

BIOMAG - 2018 Challenge

Localization of MEG seizures onset

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<https://github.com/massich/epilepsy-biomag-2018>



Methodology

Our pipeline consists in the following steps:

1. Clean up data (Select time segment and mark bad channels)
2. Compute ICA and manually select a component: dipolar and matching the seizure onset
3. Compute forward model using 1 Layer BEM
4. Fit an equivalent current dipole (ECD) to the ICA topography

Remark: All analysis was done using [MNE-Python](#), [FreeSurfer](#) and [Nilearn](#).

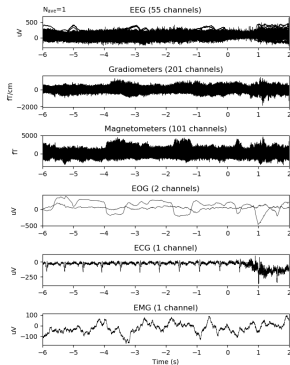
Remark: We only used the MEG channels

Remark: We used [Picard](#)¹ to compute ICA

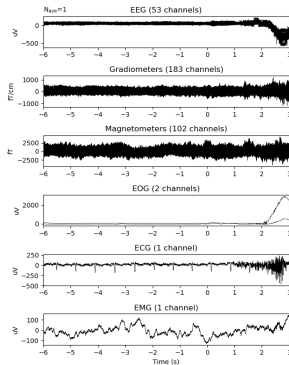
¹Pierre Ablin, Jean-Francois Cardoso, Alexandre Gramfort Faster independent component analysis by preconditioning with Hessian approximations IEEE Transactions on Signal Processing, 2018

Raw cleaned data

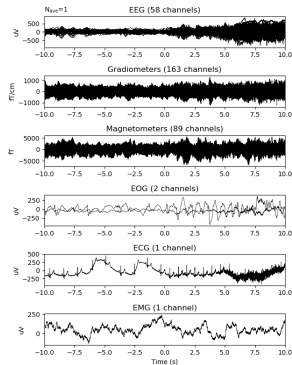
226



245



251

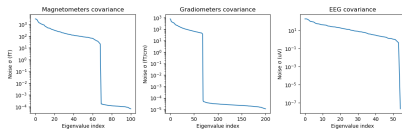
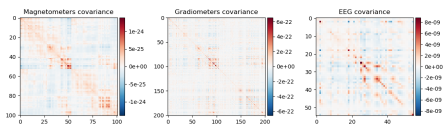


Remark: We used visual inspection of the signal to select the time of interest and mark bad channels. Here follows a summary:

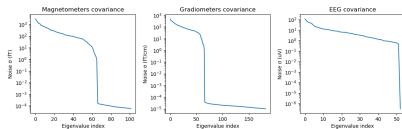
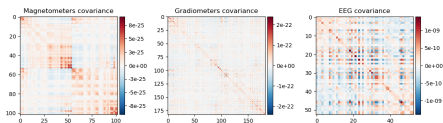
	226	245	251
time interval (in sec.):	(-6, 2)	(-6, 3)	(-10, 10)
num. of bad channels:	14	32	61

Noise covariance analysis

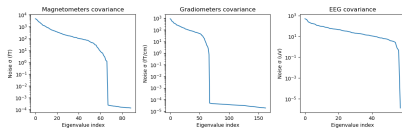
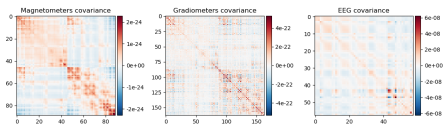
226



245



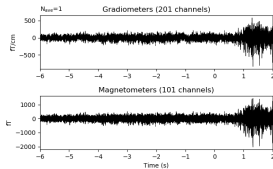
251



Remark: We also used the covariance of the noise to spot high-variance channels that we marked as bad (left figure shows final results). Finally we use the rank of the resulting noise covariance matrices (right figures) to set the number of ICA components.

Manually selected ICA component

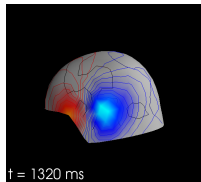
226



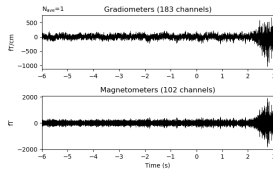
ICA components
ICA033



ICA components
ICA033



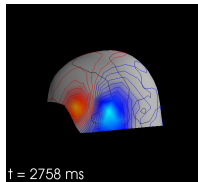
245



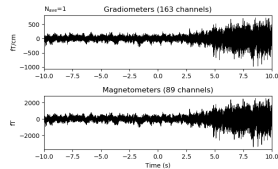
ICA components
ICA035



ICA components
ICA035



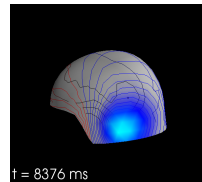
251



ICA components
ICA023



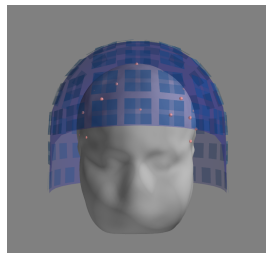
ICA components
ICA023



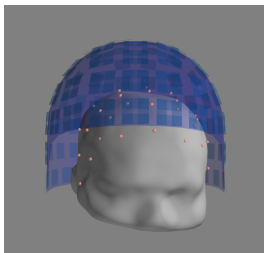
Remark: From all the ICA components, we manually selected the one which was both dipolar and temporally correlated with the seizure onset.

Coregistration

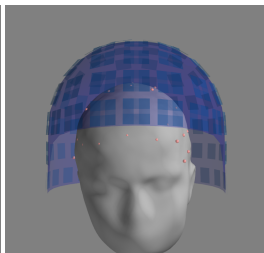
226



245



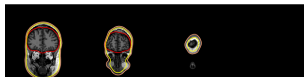
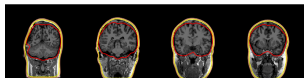
251



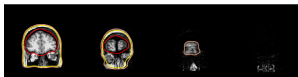
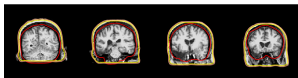
Remark: Coregistrations for 245 and 251 exhibit tilted heads which could suggest poor alignment of the MRI-device coordinates. Although it is hard to assess without pictures of the acquisition.

Boundary Element Model

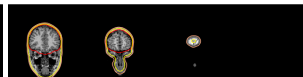
226



245



251

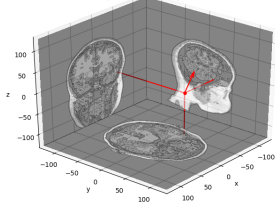


Remark: We use a Boundary Element Method (BEM) with one layer to solve the forward problem.

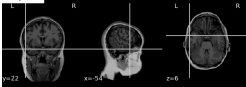
Fit an equivalent current dipole (ECD)

226

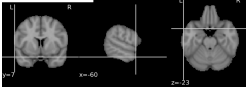
Dipole #1 / 1 @ 1.320s, GOF: 0.0%, 0.1nAm
(-53.7, 14.9, -25.7) mm



Subj: 226

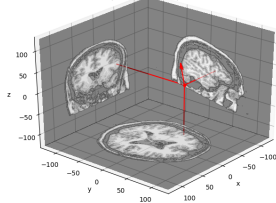


Subj: 226 (MNI Space)

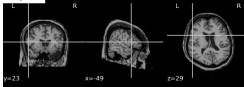


245

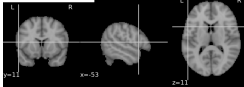
Dipole #1 / 1 @ 2.759s, GOF: 0.0%, 0.1nAm
(-48.1, 15.3, -3.6) mm



Subj: 245

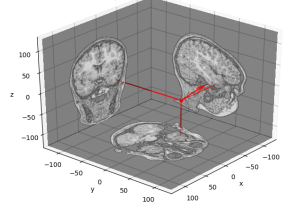


Subj: 245 (MNI Space)

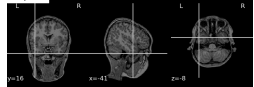


251

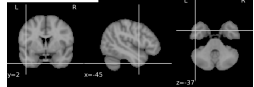
Dipole #1 / 1 @ 8.376s, GOF: 0.2%, 1.1nAm
(-40.5, 8.9, -40.1) mm



Subj: 251



Subj: 251 (MNI Space)



1st row: Dipole location in subject's MRI in 3D.

2nd row: Dipole location in subject's MRI coordinates (2D slices)

3rd row: Dipole location in subject's MNI template brain (2D slices)

Results Summary

	MNI			TAL		
	x	y	z	x	y	z
226:	-60	7	-23	-58	2	-17
245:	-53	11	11	-50	8	12
251:	-45	2	-37	-44	-2	-29

Table 1: ECD location for each subject using MNI and TAL template brain coordinates.

Remark: TAL coordinates were computed from MNI coordinates using this [Bioimage Suit](#) webtool.