

A Typical User

SEDER SOFTWARE

A typical series of steps:

- 1. Make a study
- 2. Add a subject
- 3. Collect data
- 4. Add MEG data
- 5. Prepare analysis
- 6. Perform analysis
- 7. Add final notes

STEP 1: Make a study

- What will you call your study?
- Run the command:
 - `seder_new_study`

STEP 2: Add a subject

- You must know the subject's name.
- You must also have an existing study available.
- Then use this:
 - `seder_new_subject`

STEP 3: Collect data

- Collect whatever data you like.
- Some examples:
 - MEG
 - MRI
 - fMRI
 - DTI

STEP 4: Add MEG data

- If you collected MEG data, you must connect the data to the Seder system.
- To do that, you must know:
 - the subject ID
 - the ID used with the MEG system
 - the year, month and day of data collection
 - the study
 - which MEGRAID was the data stored on
- Use this:
 - `seder_new_meg_raw`

STEP 5: Prepare analysis

- Now you want to analyze the data.
- Decide what form of analysis you will use.
- Examples:
 - dspm
 - freesurfer
 - dip_sandbox
 - dip_clin
 - clinical_reports

STEP 5: Prepare analysis (continued)

- Know what types of data this analysis is dependent on. For example:
 - meg_raw/epilepsy_2004_02_30
 - freesurfer/epilepsy_2004_03_23
- Have a general goal in mind (optional)
- Use the command:
 - seder_new_dataform
- Enter in the dependencies and initial notes

STEP 6: Perform the analysis

- Do whatever analysis you want to do in the newly created folder for that purpose.
- If you perform a new kind of analysis, be sure to go back to Step 5.
- Keep in mind the key results of your analysis.

STEP 7: Add final notes

- Every analysis folder created with Seder software will have a file called:
SEDER_FINAL_README.txt
- This file should be used to record two things:
 - The commands that you used to perform the analysis
 - Any final results of the analysis