

NeuroHackademy 2025

DIPY

Overview of Diffusion imaging pipeline using DIPY

Serge KOUDORO

Intelligent Systems Engineering, Indiana University



National Institutes
of Health

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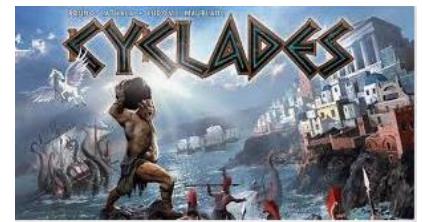
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AND ENGINEERING



Serge Koudoro

Research Software Engineer

10y+

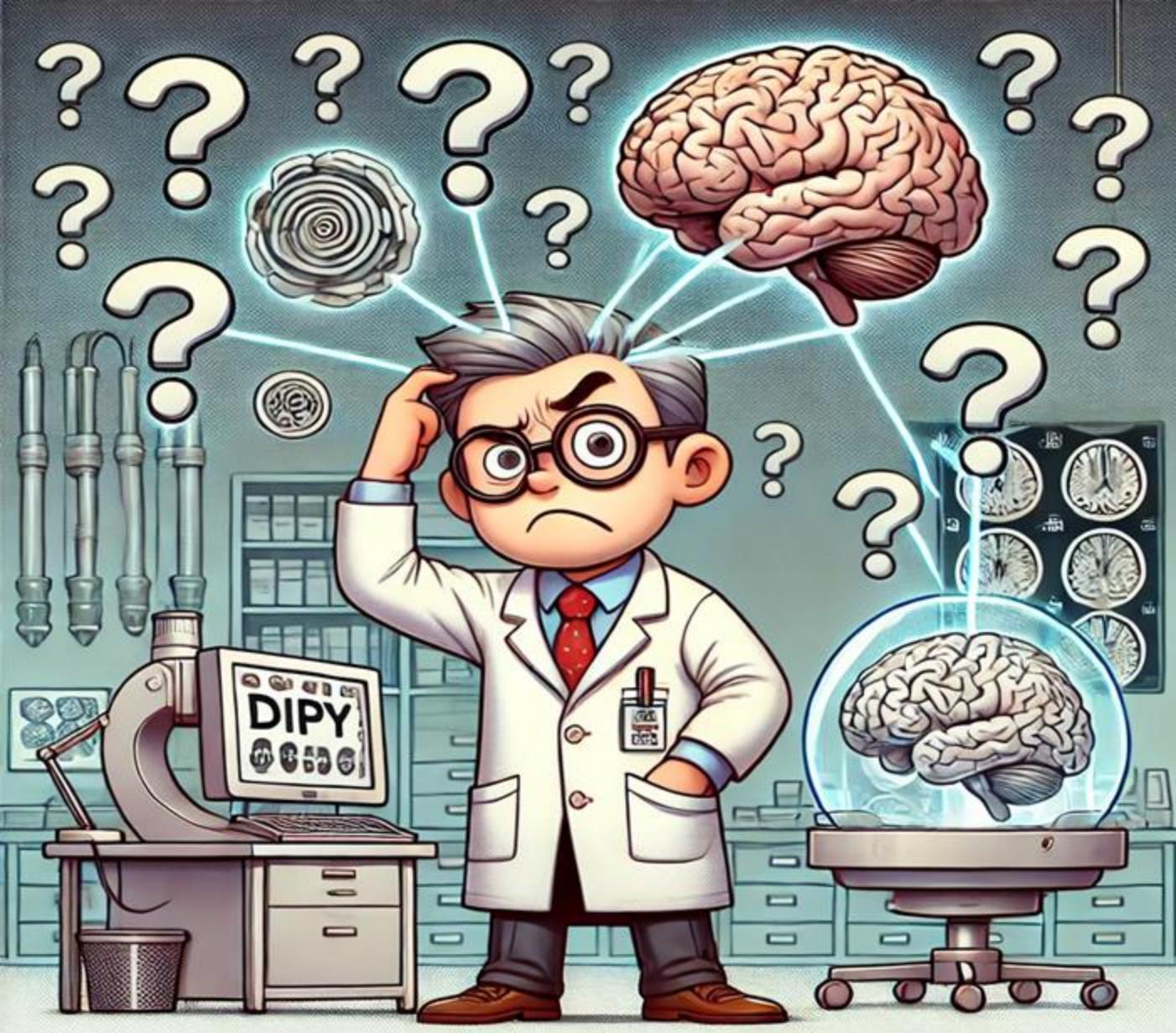
A screenshot of Visual Studio Code showing Python code for dipy tests. The code includes imports like numpy and dipy, and defines functions for testing masked array operations and gradient calculations.

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Key Learning Objectives

- Understand the fundamentals of diffusion MRI
- Explore DIPY and its command-line interface (CLI)
- Identify the essential blocks in a diffusion imaging pipeline
- Build your own diffusion imaging pipeline



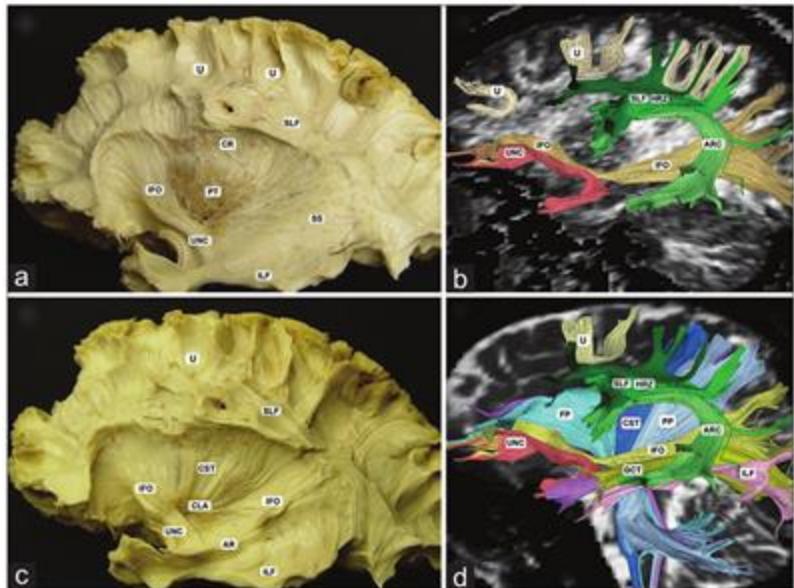


Let's start
from the
beginning



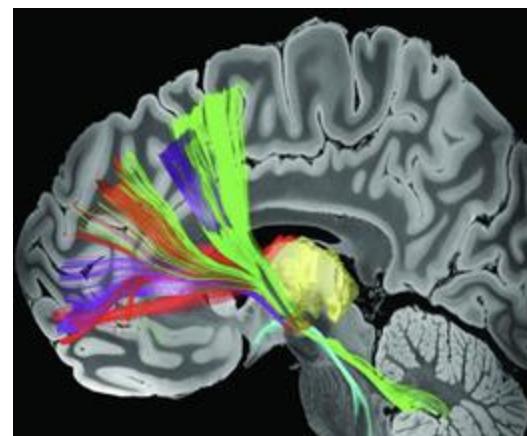
Why study the white matter?

- Brain functions rely on the network interactions between different regions.

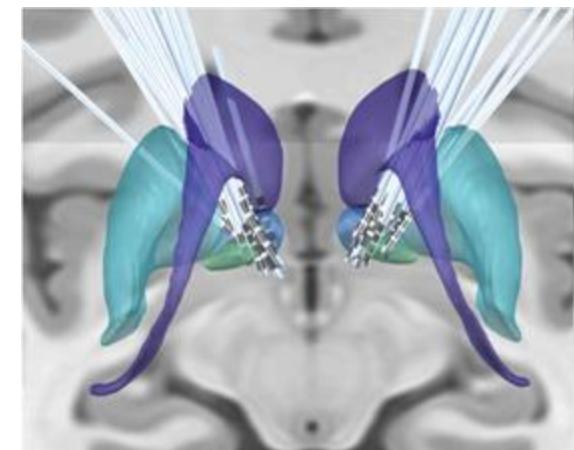


[Dini et al. Neurosurg. Intern. 2013]

- The precise information of fiber pathways are critical for clinical interventions.
- Example: guidance for electrode placement in deep brain stimulation.



Middlebrooks et al., *American Journal of Neuroradiology*, 2020



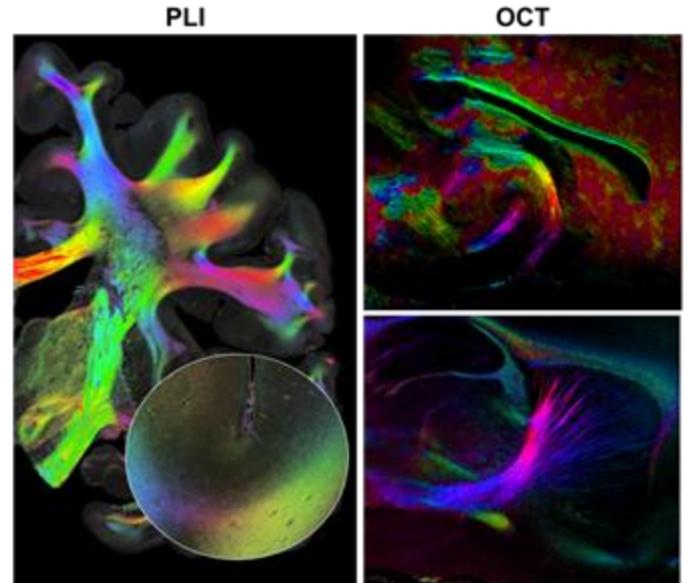
Li et al., *Nature Communications*, 2020



How do we track connections in the human brain ?

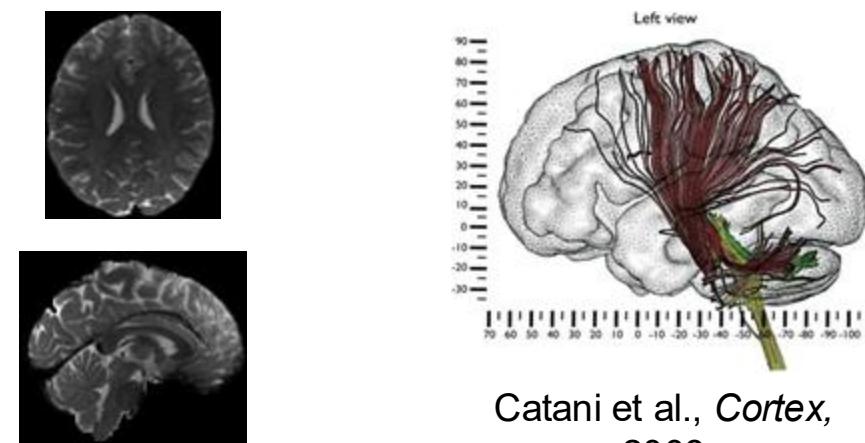
=> Polarized light imaging (PLI) & Optical coherence tomography (OCT):

- First developed in the 1990s
- Postmortem
- Resolution: micrometer
- PLI: birefringent (reflective) properties of myelinated fibers
- OCT: interference of light backscattered from the tissue



=> Diffusion Magnetic Resonance Imaging (dMRI):

- First developed in the 1990s
- *in vivo*
- Resolution: millimeter
- anisotropic diffusivity of water in the axons



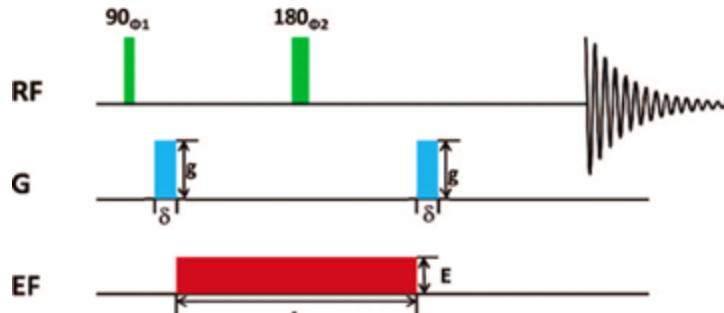
Catani et al., Cortex,
2008



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Pulsed-gradient spin echo experiment



Stejskal and Tanner
(1965)

$$\frac{S(TE, \gamma, G, \Delta, \delta)}{S(TE)} = e^{-\gamma^2 G^2 \delta^2 (\Delta - \frac{\delta}{3}) D}$$

$$\frac{S(b)}{S_0} = e^{-bD}$$

MR diffusion tensor spectroscopy and imaging

P J Basser¹, J Mattiello, D LeBihan

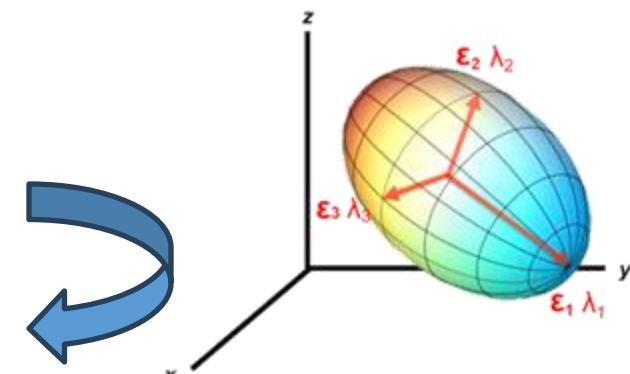
Affiliations + expand

PMID: 8130344 PMCID: PMC1275686 DOI: 10.1016/S0006-3495(94)80775-1

$$\ln \left(\frac{S(\theta)}{S_0} \right) = -b \mathbf{g}^T \mathbf{D} \mathbf{g}$$

↓
Fitted as a linear model → \mathbf{D}

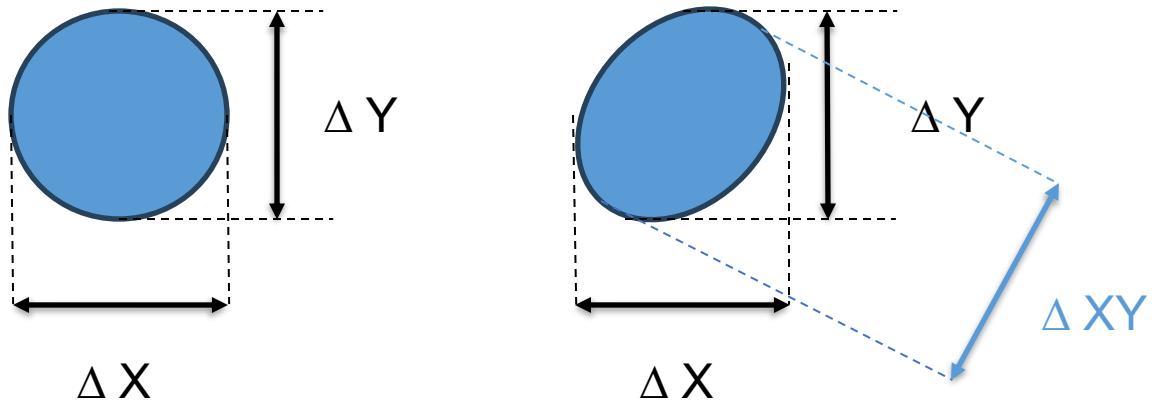
Eigen decomposition



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Why do we need tensor representation?



$$\begin{bmatrix} D_{xx} & D_{xy} \\ D_{yx} & D_{yy} \end{bmatrix}$$

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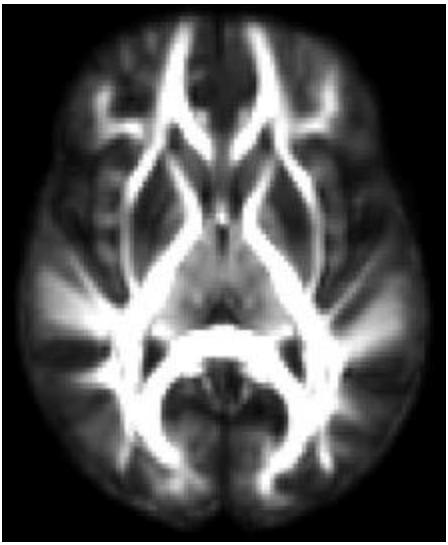


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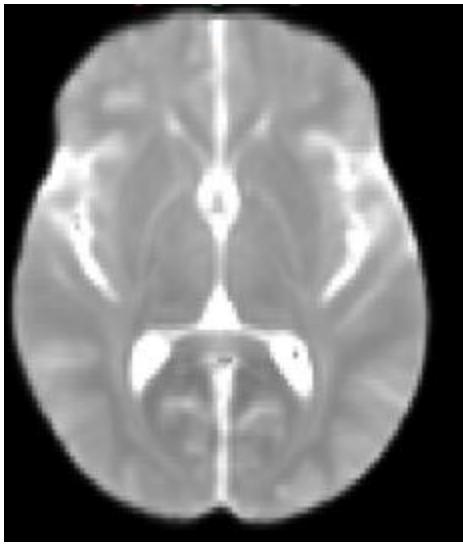
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FA map



MD map



$$FA = \sqrt{\frac{3}{2}} \cdot \frac{\sqrt{(\lambda_1 - \lambda_{mean})^2 + (\lambda_2 - \lambda_{mean})^2 + (\lambda_3 - \lambda_{mean})^2}}{\sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}$$

- Useful for detecting neuro-degeneracies
- Useful for detecting tracts and their connectivity patterns
- Assess white matter integrity

$$MD = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3}$$

- Detect tissue changes
- Useful for analyzing edema
- Assess different pathologies and axonal density

Software

- FSL (2000)
- Camino (2005)
- Mrtrix1 (2009) , Mrtrix3 (2019)
- Explore-DTI (2009)
- Tortoise (2007)
- DIPY (2011)



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DIPY

Free and open source software project for computational anatomy in Python.

It focuses on diffusion MRI analysis but also contains algorithms that are generic for medical imaging e.g. denoising, registration.

Created in 2011, DIPY is an international project which brings together scientists **across labs and countries ...**

... to share their **state-of-the-art code** and expertise in the same codebase, accelerating scientific research in medical imaging.

Specialized: **Diffusion MRI**

- Data preprocessing (P2S, Gibbs, ...)
- Voxel signal reconstruction (DKI, QTI, ...)
- Tracking algorithms (PFT, ...)
- Tractography Segmentation (QB, RB, ...)
- Tractography Registration (SLR, BundleWarp, ...)
- Statistical analysis and tractometry (BUAN, AFQ, ...).

General: **Medical Imaging**

- Affine and Nonrigid registration (SyN, ...)
- Denoising (NLMeans, ...)
- Visualization (Horizon, FURY, ...)
- Tissue segmentation & classification (HMRF, ...)

Garyfallidis, Eleftherios, Matthew Brett, Bagrat Amirbekian, Ariel Rokem, Stefan Van Der Walt, Maxime Descoteaux, and Ian Nimmo-Smith. "Dipy, a library for the analysis of diffusion MRI data." *Frontiers in neuroinformatics* 8 (2014): 8.

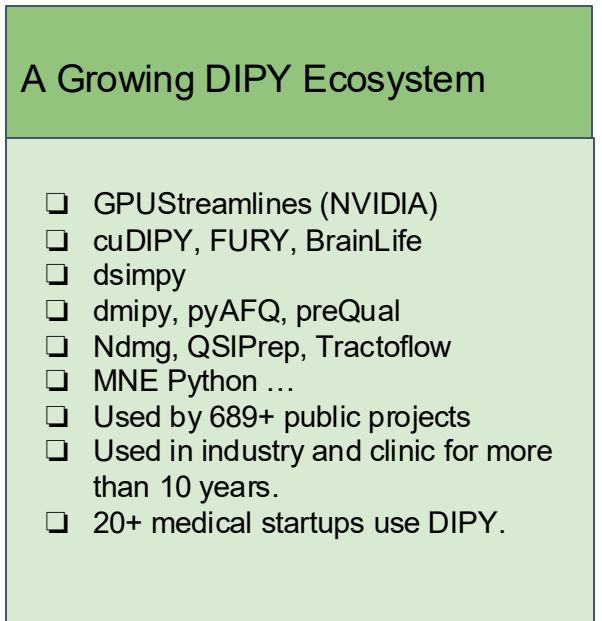
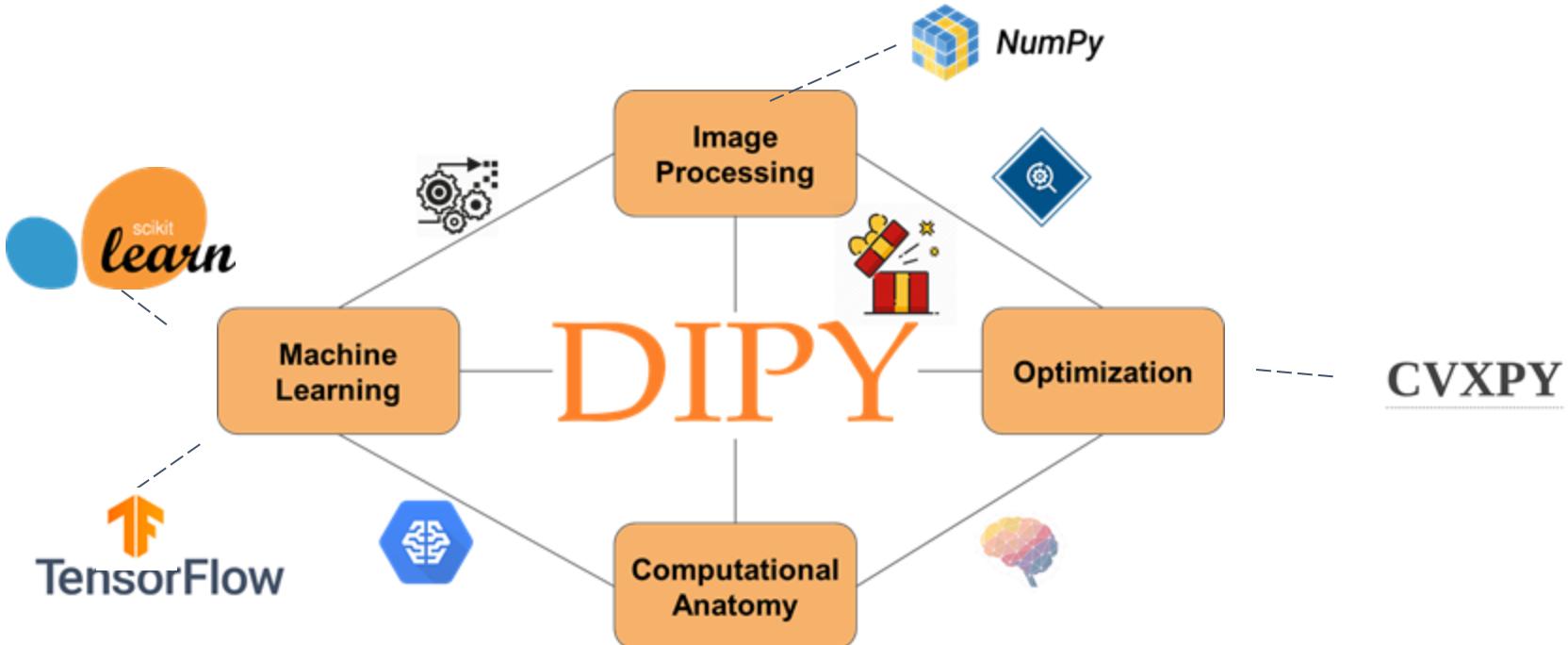


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DIPY Dependencies & Ecosystem

DIPY has been developed in parallel with NiBabel to provide access to Pythonic APIs for Neuroimagers and Data Scientists.



Garyfallidis, Eleftherios, Matthew Brett, Bagrat Amirbekian, Ariel Rokem, Stefan Van Der Walt, Maxime Descoteaux, and Ian Nimmo-Smith. "Dipy, a library for the analysis of diffusion MRI data." *Frontiers in neuroinformatics* 8 (2014): 8.



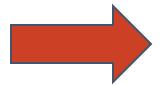
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Growing the TRL (Technology Readiness Level)

TRL	Software-Specific Definition	Indicators	What Does it means for DIPY ?
TRL-1	Basic research and concept formulation. No code exists yet.	Theoretical models, academic papers, white papers, proof-of-concept ideas.	Literature review
TRL-2	Algorithm development and feasibility studies. No practical implementation.	Early algorithm descriptions, feasibility tests, and simulations.	Algorithm Development: Core diffusion MRI methods are based on well-established academic research.
TRL-3	Prototype or preliminary code implemented in a controlled, test environment.	Alpha version of software, preliminary validation using synthetic data.	
TRL-4	Functional prototype with basic usability. Demonstrated in a lab setting, not tested externally.	First public release, early validation against real-world data, but limited users.	Code Implementation: Open-source implementation with robust Python support. <ul style="list-style-type: none">- Strong Software Engineering principle + core API vs UI- Heavy Testing + Detail documentation +Community- Great and sustainable software to help researchers.
TRL-5	Software validated in a relevant environment (e.g., used in research).	Beta version, limited external users, integrated with test datasets, early debugging.	

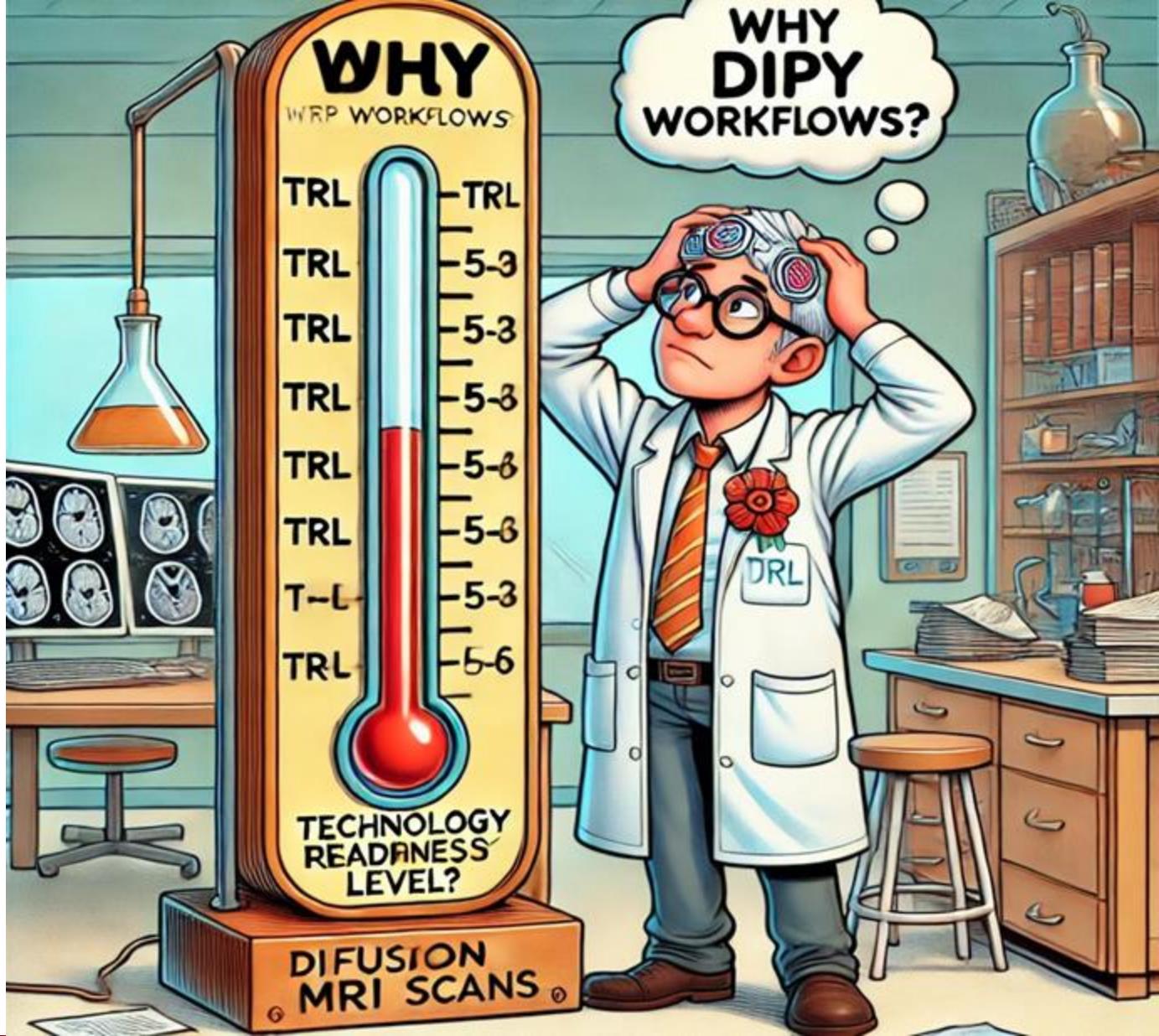


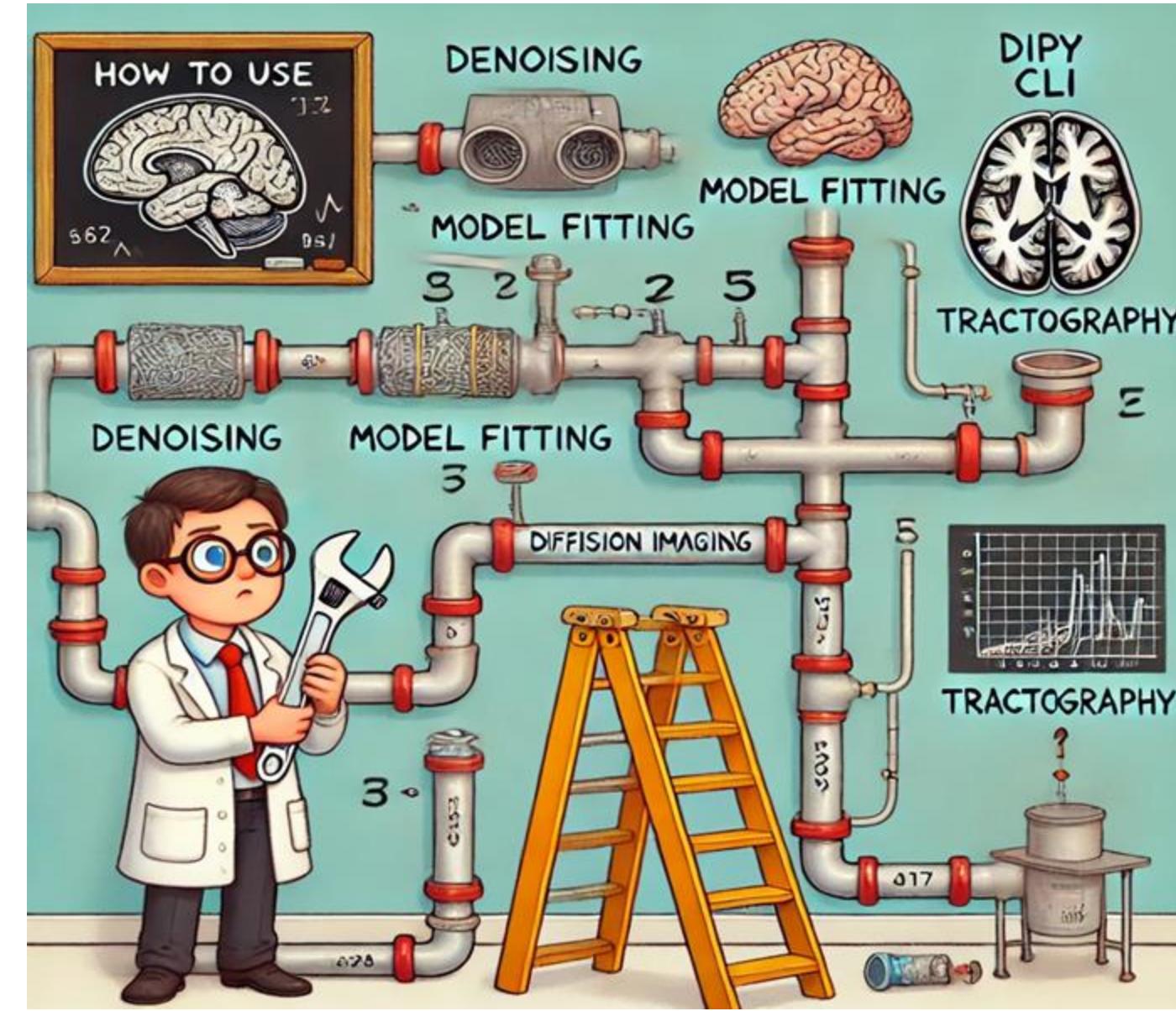
Growing the TRL (Technology Readiness Level)

TRL	Software-Specific Definition	Indicators	What Does it means for DIPY ?
TRL-6	Software tested in a real-world research setting, but not fully adopted or standardized.	Multiple research groups use it, academic publications cite it, early real-world applications.	Research Validation: Used in academic research, validated in studies.
TRL-7	Operational prototype demonstrated in a real environment, but not yet a commercial or clinical standard.	Widespread academic use, reliable documentation, community contributions, open-source adoption.	Operational Deployment: Widely used in neuroscience, but limited clinical deployment.
TRL-8	Software is fully validated and used in production, but not yet a formal regulatory or enterprise standard.	Software integrated into commercial or clinical systems, tested on a broad scale.	Industry Adoption & Regulatory Compliance: No FDA/CE approval yet for medical diagnostics, not embedded in commercial MRI systems.
TRL-9	Fully deployed in operational environments, meeting industry or regulatory standards.	Regulatory approval (e.g., FDA, ISO), integration into commercial software suites.	Regulatory Approval: FDA clearance or CE marking - Enterprise Integration - Long-Term Clinical Validation - Security & Compliance - Broader Adoption Beyond Academia :

→ TR-7: Operational Deployment

- Reduces manual effort by enabling automation and scripting
- Accessible to non-programmers
- Enhances reproducibility
- Scale efficiently for large datasets / Optimized for efficiency and scalability





How to build your diffusion imaging pipeline ?

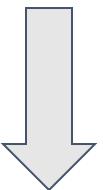


First things first, dcm2nix => DICOM to NIFTI

```
dcm2niix -z y -f %p_%t_%s -o /path/output /path/to/dicom/folder
```

```
(boystown) [pi09@k1:/nobackup/pi09/boystown/ABC Protocol/M68103049/t1w_32ch_mpr_1mm_0005] $
```

```
SeriesR-0005-0001-1.dcm SeriesR-0005-0015-1.dcm SeriesR-0005-0029-1.dcm SeriesR-0005-0043-1.dcm SeriesR-0005-0057-1.dcm SeriesR-0005-0071-1.dcm SeriesR-0005-0085-1.dcm SeriesR-0005-0099-1.dcm SeriesR-0005-0113-1.dcm SeriesR-0005-0127-1.dcm SeriesR-0005-0141-1.dcm SeriesR-0005-0155-1.dcm SeriesR-0005-0169-1.dcm SeriesR-0005-0183-1.dcm
SeriesR-0005-0002-1.dcm SeriesR-0005-0016-1.dcm SeriesR-0005-0030-1.dcm SeriesR-0005-0044-1.dcm SeriesR-0005-0058-1.dcm SeriesR-0005-0072-1.dcm SeriesR-0005-0086-1.dcm SeriesR-0005-0109-1.dcm SeriesR-0005-0114-1.dcm SeriesR-0005-0128-1.dcm SeriesR-0005-0142-1.dcm SeriesR-0005-0156-1.dcm SeriesR-0005-0170-1.dcm SeriesR-0005-0184-1.dcm
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SeriesR-0005-0012-1.dcm SeriesR-0005-0026-1.dcm SeriesR-0005-0040-1.dcm SeriesR-0005-0054-1.dcm SeriesR-0005-0066-1.dcm SeriesR-0005-0082-1.dcm SeriesR-0005-0096-1.dcm SeriesR-0005-0110-1.dcm SeriesR-0005-0124-1.dcm SeriesR-0005-0138-1.dcm SeriesR-0005-0152-1.dcm SeriesR-0005-0166-1.dcm SeriesR-0005-0180-1.dcm
SeriesR-0005-0013-1.dcm SeriesR-0005-0027-1.dcm SeriesR-0005-0041-1.dcm SeriesR-0005-0055-1.dcm SeriesR-0005-0069-1.dcm SeriesR-0005-0083-1.dcm SeriesR-0005-0097-1.dcm SeriesR-0005-0111-1.dcm SeriesR-0005-0125-1.dcm SeriesR-0005-0139-1.dcm SeriesR-0005-0152-1.dcm SeriesR-0005-0167-1.dcm SeriesR-0005-0181-1.dcm SeriesR-0005-0193-1.dcm
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```



```
M68103049_t1w_32ch_mpr_1mm_20240501174427_5.json  
M68103049_t1w_32ch_mpr_1mm_20240501174427_5.nii.gz
```

Li X, Morgan PS, Ashburner J, Smith J, Rorden C (2016) The first step for neuroimaging data analysis: DICOM to NIfTI conversion. J Neurosci Methods. 264:47-56. doi: 10.1016/j.jneumeth.2016.03.001. PMID: 26945974



Installation

Official latest stable

```
>>> pip install -U dipy
```

```
>>> conda -c conda-forge dipy
```

Official developer / unstable

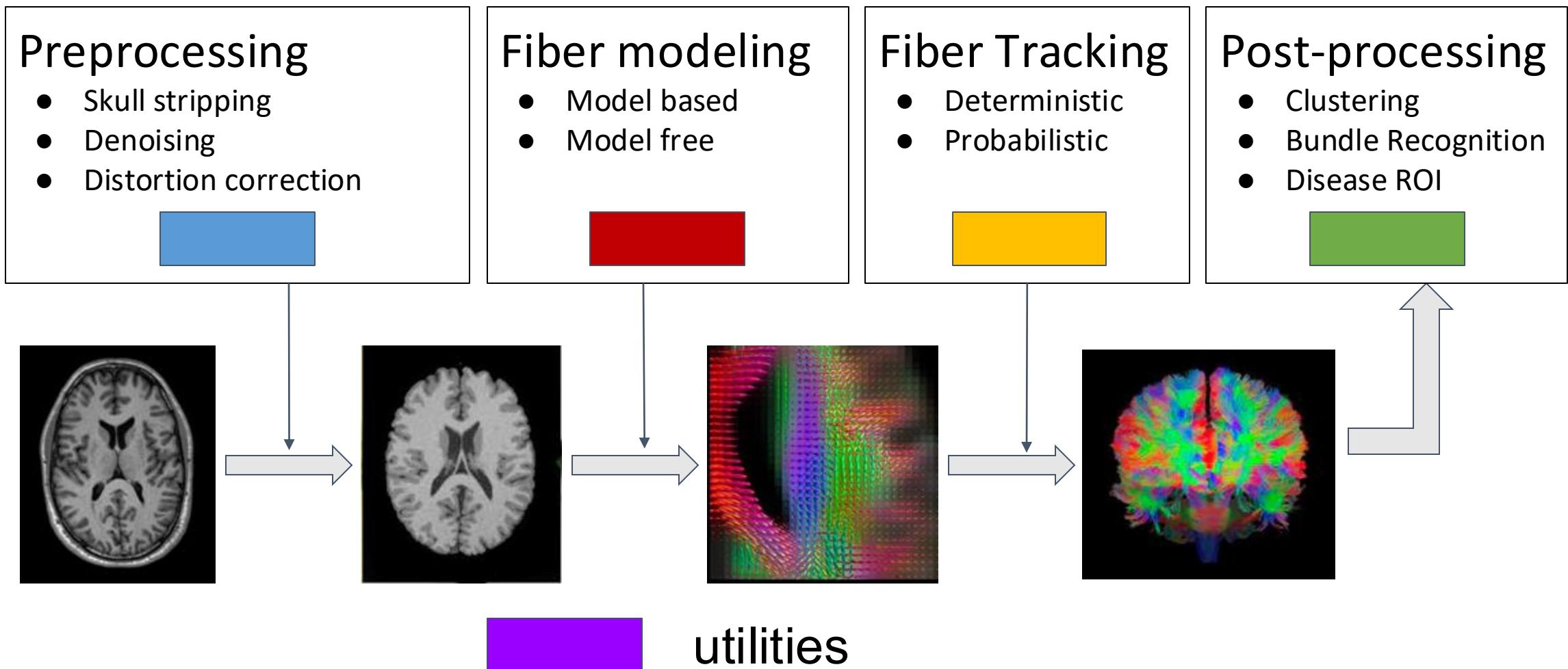
```
>>> pip install --upgrade --progress-bar off --extra-index-url  
"https://pypi.anaconda.org/scientific-python-nightly-wheels/simple" "dipy==1.12.0.dev0"
```



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CLI Diffusion MRI pipeline



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→ Currently, 50+ DIPY Workflows for diffusion MRI analysis. More to come....

dipy_align_affine
dipy_align_syn
dipy_apply_transform

dipy_buan_ellip
dipy_buan_profiles
dipy_buan_shapes
dipy_bundlewarp

dipy_concatenate_tractograms
dipy_convert_tensors
dipy_convert_tractograms
dipy_correct_motion

dipy_denoise_lPCA
dipy_denoise_mPPCA
dipy_denoise_nlmeans
dipy_denoise_patch2self
dipy_evac_plus

dipy_fetch
dipy_fit_csa
dipy_fit_csd
dipy_fit_dki
dipy_fit_dsi
dipy_fit_dtI

dipy_fit_ivim
dipy_fit_mapmri

dipy_gibbs_ringing
dipy Horizon
dipy_info

dipy_labelsbundles
dipy_mask
dipy_median_otsu
dipy_nifti2pam
dipy_pam2nifti
dipy_recobundles

dipy_reslice
dipy_sh_convert_mrtrix

dipy_slr
dipy_split
dipy_tensor2pam
dipy_track
dipy_track_pft

Preprocessing

Tractometry

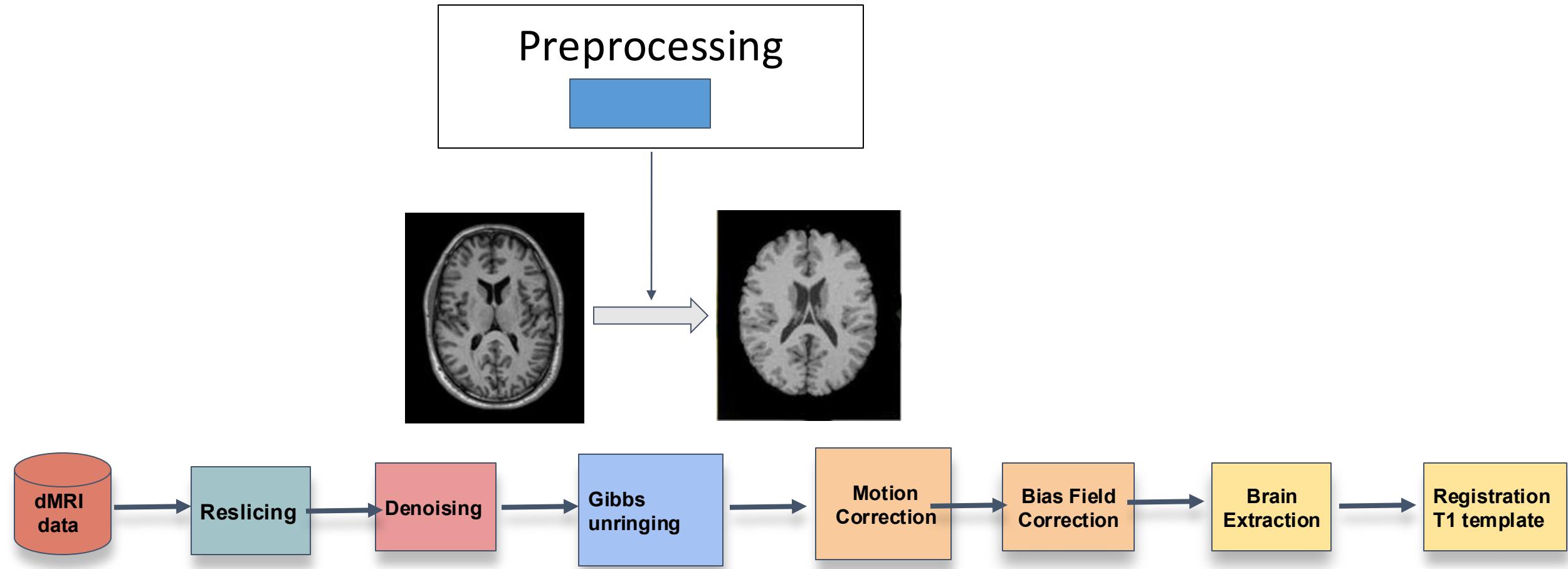
utilities

Reconstruction

Tractography



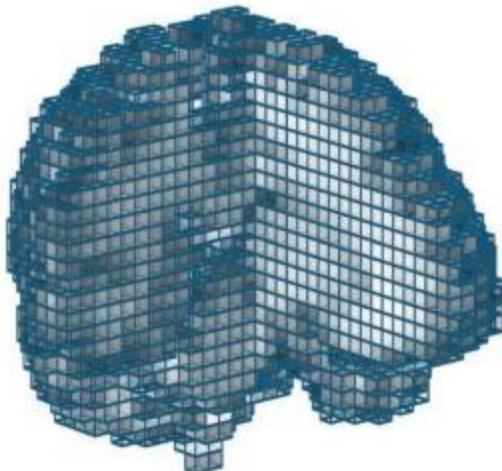
dMRI pipeline: Why Preprocessing ?



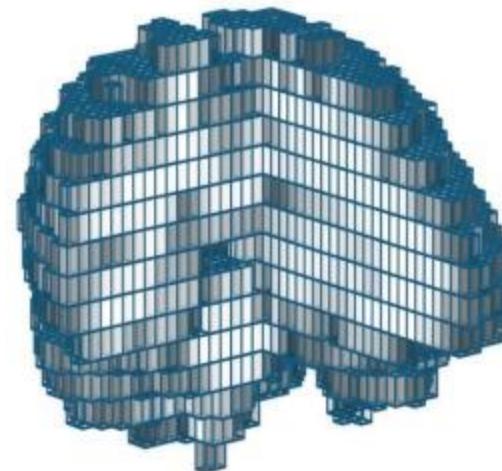
Reslice (Interpolate)



Isotropic voxels



Anisotropic voxels



```
>>> dipy_info my_nifiti_files.nii.gz  
>>> dipy_reslice
```





Understand Your Data: >>> dipy_info

```
> dipy_info ../../dipy/stanford_hardi/HARDI150.nii.gz
INFO:-----
INFO:Looking at ../../dipy/stanford_hardi/HARDI150.nii.gz
INFO:-----
INFO:Data size (81, 106, 76, 160)
INFO:Data type int16
INFO:Data min 0 max 13157 avg 330.8058252724754 of vol 0
INFO:2nd percentile 0.0 98th percentile 2202.0 of vol 0
INFO:Native coordinate system RAS
INFO:Affine Native to RAS matrix
[[ 2.    0.    0.   -80.]
 [ 0.    2.    0.  -120.]
 [ 0.    0.    2.   -60.]
 [ 0.    0.    0.    1.]]
INFO:Voxel size [2. 2. 2.]
```



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Understand Your Data: >>> dipy_info

```
> dipy_info ../../data/sunita/Dipy/abcdefg.nii.gz
INFO:-----
INFO:Looking at ../../data/sunita/Dipy/abcdefg.nii.gz
INFO:-----
INFO:Data size (128, 128, 88, 33)
INFO:Data type float64
INFO:Data min 0.0 max 25449.873025417328 avg 715.9515434390219 of vol 0
INFO:2nd percentile 0.0 98th percentile 5394.503000259399 of vol 0
INFO:Native coordinate system LAS
INFO:Affine Native to RAS matrix
[[ -1.868 -0.147 -0.057 121.132]
 [ -0.152 1.862 0.174 -78.635]
 [ -0.04 -0.167 1.992 -99.582]
 [ 0. 0. 0. 1. ]]
INFO:Voxel size [1.875 1.875 2. ]
WARNING:Voxel size is not isotropic. Please reslice.
```



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Denoising

```
>>> dipy_denoise_nlmeans
```

Self-Similarity:

Images are often self-similar, in that each patch in an image is similar to many other patches from the same image.

Image denoising with **block-matching and 3D filtering** (Dabov, 2006)

NL-Means (Buades et. al. 2005) and its variants ONLM, AONLM, etc.
BM3D (Dabov et al., 2007) thresholds in frequency space.

```
>>> dipy_denoise_lPCA  
>>> dipy_denoise_mPCA
```

Low Rank Approximations:

Approximate the data to a smaller basis, typically via a low-rank approximation and then reconstruct from the low rank approximations.

Rank 'r' is the parameter that needs to be found for doing such an approximation. Typically done via PCA for Diffusion MRI.

Local PCA (Manjon et. al., 2013)

Marchenko Pastur PCA (Veraart et. al., 2016)

Not implemented

Sparsity:

Images are often sparse and this property can be leveraged for denoising the data. These methods require a predetermined basis set to do the denoising such as DCT, DWT, etc. or by learning the basis from the data, known as dictionary learning.

K-SVD Overcomplete Dictionary Learning - Aarhon and Elad 2006

Denoising and fast diffusion imaging with physically constrained sparse dictionary learning, Gramfort, et. al., 2014

```
>>> dipy_denoise_patch2self
```

Statistical Independence:

Since noise originates from random fluctuations, noise in one subset of an image can be assumed to be statistically independent of the noise in another subset. Using one subset to predict the other gives denoising performance.

Patch2Self, Fadnavis, et. al. 2020

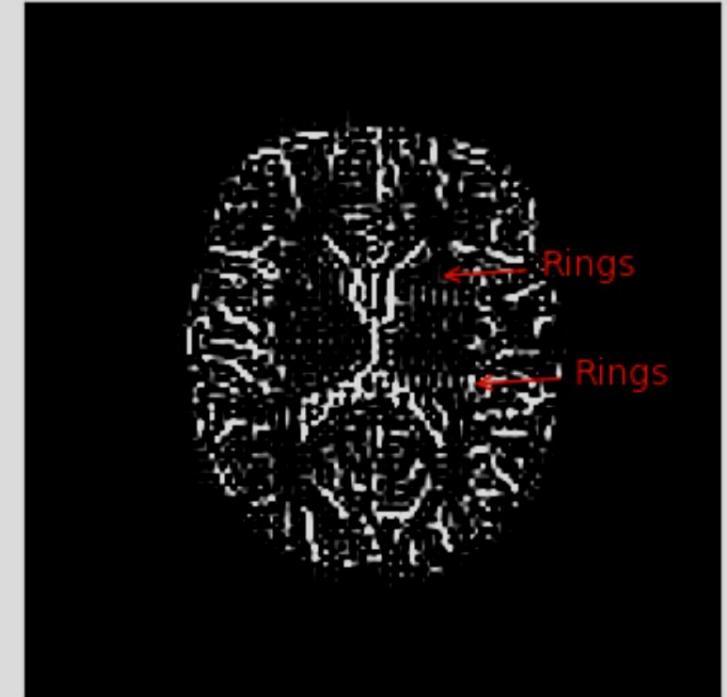
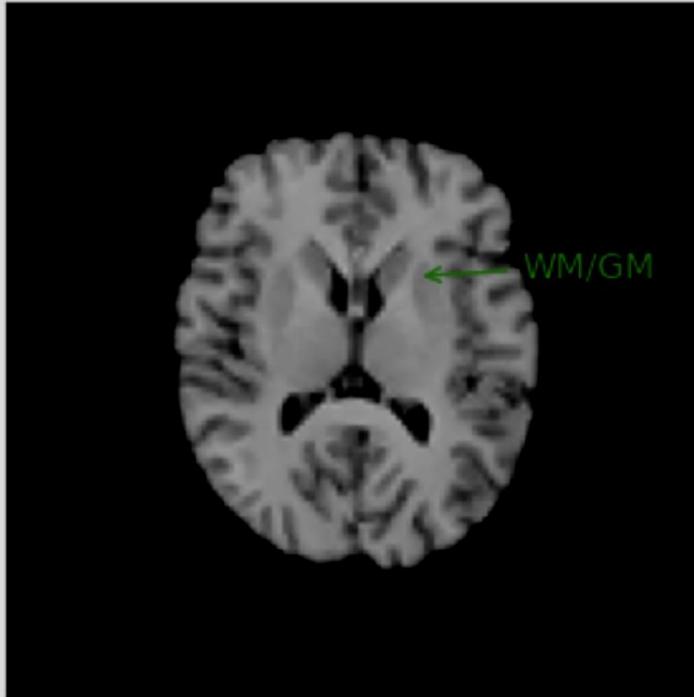
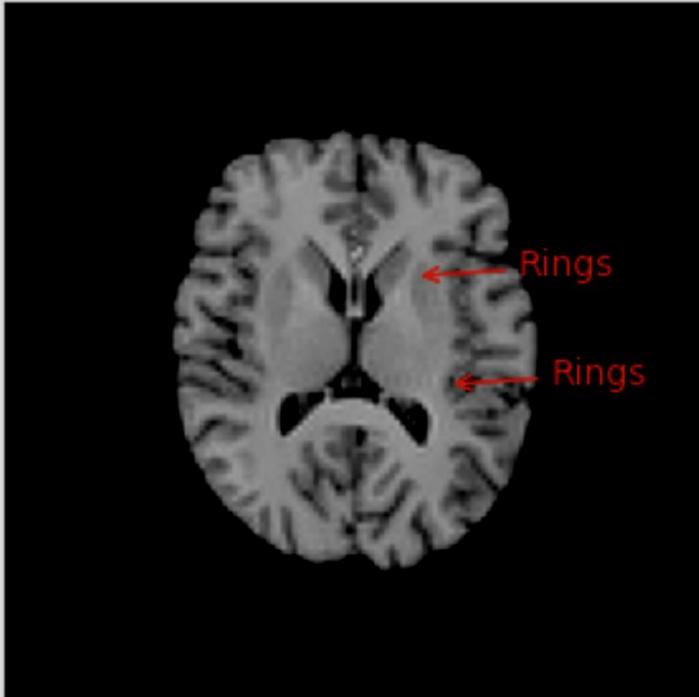
Noise2Self, Batson, et. al. 2019

Noise2Noise, Lehtinen, et. al. 2018



Gibbs Unringing

```
>>> dipy_gibbs_ringing input_files
```



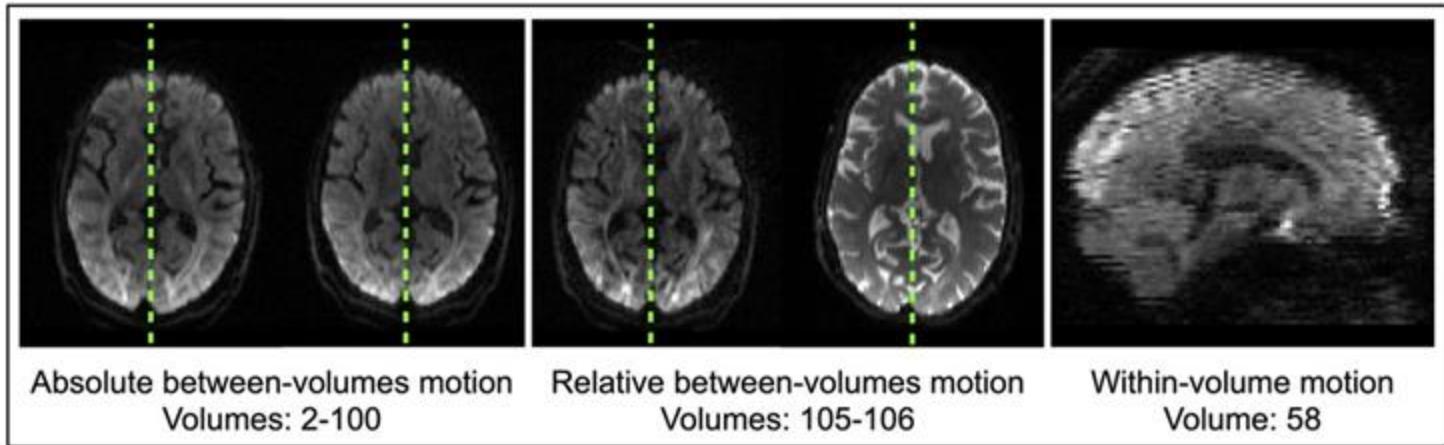
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Motion Correction

```
>>> dipy_correct_motion
```

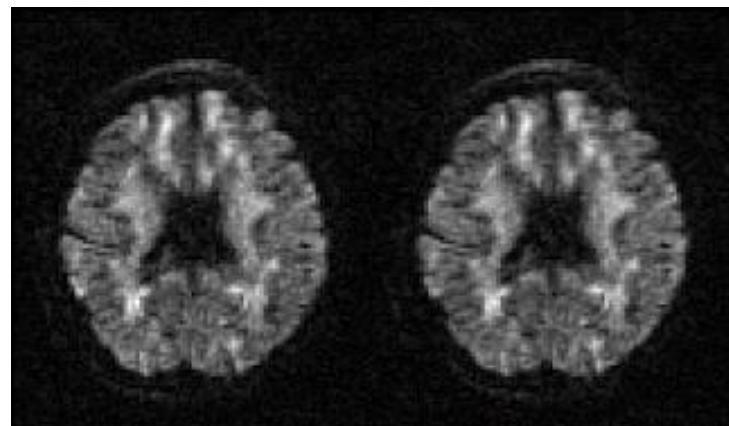
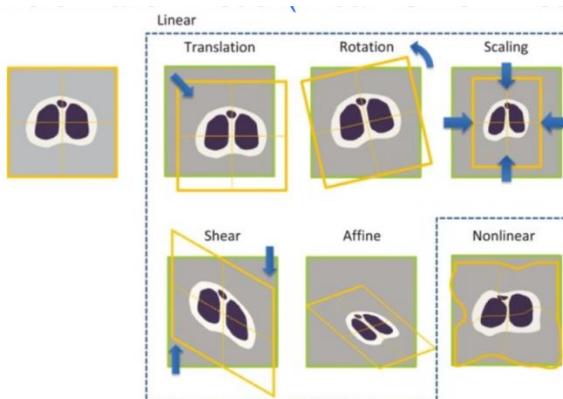
Eddy current correction



Affine Transformation

	Before	After	Preserves
Translation (3 dof)			orientation
Rotation (3 dof)			lengths
Rigid (6 dof)			lengths
Homogeneous Transformations			angles
Similarity (7 dof)			
Affine (12 dof)			parallelism

DIP'



Serge Koudoro

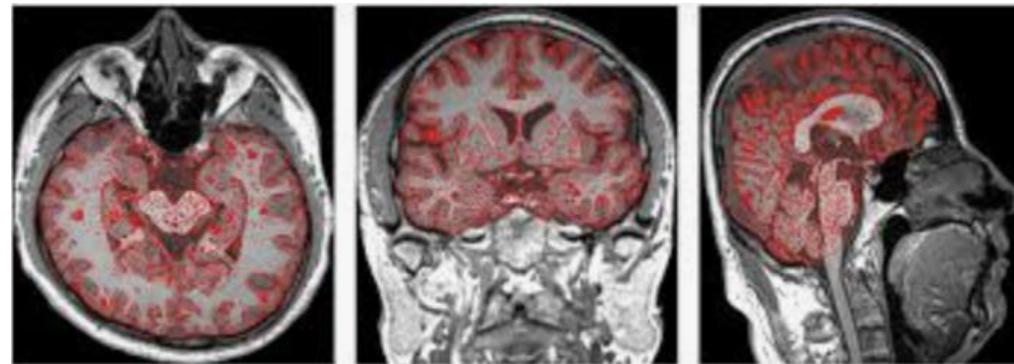
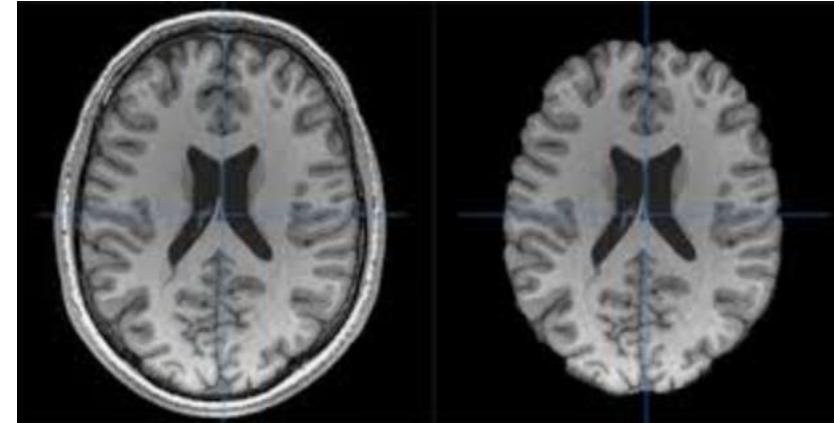


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Brain extraction

```
>>> dipy_median_otsu (for dwi)  
>>> dipy_evac_plus (for T1)
```

SynthSeg
BET



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Huge topic

Register T1- Template

```
>>> dipy_align_affine  
>>> dipy_align_syn
```

Bias field Correction

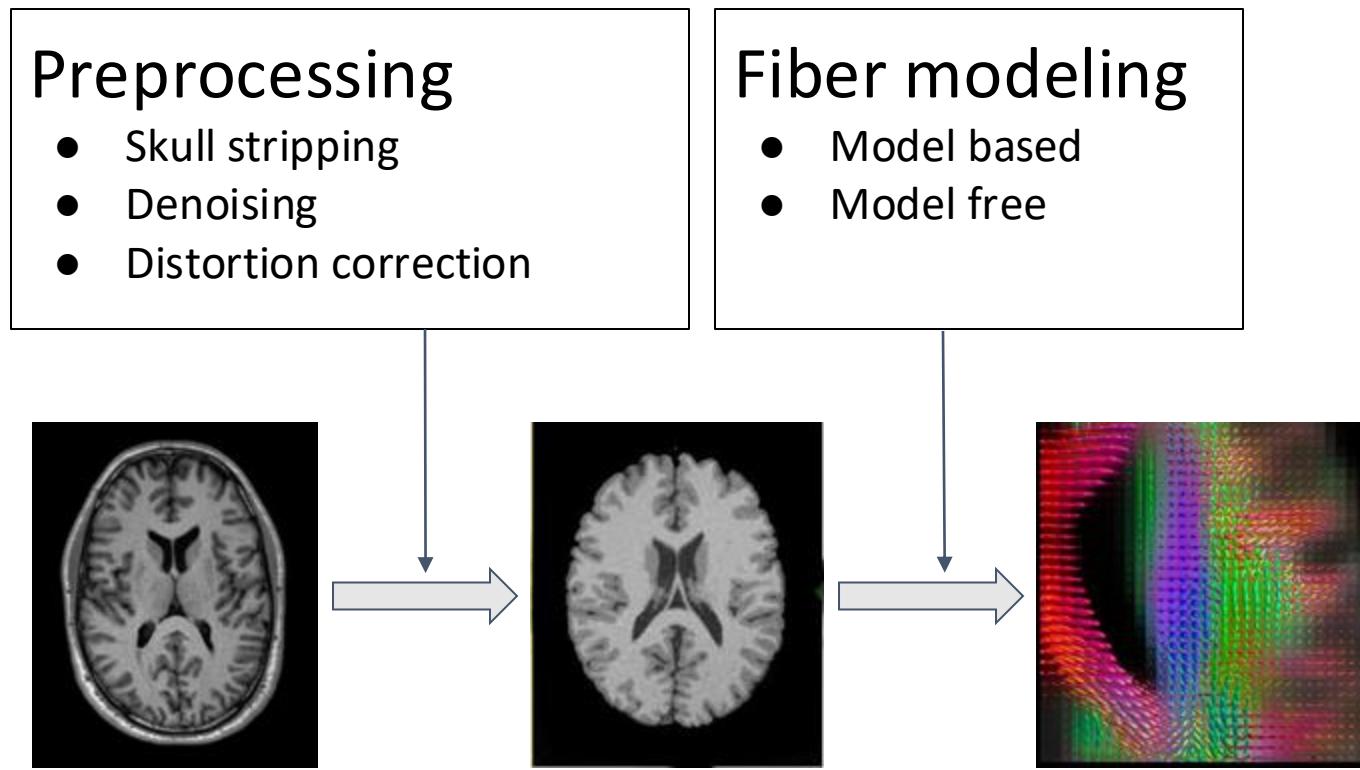
```
>>> dipy_correct_biasfield
```

Tax CMW, Bastiani M, Veraart J, Garyfallidis E, Okan Irfanoglu M. What's new and what's next in diffusion MRI preprocessing. *Neuroimage*. 2022 Apr 1;249:118830. doi: 10.1016/j.neuroimage.2021.118830. Epub 2021 Dec 26. PMID: 34965454; PMCID: PMC9379864.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9379864/>



dMRI pipeline: Reconstruction



Reconstruction

```
>>> dipy_fit_dt
>>> dipy_fit_csa
>>> dipy_fit_csd
>>> dipy_fit_dki
>>> dipy_fit_dsi
>>> dipy_fit_ivim
>>> dipy_fit_mapmri
>>> dipy_fit_forecast
>>> dipy_fit_rumba
>>> ....
>>> 30+ models
```



A bit of theory

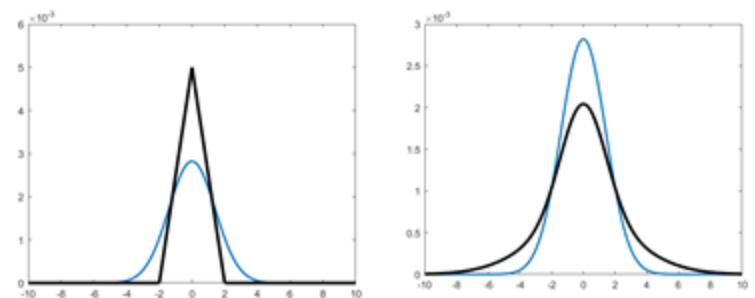
- **Phenomenological models** - Represent observable properties without assuming hidden mechanisms
 - eg - DTI, DKI
- **Mechanistic models** - Postulate hidden mechanism. In case of brain, fiber orientations and density of neural tissues
 - eg - NODDI

Gaussian diffusion Modeling

$$\text{DTI} \quad \ln\left(\frac{S(\theta)}{S_0}\right) = -b\mathbf{g}^T \mathbf{D} \mathbf{g}$$

$$\text{DKI} \quad \log\frac{S(b,n)}{S_0} \approx -bD(\mathbf{n}) + \frac{1}{6}b^2D(\mathbf{n})^2K(\mathbf{n})$$

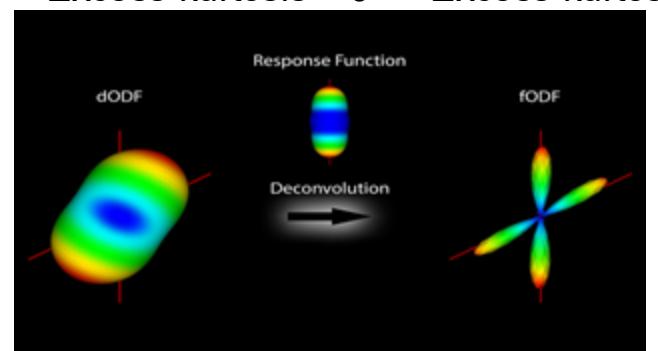
DTI has 6 parameters
DKI has 15 parameters



Orientation Distribution Modeling

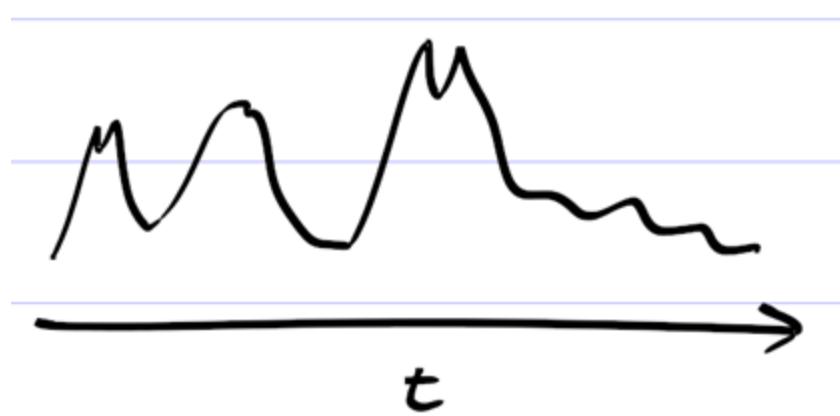
$$\text{CSA} \quad \text{ODF}(\mathbf{n}) = \int_{\mathbb{R}^3} E(\mathbf{q})\delta(\mathbf{q} \cdot \mathbf{n} - r) d\mathbf{q}$$

$$\text{CSD} \quad S(\mathbf{q}) = \int_{S^2} R(\mathbf{q}, \mathbf{n})f(\mathbf{n}) d\mathbf{n}$$



Demystifying Spherical Harmonics

- A spherical harmonic transform is simply the Fourier Transform constrained by the fact that the domain of the signal is a sphere.
- Spherical harmonics are Fourier basis functions on the sphere.



Standard 1D signal where we could apply the Fourier Transform



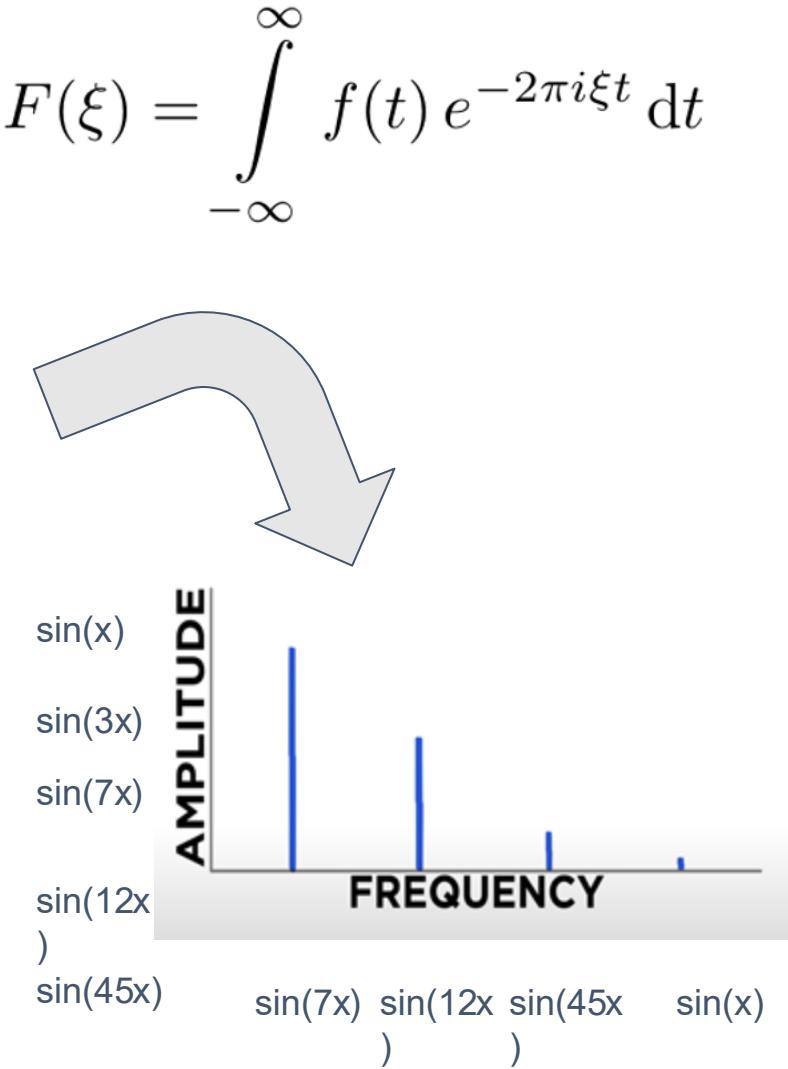
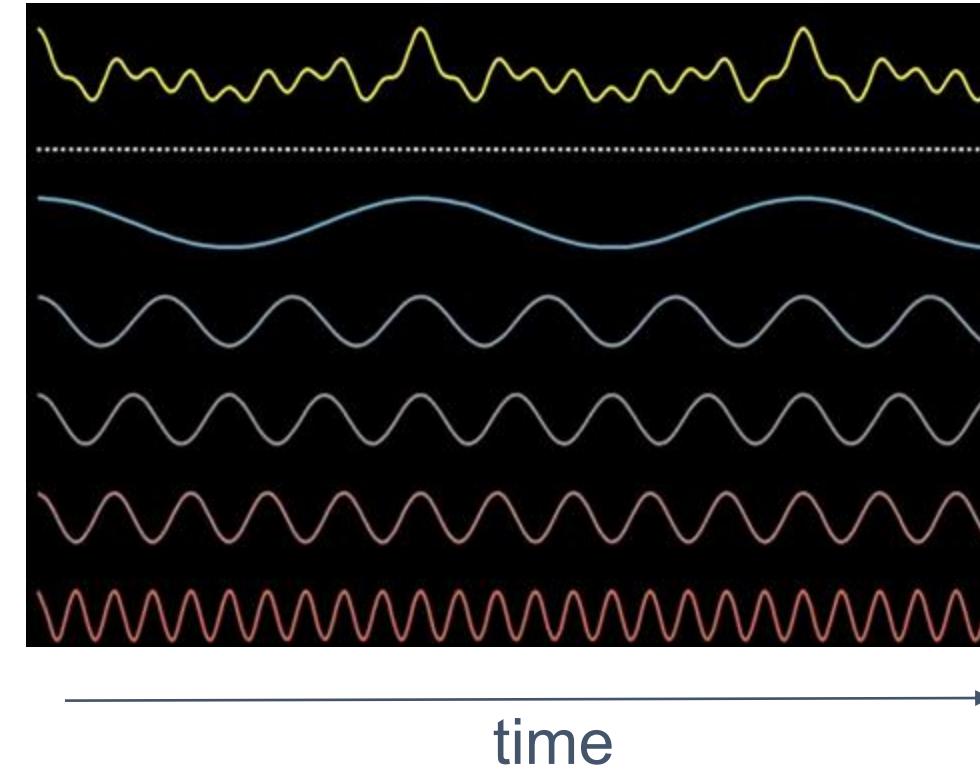
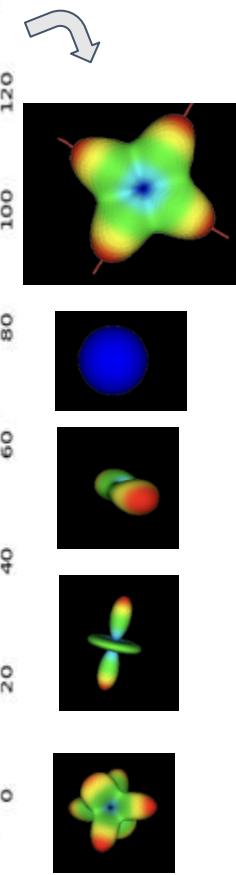
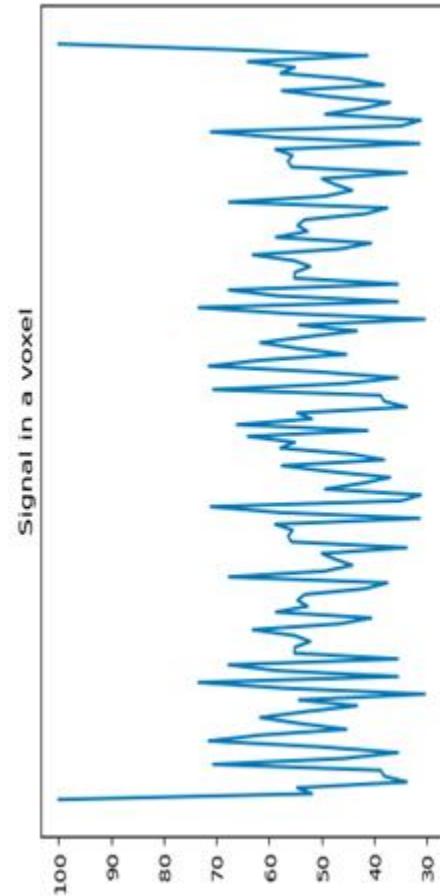
Spherical signal (showing only a slice of that sphere) - Signal wraps around the sphere.



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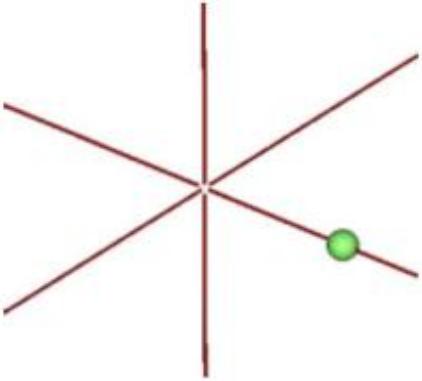
But what is the Fourier Transform? $\mathcal{F}\{f(t)\} = F(\xi) = \int_{-\infty}^{\infty} f(t) e^{-2\pi i \xi t} dt$



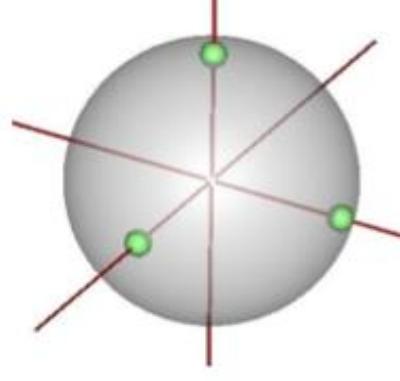
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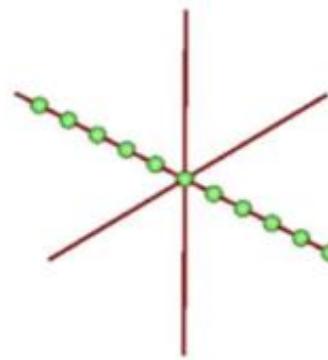
History of q-space sampling



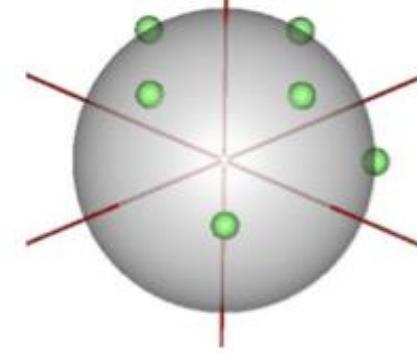
Pulsed Gradient Spin Echo
Stejskal & Tanner, 1965



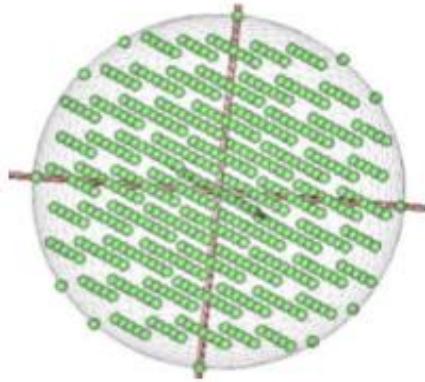
Diffusion-weighted imaging
Le Bihan, 1986



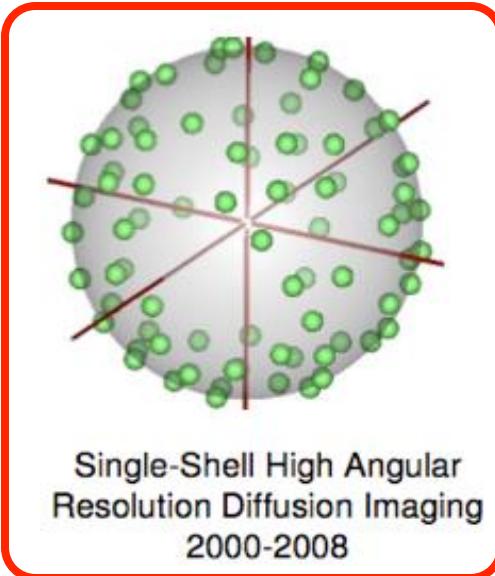
Diffusion spectrum
Callaghan, 1991



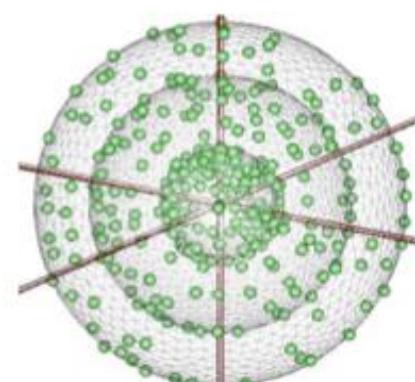
Diffusion tensor imaging
Basser, 1994



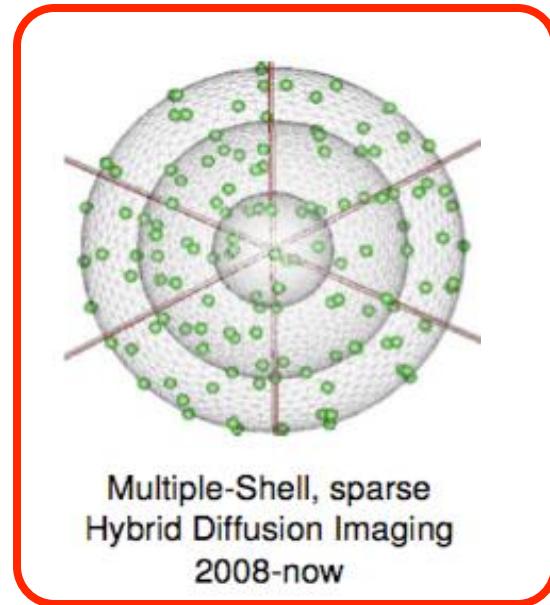
Diffusion spectrum imaging
Van Wedeen, 2000



Single-Shell High Angular
Resolution Diffusion Imaging
2000-2008



Multiple-Shell Diffusion
Propagator Imaging
2008-now



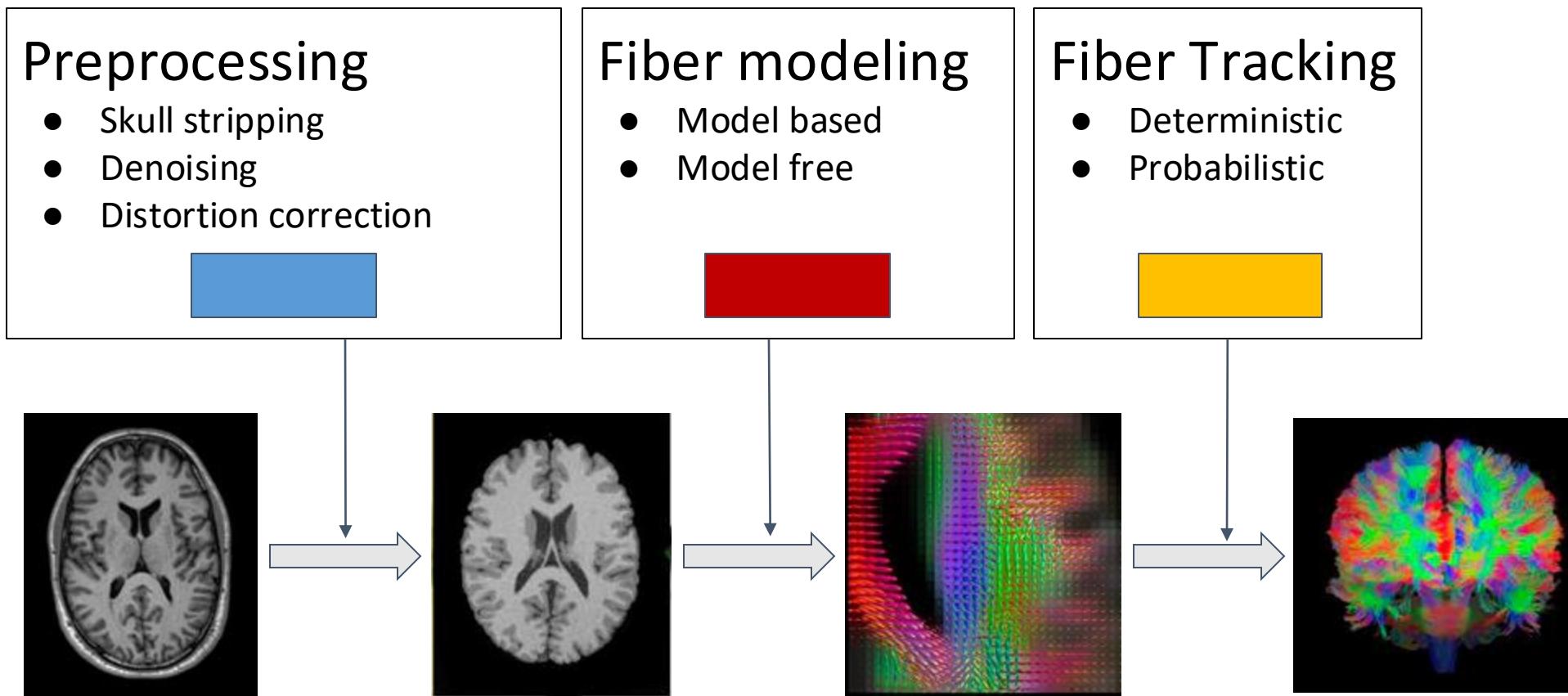
Multiple-Shell, sparse
Hybrid Diffusion Imaging
2008-now

```
>>> dipy_fit_dti
>>> dipy_fit_csa
>>> dipy_fit_csd
>>> dipy_fit_dki
>>> dipy_fit_dsi
>>> dipy_fit_ivim
>>> dipy_fit_mapmri
>>> dipy_fit_forecast
>>> dipy_fit_gqi
>>> ....
>>> 30+
```

Method	Single Shell	Multi Shell	Cartesian	Paper Data Descriptions	References
DTI (SLS, WLS, NNLS)	Yes	Yes	Yes	Typical b-value = 1000 s/mm ² , maximum b-value 1200 s/mm ² (some success up to 1500 s/mm ²)	Basser <i>et al.</i> [BMLeBihan94b]
DTI (RESTORE)	Yes	Yes	Yes	Typical b-value = 1000 s/mm ² , maximum b-value 1200 s/mm ² (some success up to 1500 s/mm ²)	Chang <i>et al.</i> [CJP05], Chung <i>et al.</i> [CLH06], Yendiki <i>et al.</i> [YKK+14]
FwDTI	No	Yes	No	DTI-style acquisition, multiple b=0, all shells should be within maximum b-value of 1000 s/mm ² (or 32 directions evenly distributed 500 s/mm ² and 1500 s/mm ² per Neto Henriques <i>et al.</i> [NetoHenriquesRG+17])	Pasternak <i>et al.</i> [PSG+09], Neto Henriques <i>et al.</i> [NetoHenriquesRG+17]
DKI - Standard	No	Yes	No	Dual spin echo diffusion-weighted 2D EPI images were acquired with b values of 0, 500, 1000, 1500, 2000, and 2500 s/mm ² (max b value of 2000 suggested as sufficient in brain tissue); at least 15 directions	Jensen <i>et al.</i> [JHR+05]
DKI+ Constraints	No	Yes	No	None	Dela Haije <i>et al.</i> [DelaHaijeOzarslanF20]
DKI - Micro (WMTI)	No	Yes	No	DKI-style acquisition: at least two non-zero b shells (max b value	Fieremans <i>et al.</i> [FJH11], Tabesh <i>et al.</i> [TJAH11]



CLI Diffusion MRI pipeline

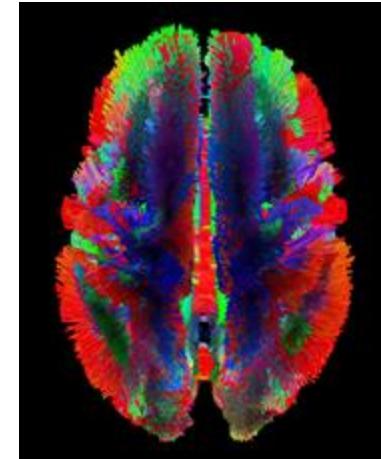
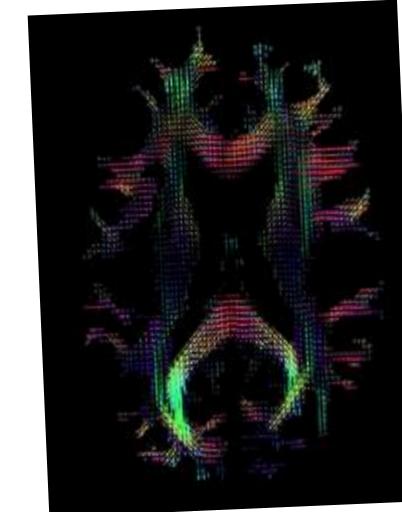
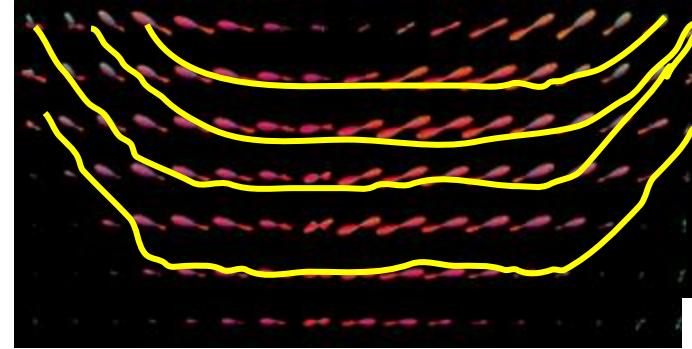
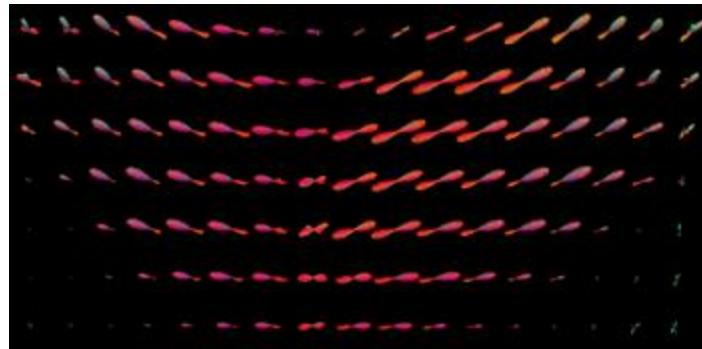


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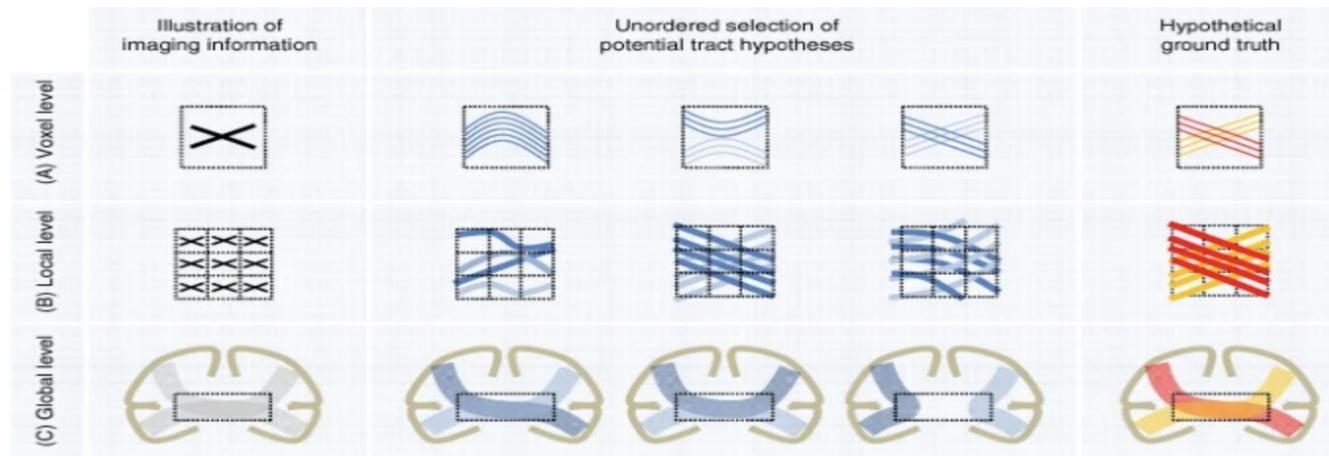
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Tracking

A) Fiber Orientation Distribution Function B) Fiber Tracking



Requirements for streamline tractography

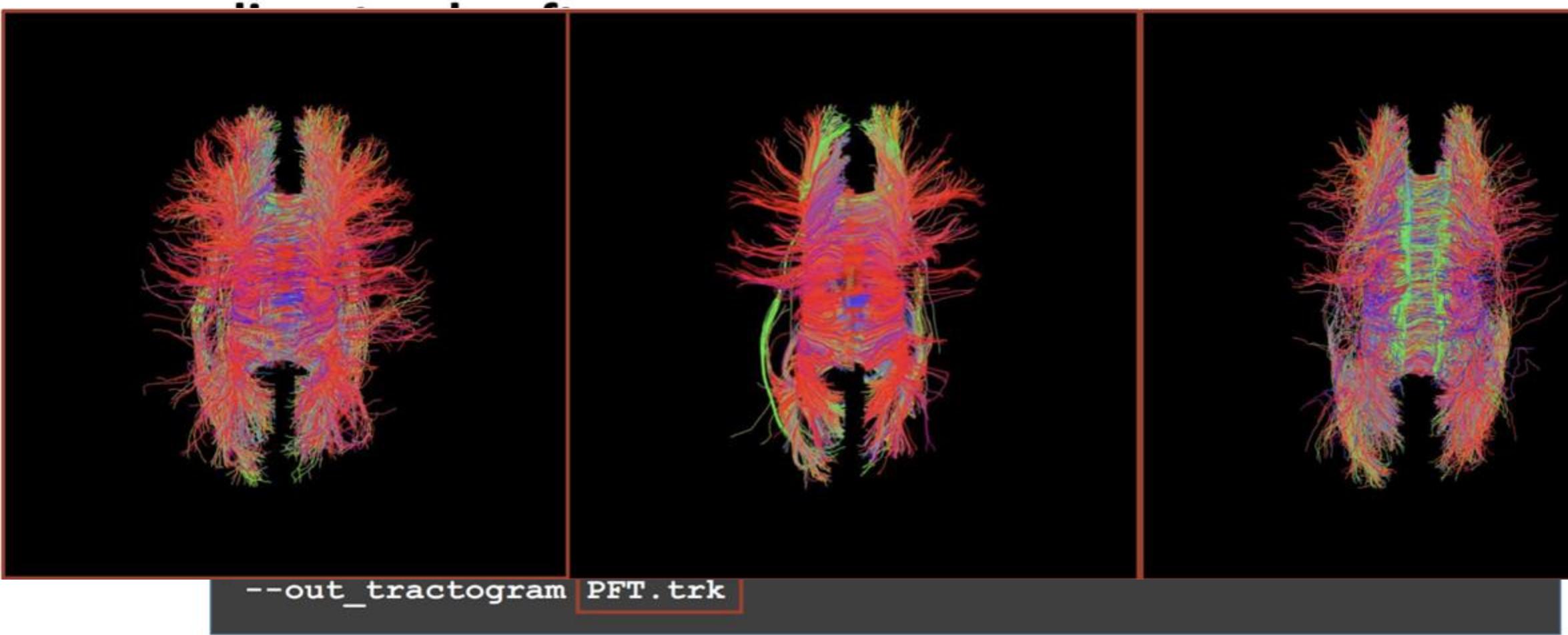


Maier-Hein, K.H., Neher, P.F., Houde, J.C. et al. The challenge of mapping the human connectome based on diffusion tractography. *Nat Commun* 8, 1349 (2017). <https://doi.org/10.1038/s41467-017-01285-x>

- **Images of the white matter orientation**
e.g. tensors, ODFs, fiber ODFs, peaks/maxima
- **Direction selection strategy - DirectionGetters**
e.g. highest value, probabilistic approaches
- **Tracking Mask – StoppingCriterion**
e.g. white matter volume -> estimated from the anatomical Image or DTI
- **Seeding Mask**
e.g. region of interest, white matter volume
- **Step size, maximum curvature and interpolation method**
e.g. nearest neighbour, tri-linear



→ Tractography



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→ Visualize Tractography results

Execution examples

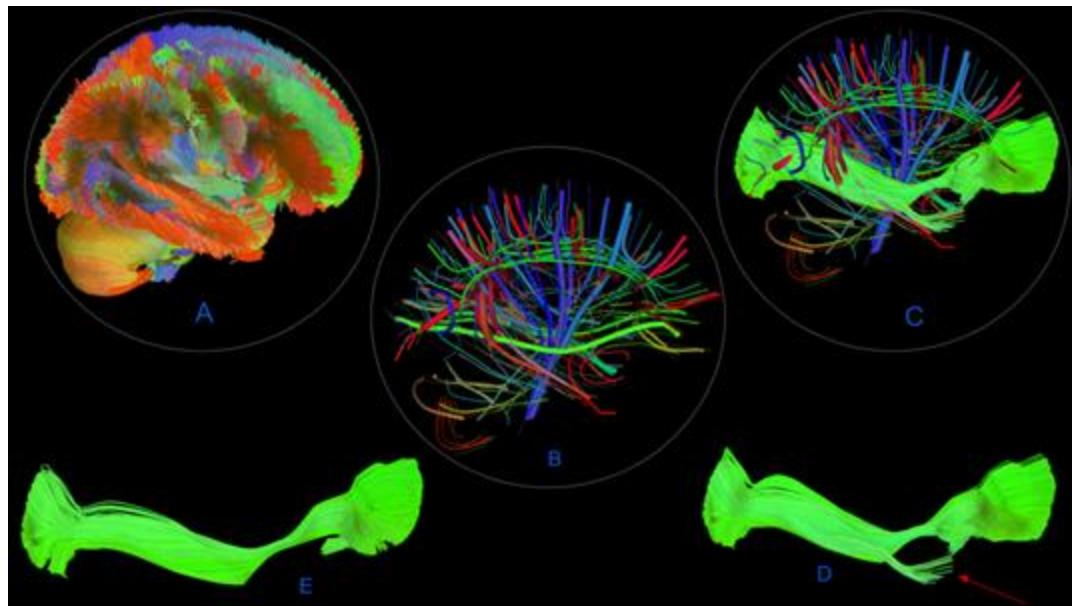
```
$ dipy_horizon tractogram.trk
```

```
$ dipy_horizon bundle1.trk bundle2.trk
```

```
$ dipy_horizon image.nii.gz
```

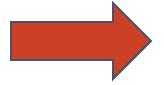
```
$ dipy_horizon tractogram.trk image.nii.gz --cluster --cluster_thr 15
```

```
$ dipy_horizon bundle1.trk bundle2.trk --cluster --cluster_thr 15
```

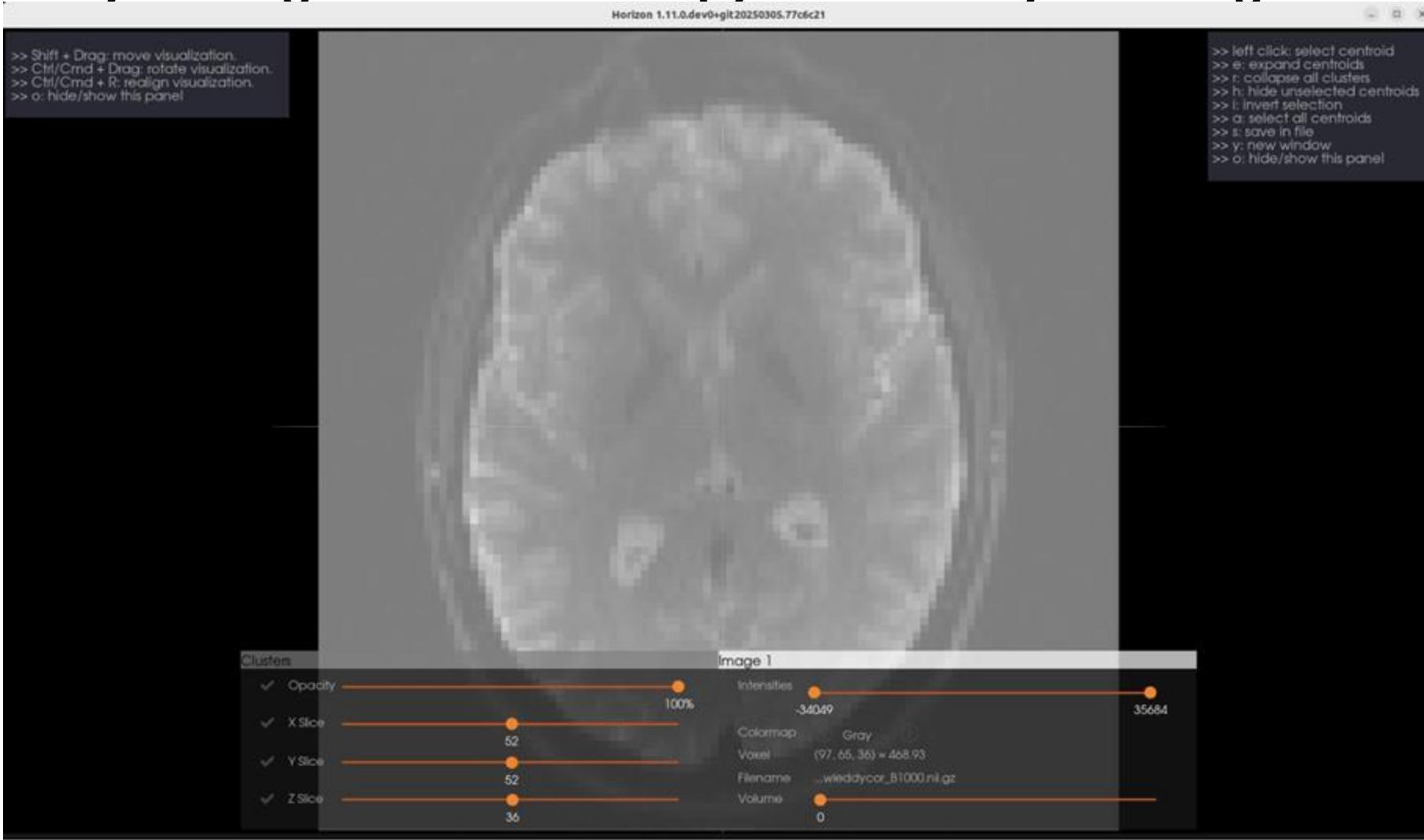


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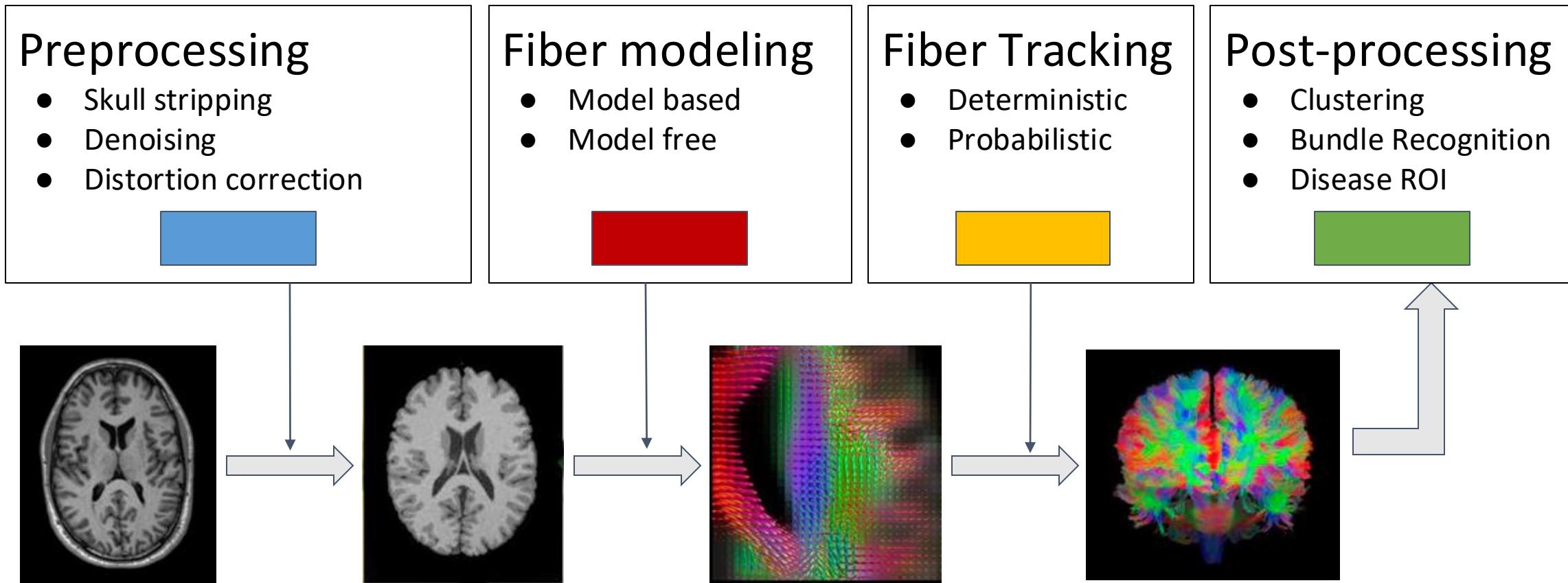
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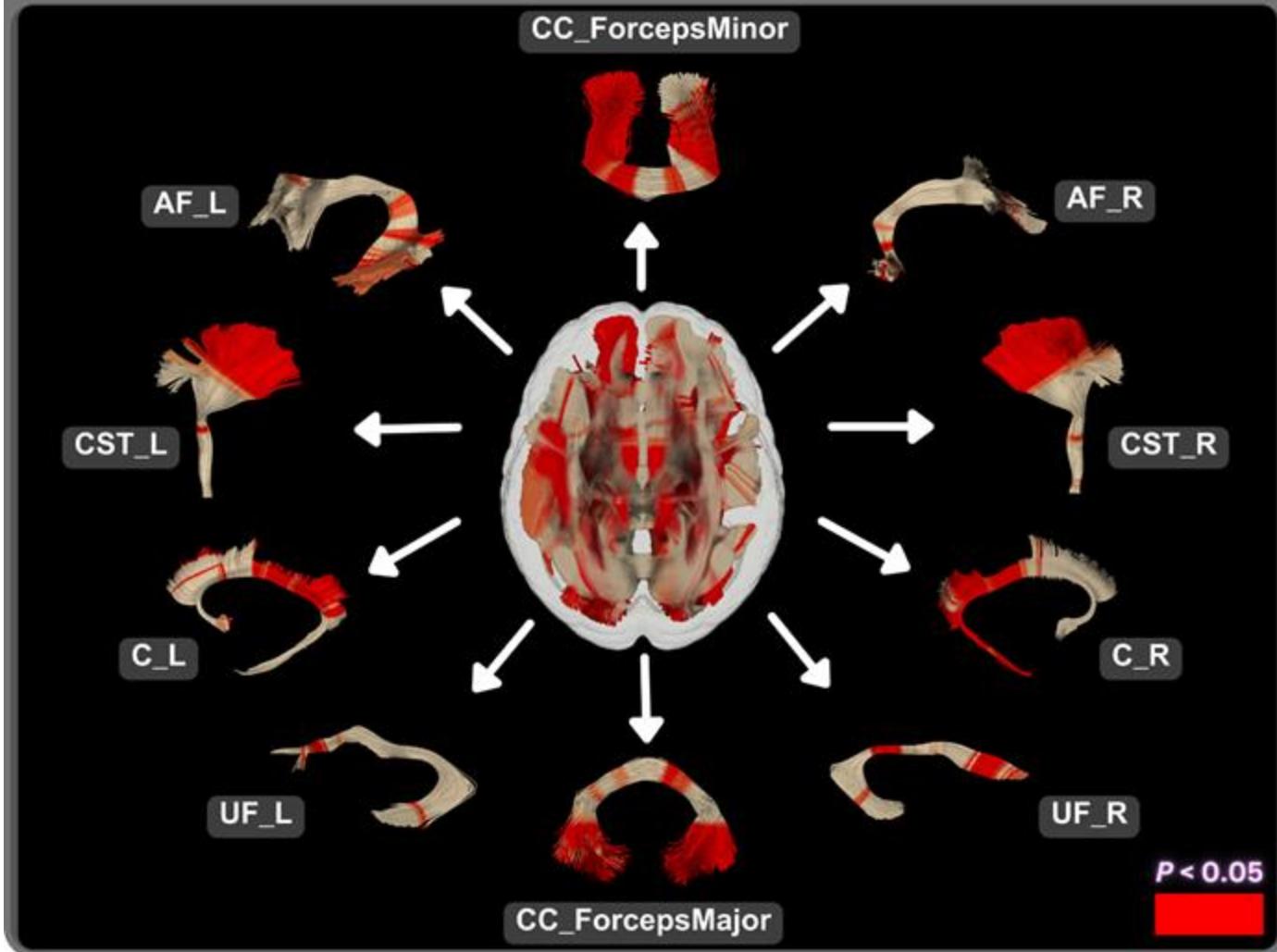
Visualize your original data: >>> dipy horizon my file.nii.gz



Post-Processing: Clustering Analytics



Strongest Signal Detected by Tau and MD Metric



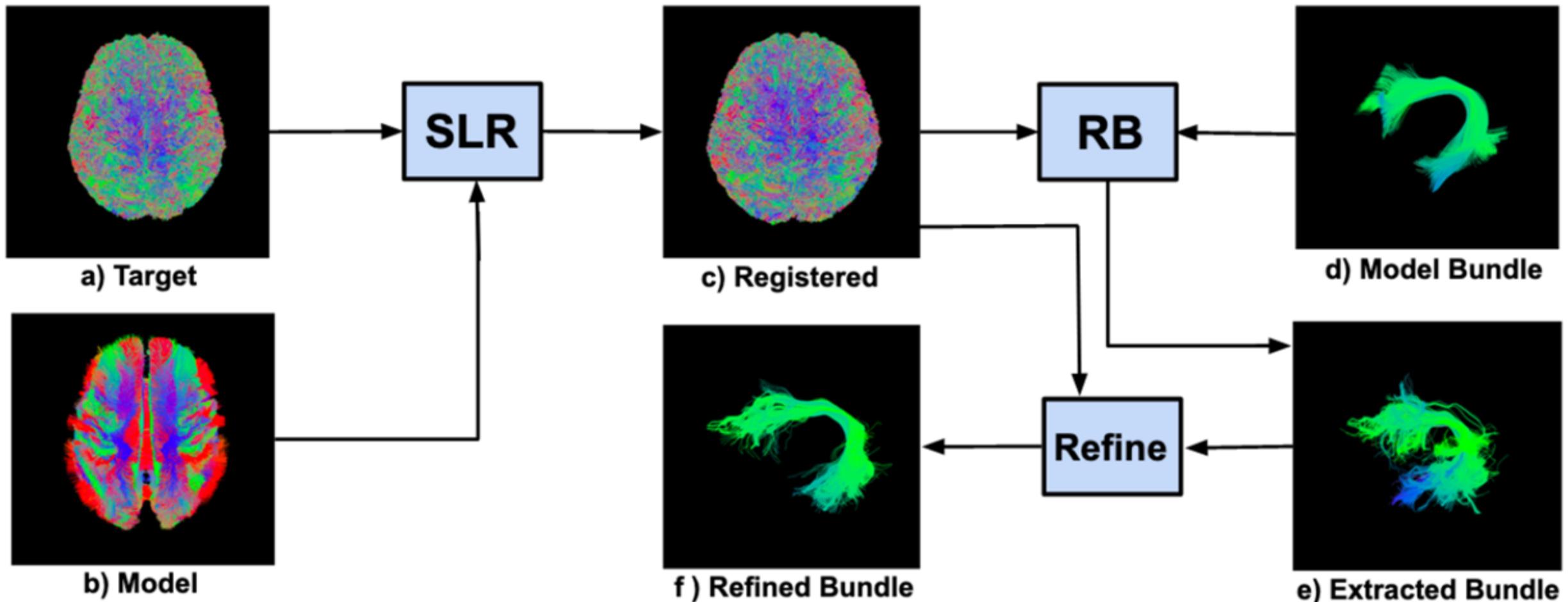
ADNI3 - 730 subjects

Chandio, B. Q., Villalon-Reina, J. E., Nir, T. M., Thomopoulos, S. I., Feng, Y., Benavidez, S., ... & Alzheimer's Disease Neuroimaging Initiative. (2024). Amyloid, Tau, and APOE in Alzheimer's Disease: Impact on White Matter Tracts. *PSB*, 2025



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→ Recognize bundle



Tractometry

Location

Significance

Detail

dipy_buan_profiles bundles/ subjects_small/ --out_dir "bundle_profiles"

C



dipy_buan_lmm "bundle_profiles/*" --out_dir "lmm_plots"

A

IFOF-D

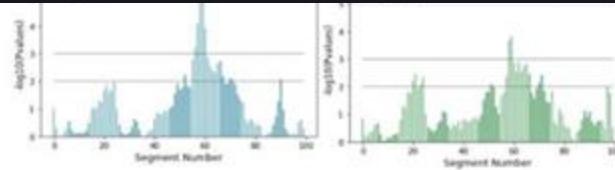
B

RD

D

IFOF-R RD-for-Dixk-38-42

dipy_buan_shapes subjects_small/ --out_dir "sm_plots"

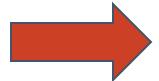


Chandio, BQ., et al. *Sci Rep* 10, 17149 (2020).



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 Utilities

```
>>> dipy_fetch my_data|list|all
>>> dipy_math "vol1+vol2" data1.nii.gz data2.nii.gz
>>> dipy_extract_b0 my_data.nii.gz
>>> dipy_extract_shell my_data.nii.gz
>>> dipy_extract_volume my_data.nii.gz
>>> dipy_mask my_data.nii.gz 0.5
>>> dipy_convert
>>> dipy_concatenate_tractogram
>>> dipy_pam2nifti ....
>>> ....
```



→ Documentation & Tutorial

The screenshot shows the DIPY documentation website. The top navigation bar includes links for Docs (highlighted with a purple border), Workshops, Community, and About. Below this, there are sections for Overview, Tutorials, Recipes, CLI / Workflows (highlighted with a red border), API, and CLI API (highlighted with a red border). The background features a large, stylized "fusion" logo.

In a terminal: \$ dipy_ ←TAB

or eg. dipy_info – help

The screenshot shows the DIPY Command Line Utilities Reference page for the `dipy_align_affine` command. The page has a dark theme with orange text highlights. It includes a Section Navigation sidebar with links to other commands like `dipy_align_syn`, `dipy_apply_transform`, etc. The main content area shows the command usage: `dipy_align_affine [OPTIONS] static_image_files moving_image_files`. It also lists Input Parameters (`static_image_files` and `moving_image_files`) and General Options. A note at the bottom says "Move to the folder with the data:".





What's Next ?



→ Continue to grow to achieve TRL 7-8 from our current status TRL 6.8

→ To do so:

→ Increase the number of DIPY Workflows

→ Introduces basic User Interfaces

→ Increased validation against clinical gold standards

→ BE PART of the COMMUNITY !!!

→ By providing feedback of your clinical need/challenges

→ By sharing data, building collaboration at every level



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March 16th – March 20th

Coming Soon

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Please enter your email

Notify Me

Notify me when the workshop registrations are available.

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March 17th - 21st

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▶ Previous Workshops

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DIPY

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Documentation at dipy.org