System design considerations for biomagnetic applications using optically pumped magnetometers

Tilmann H. Sander, Physikalisch-Technische Bundesanstalt, Berlin, Germany, tilmann.sander-thoemmes@ptb.de
Maik Liebl, Physikalisch-Technische Bundesanstalt, Berlin, Germany, maik.liebl@ptb.de
Frank Wiekhorst, Physikalisch-Technische Bundesanstalt, Berlin, Germany, frank.wiekhorst@ptb.de
Thomas Middelmann, Physikalisch-Technische Bundesanstalt, Berlin, Germany, thomas.middlemann@ptb.de

Introduction

A string of innovations in the field of optically pumped magnetometers (OPMs) lead to high expectations for simplified biomagnetic devices. Since OPM sensors are currently available only as single-units with inter-sensor synchronization or at most common support electronics the current OPM setups require considerable experimental expertise. This contrasts with turnkey multichannel SQUID systems with often integrated software suites.

Methods

Typical magnetically shielded rooms are optimized for SQUIDs, which can have a large dynamic range of up to several 100 nT. Therefore, the decreasing shielding effectiveness of mu-metal below 1 Hz is not a severe problem for SQUIDs. The shielding requirements for OPMs are almost the opposite as field fluctuations above 10 nT saturate them.

Results

Using the active compensation on the outer edge of a two-layer shielded room of type Ak3b commercial OPMs can be operated without saturation. Auditory evoked fields close to 1 pT were measured confirming the potential of OPMs for MEG. For flow investigations using magnetic microspheres an existing phantom was surrounded by OPM sensors distributed on a cylindrical surface. The magnetic field of a moving probe metallic sphere was detected on the cylinder surface.

Conclusion

OPMs allow a range of new measurement setups for biomagnetism and the flexibility in placing them around a field source is outstanding, but it is not clear whether OPMs will replace or complement existing SQUID installations. Particularly for MEG the requirements for sensor calibration and geometric precision might be difficult to meet with OPMs. New high dynamic range OPMs have been announced and might alleviate the saturation problem.

Real-time time-frequency analysis in MNE-CPP

Johannes Vorwerk, Institute of Electrical and Biomedical Engineering, UMIT – Private University for Health Sciences, Medical Informatics and Technology, Hall in Tirol, Austria, johannes.vorwerk@umit.at
Lorenz Esch, Massachusetts Institute of Technology, Harvard Medical School, Athinoula A. Martinos Center for Biomedical Imaging, Charlestown, MA, USA
Matthias Klemm and Jens Haueisen, Institute of Biomedical Engineering and Informatics, Technische Universität Ilmenau, Ilmenau, Germany
Daniel Baumgarten, Institute of Electrical and Biomedical Engineering, UMIT – Private University for Health Sciences, Medical Informatics and Technology, Hall in Tirol, Austria

Introduction

Real-time EEG processing has the potential to become of tremendous interest to the neuroscience community due to its unique time resolution and the possibilities it offers for a fundamental change in neuroscientific work - away from experiments with fixed paradigms in favor of highly dynamic and adaptable paradigms depending, e.g., on the current state of a brain property of interest. Currently, many applications of real-time EEG processing – from brain computer interfaces (BCI) to brain-state dependent stimulation – are based on real-time time-frequency analysis. We present the implementation and possible application of real-time time-frequency analysis in the open-source toolbox MNE Scan.

Methods

MNE Scan is an open-source and cross-platform application that allows for the real-time processing of EEG/MEG measurements (Esch et al., 2018). Besides EEG/MEG preprocessing steps, such as signal filtering and averaging, MNE Scan offers complex processing steps such as real-time source localization and connectivity analysis (Dinh et al., 2015). Due to its modular structure, MNE Scan is easily extendable. We implemented real-time time-frequency analysis in MNE-CPP and demonstrate a possible use case.

Results

We outline the implementation of real-time time-frequency analysis in MNE-CPP. In combination with MagCPP, which allows for the external control of Magstim TMS devices, this newly implemented feature allows to set up a processing pipeline for brain-state-dependent closed-loop TMS. We demonstrate such a pipeline for closed-loop TMS stimulation based on the detection of ß event-related desynchronizations (ERDs).

Conclusion

The implementation of real-time time-frequency analysis in MNE Scan is an easily accessible and affordable solution for EEG-based closed-loop TMS paradigms. It allows to easily adopt novel study designs, but could also help to improve further existing TMS paradigms.

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A Fourier transformation based convolutional neural network layer for physics-informed deep learning of magnetic dipole inversion

Nora Küchler, Department of Computer Science and Automation, Technische Universität Ilmenau, Ilmenau, Germany, nora.kuechler@tu-ilmenau.de
Jens Haueisen, Department of Computer Science and Automation, Technische Universität Ilmenau, Ilmenau, Germany, jens.haueisen@tu-ilmenau.de
Ferdinand Schweser, Buffalo Neuroimaging Analysis Center, Dept. of Neurology, Jacobs School of Medicine and Biomedical Sciences, University at Buffalo, The State University of New York, Buffalo, NY, United States; Center for Biomedical Imaging, Clinical and Translational Science Institute, University at Buffalo, The State University of New York, Buffalo, NY, United States, schweser@buffalo.edu
Thomas Jochmann, Department of Computer Science and Automation, Technische Universität Ilmenau, Ilmenau, Germany, thomas.jochmann@tu-ilmenau.de

Introduction

When biological tissue is brought into an externally-applied magnetic field it magnetizes and perturbates the applied field. This perturbation can be mapped with magnetic resonance imaging and subsequently be used to calculate the underlying magnetic susceptibility distribution. Magnetic susceptibility promises to provide insights into disease processes that alter the tissue chemical composition.

Iterative numerical methods for solving the mathematical inverse problem posed by susceptibility mapping require a fast simulation of the field perturbation caused by a given susceptibility distribution. The perturbation field (f) can be approximated by a three-dimensional spatial convolution (*) of the magnetic dipole (d) and the magnetic susceptibility distribution (χ):

$$f = d * \chi \,.$$

Discrete, numerical convolution in the spatial domain is fast when the convolutional kernel is small. For large kernels, such as d, a computationally more efficient approach is to perform the convolution in the Fourier domain:

$$f = \mathrm{F}^{-1}\{\mathrm{F}\{d\} \bullet \mathrm{F}\{\chi\}\},$$

where F denotes the Fourier transform and • the point-wise multiplication.

Here we present a GPU-accelerated approach to dipole convolution, embedded in a neural network layer.

Methods

We developed a Fourier transformation based convolutional layer for tf.keras (Python, Tensorflow 2.0). The non-trainable weights of the convolutional kernel are defined by the physical problem (magnetic dipole). All matrix operations are implemented with Tensorflow methods, omitting Numpy, in order to fully operate on graphics processing units (GPUs) with NVIDIA CUDA support. We validated the results against theoretical predictions and solutions from an established CPU-based MATLAB implementation.

Results

The numerically-achieved perturbation from a uniform cylinder resembled the theoretical prediction. Our GPU implementation was 60 times faster than the CPU version (160×160×160 voxels) with differences only at the level of numerical accuracy ($\max(|f_{\mathrm{MATLAB}} - f_{\mathrm{TensorFlow}}|) / \mathrm{SD}(f_{\mathrm{TensorFlow}}) < 5 \cdot 10^{-6}$).

Conclusion

Our GPU-based implementation of the magnetic dipole convolution reduces computation times by more than an order of magnitude and therewith enables novel numerical approaches with physics-informed deep learning.

PyRates – A Python Toolbox for Neurodynamic Systems Modeling

Richard Gast, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, rgast@cbs.mpg.de
Daniel Rose, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany
Thomas R. Knösche, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany

Introduction

In neuroscience, computational modeling has become an important source of insight into brain states and dynamics. Typical workflows in computational neuroscience include the definition of the model via differential equations, numerical simulations of the model behavior, optimization of model parameters and different types of analysis of the model behavior. In this work, we present PyRates, a Python framework that provides the means to build, optimize and analyze a large variety of dynamical systems. Using the example of the Jansen-Rit model, we explain the mathematical formalism, software structure and key features of PyRates (Jansen and Rit, Biol. Cybernetics 1995).

Methods and Results

The Jansen-Rit model is a neural mass model that describes the average membrane potential fluctuations inside a cortical column (Jansen and Rit, Biol. Cybernetics 1995). It is composed of 3 populations (pyramidal cells, excitatory interneurons, inhibitory interneurons), which are modeled via a set of 6 coupled nonlinear, first-order, ordinary differential equations. This model is implemented via the YAML interface of PyRates. We then simulate its numeric behavior for the standard parametrization reported in (Jansen and Rit, Biol. Cybernetics 1995), using the PyRates interface to the initial value problem solver of *scipy*. Subsequently, we perform a simple parameter optimization, using the genetic optimization functionality that comes with PyRates. Finally, we demonstrate how to perform bifurcation analysis via the Auto-07p interface of PyRates. At each step, we replicate results from the literature and thereby validate the accuracy of the computations performed via PyRates.

Conclusion

We conclude that PyRates is a powerful tool for dynamical systems modeling that provides (1) generic, reusable and easy-to-share model definition interfaces, (2) access to a number of efficient differential equations solvers, (3) extensive functionalities for parameter sweeps, optimizations and continuations, (4) convenience functions for timeseries analysis and visualization, and (5) various parallelization possibilities.

Efficiently localizing cortical representations by combining bi-ophysiological measurements with electric field simulations of TMS

Ole Numssen, Lise Meitner Research Group “Cognition and Plasticity”, Max Planck Institute for Human Cognitive and Brain Sciences Leipzig, Germany, numssen@cbs.mpg.de
Gesa Hartwigsen, Lise Meitner Research Group “Cognition and Plasticity”, Max Planck Institute for Human Cognitive and Brain Sciences Leipzig, Germany, hartwigsen@cbs.mpg.de
Thomas R. Knösche, Methods and Development Group “Brain Networks”, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, knoesche@cbs.mpg.de
Konstantin Weise, Methods and Development Group “Brain Networks”, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, kweise@cbs.mpg.de

Introduction

Despite the widespread use of transcranial magnetic stimulation (TMS), the precise cortical locations underlying the resulting physiological and behavioural effects are only coarsely known. We present a novel method, which combines physiological measurements with numerical electric field simulations to determine the effectively stimulated cortical site at the individual subject level. We applied this method on the primary motor cortex (M1) and show its performance by discriminating hand-muscle representations on the individual level.

Methods

Based on previous work (Weise & Numssen, 2020), we assume that at the cortical site of activation the relationship between electric field and MEP follows a sigmoidal shape. We applied single biphasic TMS pulses to 15 subjects with random intensities and random coil positions/orientations around M1 using a MagPro X100 stimulator (MagVenture) and a neuronavigated MCF-B65 figure-of-eight coil. For each pulse, we calculated the corresponding electric field distribution with SimNIBS. We performed a voxel-wise nonlinear regression analysis between the electric field and the measured MEPs for three different hand muscles in the center of grey matter. We used voxel-wise goodness-of-fits to identify the cortical bases of the physiological responses.

Results

We were able to determine independent hotspots for the different hand muscles on the sulci and the gyral crowns of M1. Importantly, we could show that with a subset of about 200 pulses qualitatively identical results can be obtained with a derivation of about 5%.

Conclusion

We introduced a new and very efficient TMS protocol for motor cortex mapping. We successfully identified cortical hotspots on the individual subject level for different hand muscles. Currently, we are working on the validation, where we will target each estimated cortical hotspot with optimized coil positions. Given the efficiency of the proposed methods, mappings of high-level processes might be targeted in the future.

Reconstructing Network dynamics from MEG Signals

Shih-Cheng Chien, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, vchien@cbs.mpg.de
Richard Gast, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, rgast@cbs.mpg.de
Burkhard Maess, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, maess@cbs.mpg.de
Thomas R. Knösche, Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany, knoesche@cbs.mpg.de

Introduction

MEG and EEG are macroscopic recordings that are often used to study human cognition. Reconstructing the corresponding mesoscopic activities (e.g., firing rates of excitatory and inhibitory neural populations) can help to understand the underlying neural computation. To associate macro- and mesoscopic activities, we use neural mass modeling to investigate the proportions of the primary currents through pyramidal cells (i.e., source of MEG signal) that are initiated by three types of neural populations.

Methods

The primary currents through pyramidal cells can be approximated by the weighted sum of excitatory/inhibitory ion currents from apical/basal dendrites. The simulation of MEG signals is done in our network model that consists of pyramidal (PYR), somatostatin-expressing (SOM), and parvalbumin-expressing (PV) neural populations. The PYR-to-PYR connections can be apical or basal, and the SOM-to-PYR and PV-to-PYR connections are apical and basal, respectively. Short-term depression (STD) is applied to PYR-to-PYR connections, and short-term facilitation (STF) is applied to PYR-to-SOM connections. The simulated MEG is fitted to the target MEG recordings, and the network dynamics after fitting are examined.

Results

The MEG recordings are adapted from a human auditory study, where the participants passively listened to the regular and random tonal sequences (Andreou et. al., Neuroimage, 2015). The MEG amplitude shows an onset peak followed by a rising curve that plateaus at a level that reflects the predictability of the sequences. Our simulated MEG successfully reproduces the MEG recording. The resulting network dynamics show that the onset peak is mainly contributed by the PYR-to-PYR currents, while the rising curve and the long-lasting plateau are mainly contributed by the SOM-to-PYR currents.

Conclusion

Considering both excitatory and inhibitory currents in MEG simulation provides better fitting to the MEG recordings. The resulting network dynamics reveal the involvement of SOM interneurons in the encoding of sequential patterns of sound.