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MNE: Software for Acquiring, Processing and Visualizing MEG/EEG Data

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Abstract

The methods for acquiring, processing, and visualizing Magnetoencephalography (MEG) and Electroencephalography (EEG) data are rapidly evolving. Advancements in hardware and software development offer new opportunities for cognitive and clinical neuroscientists but at the same time introduce new challenges as well. In recent years the MEG/EEG community has developed a variety of software tools to overcome these challenges and cater to individual research needs. As part of this endeavour, the MNE software project, which includes MNE-C, MNE-Python, MNE-CPP, and MNE-MATLAB as its subprojects, offers an efficient set of tools addressing certain common needs. Even more importantly, the MNE software family covers diverse use case scenarios. Here, we present the landscape of the MNE project and discuss how it will evolve to address the current and emerging needs of the MEG/EEG community.

Keywords: Magnetoencephalography (MEG), Electroencephalography (EEG), Software, Analysis tools, Open-Source, Real-time analysis, Signal processing, Machine Learning

1. MEG/EEG Data Analysis in Research and Clinical Settings

The field of neuroscience is rapidly expanding through interdisciplinary efforts and has enabled studies of the nervous system at several scales, starting from the molecular level and the study of single neurons in animals and extending to recording and manipulating large-scale human brain networks. Brain activity can be studied with a wide variety of temporal and spatial resolutions using diverse techniques. The research community thus has access to a growing amount of shared multi-modal as well as multi-scale brain data. MEG and EEG have a unique position in this endeavor as the only non-invasive means for studying electrophysiological activity. Both methods can track neuronal dynamics at millisecond resolution and, hence, capture behaviorally relevant fast changes inaccessible to hemodynamic methods, e.g., functional magnetic-resonance imaging (fMRI). While MEG can have a higher spatial resolution due to absence of the smearing effects present in EEG, it is also more selective by favoring signals from cortical pyramidal neurons in the walls of the sulci (Baillet, 2017). MEG and EEG, therefore, have a complementary

nature, and it has been suggested that improved results can be obtained when combining the two methods (Sharon et al., 2007). The research in non-invasive electrophysiology can be systematized by considering at least two aspects.

First, how MEG and EEG are used depends substantially on the broader practical context of data *acquisition*. Common settings range from basic academic research to clinical studies aiming at diagnostics of individual patients to inform subsequent treatment choices. The interaction with data and the optimal software tools will, therefore, assume a different form for the researcher attempting to, e.g., decode low-level visual features from gamma band sensor level dynamics (Westner et al., 2018) than for a clinician employing MEG for pre-surgical assessment of an epileptic patient (De Tiège et al., 2012). In the first case, a researcher may want to compose an appropriate sequence of *processing* operations that will preserve the effects of interest and lead to best decoding performance. On the other hand, in clinical practice, a fixed set of tools are required emphasizing interactive *visualization* for effective identification of the salient epileptiform activity. For this purpose, a stand-alone medical software application with a graphical user interface (GUI) with limited customization options is likely to be preferred.

Second, the MEG and EEG communities follow the recent trend toward data-centric research in the biomedical sciences (Leonelli, 2016). This trend is characterized by the increasing volume of publicly available curated scientific data (Poldrack et al., 2017) and their reuse by teams who have not been involved in the acquisition of the data. Accordingly, new consortia keep emerging that curate large-scale MEG and EEG datasets (Niso et al., 2016; Zhang et al., 2018; Van Essen et al., 2013; Taylor et al., 2017). As a result, researchers from diverse backgrounds can now work on human electrophysiology data without having access to MEG and/or EEG acquisition infrastructure. A researcher who acquires MEG data in a semantic auditory processing experiment with a limited number of subjects would need a different set of tools than one who studies cognitive aging employing thousands of MEG recordings from a database (Taylor et al., 2017; Van Essen et al., 2013; Niso et al., 2016). The former would use a combination of GUIs for assessment of data quality, setting annotations, scripting for preprocessing and data analysis backed by reporting tools for quality assessment. The latter would almost solely rely on scripts, emphasize automated processing (Engemann and Gramfort, 2015; Jas et al., 2017) and utilize dedicated libraries for classical machine learning (Pedregosa et al., 2011), deep learning, and specialized forms of data visualization.

In the following, we will discuss how the research and software development activities in the MNE community have responded to the variety of needs. We will first briefly summarize the history of the MNE software (Esch et al., 2018; Gramfort et al., 2014, 2013a; Jas et al., 2018) and then cover the different MNE packages. We will detail how each of the MNE software packages responds to the needs of different types of MEG/EEG users. Subsequently, we will discuss emerging data analysis use cases that require novel innovations in software, or even some rethinking of the way MEG/EEG data are visualized and analyzed. With this perspective, we will discuss how the MNE software tools can already partially address these new needs and what could be a path forward.

2. MNE and its history

MNE is a software package that provides complete data analysis pipelines for MEG/EEG data processing. In comparison to other (MATLAB-based) software packages for MEG/EEG data processing, e.g., Brainstorm (Tadel et al., 2011), EEGLAB (Delorme and Makeig, 2004; Delorme et al., 2011), FieldTrip (Oostenveld et al., 2011), NutMeg (Dalal et al., 2011), and SPM

(Litvak et al., 2011), MNE comes in multiple flavors, i.e., MNE-C (historically referred simply to as MNE), MNE-CPP, MNE-MATLAB and MNE-Python, each addressing needs from different segments of the academic and clinical communities. While the original MNE-C was started by Matti Hämäläinen at MGH in 2001 and made publicly available in 2006, the other MNE packages started later (MNE-CPP in 2010 and MNE-Python in 2011), incorporating the same core features as MNE-C, such as direct integration with the anatomical reconstruction provided by the FreeSurfer software (Fischl et al., 1999).

Figure 1 illustrates the landscape of different MNE flavors and their different roles. All MNE packages are currently engaged in the original context of MEG/EEG processing (second quadrant), where “original context” refers to well-established workflows ranging from the actual experimental design, data acquisition, processing, to analysis for basic research purposes. The first quadrant includes the MNE-C and MNE-CPP packages that use the C and CPP, a.k.a. C++, programming languages. Both are used in translational research bringing state-of-the-art methods to clinical applications and practice. Here, high-level graphical user interface controls provide tools for clinicians and researchers with minimal or non-existent programming background. The need for large scale data (big data) analysis is covered by MNE-Python, paving the way for more computer intensive data science and machine learning approaches (third quadrant). MNE-Python and its growing support for EEG and machine learning methods has recently enabled large-scale analysis of clinical EEG in neurology (Engemann et al., 2018). The future tools, discussed in greater detail in section 4, could specifically respond to the needs of clinical practice powered by data-driven methods and recycling of consortium data (quadrant four). Different features of the MNE packages are summarized in Table 1: All packages read and write data in the same file format, enabling users to use the tool that is best suited for each processing step. In this table, ECD stands for equivalent current dipole, LCMV for linearly constrained minimum-variance (Van Veen et al., 1997), DICS for dynamic imaging of coherent sources (Gross et al., 2001), MxNE for mixed-norm estimates (Gramfort et al., 2013b), MVPA for multivariate pattern analysis (often referred to as decoding) (KING et al., 2018), BEM for Boundary Element Method, MUSIC for MULTiple SIGNAL Classification (Mosher and Leahy, 1999), and we refer to (Wipf and Nagarajan, 2009) for details on γ -MAP.

As illustrated in Figure 1, MNE-Python offers a unique opportunity to connect the data science and machine learning communities with the MEG and EEG data processing challenges. This is presently possible thanks to the modern open source Python tools that are now available for advanced statistical computations and analysis of big data.

3. The scope and features of the MNE packages

3.1. Off-line analysis with MNE-C GUIs and command line tools

The original MNE-C, conceived and written at the Martinos Center at Massachusetts General Hospital, consists of command line programs that can be used in shell scripts for automated processing and two GUI applications for interactive data processing and inspection. MNE-C supports band-pass, low-pass, and high-pass filtering. The GUI `mne_browse_raw` also allows previewing the filtered data, so one can investigate the impact of the filter on the signal, as well as the interactive creation of the projection operator for the Signal-Space Projection (SSP) method using a Singular Value Decomposition (SVD) of a selected portion of the data (Uusitalo and Ilmoniemi, 1997). The same software module can also be used for computing averages over multiple trials and for the estimation of the noise-covariance matrix.

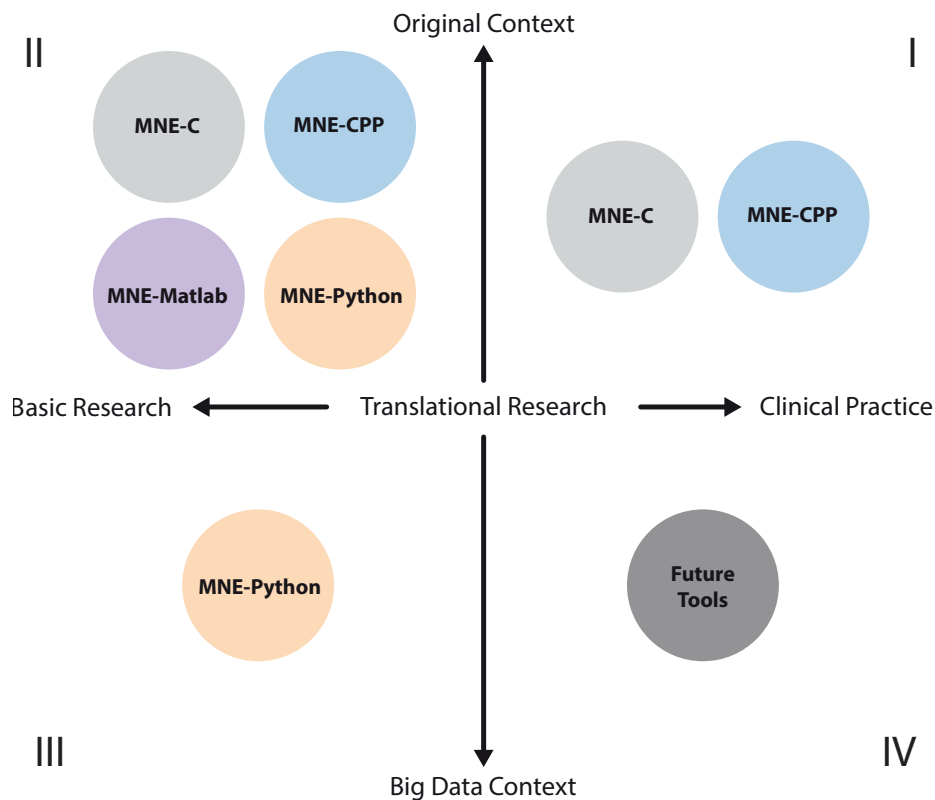


Figure 1: The MNE landscape. The quadrants are populated by the four MNE packages based on their individual scope and key qualifications. The individual MNE packages have slightly different mission statements focusing on different user needs and research questions.

The other GUI `mne_analyze` allows the interactive alignment of the MRI and MEG coordinate systems, the so-called coregistration step, as well as the interactive exploration of cortically constrained source estimates obtained by MNE, dSPM, and sLORETA inverse methods. The command line tools can be assembled in Unix shell scripts for non-interactive analysis. The usage of the MNE-C software is primarily described in the PDF manual: <https://www.martinos.org/meg/manuals/MNE-manual-2.7.pdf>.

3.2. Off-line analysis with MNE-MATLAB

The MNE-MATLAB toolbox (compatible with MATLAB versions 7.0 or later) started from a desire of the MNE user community to go beyond the possibilities made available by the compiled MNE-C tools. It is a collection of m-files to facilitate interfacing with binary file formats of the MNE software and is redistributed as a part of several MATLAB-based MEG/EEG software packages (Brainstorm, FieldTrip, NutMeg, and SPM). The included functionality can be roughly divided into following four categories: (1) High-level reading and writing routines, which provide interfacing with binary file formats like `.fif`, `.stc`, `.label`, and `.w` files. (2) Signal processing routines, which implement the software gradient compensation and signal-space

Table 1: Overview of the features provided by the different MNE packages (\checkmark = supported).

Software package	MNE-C	MNE-MATLAB	MNE-CPP	MNE-Python
Data acquisition			\checkmark	
Stand-alone applications with GUI	\checkmark		\checkmark	
Real-time analysis and visualization			\checkmark	\checkmark
Filtering	\checkmark		\checkmark	\checkmark
Signal space projection (SSP)	\checkmark	\checkmark	\checkmark	\checkmark
Maxwell filtering (SSS)				\checkmark
Indep. component analysis (ICA)				\checkmark
Coregistration of MEG and MRI	\checkmark			\checkmark
Forward modeling (BEM)	\checkmark		\checkmark	\checkmark
Time-frequency analysis			\checkmark	\checkmark
Dipole modeling (single ECD)	\checkmark		\checkmark	\checkmark
Minimum-norm estimation (ℓ_2)	\checkmark	\checkmark	\checkmark	\checkmark
Beamforming (LCMV, DICS)				\checkmark
MUSIC			\checkmark	\checkmark
Sparse source imaging (MxNE, γ -MAP)				\checkmark
Surface- and volume-based spatial morphing	\checkmark	\checkmark		\checkmark
Connectivity estimation			\checkmark	\checkmark
Statistics (Univariate, MVPA)				\checkmark

projection. (3) Utility functions, which include auxiliary functions to reading and writing binary files, transforming data between coordinate systems, assembling inverse operators, proving coil definition for various sensor types, etc. (4) Examples demonstrating the use of the toolbox, which form a basis for user-specific processing routines. The MNE-MATLAB code is available online at <https://github.com/mne-tools/mne-matlab>.

3.3. Off-line analysis and scripting with MNE-Python

The growing popularity of the Python stack for data science in academia and industry has prompted the development of MNE in Python as an alternative for the MNE-C tools. Since its inception, MNE-Python (Gramfort et al., 2014) has grown from replicating most of the MNE-C functionality to implementing many popular but also novel advanced analysis tools while fully supporting EEG analysis. MNE-Python was built to support analysis of multiple imaging modalities beyond MEG/EEG and now has some support for stereotactic electroencephalography (sEEG), functional near-infrared spectroscopy (fNIRS), and electrocorticography (ECoG) data as well.

Figure 2 highlights some of the key features of MNE-Python. It implements input/output (IO) routines for reading a variety of MEG/EEG file formats (<http://martinos.org/mne/stable/manual/io.html>), advanced preprocessing tools such as the Signal Space Separation (SSS) algorithm, and XDAWN (Taulu and Kajola, 2005; Rivet et al., 2009), a dedicated decoding module for MEG/EEG (King et al., 2018), Bayesian and sparse source imaging methods (Gramfort et al., 2013b; Wipf and Nagarajan, 2009), beamforming, and scanning methods such as LCMV, DICS or RAP-MUSIC (Van Veen et al., 1997; Mosher and Leahy, 1999; Gross et al., 2001), statistics (Maris and Oostenveld, 2007; Kriegeskorte et al., 2008), real-time analysis of data (http://martinos.org/mne/stable/auto_examples/#real-time-m-eeg-acquisition), and

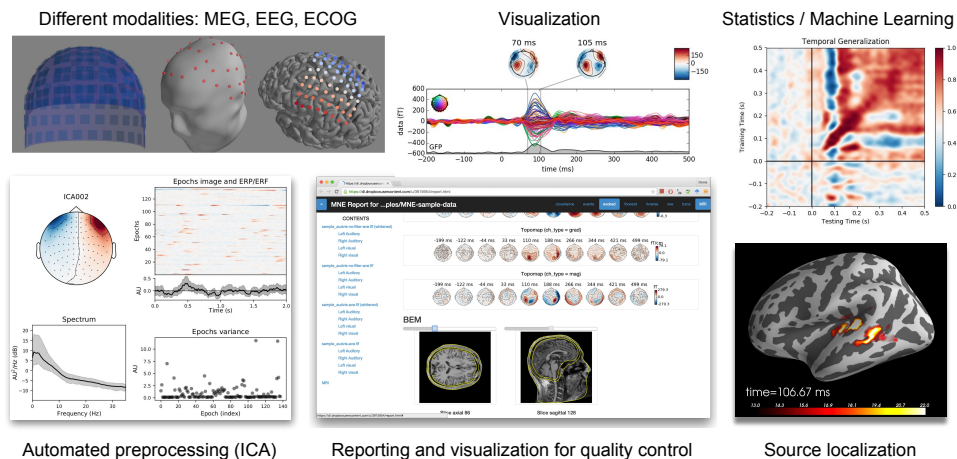


Figure 2: MNE-Python: processing and visualizing electrophysiology data

quality assurance and reporting tools (Jas et al., 2018). The decoding module is built to facilitate the use of the popular `scikit-learn` (Pedregosa et al., 2011) software, which provides simple and effective programmatic access to a wide array of classical machine learning algorithms and procedures in Python. Like `scikit-learn`, MNE-Python is distributed under a permissive Berkeley Software Development (BSD) license and readily supports academic as well as commercial reuse.

The code is available online at <https://github.com/mne-tools/mne-python>. More than 80 people have so far contributed to the MNE-Python source code. Online documentation is available at <http://martinos.org/mne/stable/documentation.html> with examples continuously updated thanks to `sphinx` and `sphinx-gallery` (<https://sphinx-gallery.readthedocs.io/en/latest/>) packages.

3.4. Acquisition and real-time analysis with MNE-CPP

MNE-CPP provides a cross-platform framework which allows the development of software applications for real-time MEG/EEG data acquisition, processing and visualization. The project is open-source BSD licensed (3-clause). It can be used to develop stand-alone applications on Windows, MacOS, and Linux. MNE-CPP builds upon two external dependencies: The Qt framework (QtProject, 2018) for GUI programming and the Eigen library (Guennebaud et al., 2018) for linear algebra. All MNE-CPP tools are designed to function in off-line as well as in real-time scenarios. In addition to giving experienced C++ developers the opportunity to create their own applications, MNE-CPP offers pre-developed stand-alone applications with GUIs. Currently, three applications are being developed: MNE Scan (Esch et al., 2018), MNE Browse, and MNE Analyze. All three are available as pre-built binaries for Windows, MacOS, and Linux.

MNE Scan is a plug-in based tool that can be used to acquire data from MEG/EEG devices and store the received data to a file and/or provide real-time data streams. Acquisition and processing tasks are developed as individual units. The workflow follows a pipeline approach where the user can select and connect the acquisition plug-in and subsequent real-time processing plug-ins. The acquisition plug-ins offer connections to MEG (Elekta Neuromag, BabyMEG) and EEG (TMSI Refa, EEGoSports, gTec USB, BrainAmp, and Natus) devices. It is also possible to stream in

recorded data from a file to imitate an ongoing measurement session. This is especially useful when debugging and testing new plug-ins. The processing plug-ins include real-time capable implementations for temporal filtering, SSP, SPHARA (Graichen et al., 2015), software gradients, averaging, source localization, connectivity estimation, and a Brain Computer Interface (BCI). A clinically oriented use case for MNE Scan is its use in the BabyMEG system. The BabyMEG (Okada et al., 2016) is a 375-channel, whole-head pediatric MEG instrument. It is used in a clinical environment at Boston Children’s Hospital for both patients and healthy neonates, infants, and preschool children up to three years of age. Another use case of MNE Scan is the computation and visualization of source estimates in real-time (Dinh et al., 2015, 2018) via a dedicated plug-in. The estimated source activity is visualized on a cortical surface reconstructed with the Freesurfer software (Fischl et al., 1999). Fig. 3 shows a snapshot of MNE Scan during real-time source localization setup. MNE Scan can also be used in neurofeedback research and applications. For example, the SSVEP BCI plug-in provides a visual reactive BCI to control a virtual keyboard.

Similar to MNE Scan’s offline counterparts, MNE Browse and MNE Analyze are also inspired by their MNE-C counterparts. With their reimplementations MNE-CPP targets to make them future proof, available on Windows machines, more community driven and extensible with new state-of-the-art analysis methods. Both MNE Browse and MNE Analyze are designed to process and visualize MEG/EEG data offline and are solely based on MNE-CPP libraries, Eigen and Qt. MNE Browse functions as a lightweight analysis tool and features basic processing steps such as the loading and visualization of data, channel management, annotation and temporal filtering. On the contrary, MNE Analyze provides more sophisticated analysis tools such as dipole fitting, distributed source localization, and computation of confidence intervals. MNE Analyze’s underlying architecture implements plug-ins for maintainability and easy feature inclusion. MNE Browse and MNE Analyze, as part of the MNE-CPP project, are still in an early development phase. The MNE-CPP code is available online at <https://github.com/mne-tools/mne-cpp> and www.mne-cpp.org.

4. The needs for future MEG/EEG data processing

The MNE environment with its different packages is able to cover a wide variety of use case scenarios. MNE-C will continue to function as the code backbone of MNE-Python and MNE-CPP. Its longstanding acceptance and tested features throughout the community will keep guiding new and ported features. MNE-MATLAB will continue to ensure the usage of MNE data structures in the MATLAB ecosystem dominated by the Fieldtrip, Brainstorm, NutMeg, and SPM toolboxes. We envision new usage scenarios will emerge at the intersection of already known practices, imposing new demands for acquiring, processing, and visualizing MEG/EEG data. In the following we shall discuss a few likely scenarios.

Browsing of remote databases. The advent of large datasets poses new challenges for interactive visualization. In particular, it will not be feasible to duplicate the data on a local workstation. Currently, users who want to browse through large data sets must restrict themselves to a subset of data. Subsequently, they would need to load each file separately from the command line or the GUI menu, disrupting the workflow. Future versions of MEG/EEG data browsers will therefore have to operate over the network and include functionality that facilitates navigation through thousands of MEG/EEG recordings. This would at least include an effective file-search, scheduling functionality to specify a set of files to visit sequentially, as well as cross-data set navigation controls to enable seamless browsing. In the current software ecosystem, MNE-Python could most naturally extend to this domain given how much the Python language is used for web

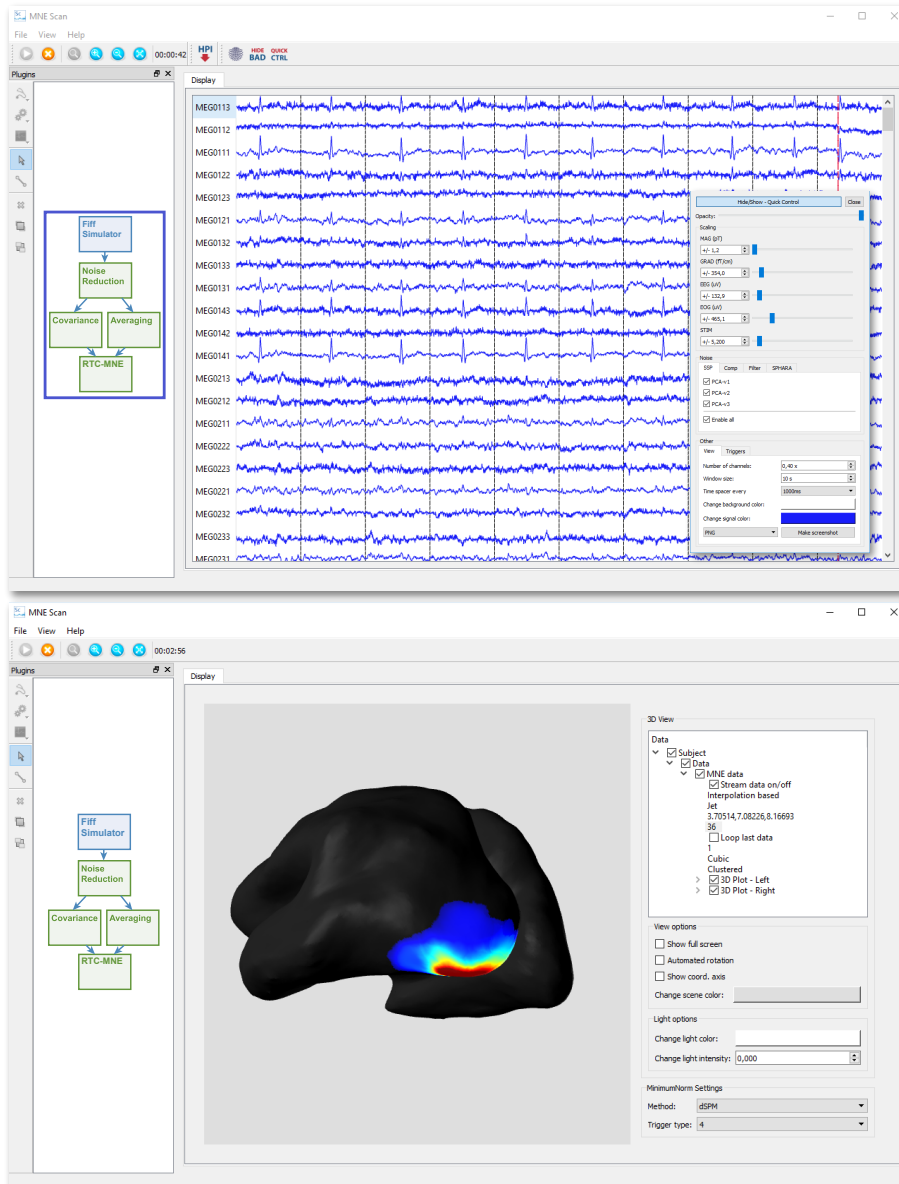


Figure 3: Real-time source localization setup in MNE Scan: In the presented pipeline (see blue rectangle) the FiffSimulator imitates a real-time data stream based on pre-recorded data (see upper screenshot). After the data was filtered the data stream is forwarded to an averaging and covariance plug-in. Subsequently, the averaged (25 moving average) and noise covariance results are sent to the RTC-MNE plug-in. Finally, the source estimates are plotted on an inflated brain surface mesh and can be made available to connected plug-ins (see lower screenshot).

applications, and the ability to communicate with remotely running Python kernels as done with the Jupyter software (<https://jupyter.org/>).

Integration of advanced analysis tools during clinical MEG/EEG acquisition. The search for biomarkers using machine learning on large, socially heterogeneous samples has become an active area of research (Allen et al., 2012; Drysdale et al., 2017; Liem et al., 2017; Khan et al., 2015, 2018). In the near future, medical professionals may develop machine learning models pre-trained offline and apply these models online during MEG/EEG data acquisition to help detect abnormal brain signals and supplement diagnostics. Software tools could thus support extensions for models specified and trained using machine learning tools. In a second, related scenario, medical doctors and data scientists may work together to include custom data processing routines at the acquisition level. For example, the clinical experimenter may launch a software pipeline for automated preprocessing from within the acquisition GUI to obtain clean data and a visual quality control report (Engemann and Gramfort, 2015; Jas et al., 2018). This could be implemented via modular extensions of the acquisition software in C++ to execute custom routines written in Python, thereby integrating MNE Scan and MNE-Python.

General Real-Time Processing. Real-time processing can become of interest as it has the potential for creating highly dynamic and adaptable paradigms depending mainly on the current brain state or condition of interest. Neurofeedback enables researchers to test hypotheses about specific brain conditions, e.g., the state of specific brain areas, by monitoring this condition, and adapting the experimental interventions accordingly. This opens up a new way to investigate basic mechanisms of brain functions and can give the subject a chance to learn and modify their neuronal activity patterns (Wolpaw et al., 1991). Latter is a valuable tool in neurorehabilitation (Mohanty et al., 2018). Moreover, real-time data analysis allows an early assessment of the measurement setup, the subject's response to the introduced paradigm, and the feasibility of a research idea. Early correction of badly designed measurement setups and paradigms can contribute to saving time and resources. Thus, the promotion of real-time analysis tools as a preemptive indicator for problems can become of increasing interest to the MEG/EEG community. A more general and long-term goal for real-time data analysis can also be found in clinical environments. Here it is of special interest to further utilize MEG/EEG in clinical diagnosis, where speed is often essential. Sophisticated analysis tools such as real-time source estimation could lead to a faster diagnosis and better monitoring of the condition of a patient.

Brain-computer interfaces and hyperscanning. Two emerging approaches in rehabilitation science, social neuroscience, and computational psychiatry are BCIs (Höhne et al., 2014; Mohanty et al., 2018) and hyperscanning (Bilek et al., 2017; Ahn et al., 2018; Goldstein et al., 2018; Zhdanov et al., 2015). It is likely that soon new acquisition paradigms will emerge both for basic research and clinical practice in which BCI and hyperscanning will be combined, such that the stimulation will be driven by brain activity of several individuals (Rao et al., 2014; Jiang et al., 2018). The acquisition software, in this scenario, will need not only modular extensions for real-time stimulation and machine learning, but also flexible visualization functionality that supports the appropriate abstractions for co-representing activity from several brains.

Cloud computing. Data analysis aiming at diagnostics is difficult to generalize due to the different platforms, complex data acquisition, and processing involved. In this context, community standards will play a crucial role (Gorgolewski et al., 2016; Niso et al., 2018). The newly established Brain Imaging Data Structure (BIDS) for organizing data is already promising as it simplifies the process of creating portable pipelines – the so-called BIDS Apps (Gorgolewski et al., 2017b). As already started by some fMRI software stacks (Esteban et al., 2017a, 2018; Gorgolewski et al., 2017a; Esteban et al., 2017b; Yarkoni et al., 2011; Glatard et al., 2018), one

would need to develop cloud based automated pre- and postprocessing applications, that could even be integrated with acquisition and analysis software platforms. This would significantly increase the ease and efficiency of acquiring, monitoring, analyzing, and integrating various types of clinical electrophysiology data with anatomical structures. Tighter integration with BIDS will allow MNE to interface easily with applications in the cloud but also amongst its different flavors and with other MEG/EEG analysis software. Acquisition and analysis plug-in interfaces could be enabled to communicate with the cloud application programming interface to retrieve preprocessed volume reconstructions and to upload the acquired data again to the cloud. In addition to source localization, automated cloud-based post-processing will also enable the extraction of biomarkers to support diagnosis (Engemann et al., 2018). Through the modular concepts used in the cloud processing pipelines, it will be readily extensible by the scientific community with new processing steps.

In conclusion, the different MNE projects continue to have specific roles in order to cover all the varied aspects of MEG/EEG data processing. We envision that many of the new developments will necessitate integration of several packages for optimal implementation. For example, machine-learning tools can be readily developed in MNE-Python using large data sets as input and implemented for clinical use as plug-ins in MNE-CPP. MNE as a whole continues to provide freely accessible and multi-purpose software tools for the acquisition, processing, and visualization of MEG/EEG data for both basic and clinical research as well as for clinical applications.

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