NOTE: pick\_channels() & pick tupes is a legacy function. New code should use inst.pick(...).

“EEG, MEG, HEOG, VEOG, ECG, MISC006, MISC007”

Make find bads use only the first 20 seconds

What can we do to improve EEG? SSP or SSS? Or is it just generally poor?

Compare dataset 3 and dataset 4

Compare 4 and 8 repetiotions….

why is dataset 4 not as good even though it is twice as much data?

Delay for short term loudness - is this an boredom effect?

Compare number of reps (and first four and last four averaged)

What makes a “good recording?”

Signal to noise ratio?

Movement in the MEG?

Individuals but on source space…

Double vs short format for Fifs… does this make a difference?

* re-referencing?
* Main line removal?
* ICA?
* Why are ‘0 projection items activated’ when evoking? Have they already been removed dueing maxfilter? (Similar: No projector specified for this dataset. Please consider the method self.add\_proj.)
* Put VEOG/HEOG thresholds back to where they were for Russian (I think I have increased them) - how many deleted – does this make a difference?
* What should we use for high pass? Currently I am using 0.1 – is this too high? (others are using 0.01)
* Check both this (high pass and low pass as well (currently 330Hz))
* Can we use ‘short’ (32 bit )instead of single (16bit) for the fifs (we used 16 for the Russian data so perhaps it makes no difference)

No referenceing for Source space?

Comparison of individuals

Loudness?

Why are some poor?

How similar are the IPPMs for individuals?

SSS vs SSP! (Runhoa’s paper says that SSP is better! [https://www.biorxiv.org/content/10.1101/2023.09.21.558786v1](https://eur03.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.biorxiv.org%2Fcontent%2F10.1101%2F2023.09.21.558786v1&data=05%7C01%7Cacgt2%40universityofcambridgecloud.onmicrosoft.com%7C7c36ec133c4d45ea92dd08dbc5bddbc3%7C49a50445bdfa4b79ade3547b4f3986e9%7C1%7C0%7C638321191765399343%7CUnknown%7CTWFpbGZsb3d8eyJWIjoiMC4wLjAwMDAiLCJQIjoiV2luMzIiLCJBTiI6Ik1haWwiLCJXVCI6Mn0%3D%7C3000%7C%7C%7C&sdata=S44gw%2F9Pj8XK1sEKUtICt8CJfsQKrDzaT8N2ty9evRQ%3D&reserved=0))

Should we be getting rid of bads with highish frequencies in the EEG during the viewing stage?? (does it improve or make things worse?)

* What are the weird spikes in the EEG? That becomes obvious after EEG average refencing? Muscle artifact or bad channel? (actually, I can see them before the channel before referencing?)
* Is interpolation of EEG the way to go, or should we just ignore them?

Implememnt BIDS

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<https://mne.tools/stable/overview/implementation.html#minimum-norm-estimates>

*Source Improvements…?*

* Reduce noise in different ways
  + For each trial, bad those channels that are above 150/200, if EEG & less than 5 – \*Don’t drop\*
  + Interpolation
  + Only do ICA on those above 150/200, if eeg & less than 5.
  + Use AAR component separation

Can we/should we remove comp/move and other channels to reduce file size?

**Source Improvements**

* Added support for automated SNR estimation?
* New apply inverse options:
  + RANK
  + Add patch statistics for use with depth
  + Limit depth\_chs
* -csd (improvement?)
* Diag
* *Cov+gcov = “baseline”- preexperiment - > empty-room MEG, and diag EEG – not stimulus*
* Add SSP
* SNR
* Depth – it is still not clear to me what this really is – Should it be 0.5? How can we work out what it should be?

Can we replace the command-line

Flash vs normal CBU-MPRAGE:

https://mne.tools/dev/overview/implementation.html

Inner two for Flash

Outer one T1 (too time consuming?)

*# Convert each echo into mgz files for flash5 and flash30 sequences*

mri\_convert your\_nifti\_file\_name\_megre5\_echoX.nii.gz megre5\_X.mgz

*# Average echos and store the average files into mri/flash/parameter\_maps folder of your freesurfer directory of the subject*

mri\_average -noconform megre5\_1.mgz megre5\_2.mgz megre5\_3.mgz megre5\_4.mgz megre5\_5.mgz megre5\_6.mgz megre5\_7.mgz megre5\_8.mgz ${SUBJECTS\_DIR}/${SUBJECT}/mri/flash/parameter\_maps/flash5.mgz

mri\_average -noconform megre30\_1.mgz megre30\_2.mgz megre30\_3.mgz megre30\_4.mgz megre30\_5.mgz megre30\_6.mgz megre30\_7.mgz megre30\_8.mgz ${SUBJECTS\_DIR}/${SUBJECT}/mri/flash/parameter\_maps/flash30.mgz

*# In python terminal, make the BEM models*

**from** mne.bem **import** make\_flash\_bem

subject = "XZJ7KI"

subjects\_dir = "your\_freesurfer\_directory"

make\_flash\_bem(subject, overwrite=False, show=True, subjects\_dir=subjects\_dir,

flash\_path=None, copy=True, verbose=None)