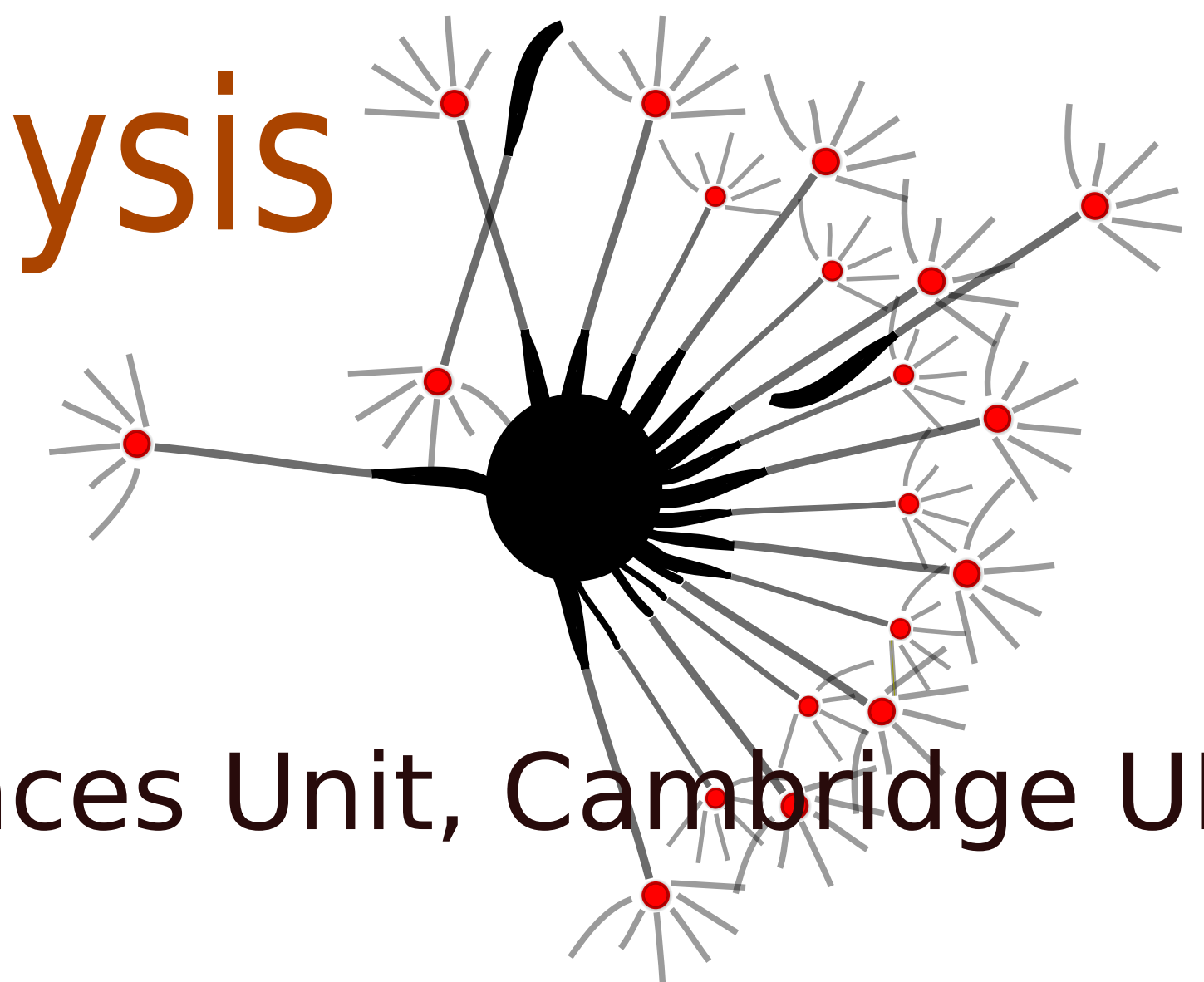# Building an open platform for advanced diffusion MRI analysis

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Background

Diffusion-weighted MR imaging (dMRI) is a non-invasive technique which can reveal important information about the directional organisation of the white matter fibres of the brain.

Tractography is a way to approximate these neuronal pathways using streamlines and connectivity profiles.

Deriving tractography from the raw MR data calls for a wide range of signal processing, medical imaging and machine learning techniques. These we have provided in the dipy toolbox.

Overview

Dipy stands for diffusion imaging in python and is a free, open source, python toolbox.

It provides a library of algorithms to give a full data processing pathway from raw diffusion magnetic resonance data to tractographies, with several novel algorithms for analysing, comparing and displaying tractographies.

Our algorithms are designed to allow very quick analyses of the huge datasets that typically are involved in tractography.

Dipy operates across all standard platforms and inter-operates with the file formats of a wide range of other brain imaging software.
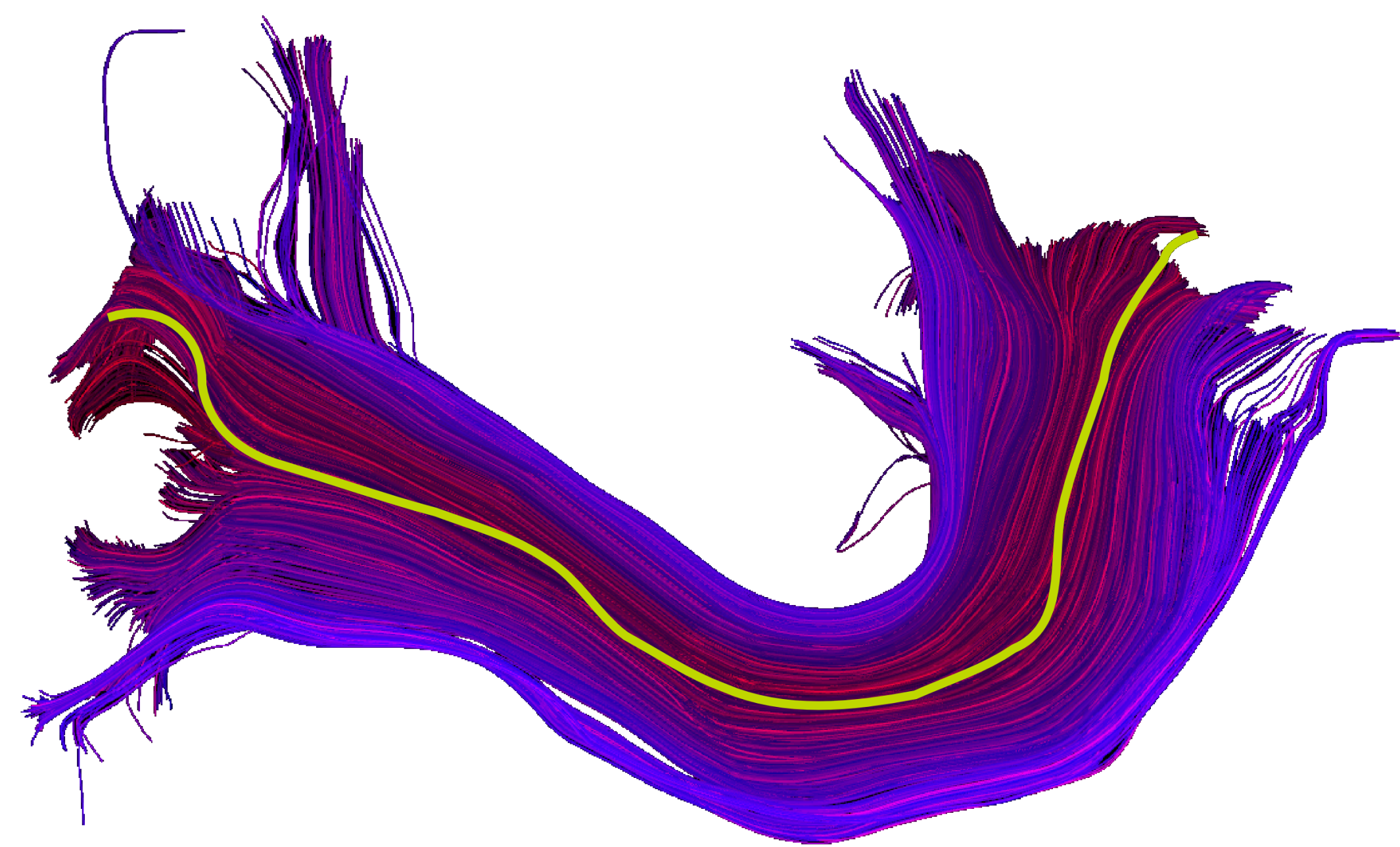
Purpose

The aim of dipy is to make it easier to do better diffusion MR imaging research.

This it achieves by clearly written, and clearly explained, code with a good fit to the underlying concepts, designed in a way that fosters large scale collaborative development using the latest software engineering principles.

We believe that by understanding the underlying anatomy in vivo and by providing the tools to compare different populations we will be able to help researchers and medical practitioners with new ways to investigate and understand the structure of the complex neuronal pathways in the brain in health or disease.
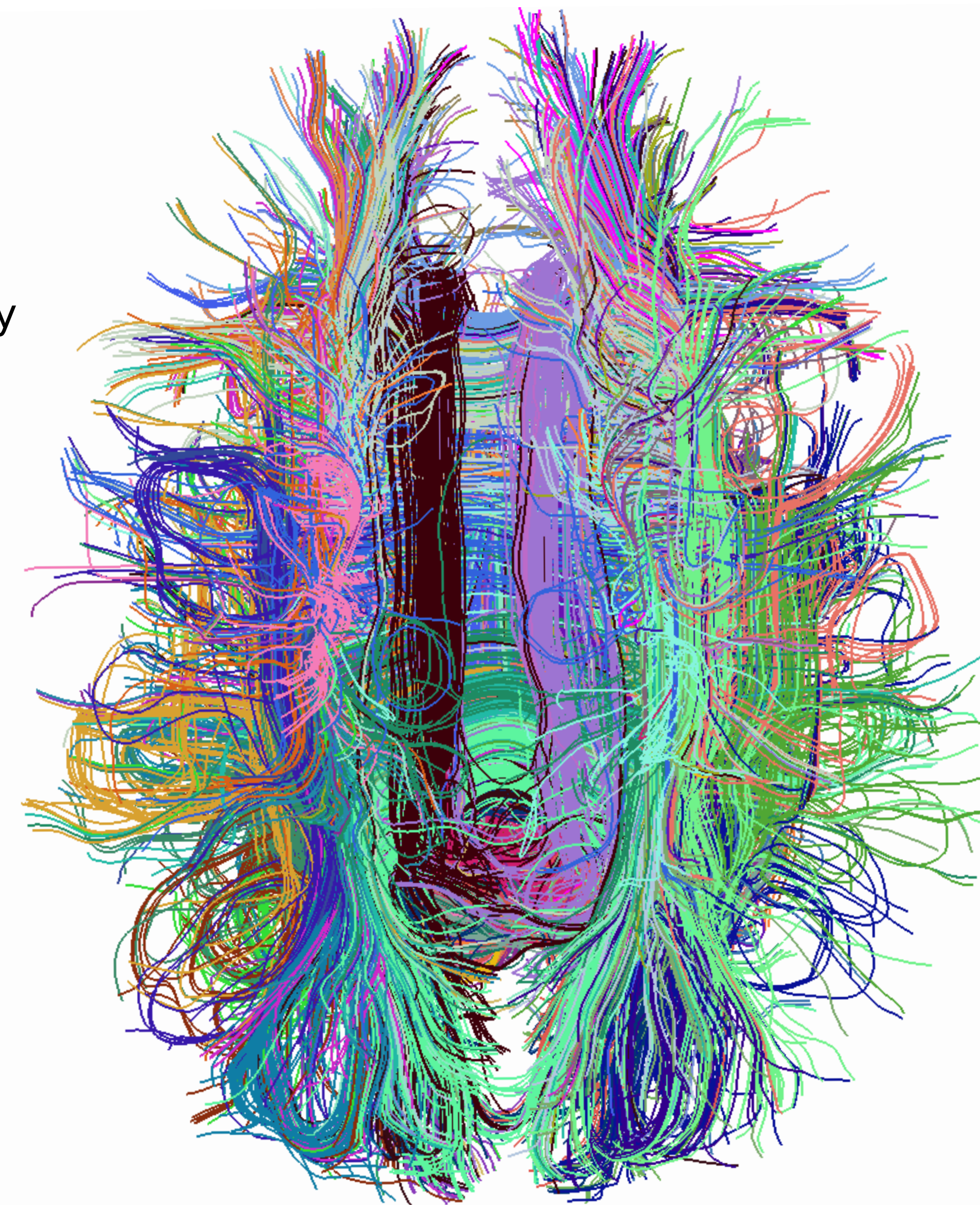
Version 0.5.0 Just Released !!!

www.dipy.org

Available options

* Reconstruction algorithms, e.g. GQI, DTI

* Tractography generation algorithms, e.g. EuDX

* Intelligent downsampling of tracks

* Ultra fast tractography clustering

* Resampling datasets

* Visualizing multiple brains simultaneously

* Inter-brain track correspondence

* Warping tractographies

* Reading many different file formats

* Dealing with huge tractographies

* Playing with datasets interactively

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