* Confirm that the new SSS and old SSS files look the same and that the rejection rates are the same (or better)
* Should we use the new SSS and cal in the newer data? Ask Olaf. If so, add in checker?
* 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 trails due to thresholds?

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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?