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

EEG, MEG, HEOG, VEOG, ECG, MISC006, MISC006

Compare old and new maxfilter (select bads beforehand)

Implement hpi removal

Implement pos finding

Implement better bad channel finding

Compare dataset 3 and dataset 4

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

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

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

EEG vs MEG

Play with PCA components - some of them look like external noise items

Why are ‘0 projection items activated’ when evoking? Have they already been removed dueing maxfilter?

Check is EEG or MEG better?

Compare old matlab Russian and new matlab Russian, and python Russian maxfilter – which is different/better and why?

Put VEOG/HEOG thresholds back to where they were for Russian (I think I have increased them)

Make use of New version of Maxfilter (2.2.22 or whatever it is)

In the new python script, EEG are not having bad channels applied, as we miss out the step for maxfilter.

Using thresholds (how many deleated?)

If we re-reference EEG – is this what is making imagined speech worse that old russian? Should we therefore be avoiding it for reconstruction?

Do EEG bad selection AFTER referencing – makes it easier to see?

Why does the ICA code occasionally crash?

Compare the spectrograms of the Russian and English data (). Is the the Russian is better (ie flatter)? If so, why?: English:

A graph of a graph of a graph

Description automatically generated

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))

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))

* Confirm that the new SSS and old SSS files look the same and that the rejection rates are the same (or better)
* 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)
* 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?

<https://www.nature.com/articles/s41598-023-27528-0> claims we should leave everything alone, including:

* re-referencing?
* Main line removal?
* ICA?
* Dropping trials due to thresholds?

Implememnt BIDS

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<https://mne.tools/stable/overview/implementation.html#using-flash-images>

Use 3 layer BEM

Source alignment: https://mne.tools/dev/auto\_tutorials/forward/20\_source\_alignment.html

Use –accurate in the forward model <https://mne.tools/stable/overview/implementation.html#minimum-norm-estimates>

READ ALL NME DOCUMENTATION

Surface is watershead/freesurfer/MPRAGE (from XXX) other 2 from are flash

Watershead:

Flash:

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

Inner two for Flash

Outer one T1

*# 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)

MRI slice overlay

*Improvements…?*

* Reduce noise in different ways
  + Do with ‘ICA’ blinks
  + Does ECG python removal help?
  + 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
* 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?