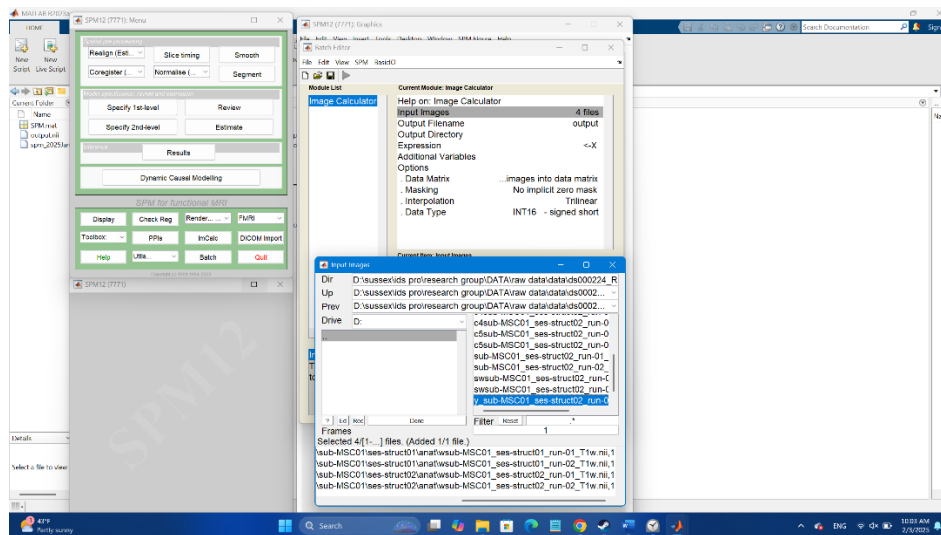


## Anatomical averaging:

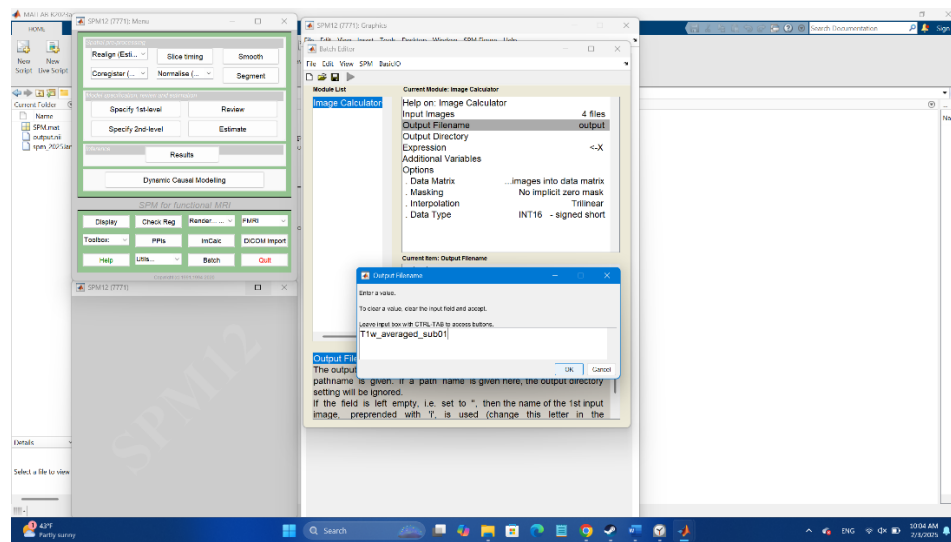
- ImClac batch folder will be selected, this batch will be used for averaging a number of images.



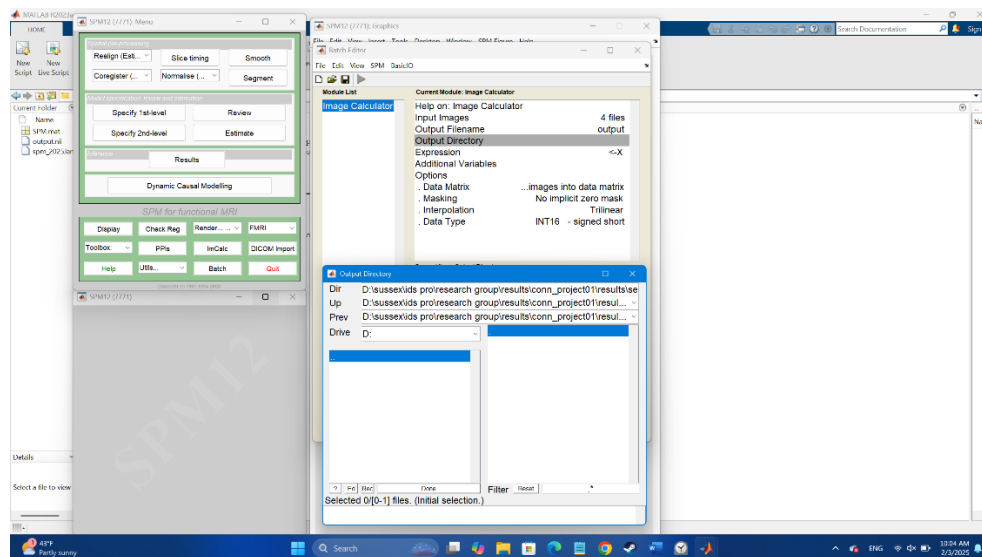
- In the input images, 4 normalized images will be selected including images with “w” prefixes from 2 sessions and their 2 runs (not adding images with “sw” prefixes, however, deciding the use of which image depends on your research-related factors and decision, in some cases “sw” images will be used).



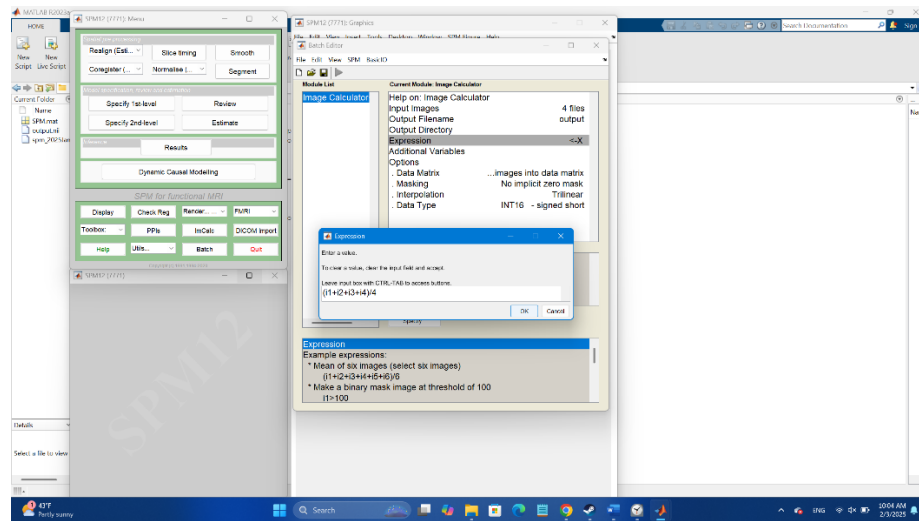
- The output file's name will be selected (e.g., T1w\_averaged\_sub01)



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

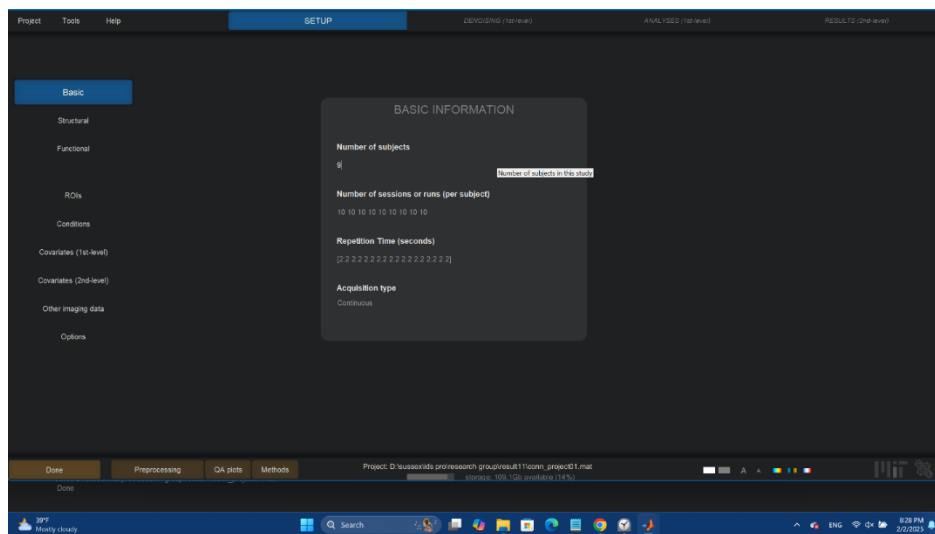


- In the expression section, you need to add the formula for your averaging. As is presented in the following image, since 4 images exist, the sum of all images was divided by the number of images.

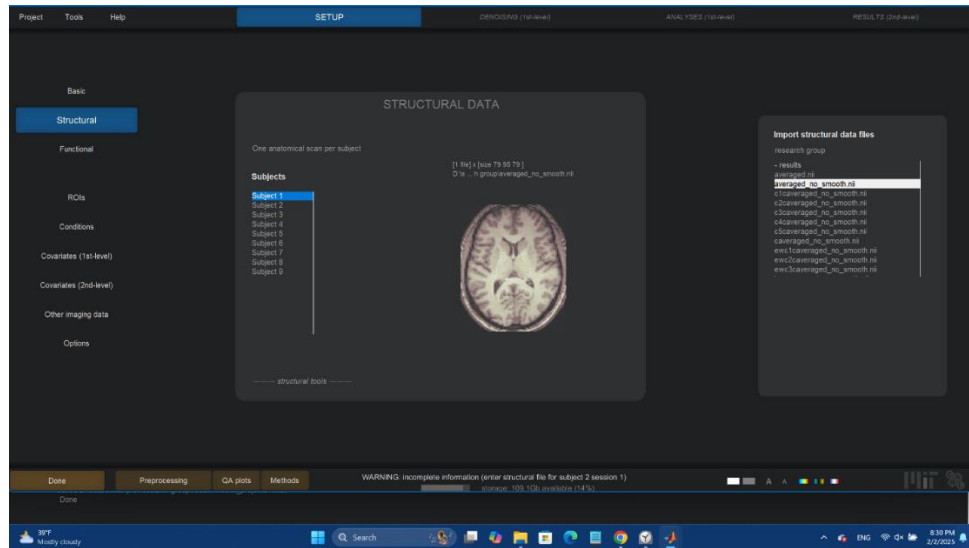


## CONN preprocessing:

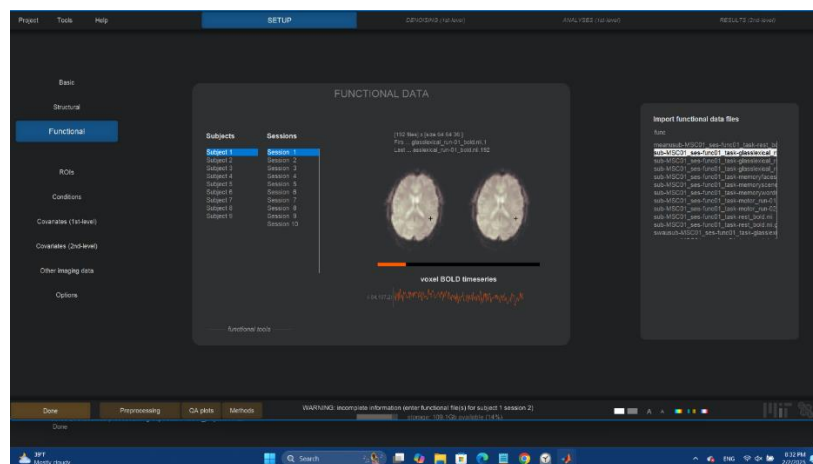
- 9 subjects with 10 sessions and TR = 2.2 (according to Json files) will be entered.



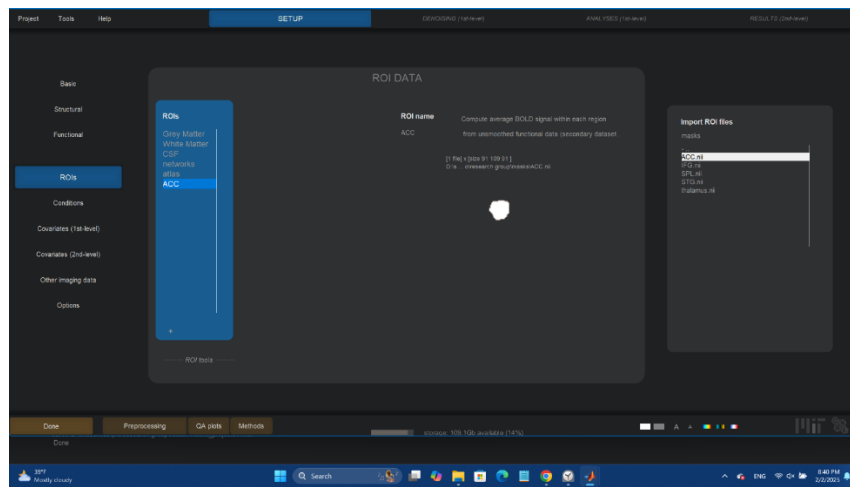
- For each subject, its corresponding averaged anatomical data will be added in the structural step.



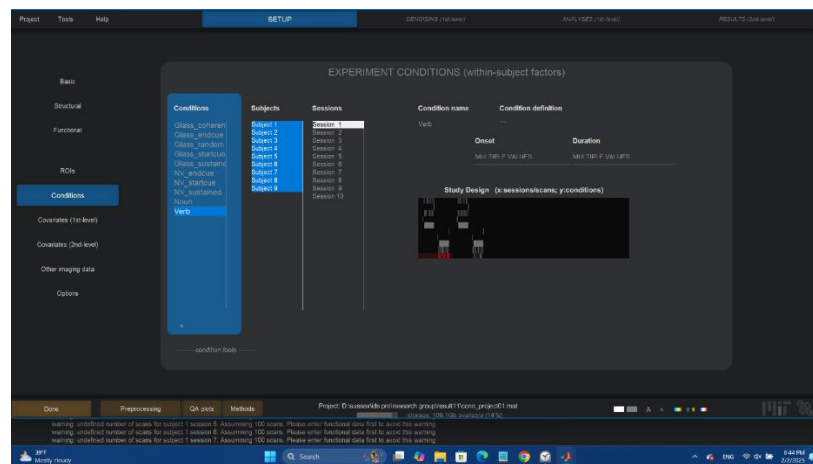
- For the functional part, functional images (bold images) for each session for all subjects will be added.
- Our functional images include: 1) rest, 2) motor tasks (2 runs), 3) glass lexical tasks (2 runs), 3 memory tasks.
- Solution for consideration: two approaches can be applied in our dataset, 1) assuming each task as a separate session and adding all tasks in one run of CONN's preprocessing (e.g., subject 1 has 10 sessions and 8 tasks in each session. To run the CONN preprocessing only once, we can assume that we have 80 sessions (each session includes different tasks or the same task from different sessions). The other way to do that is to run preprocessing for each task separately.



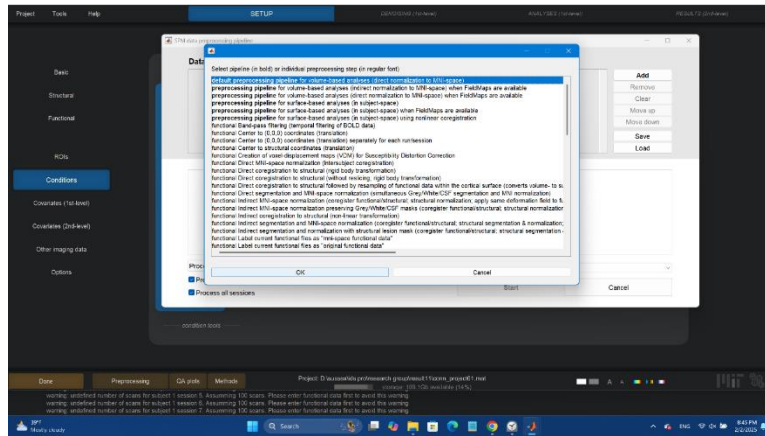
- In the ROI section, pre-defined ROIs will be imported from your local directory.



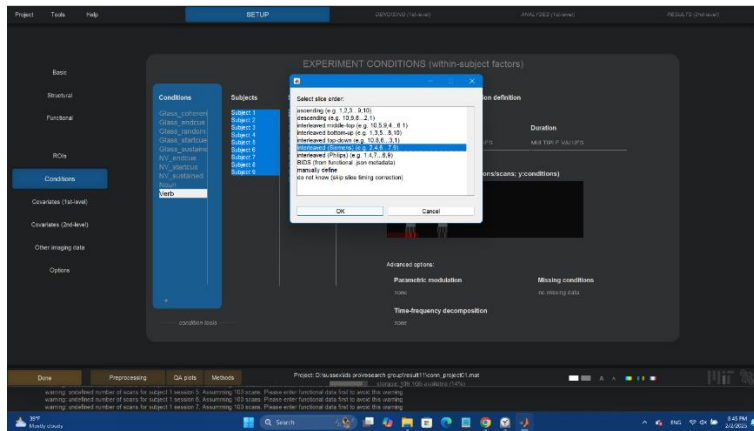
- All conditions will be imported automatically using condition tools > import conditions info from text files > BIDS compatible (one \*\_tsv ...)



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

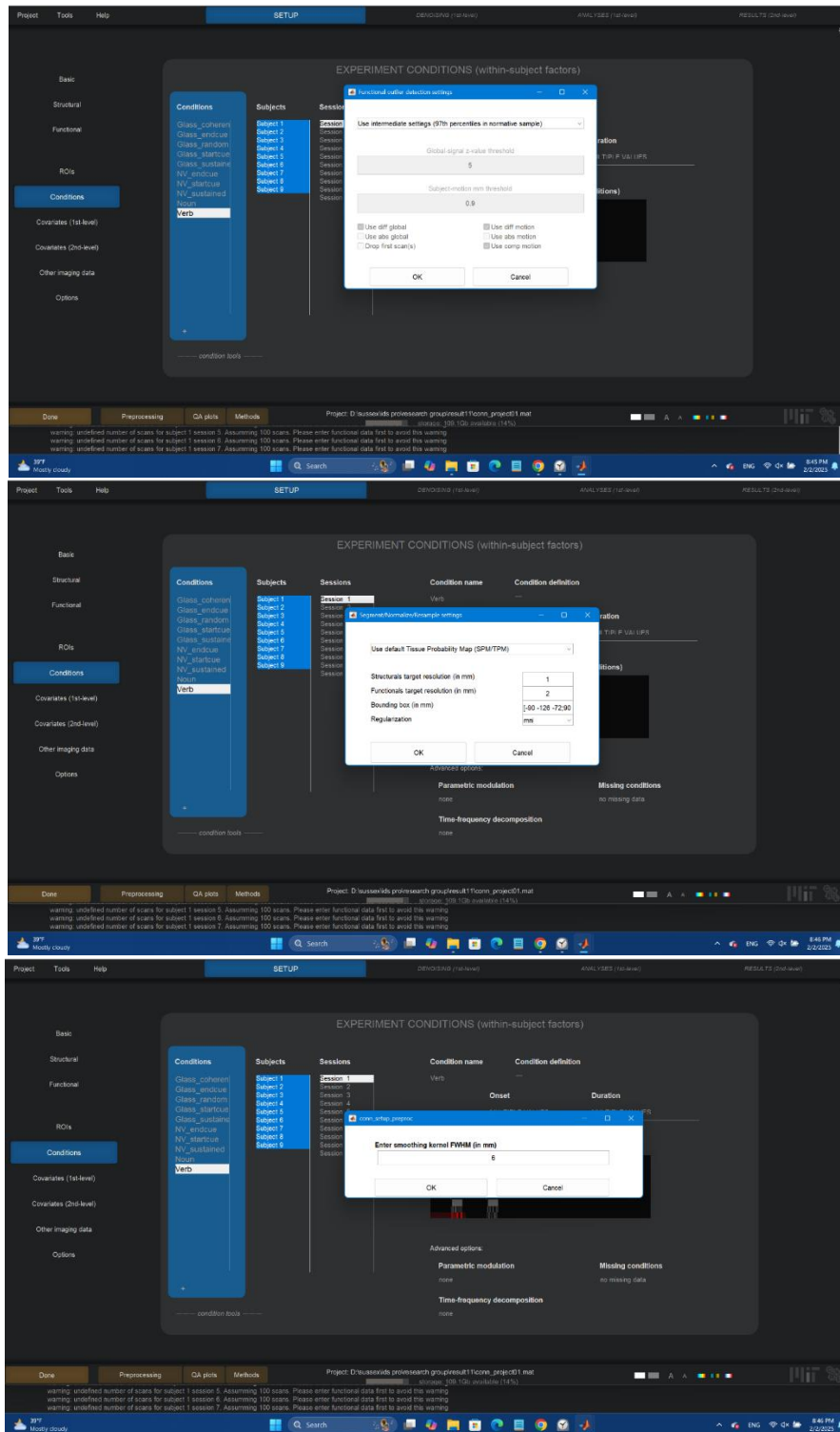


- According to the JSON file, interleaved (Simens) will be selected as slice order.

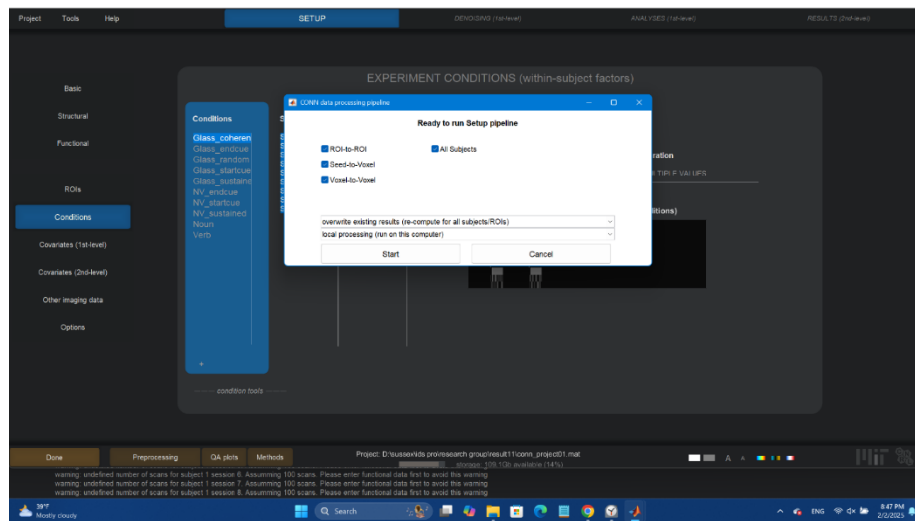




- All other parts would be set as default (only the Gaussian kernel will be set to 6mm)



- 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.

