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# Mipy: An Open-Source Framework to improve reproducibility in Brain Microstructure Imaging

**Submission No:**

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Abstract Submission

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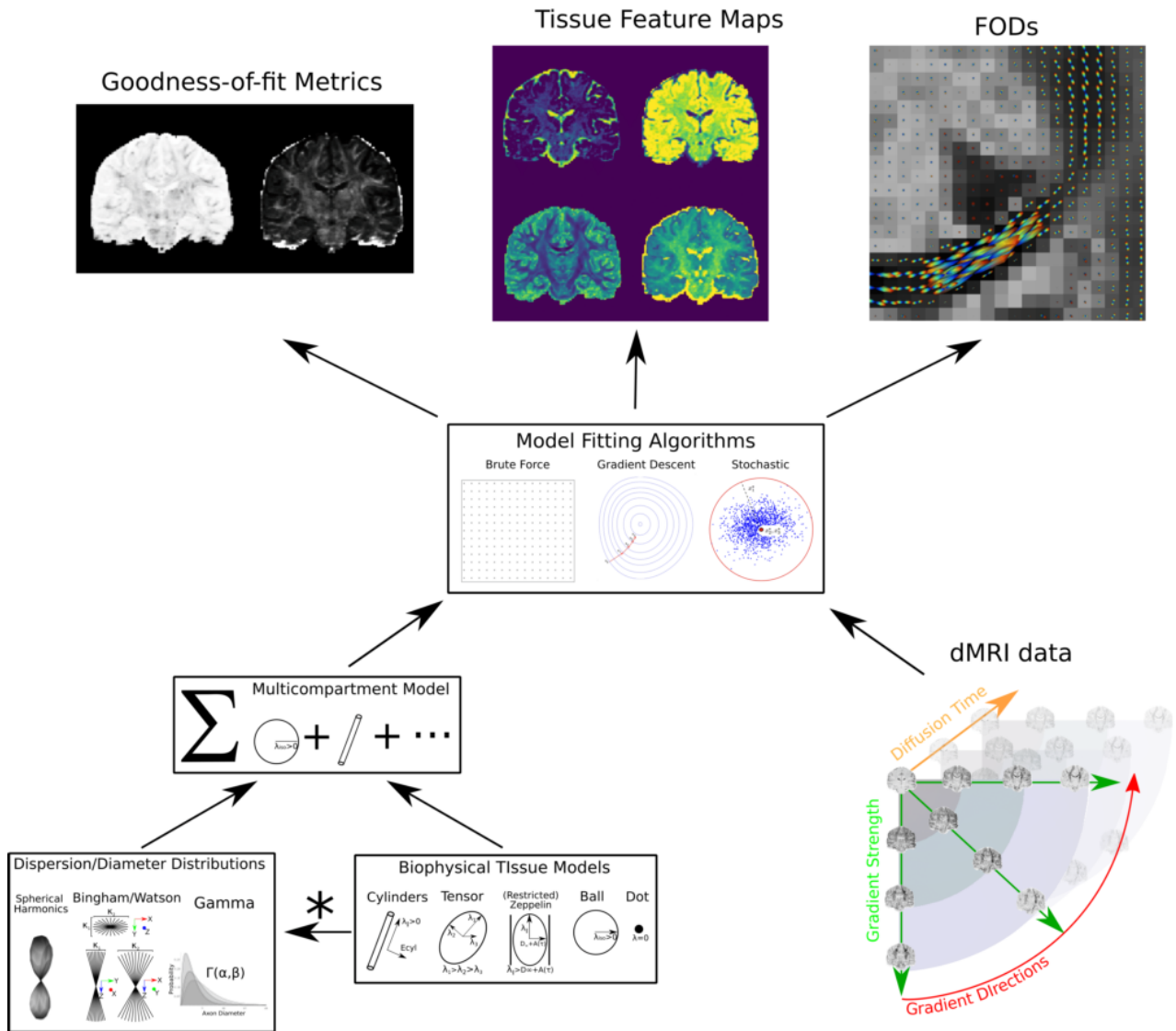
**Introduction:**

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

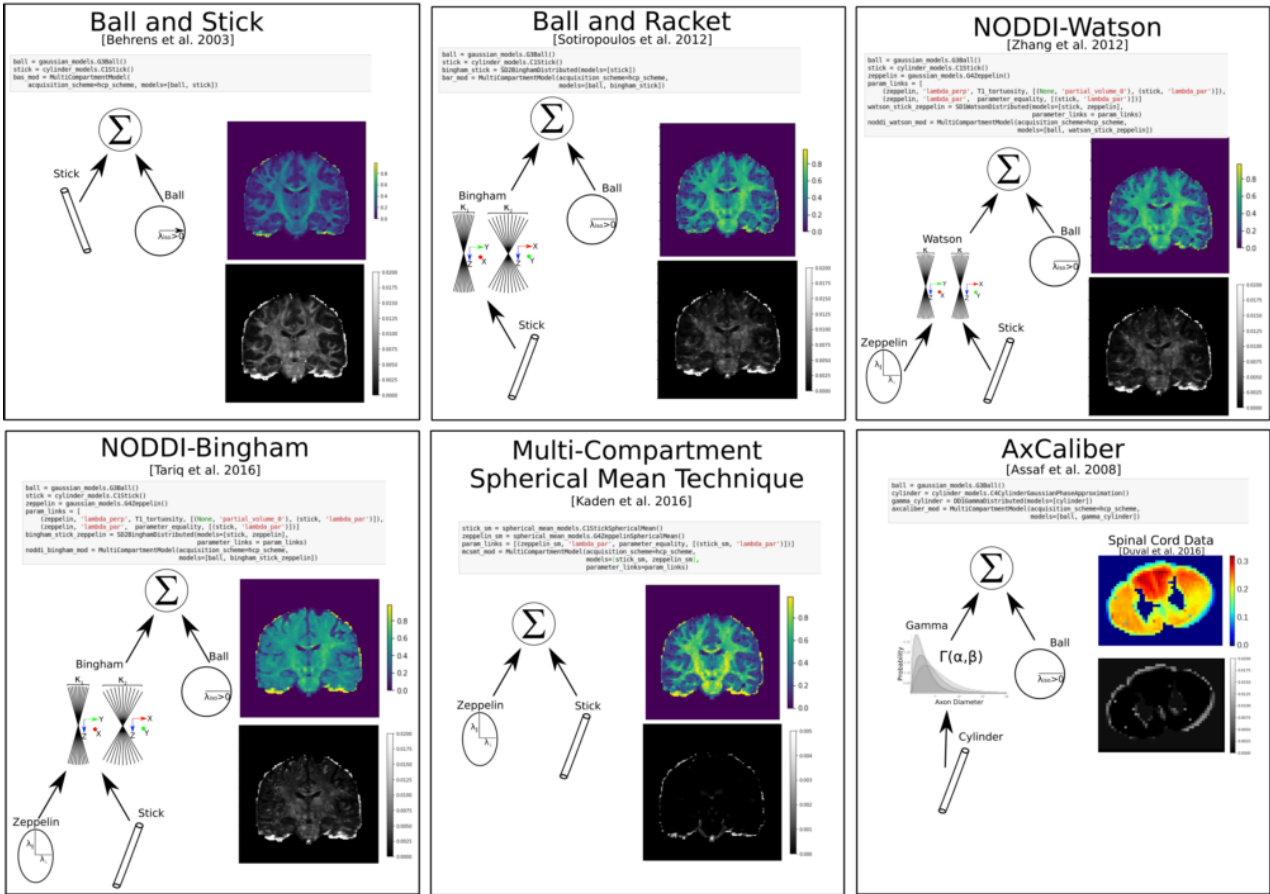


·Overview of Mipy workflow.

## Results:

Creating and fitting MC-models is very easy in Mipy - often taking no more than 10 lines of code. As a 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 sen 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.

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**Imaging Methods:**

Diffusion MRI

**Modeling and Analysis Methods:**

Diffusion MRI Modeling and Analysis <sup>1</sup>  
 Methods Development  
 Multivariate modeling <sup>2</sup>

**Keywords:**

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

<sup>1</sup><sup>2</sup>Indicates the priority used for review

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**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**

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