Mipy: An Open-Source Framework to improve reproducibility in Brain Microstructure Imaging
Rutger Fick, Demian Wassermann, Rachid Deriche

To cite this version:

HAL Id: hal-01722146
https://hal.archives-ouvertes.fr/hal-01722146
Submitted on 3 Mar 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Mipy: An Open-Source Framework to improve reproducibility in Brain Microstructure Imaging

Submission No:
1628

Submission Type:
Abstract Submission

Authors:
Rutger Fick1, Demian Wassermann2, Rachid Deriche1

Institutions:
1INRIA, Sophia Antipolis, France, 2INRIA, Paris, France

First Author:
Rutger Fick - Lecture Information | Contact Me
INRIA
Sophia Antipolis, France

Introduction:
The recovery of microstructure-related features of the brain's white matter is a current challenge in diffusion MRI (dMRI). In particular, multi-compartment (MC)-based models have been a popular approach to estimate these features. However, the usage of MC-models is often limited to those hard-coded in publicly available toolboxes. To provide access to any MC-based model and improve reproducibility in MC-based research, we propose Microstructure Imaging in Python (Mipy); a free and open source software project to robustly estimate these important features from single-shell, multi-shell, and multi-diffusion time dMRI data. Mipy follows a "building block"-based philosophy to microstructure imaging, meaning an MC-model can be constructed and fitted to dMRI data using any combination of underlying tissue models, axon dispersion- or diameter distributions, and optimization algorithms. Furthermore, only focussing on MC-modeling, Mipy emulates the workflow and is designed to be complementary to the already existing Diffusion Imaging in python (Dipy) toolbox [5], which focusses more on non-parametric dMRI modeling and tractography.

Methods:
Mipy emulates the architecture of successful python toolboxes like Dipy and Scikit-learn. We show Mipy's workflow in Figure 1. First, a multi-compartment "model" object is created by choosing one or more models to represent tissue features such as water diffusivity, axon diameter distributions, axon dispersion, axon bundle crossings and extra-axonal diffusion restriction. A constructed model object can also include custom or known parameter constraints like axon tortuosity [3]. To estimate model parameters from dMRI data, a "fit" object is created by simply using "model.fit(data)", where both classical or more recent optimization algorithms can be chosen such as Microstructure Imaging in Crossings (MIX) [4]. From the "fit" object we can recover fitted model parameters, various metrics for the goodness-of-fit and Fiber Orientation Distributions (FODs) if axon dispersion models were used. We emphasize that Mipy's modular design enables users to easily adapt and/or extend current Mipy features, allowing for the modular addition of new models or optimizers, thus improving the reproducibility of MC-modeling research.
MIPY: modular Microstructure Imaging in Python

Results:

Creating and fitting MC-models is very easy in Mipy - often taking no more than 10 lines of code. As an example of how Mipy works, we show in Figure 2 the model setup of six well-known MC-models from literature. From top to bottom and left to right, we show Ball and Stick [2], Ball and Racket [8], NODDI with Watson or Bingham Distribution [10, 9], Multi-Compartment SMT [6] and AxCaliber [1]. For each model, we give the lines of code to setup the model and a graph of the model work flow. We run “model.fit(data)”, where data is a slice of multi-shell HCP data for the first 5 models or a slice of spinal cord data for AxCaliber. We then show the estimated intra-axonal volume fraction and fitting error on the right. It can be seen that all models show larger volume fractions in white matter areas and lower ones in gray matter and CSF, but fitting errors vary for different models - implying that some models may be more appropriate for certain tissue configurations than others. In this way, Mipy allows for easy analysis of different models, giving the user the tools to experiment make an informed decision as to what approach is best for an application.
Complete Model Setup and estimation of Intra-axonal volume fraction and fitting Error using Mipy

- Mipy allows for the complete setup of complex MC-models in no more than 10 lines of code. Then, using simply “model.fit(data)” will estimate the model parameters from the dMRI data.

Conclusions:

We introduced the Microstructure Imaging in Python (Mipy) open-source software project, freely available at https://github.com/AthenaEPI/mipy. Using Mipy we hope to spark a community similar to Dipy, where fellow researchers can benchmark and add their own techniques in Mipy, finally contributing to more mature and reproducible science in dMRI-based Microstructure Imaging.

Acknowledgements: This work was partly supported by ERC Advanced Grant agreement No 694665:CoBCoM. Author Rutger Fick is affiliated with TheraPanacea, Paris, France as of 9/2017.

Imaging Methods:

Diffusion MRI

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis
Methods Development
Multivariate modeling

Keywords:

Data analysis
Design and Analysis
Experimental Design
Modeling
Multivariate
White Matter
WHITE MATTER IMAGING - DTI, HARDI, DSI, ETC

1|2|Indicates the priority used for review

My abstract is being submitted as a Software Demonstration.
If you answered yes to the question above, would you like a traditional poster in addition to the Software Demonstration?
Yes

Would you accept an oral presentation if your abstract is selected for an oral session?
Yes

I would be willing to discuss my abstract with members of the press should my abstract be marked newsworthy:
Yes

Please indicate below if your study was a "resting state" or "task-activation" study.
Other

By submitting your proposal, you grant permission for the Organization for Human Brain Mapping (OHBM) to distribute the presentation in any format, including video, audio print and electronic text through OHBM OnDemand, social media channels or other electronic media and on the OHBM website.

I accept

Healthy subjects only or patients (note that patient studies may also involve healthy subjects):
Healthy subjects

Are you Internal Review Board (IRB) certified? Please note: Failure to have IRB, if applicable will lead to automatic rejection of abstract.
No

Are you Animal Use and Care Committee (AUCC) certified? Please note: Failure to have AUCC, if applicable will lead to automatic rejection of abstract.
No

Please indicate which methods were used in your research:
Diffusion MRI

For human MRI, what field strength scanner do you use?
3.0T

Which processing packages did you use for your study?
Other, Please list - Mipy

Provide references using author date format