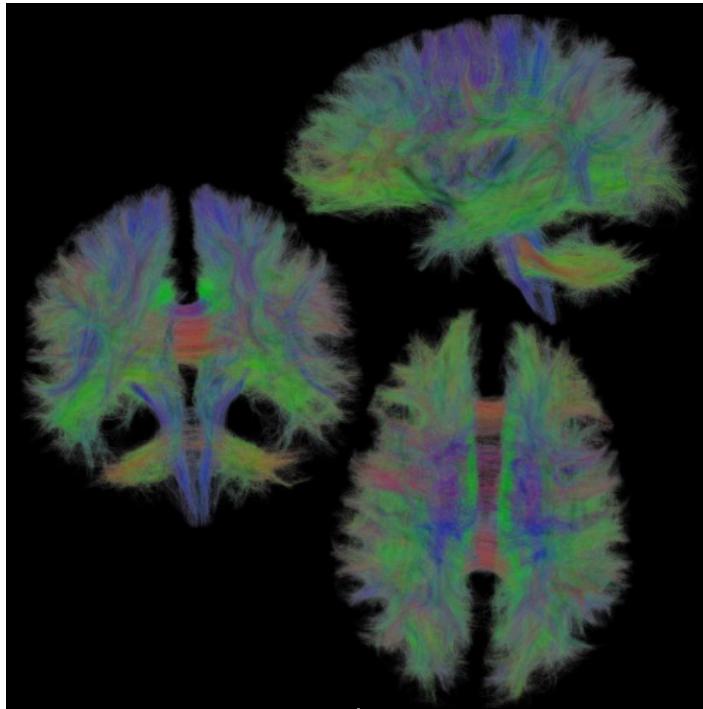




Lecture 1.2 – Diffusion and Tractography



Brain Dynamics on the Connectome
Summer School 2021

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DTU Compute, Technical University of Denmark

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École Polytechnique Fédérale de Lausanne

Lausanne, Switzerland

Danish Research Center for Magnetic Resonance

Hvidovre, Denmark

Brain dynamics on the Connectome
October 11th, 2021

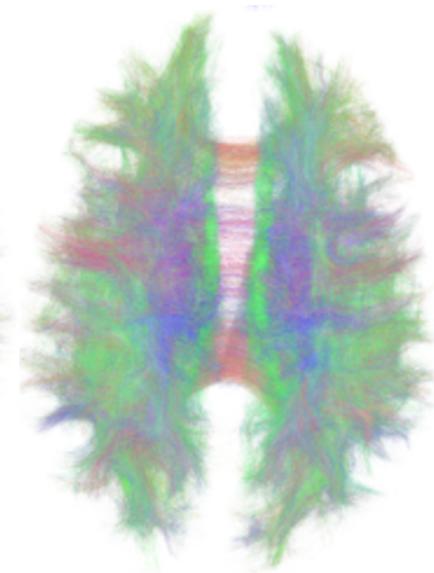
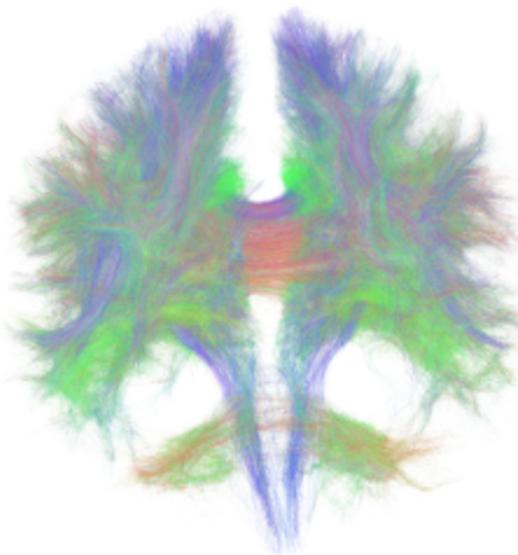
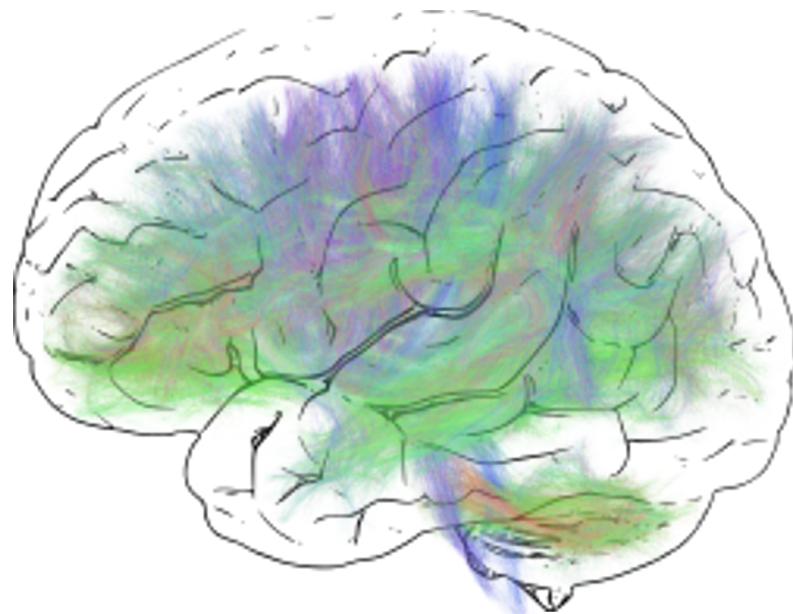


Everything into context: magnetic resonance imaging





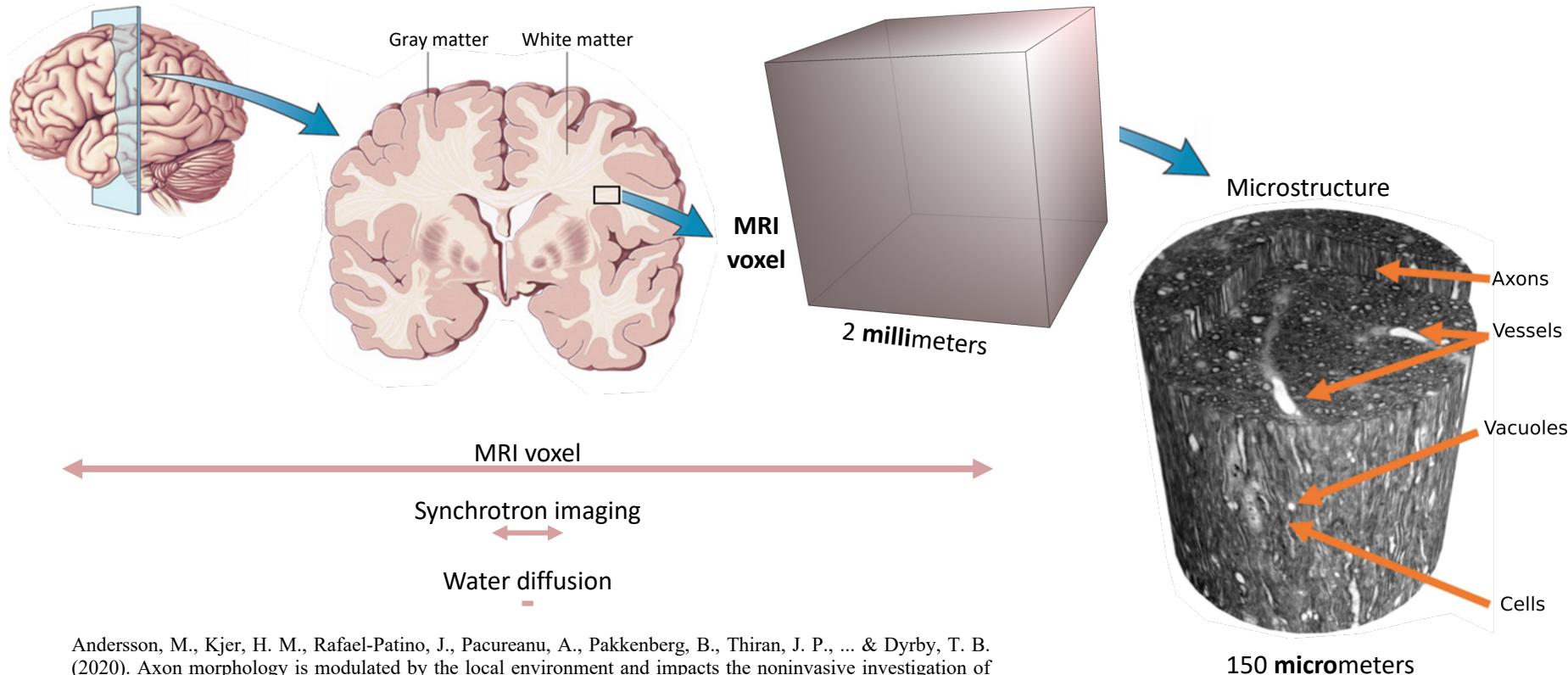
Non-invasive brain imaging through diffusion Magnetic Resonance Imaging (dMRI)



The key is to measure water diffusion



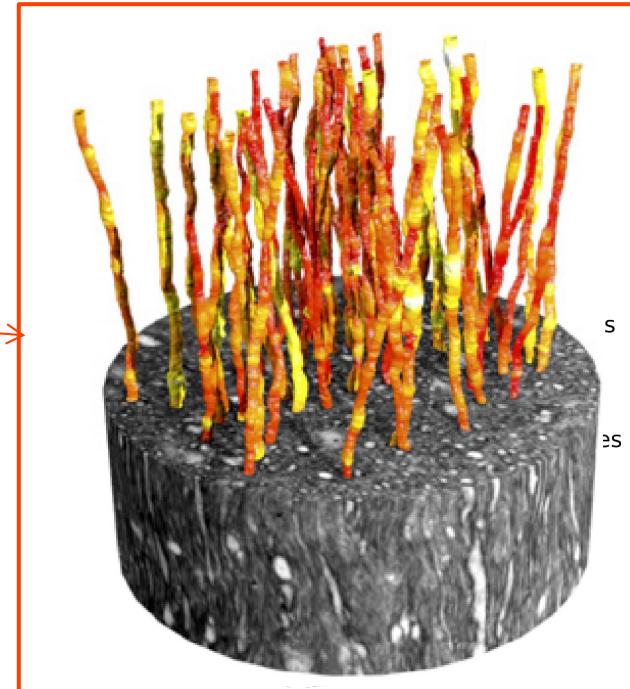
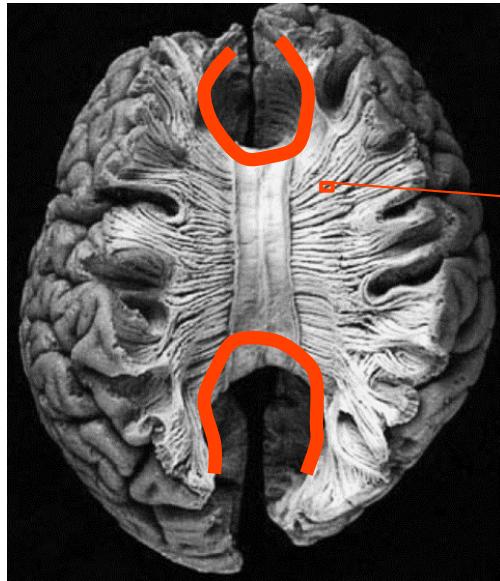
The origin of the diffusion signal: tissue's microstructure



Andersson, M., Kjer, H. M., Rafael-Patino, J., Pacureanu, A., Pakkenberg, B., Thiran, J. P., ... & Dyrby, T. B. (2020). Axon morphology is modulated by the local environment and impacts the noninvasive investigation of its structure–function relationship. *Proceedings of the National Academy of Sciences*, 117(52), 33649-33659.



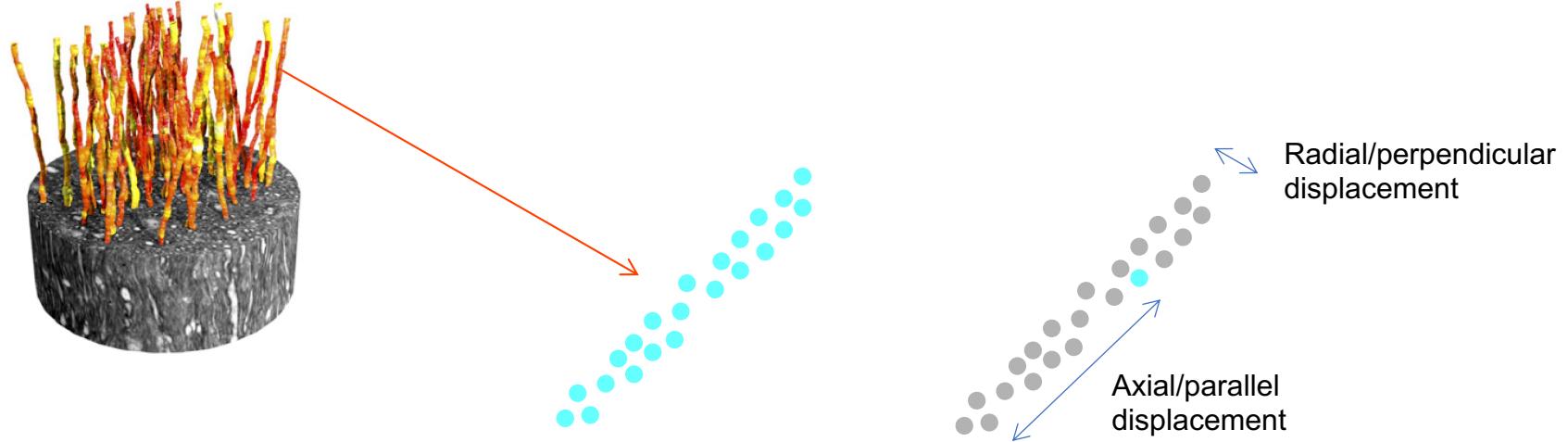
Let's focus on the major components of the white matter tissue: axons



Andersson, M., Kjer, H. M., Rafael-Patino, J., Pacureanu, A., Pakkenberg, B., Thiran, J. P., ... & Dyrby, T. B. (2020). Axon morphology is modulated by the local environment and impacts the noninvasive investigation of its structure–function relationship. *Proceedings of the National Academy of Sciences*, 117(52), 33649–33659.



Let's focus on the major components of the white matter tissue: axons

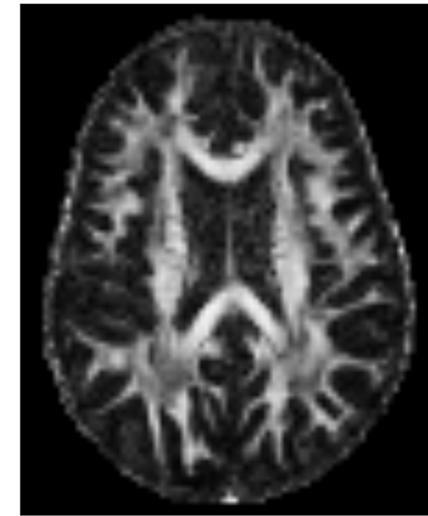
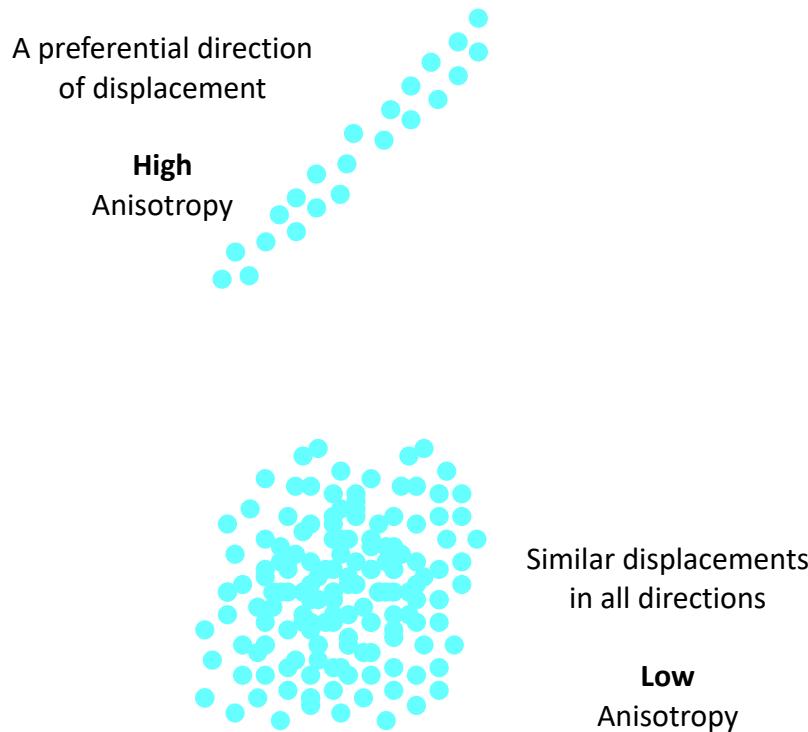


Radial/perpendicular displacement

Axial/parallel displacement



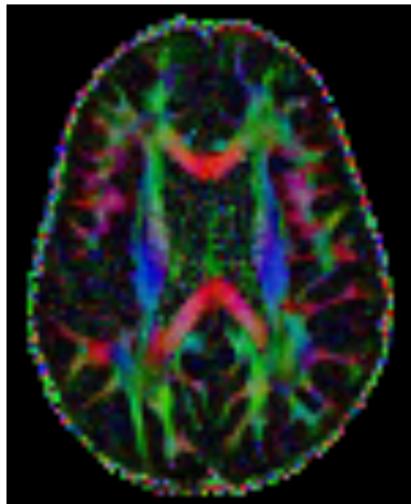
Fractional anisotropy (Diffusion Tensor Imaging)



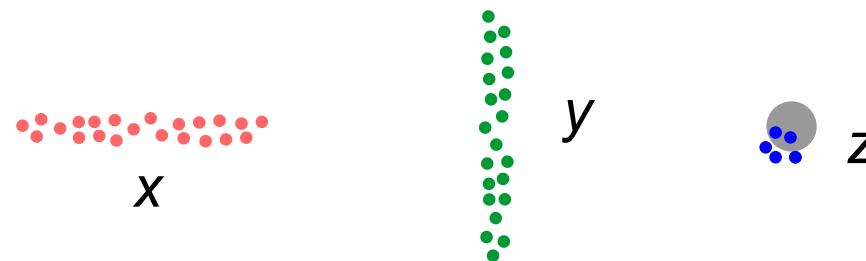
FA



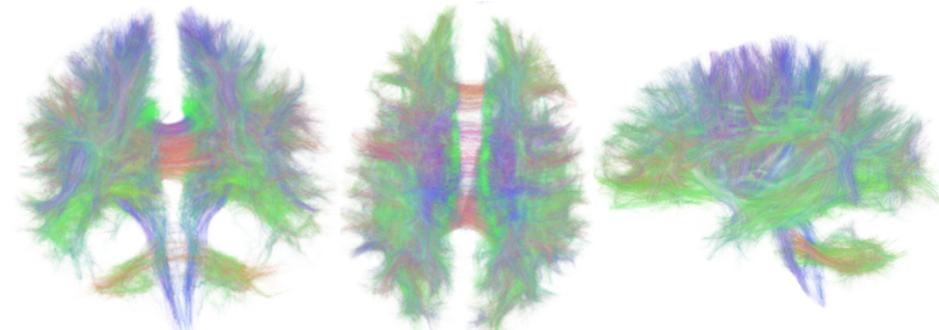
What about tractography?

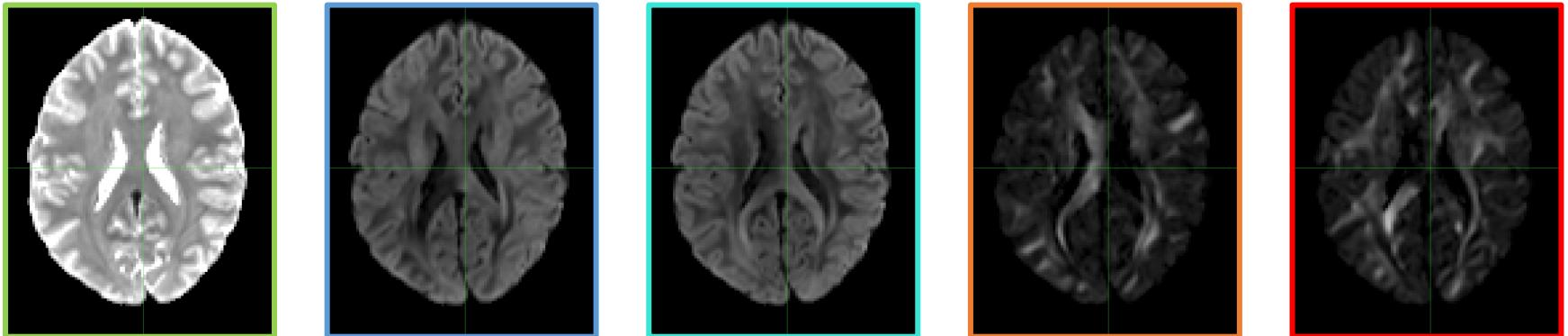
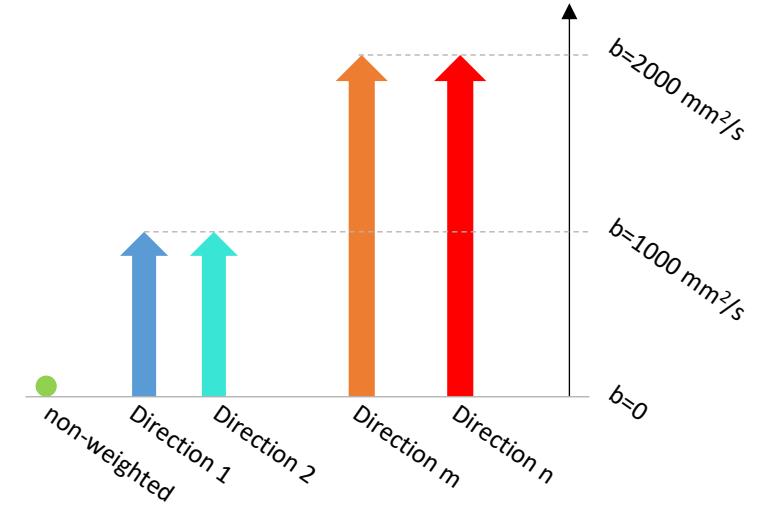
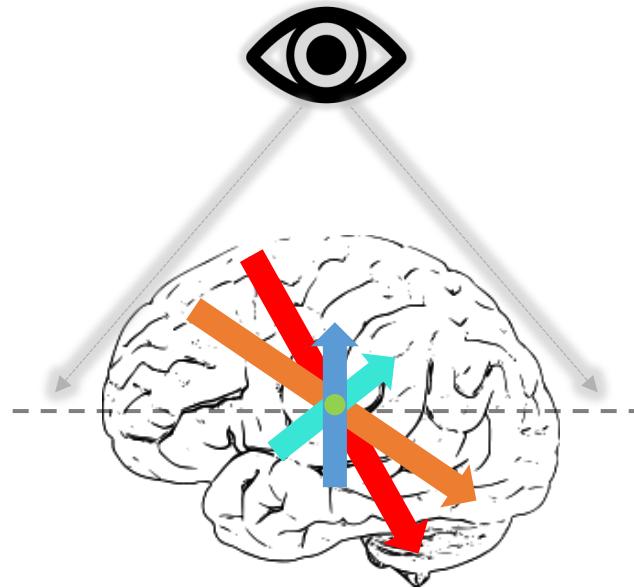


Colored FA



Directional information
about the displacement







How does it look in practice? The image metadata



bvals



bvecs

*bvals - Notepad

```
File Edit Format View Help
0
1000
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Ln 28, Col 2      100%    Unix (LF)      UTF-8
```

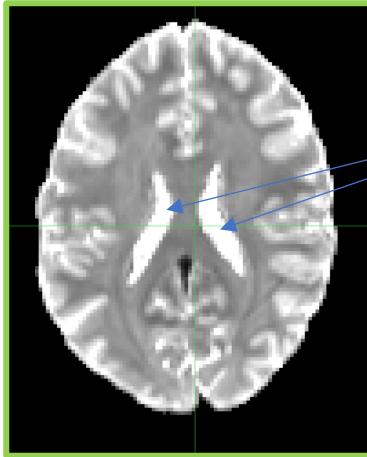
*bvecs - Notepad

```
File Edit Format View Help
0.000000 0.000000 0.000000
-0.468081 0.011522 -0.883610
0.386073 -0.257940 0.885672
-0.957682 0.126019 -0.258777
0.955580 -0.125837 0.266519
-0.521404 0.038909 0.852422
0.420465 0.056151 -0.905569
0.451700 0.891596 -0.031998
-0.291975 -0.951061 0.101157
-0.057846 0.812421 -0.580195
-0.119525 -0.824408 0.553231
0.200110 -0.377191 -0.904258
-0.198522 0.374233 0.905836
0.761319 0.555922 -0.333682
0.000000 0.000000 0.000000
-0.843221 -0.496226 0.206732
0.866279 0.298319 0.400708
-0.900413 -0.361138 -0.242559
-0.535321 -0.730931 0.423286
0.376557 0.794366 -0.476642
0.141731 -0.968735 0.203631
0.035843 0.985904 -0.163428
0.635826 -0.282588 -0.718241
-0.582269 0.494758 0.645119
0.830474 0.099351 -0.548126
-0.762316 -0.280115 0.583446
0.094249 -0.959362 -0.265972
-0.242928 0.946413 0.212810
0.000000 0.000000 0.000000
Ln 1, Col 1      100%    Unix (LF)      UTF-8
```



Remember, the presence of diffusion attenuates the signal

non-weighted

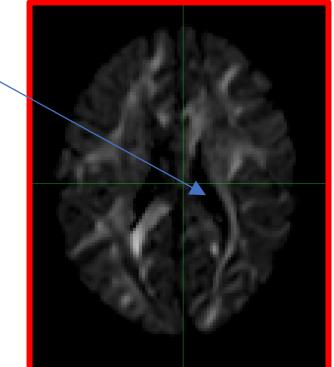
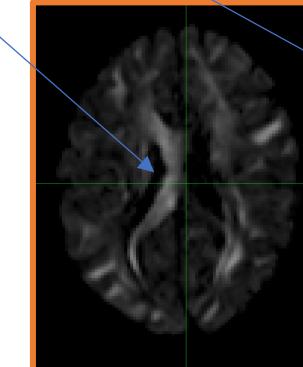
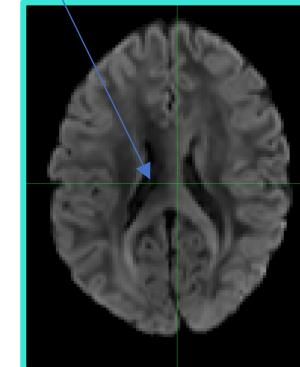
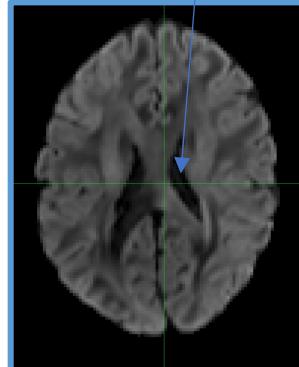


Ventricles: pools of “free” water (cerebrospinal fluid)

- diffusion is high, because water is not restricted by actual tissue structures
- Diffusion is isotropic, as it occurs equally along all directions
- They appear bright, because there is a high density of water “particles”

Indeed, no matter what is the diffusion direction, they always appear dark!

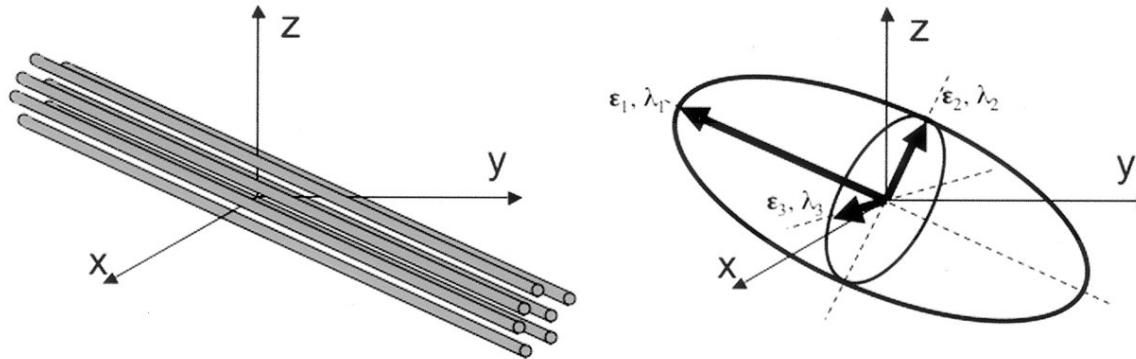
diffusion-weighted





How do we combine the images into a meaningful physical object?

Having the data, the b-values, and the b-vectors we can calculate the Diffusion Tensor



Jellison, B. J., Field, A. S., Medow, J., Lazar, M., Salamat, M. S., & Alexander, A. L. (2004). Diffusion tensor imaging of cerebral white matter: a pictorial review of physics, fiber tract anatomy, and tumor imaging patterns. American Journal of Neuroradiology, 25(3), 356-369.



<https://dipy.org/>

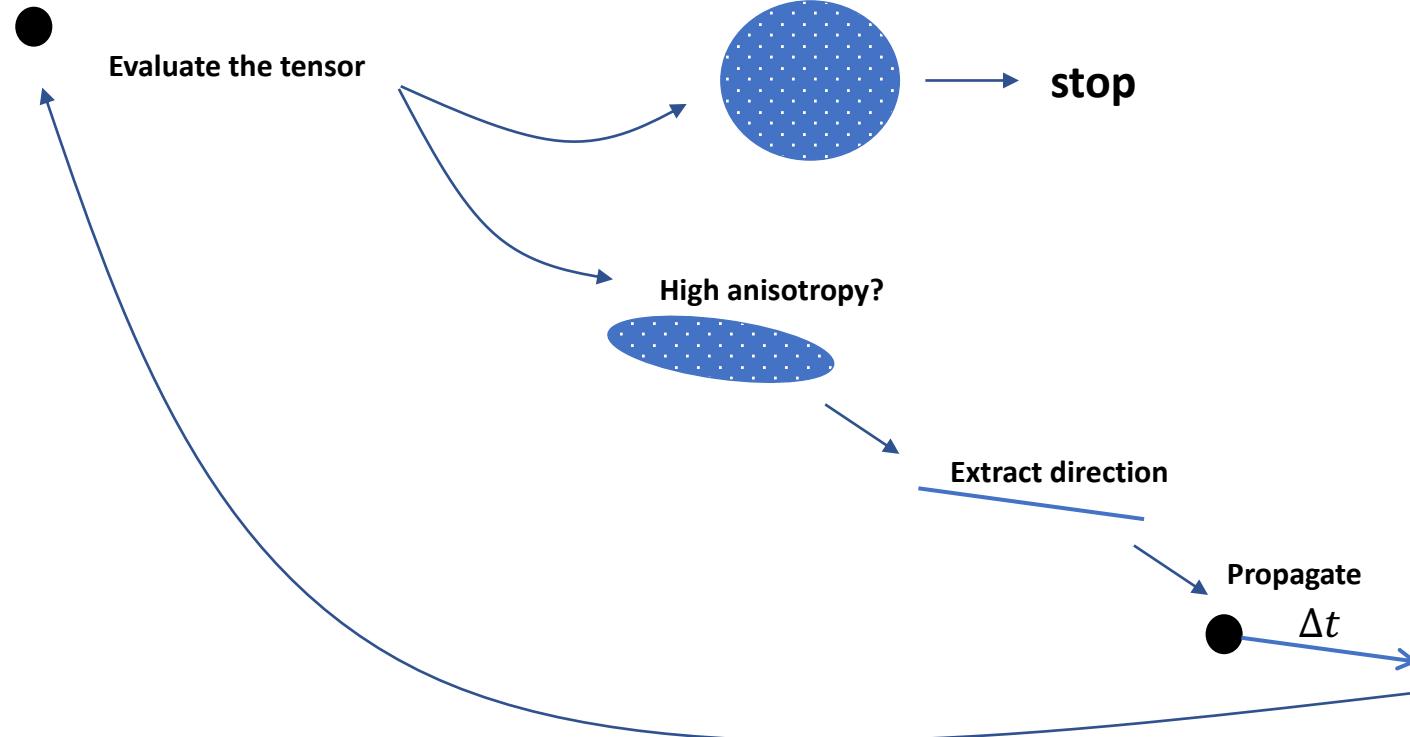
Diffusion Tensor Deterministic tractography

Mori, S., Crain, B. J., Chacko, V. P., & Van Zijl, P. C. (1999). Three-dimensional tracking of axonal projections in the brain by magnetic resonance imaging. *Annals of Neurology: Official Journal of the American Neurological Association and the Child Neurology Society*, 45(2), 265-269.



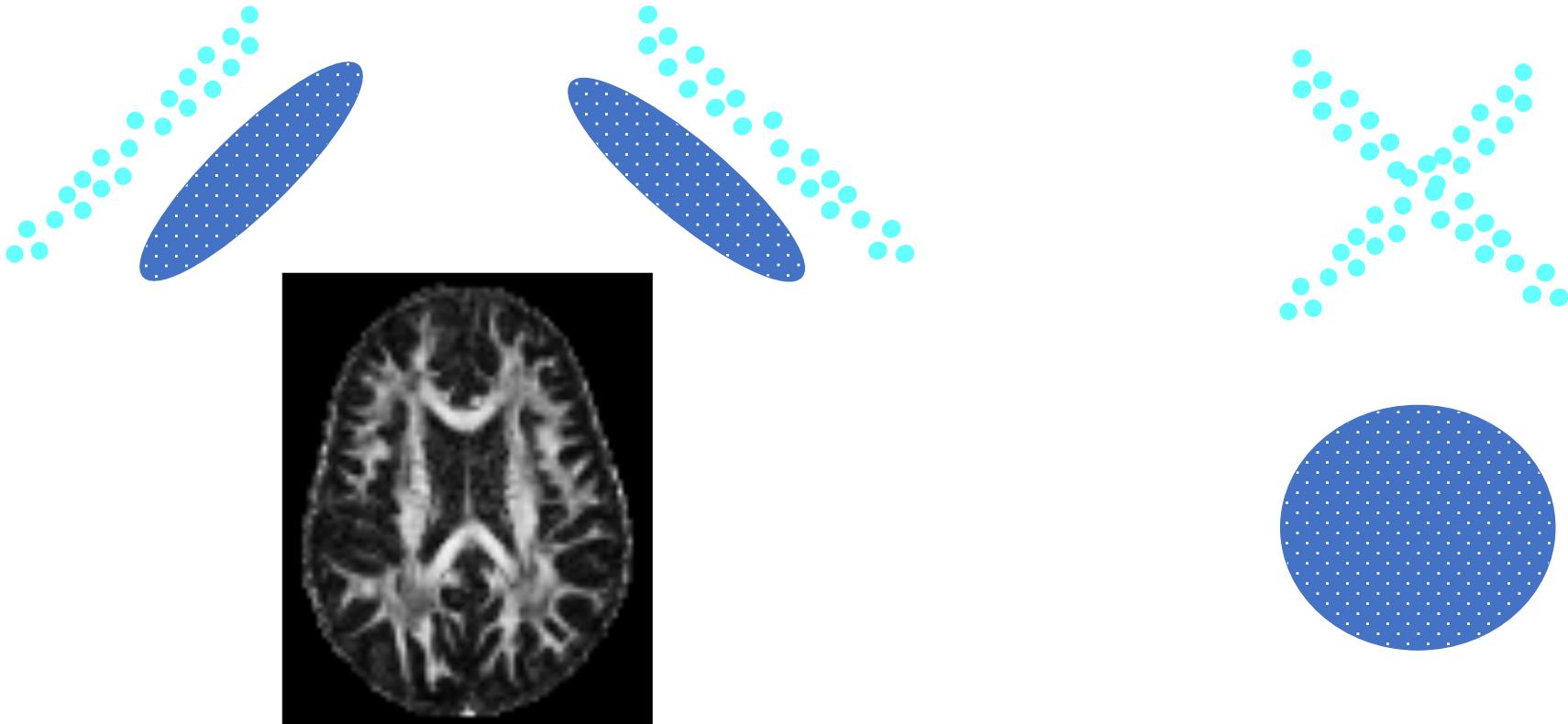
How to

Start at a point





Issues



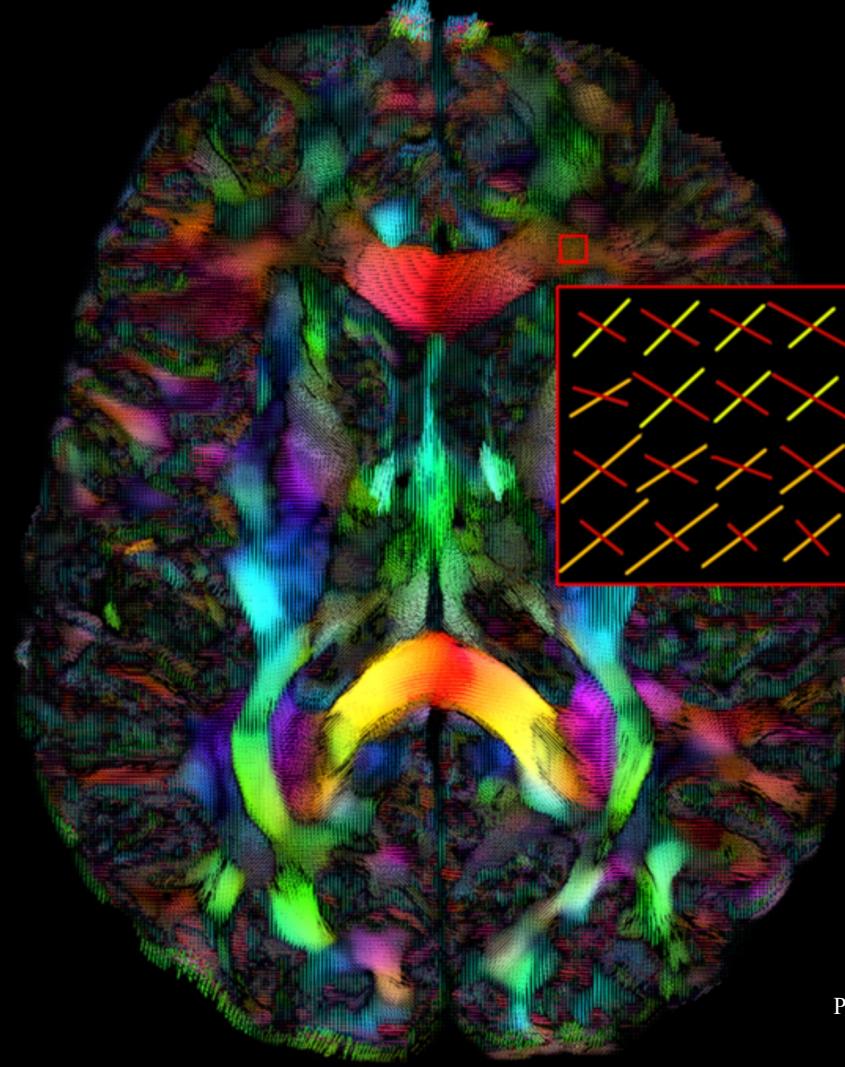
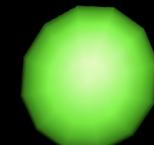
HARDI
fODF



HARDI
peaks



DTI

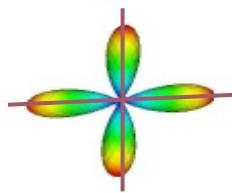


Credits:
Maxime Chamberland, PhD
Prof. Maxime Descoteaux, PhD

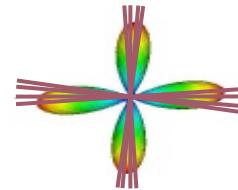


How good is tractography?

Deterministic tractography



Probabilistic tractography



Ground truth



100/0%

DTI
deterministic



20/3%

HARDI
deterministic



42/24%

HARDI
probabilistic

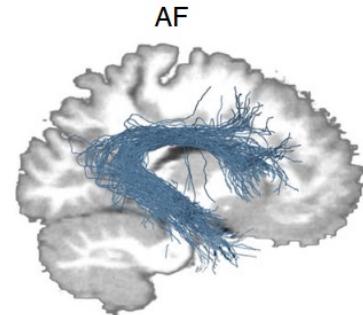


83/68%

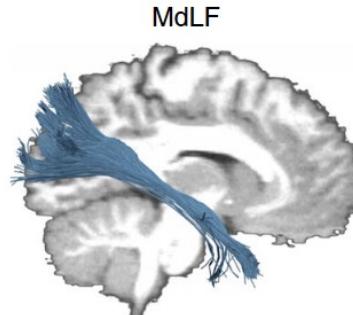
Maier-Hein, K. H., Neher, P. F., Houde, J. C., Côté, M. A., Garyfallidis, E., Zhong, J., ... & Descoteaux, M. (2017). The challenge of mapping the human connectome based on diffusion tractography. *Nature communications*, 8(1), 1-13.



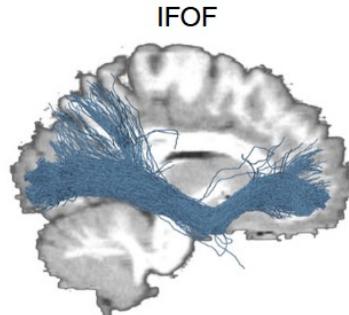
Invalid bundles



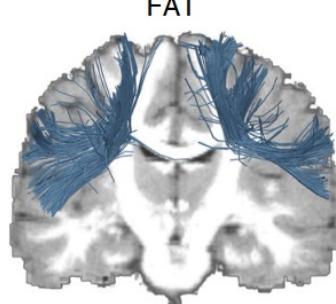
95% of submissions



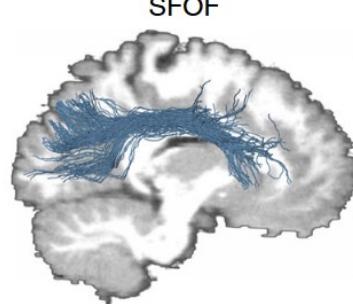
95% of submissions



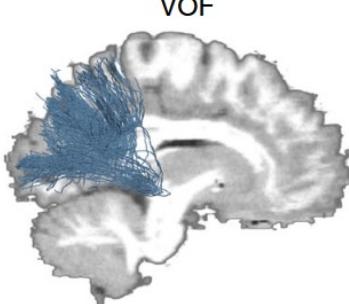
85% of submissions



88% of submissions



81% of submissions

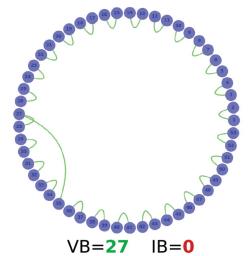
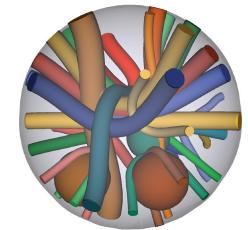


81% of submissions

Maier-Hein, K. H., Neher, P. F., Houde, J. C., Côté, M. A., Garyfallidis, E., Zhong, J., ... & Descoteaux, M. (2017). The challenge of mapping the human connectome based on diffusion tractography. *Nature communications*, 8(1), 1-13.



Tractogram filtering/optimization: false positive reduction



<https://github.com/daducci/COMMIT>

Ocampo-Pineda, M., Schiavi, S., Rheault, F., Girard, G., Petit, L., Descoteaux, M., & Daducci, A. (2021). Hierarchical microstructure informed tractography. *Brain connectivity*, 11(2), 75-88.

Docs » Connectome Mapper 3
Edit on GitHub

Connectome Mapper 3

Latest released version: v3.0.0-RC4

This neuroimaging processing pipeline software is developed by the Connectomics Lab at the University Hospital of Lausanne (CHUV) for use within the SNF Sinergia Project 170873, as well as for open-source software distribution. Source code is hosted on [GitHub](#).

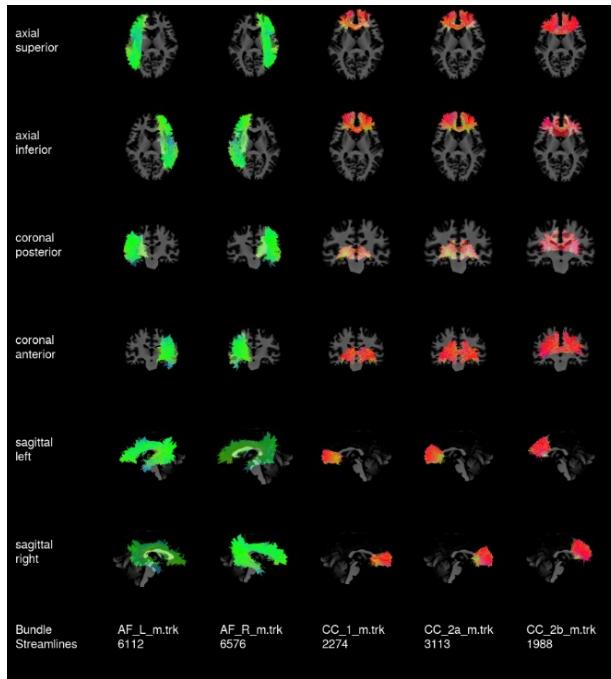
release v3.0.0-RC4 release date March DOI 10.5281/zenodo.4587906
docker v3.0.0-RC4 docker pulls 1.3k circleci passing coverage
docs passing code quality !

Smith, R. E., Tournier, J. D., Calamante, F., & Connelly, A. (2013). **SIFT**: Spherical-deconvolution informed filtering of tractograms. *Neuroimage*, 67, 298-312.



Separate/recognize bundles in your tractogram

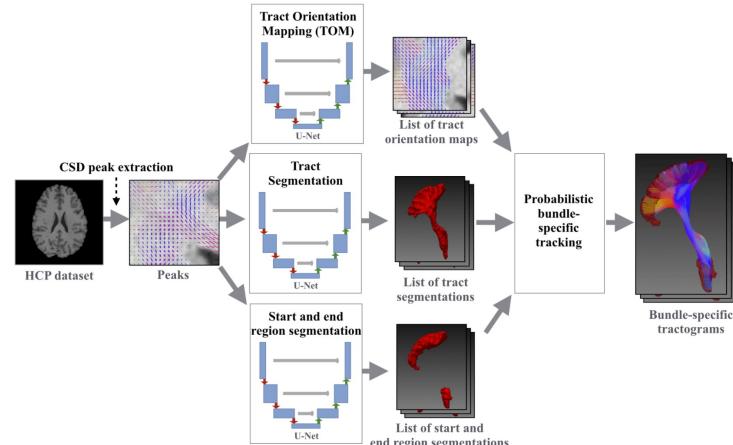
RecoBundleX



https://scil-documentation.readthedocs.io/en/latest/our_tools/recobundles.html#

Rheault, F., Poulin, P., Caron, A. V., St-Onge, E., & Descoteaux, M. (2020). Common misconceptions, hidden biases and modern challenges of dMRI tractography. *Journal of neural engineering*, 17(1), 011001.

TractSeg



<https://github.com/MIC-DKFZ/TractSeg>

Wasserthal, J., Neher, P., & Maier-Hein, K. H. (2018). TractSeg-Fast and accurate white matter tract segmentation. *NeuroImage*, 183, 239-253.



Tools (not only for tractography)

https://dipy.org/documentation/1.1.1/examples_built/reconst_csd/

DIPY

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Reconstruction with Constrained Spherical Deconvolution

Reconstruction with Constrained Spherical Deconvolution

- Reconstruction with Constrained Spherical Deconvolution
- References

This example shows how to use Constrained Spherical Deconvolution (CSD) introduced by Tournier et al. [Tournier2007]. This method is mainly useful with datasets with gradient directions acquired on a spherical grid.

The basic idea with this method is that if we could estimate the response function of a single fiber then we could deconvolve the measured signal and obtain the underlying fiber distribution.

In this way, the reconstruction of the fiber orientation distribution function (FOD) in CSD involves two steps:

1. Estimation of the fiber response function
2. Use the response function to reconstruct the FOD

Let's first load the data. We will use a dataset with 10 b0s and 150 non-b0s with b-value 2000.

```
import numpy as np
from dipy.core.gradients import gradient_table
from dipy.io.image import load_nifti
from dipy.io.gradients import read_bvals_bvecs
from dipy.io.image import load_nifti
hardi_bval_fname, hardi_bvec_fname = get_fnames('stanford_hardi')
data, affine = load_nifti(hardi_bval_fname)
bvals, bvecs = read_bvals_bvecs(hardi_bval_fname, hardi_bvec_fname)
gtab = gradient_table(bvals, bvecs)
```

<https://github.com/AthenaEPI/dmipy>

Fibre FODs with Anisotropy Index background

Notice that in white matter the FODs are nicely shaped and we have a high A_i , but in non-white matter they are very noisy and prominent. This is because the response function that we provided does not resemble the data in these areas, and we therefore get a non-sensical result, which is especially detrimental in partial-volumed voxels at the edge of the ventricles. In the following Multi-Compartment CSD example we will address this.

Multi-Shell Multi-Compartment CSD

DMipy allows to estimate multiple compartment kernels at the same time (i.e., multi-compartment CSD). The only limitation is that we only allow for one anisotropic kernel, like the Zeppelin kernel, and any number of isotropic compartments, like a Gaussian Ball or Sphere, as long as all the kernel parameters are fixed.

For this example, let us insert both a Zeppelin and a Ball into the MultiCompartmentSphericalHarmonicModel to fit the white matter and CSF, respectively.

```
In [1]:= ball = gaussian_model(0.25ball)
model_mc = MultiCompartmentSphericalHarmonicModel(
    Zeppelin(ball), sh_order=3)
model_mc.set_parameter_name('sh_order')

Out[1]:= ['01zeppelin_1_lambda_par',
         '01zeppelin_1_lambda_perp',
         '02zeppelin_1_lambda_par',
         '02zeppelin_1_lambda_perp',
         'partial_volume',
         'sh_order',
         'sh_coeff']
```

Note that we must now fix both the Zeppelin's and the Ball's diffusivities. For now, let us fix the Ball's diffusivity to free-water and keep the Zeppelin's diffusivities as before.

```
In [12]:= mod_mc.set_re_fixed_parameter('01zeppelin_1_lambda_perp', lambda_perp)
mod_mc.set_re_fixed_parameter('01zeppelin_1_lambda_perp', lambda_perp)
mod_mc.set_re_fixed_parameter('01ball_1_lambda_perp', 3e-0)
```

<https://www.mrtrix.org/>

Fibre density and cross-section - Single-tissue CSD

Docs Edit on GitHub

Fibre density and cross-section - Single-tissue CSD

This tutorial explains how to perform fibre-based analysis of fibre density and cross-section [Jaffray2017] using single-tissue spherical deconvolution. We note that high b-value (2000/mm²) is recommended to aid the interpretation of apparent fibre density (AFD) being related to the intra-axonal space. See [Jaffray2012] for more details about single-tissue AFD.

All steps in this tutorial are written in shell. All the commands are being run on a cohort of images, and make extensive use of the `for` script to simplify batch processing. If you are running this on your own machine, you will need to copy the training dataset, or repackage with one directory identifying each subject, and all files within identifying the image type, to processing step outcome. For example:

```
for sub in subjects; do
    # Run the script
    ./fibre_density_and_cross_section.sh $sub
done
```

Notes

All commands at the start of this tutorial are run from the `subjects` path. From the step where tractography is performed on the template onwards, we change directory to the `template` path.

For all Mifits scripts and commands, additional information on the command usage and available command-line options can be found by invoking the command with the `--help` option.

Pre-processing steps

If denoising and/or Gibbs ringing removal are performed as part of the preprocessing, they must be performed prior to any other processing steps; most other processing steps, in particular those that involve interpolation of the data, will invalidate the original properties of the image data that are exploited by denoising and ringing at this stage, and would render the result prone to errors.

If denoising is included, it's performed at the first step:

```
for sub in subjects; do
    denoise.sh $sub
done
```

If Gibbs ringing removal is included, it follows immediately after:

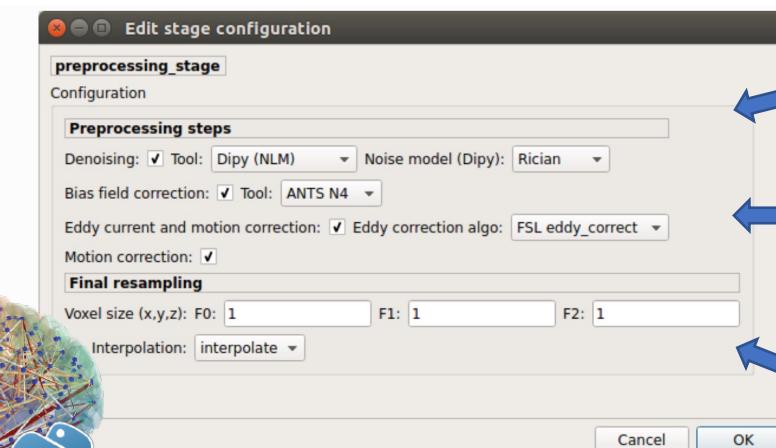
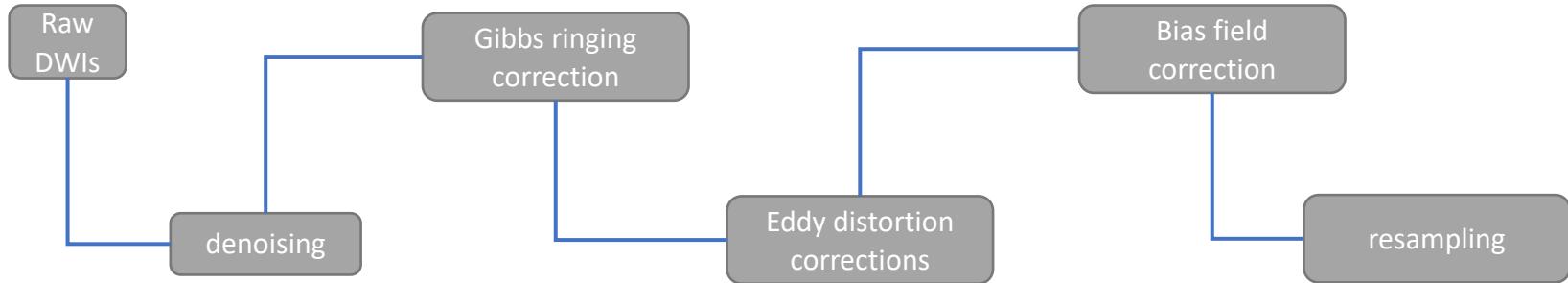
```
for sub in subjects; do
    denoise.sh $sub
    denoise_gibbs.sh $sub
done
```

If `repack` is used, it follows immediately after:

```
for sub in subjects; do
    denoise.sh $sub
    denoise_gibbs.sh $sub
    repack.sh $sub
done
```



Before tractography

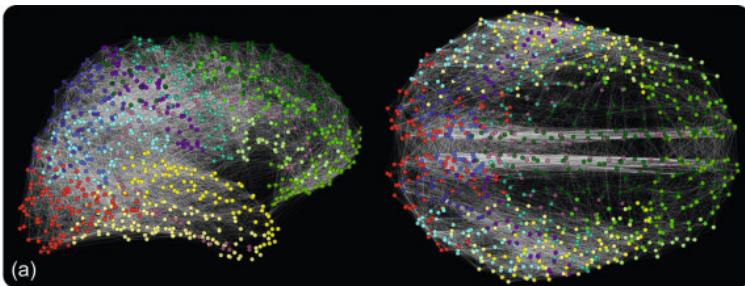


Connectome Mapper 3

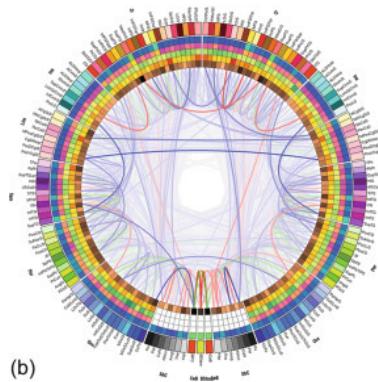


Using tractography to build the connectome

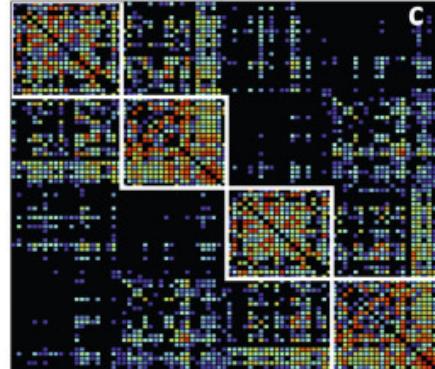
Cortical parcellation



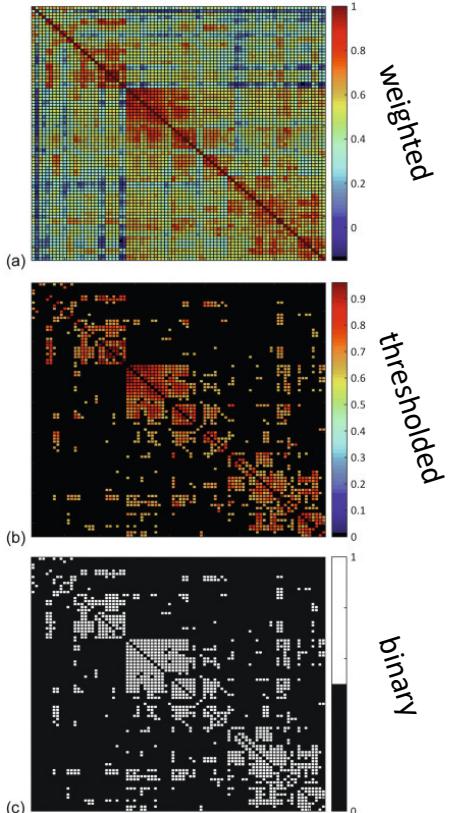
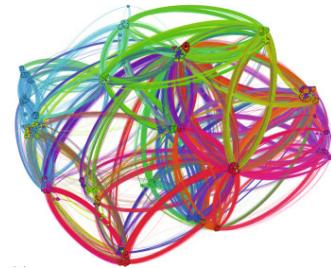
Connectogram



Structural connectivity matrix



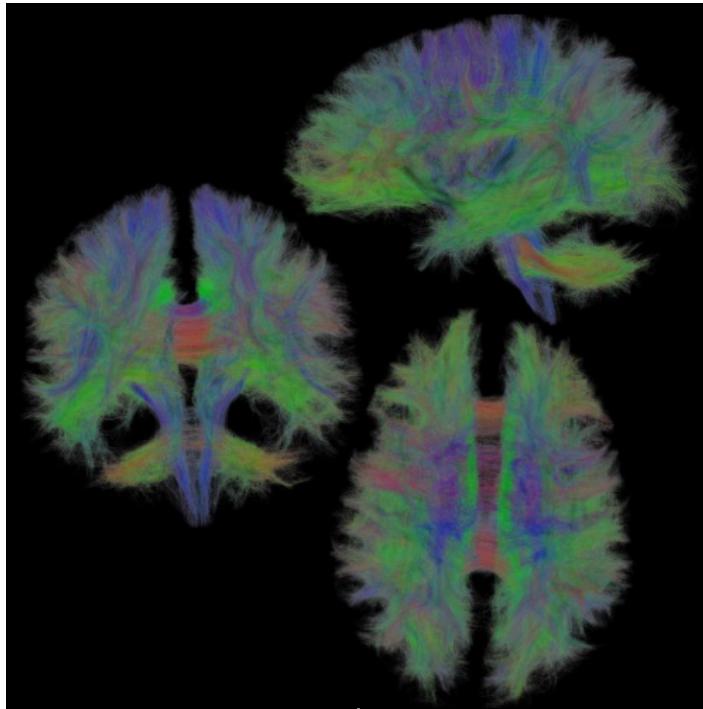
Functional connectivity
(fMRI, EEG, MEG)



Chapter 3 - Connectivity Matrices and Brain Graphs,
Editor(s): Alex Fornito, Andrew Zalesky, Edward T. Bullmore,
Fundamentals of Brain Network Analysis,
Academic Press, 2016, Pages 89-113, ISBN 9780124079083,
<https://doi.org/10.1016/B978-0-12-407908-3.00003-0>.



Lecture 1.2 – Diffusion and Tractography



Brain Dynamics on the Connectome
Summer School 2021

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Lausanne, Switzerland

Danish Research Center for Magnetic Resonance

Hvidovre, Denmark

Thank you for your attention!