

MNE-BIDS: Organizing neurophysiological data into the BIDS format and facilitating their analysis

4 November 2019

Summary

With the development of the Brain Imaging Data Structure (BIDS; (Gorgolewski et al. 2016)), the neuroscientific community received a standard to organize and share data. BIDS standardizes storage of complex experimental data by prescribing a set of file naming conventions and templates to store the associated metadata in the form of Javascript Object Notation (JSON) and tab separated value (TSV) files. It thus facilitates data sharing, eases metadata querying and enables automatic data analysis pipelines. BIDS is a rich system to curate, aggregate and annotate neuroimaging databases.

While BIDS was originally intended for Magnetic Resonance Imaging (MRI) data, it has recently been extended for magneto-encephalography (MEG; (Niso et al. 2018)), electro-encephalography (EEG; (Pernet et al. 2019)), and intracranial encephalography (iEEG; (Holdgraf et al. 2019)). In this context, many software packages for neurophysiology data analysis are now becoming BIDS compatible. For this reason, we developed a dedicated software, **MNE-BIDS** with the goal to provide a programmable interface for BIDS datasets in neurophysiology. **MNE-BIDS** allows users to re-organize data into BIDS formats, store associated metadata after anonymization, extract information necessary for pre-processing and read them into **MNE-Python** objects (Gramfort et al. 2013), ready for source localization.

Starting with a single directory full of data files with arbitrary names, **MNE-BIDS** can be used to extract existing metadata, reorganize the files into the BIDS format, and write additional metadata. All the conversion routines are thoroughly tested by running the output through the BIDS validator. Moreover, **MNE-BIDS** supports converting data formats that are not BIDS compatible into permissible formats. As a result of this, users can easily convert their datasets to BIDS in a matter of minutes, rather than hours of manual labour.

In addition to this core functionality, **MNE-BIDS** is continuously being extended to facilitate the analysis of BIDS formatted data. To name some features, it is possible to read a BIDS dataset and obtain a Python object, ready for analysis with **MNE-Python**. Users can save a T1-weighted anatomical MRI image alongside the MEG or EEG data and apply an automatic defacing algorithm for anonymization purposes. As a last example, anatomical landmark coordinates can be saved to enable coregistration between the MEG/EEG and MRI data, which is necessary for computation of forward and inverse solutions.

Users can easily install **MNE-BIDS** on all major platforms via **pip** and **conda**, and its functionality is continuously tested on Windows, OS X, and Linux. Other than the core dependencies for scientific computing (**numpy**, **scipy**) and handling of MEG/EEG data (**mne**), **MNE-BIDS** has minimal dependencies, all of which are optional. The Application Programming Interface (API) of the package is stable and extensively documented and explained in examples (<https://mne.tools/mne-bids/>). In addition, a command-line interface is provided that allows even non-Python users to benefit from some of the core functionality.

As of writing, **MNE-BIDS** has received code contributions from 15 contributors and its user base is steadily growing. Code development is active and the developer team is committed to provide timely support for issues opened on the GitHub issue tracker.

MNE-BIDS is used as a dependency in several other software packages such as the **MNE-study-template**, an automated pipeline for group analysis with MNE (Jas et al. 2018), and **Biscuit**, a graphical user interface to format BIDS data. Lastly, several large institutions have adopted **MNE-BIDS** for their workflows such as the Martinos Center for Biomedical Imaging.

The developer team is excited to improve the state of the art in data handling and looking forward to welcoming new contributors and users.

Acknowledgements

MNE-BIDS development is partly supported by the Academy of Finland (grant 310988), NIH NINDS R01-NS104585, ERC Starting Grant SLAB ERC-YStG-676943, ANR meegBIDS.fr, BRAIN Initiative and National Institute of Mental Health (1R24MH114705), the Bezos Family Foundation, the Simms Mann Foundation, and the Google Summer of Code 2019.

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