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► To cite this version:

Christelle Zielinski, Valerie Chanoine, Guillaume Auzias, Olivier Coulon, Andrea Brovelli. HGA-MarsAtlas: a toolbox for the estimate of high-resolution, single-trial source-level high-gamma activity from MEG data. Journées de l'ILCB / BLRI, May 2019, Porquerolles, France. hal-03979007v1

HAL Id: hal-03979007

<https://hal.science/hal-03979007v1>

Submitted on 8 Feb 2023 (v1), last revised 16 Feb 2023 (v2)

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HGA-MarsAtlas: a toolbox for the estimate of high-resolution, single-trial source-level high-gamma activity from MEG data

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Background

High-Gamma band activity (from 50 to 150 Hz) can be used to unravel the dynamics of functional connectivity (FC) mediating human cognitive functions [1, 2].

The approach is based on the combinaison of MEG data with a single-subject cortical parcellation scheme from individual anatomical MRI produced by the MarsAtlas model (available in the BrainVisa software) [3]. The resulting single-trial HGA from all cortical parcels can be used for functional mapping and FC analyses.

More recently, the approach has been generalized to high-resolution source models based on cortical meshes containing up to 8000 sources. Importantly, the sources within these meshes preserve inter-individual correspondences, allowing group-level analyses.

The HGA-MarsAtlas toolbox has been developed to enable automated extraction of the single-trial HGA by linking the results of anatomical analyses performed with BrainVisa and exploiting the functionalities of FieldTrip software for MEG analysis.

- Specifications
- ✓ Matlab
 - ✓ parametrizable
 - ✓ batch processing
 - ✓ optimized processing speed

We ran the HGA-MarsAtlas pipeline on the dataset from a visuomotor task analyzed in [1, 2], giving the results shown here.

Thanks to the partners!

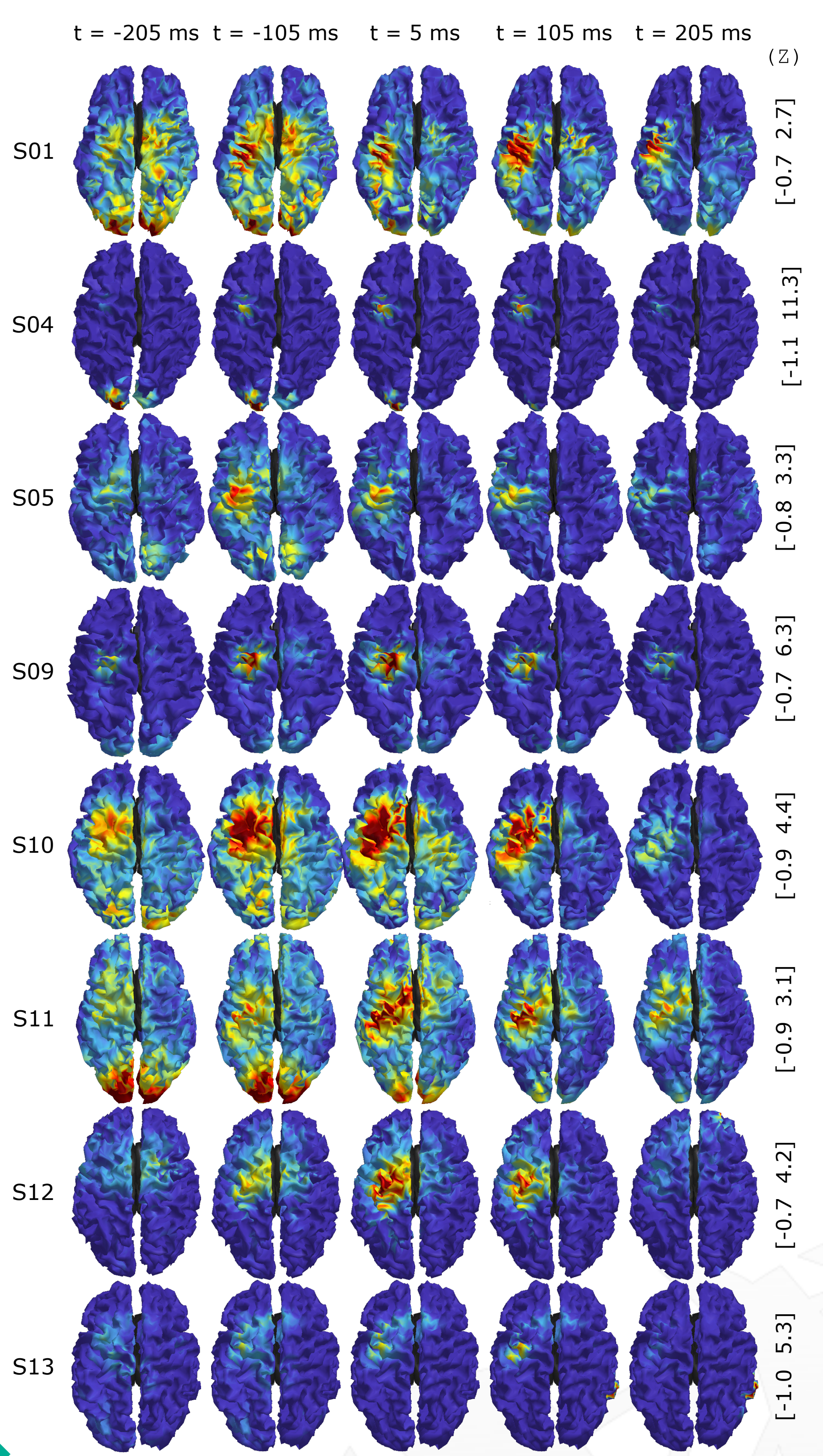


References

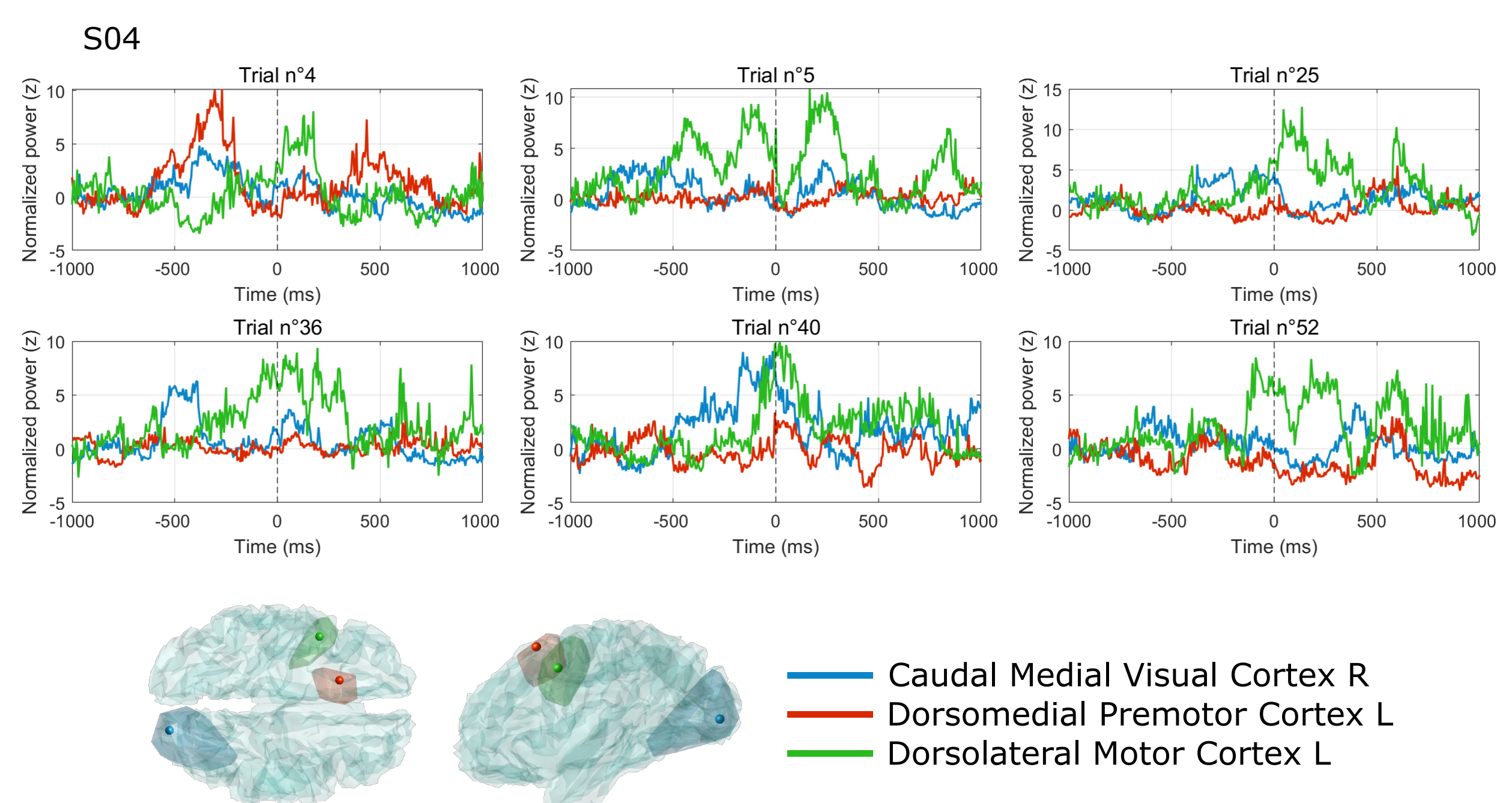
[1] Brovelli et al., 2015, Characterization of cortical networks and corticocortical functional connectivity mediating arbitrary visuomotor mapping \times 10.1523/JNEUROSCI.4892-14.2015 [2] Brovelli et al., 2017, Dynamic Reconfiguration of Visuomotor-Related Functional Connectivity Networks \times 10.1523/JNEUROSCI.1672-16.2017 [3] Auzias et al., 2016, MarsAtlas: A cortical parcellation atlas for functional mapping \times 10.1002/hbm.23121 [4] Gross et al., 2001, Dynamic imaging of coherent sources: Studying neural interactions in the human brain \times 10.1073/pnas.98.2.694 [BrainVISA: brainvisa.info] [FieldTrip: www.fieldtriptoolbox.org]

High-resolution trial-averaged HGA

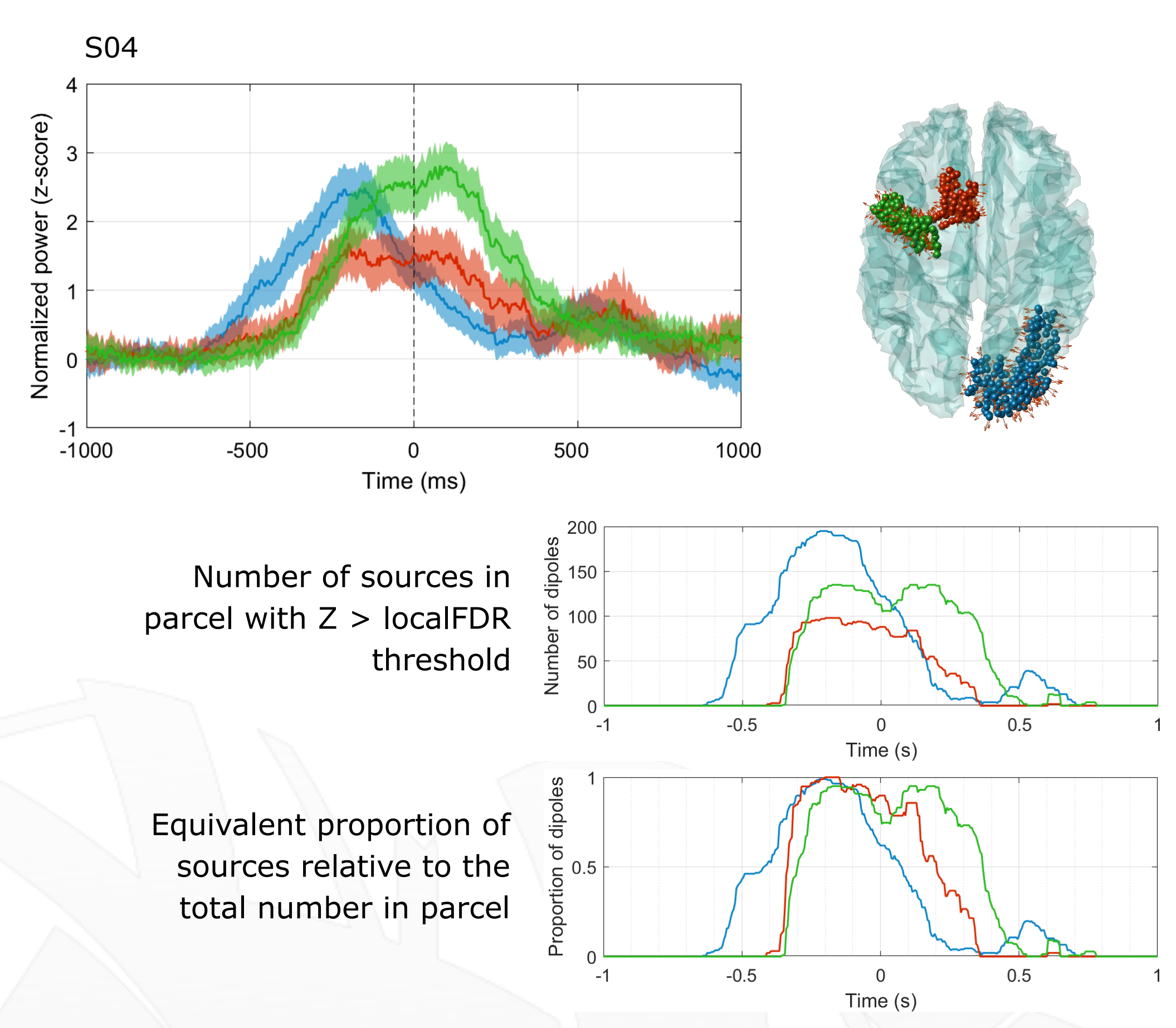
t= 0 s: participant's response (finger movement) to the visual stimulus



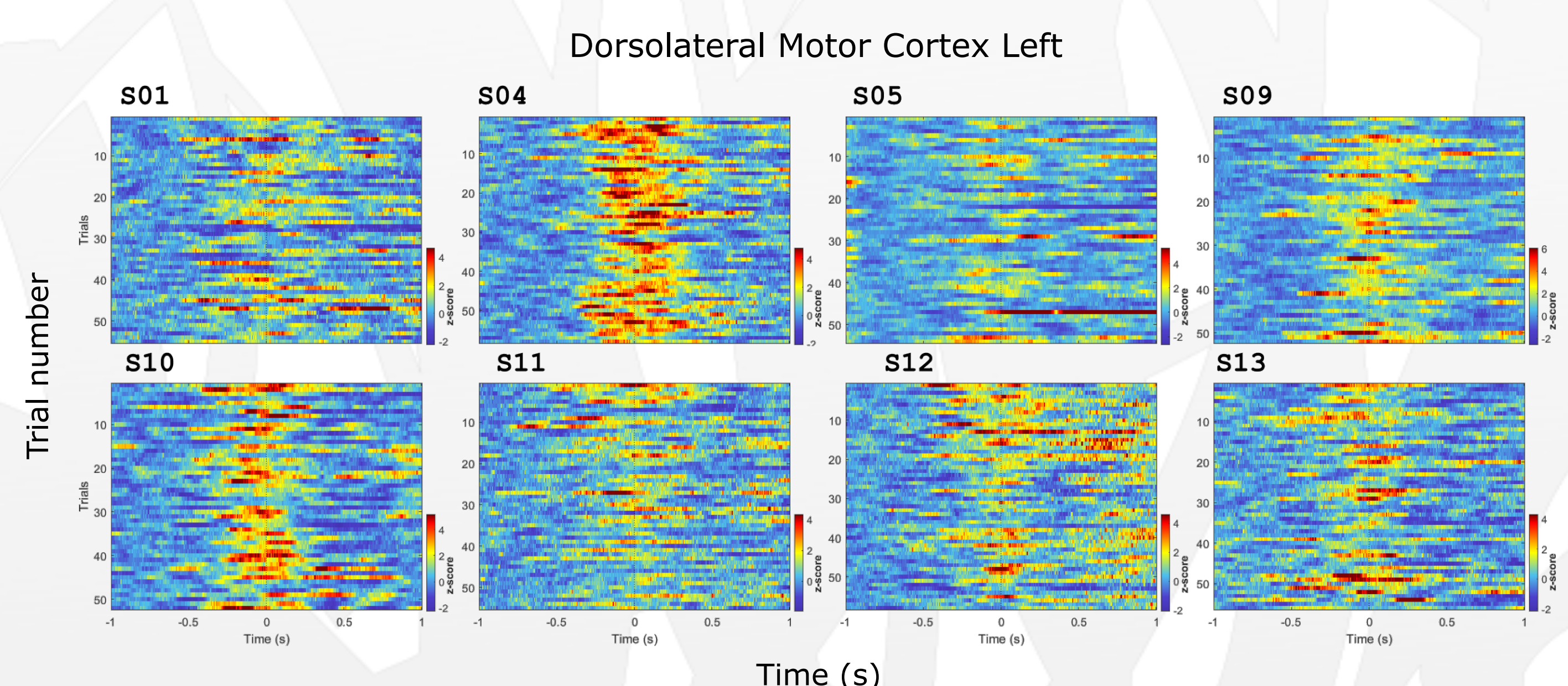
Single-trial source-level HGA



Trial-averaged HGA at parcel-level



Single-trial HGA at parcel-level



HGA-MA pipeline

MarsAtlas

- BrainVisa/FreeSurfer pipeline from individual MRI
- MarsAtlas parcellation (82 regions)
- cortical surfaces decimation (up to 8000 sources)
 - ✓ correspondences across participants

Initialization

- Parameter initialization, data importation (once):
 - ✓ MRI, MA surface & volume from BV and FS databases
 - ✓ pointers to MEG data in MEG database

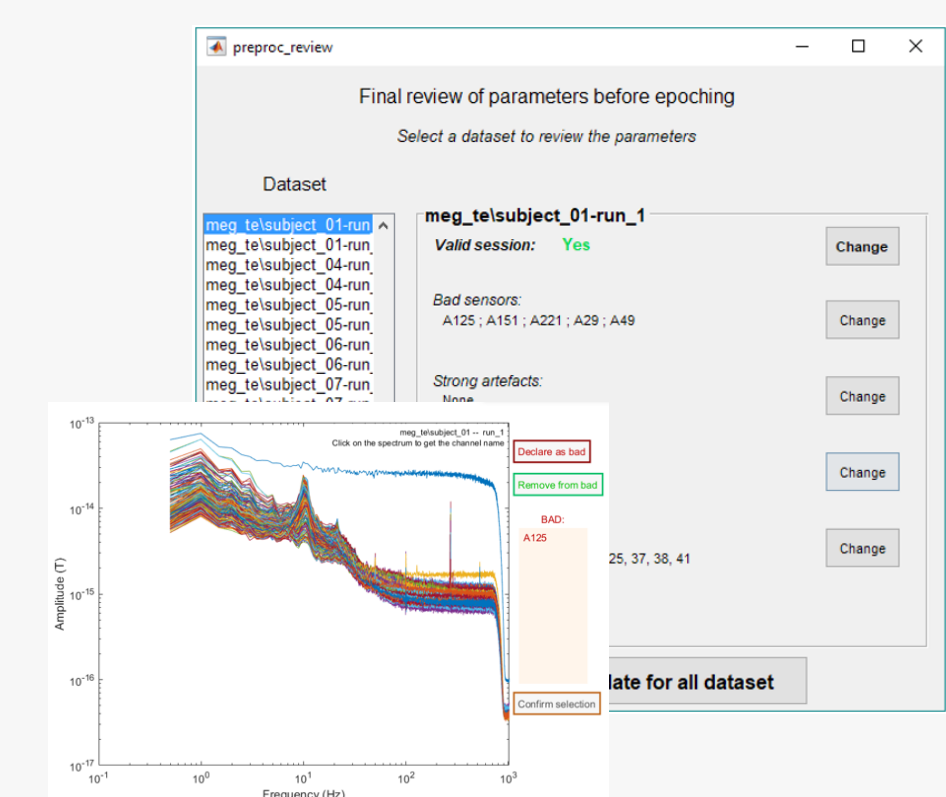
Preprocessing

Anatomical data

- Fiducial identification for coregistration [ft-manual]
- Inner skull segmentation (conduction volume) [ft-SPM]
- Sources preparation
 - ✓ cortical: surface normals
 - ✓ subcortical: k-mean in MA parcels
- Coregistration check (Left/Right flip correction)

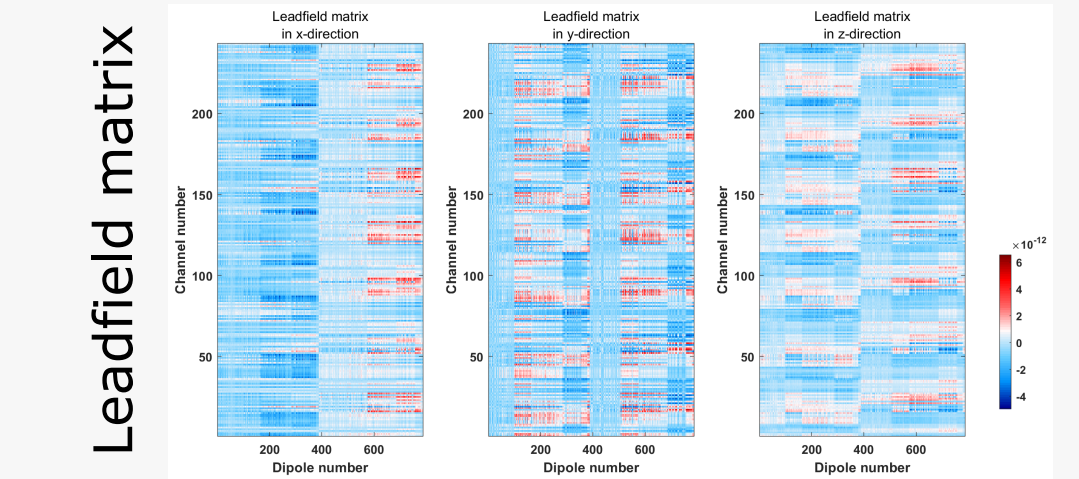
MEG data

- From a resampled data version (400 Hz)
 - Strong artefact detection
 - Bad channels
 - Artefact-linked ICA components
 - Bad trials [ft-browser]
 - Final review
- Data cleaning and backup



Source imaging

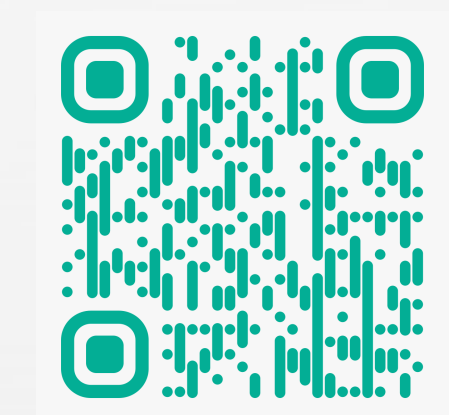
Forward model



Inverse modeling

- Power matrix** [source x trial x time]
 - Time-frequency analysis using multitapers [ft]
 - Dynamic Imaging of Coherent Sources beamformer
 - Baseline normalization (z-transform)

Beta version



Next steps

- Broad-band source-level MEG activity (LCMV beamformer)
- Cluster-based statistics to find spatio-temporal clusters of activation
- Functional connectivity dynamics
- Comparison across modalities (simultaneous MEG/SEEG)