White matter fiber bundles as a source model in the MEG inverse problem

Kostiantyn Maksymenko, Théodore Papadopoulo, Samuel Deslauriers-Gauthier

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Kostiantyn **Maksymenko***   Théodore **Papadopoulo***   Samuel **Deslauriers-Gauthier***

* Université Côte d'Azur, Inria Sophia Antipolis - Méditerranée, France

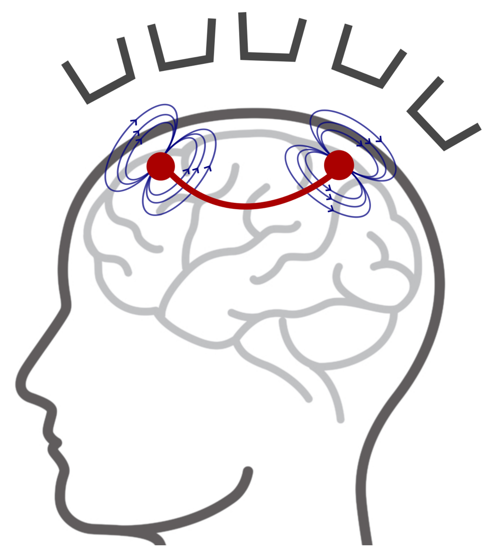
Contact - kostiantyn.maksymenko@inria.fr

http://team.inria.fr/athena/

1 INTRODUCTION

The magnetoencephalography (MEG) inverse problem, i.e. **recovering brain activity from MEG measurements**, is ill posed and **additional hypotheses** are needed to constrain the solution space.

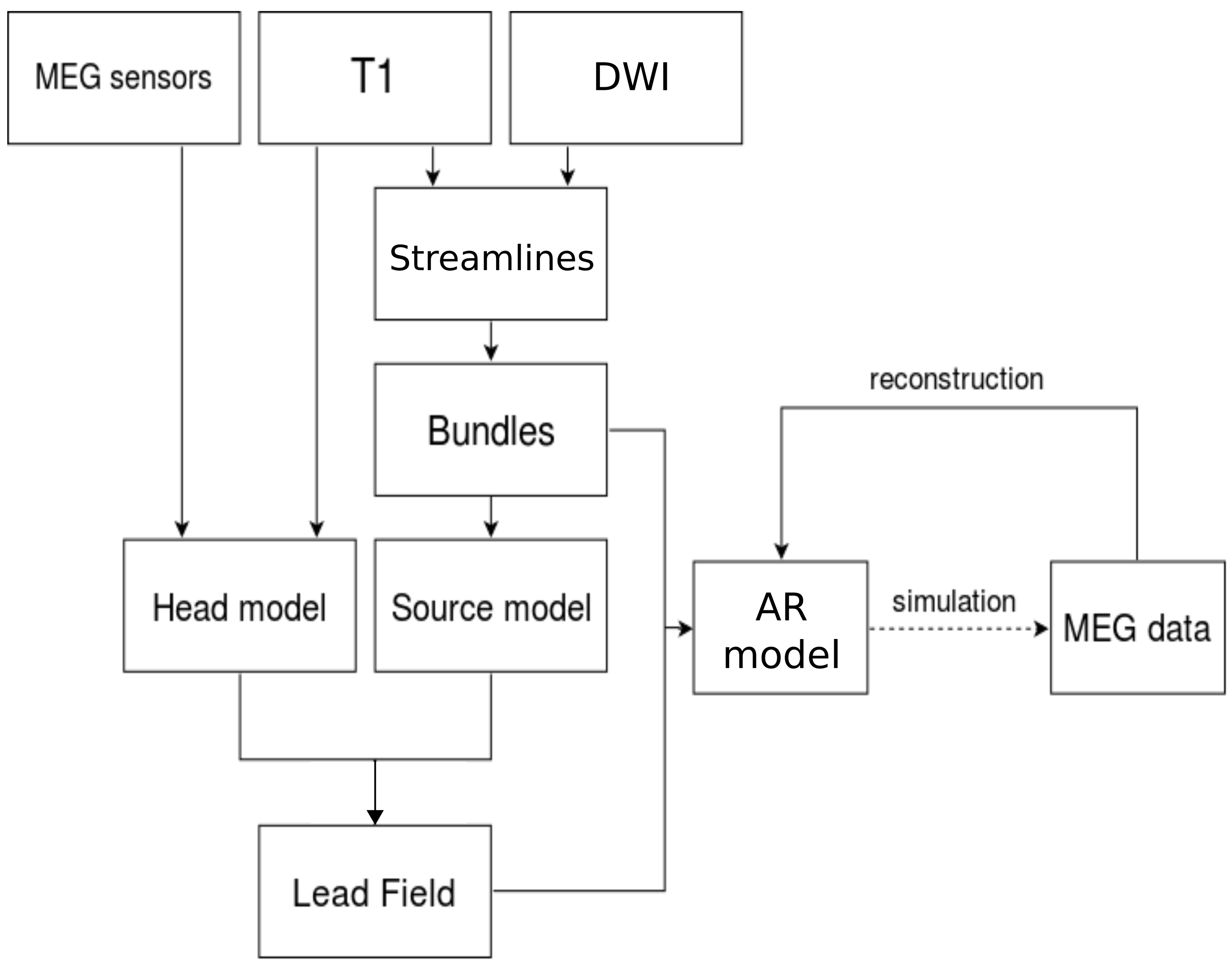
In this work, we introduce an approach which considers white matter streamlines, obtained using **diffusion magnetic resonance (MR) imaging**, as a source model for the **MEG forward problem**. To simplify the model and reduce the computational complexity we regrouped similarly shaped streamlines into bundles. The MEG data associated with a single bundle activity was simulated. The objective was to fit simulated data for each bundle and to analyze the data fitting error.



2 METHODS

- Streamlines are computed using anatomically constrained tractography [1]
- Streamlines are regrouped into bundles to reduce the number of sources [2]
- Bundle end-points are considered as MEG sources
- Realistic head model is computed based on MRI and MEG sensors locations
- Two lead fields are computed for each bundle (end-points)
- AR model (1) is used to simulate and reconstruct the MEG data (for a single bundle). Delay between two end-points is estimated based on the length of a bundle

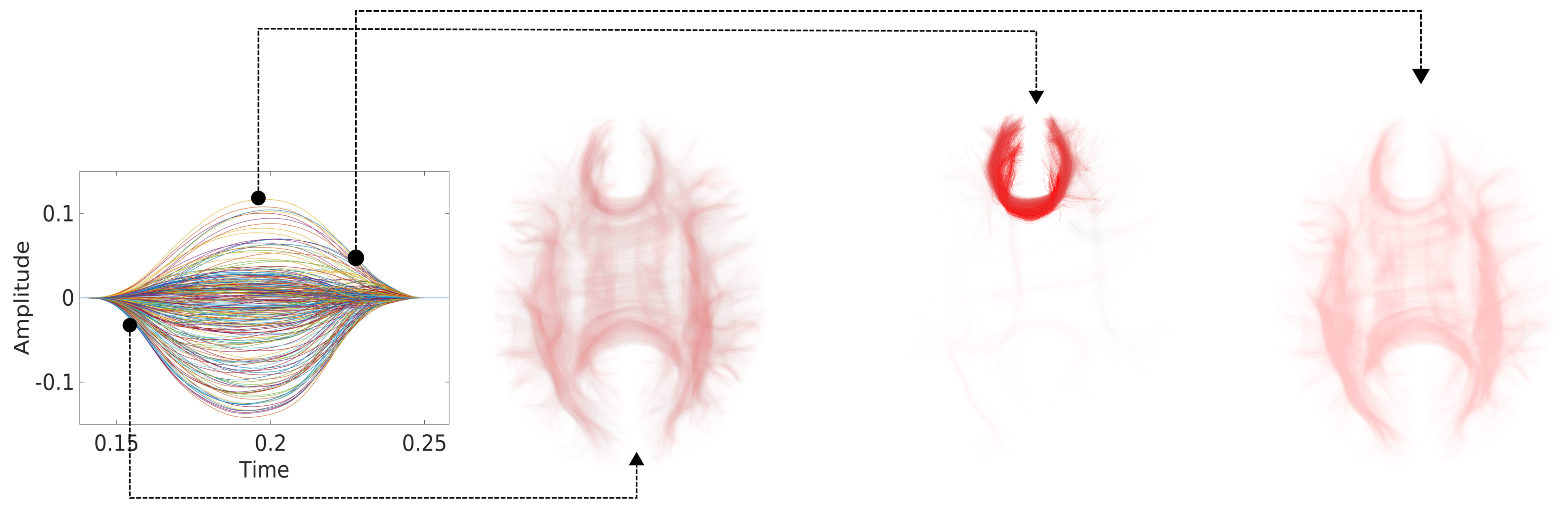
$$(1)\ y(t) = l_1 \cdot x(t) + l_2 \cdot x(t-\delta)$$



3 RESULTS

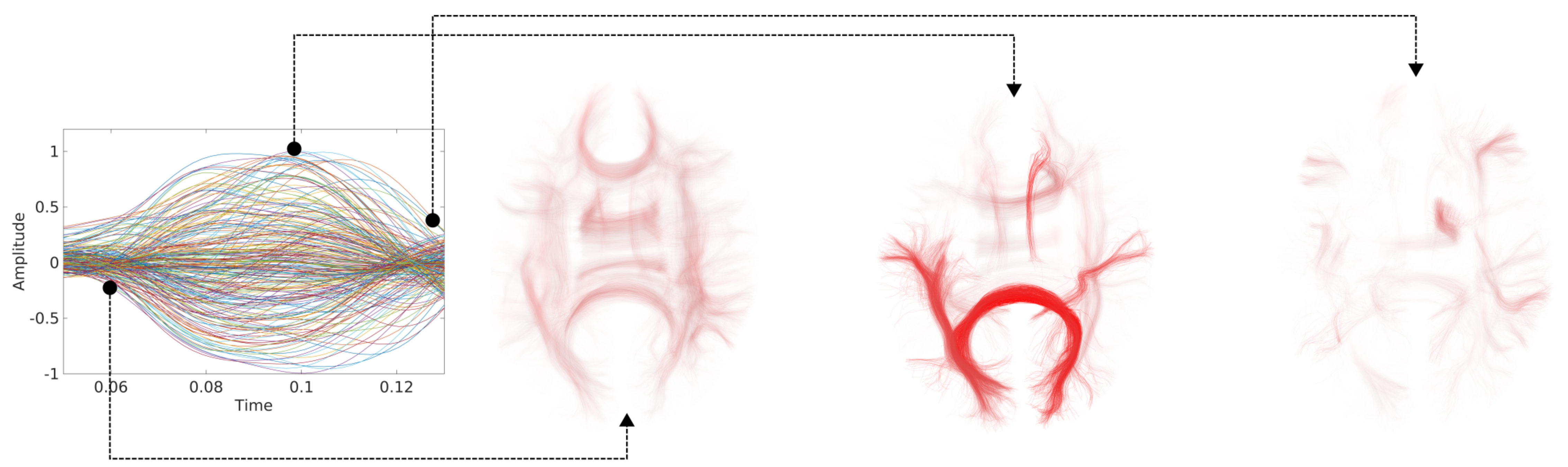
A) Simulation

- Anatomy from subject 100307 (HCP dataset)
- MEG signal simulated using (1) for one random bundle
- Least square reconstruction for each bundle
- Simulated bundle has the highest accuracy at the peak of the signal



B) Real data

- Same subject as for simulation
- Real preprocessed MEG signal corresponding to the face vs. tool visual task (first 130 ms)
- Highest accuracy corresponds to the corpus callosum through the splenium and the inferior longitudinal fasciculus



4 CONCLUSIONS

- New approach for MEG inverse problem based on the white matter fiber bundles
- Highlights reasonable bundles for real data
- Shows good performance for a single bundle simulated data
- Has natural limitations, but can be used as a preprocessing step for more complex models

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References:
[1] Girard, G., Whittingstall, K., Deriche, R., Descoteaux, M.. Towards quantitative connectivity analysis: reducing tractography biases. NeuroImage, 98, 266-278, 2014.
[2] Côté M-A., Garyfallidis, E., Larochelle, H., Descoteaux, M.. Cleaning up the mess: tractography outlier removal using hierarchical QuickBundles clustering. Proceedings of: International Society of Magnetic Resonance in Medicine (ISMRM), Toronto, Canada, 2015.