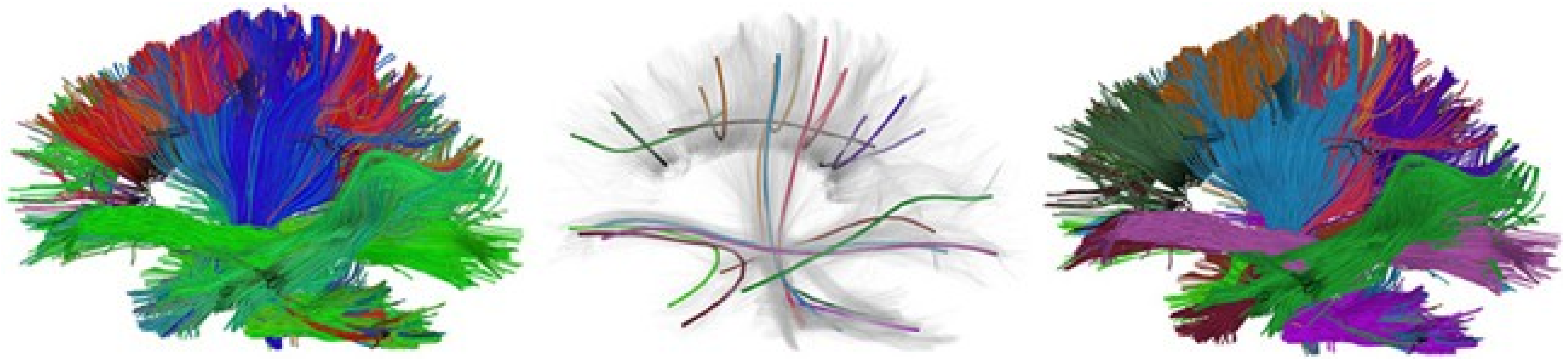
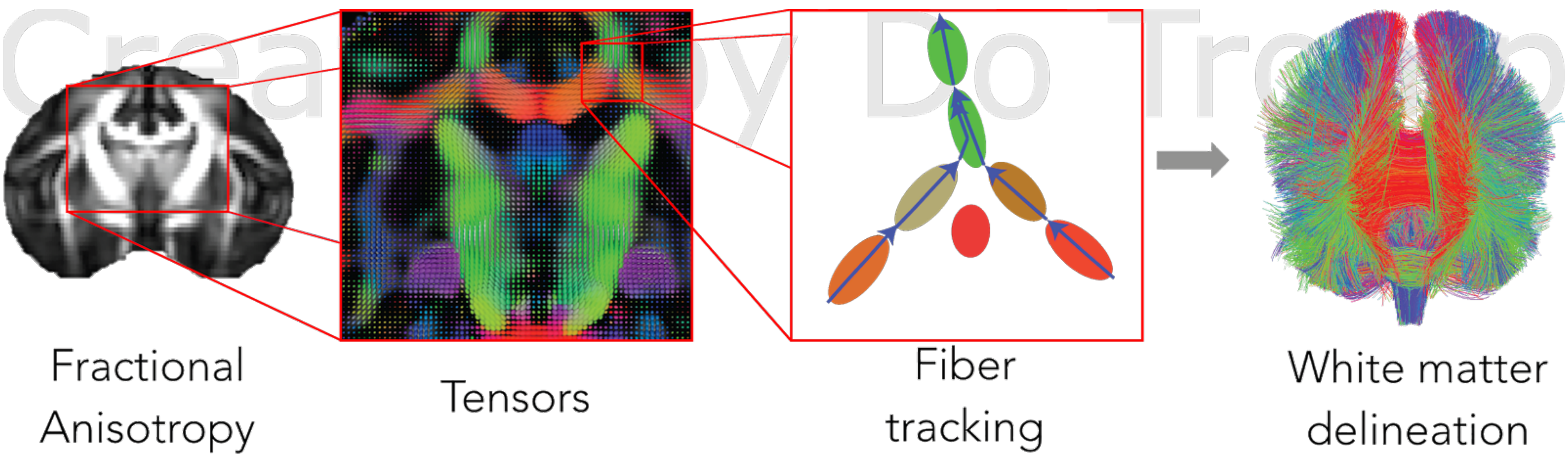
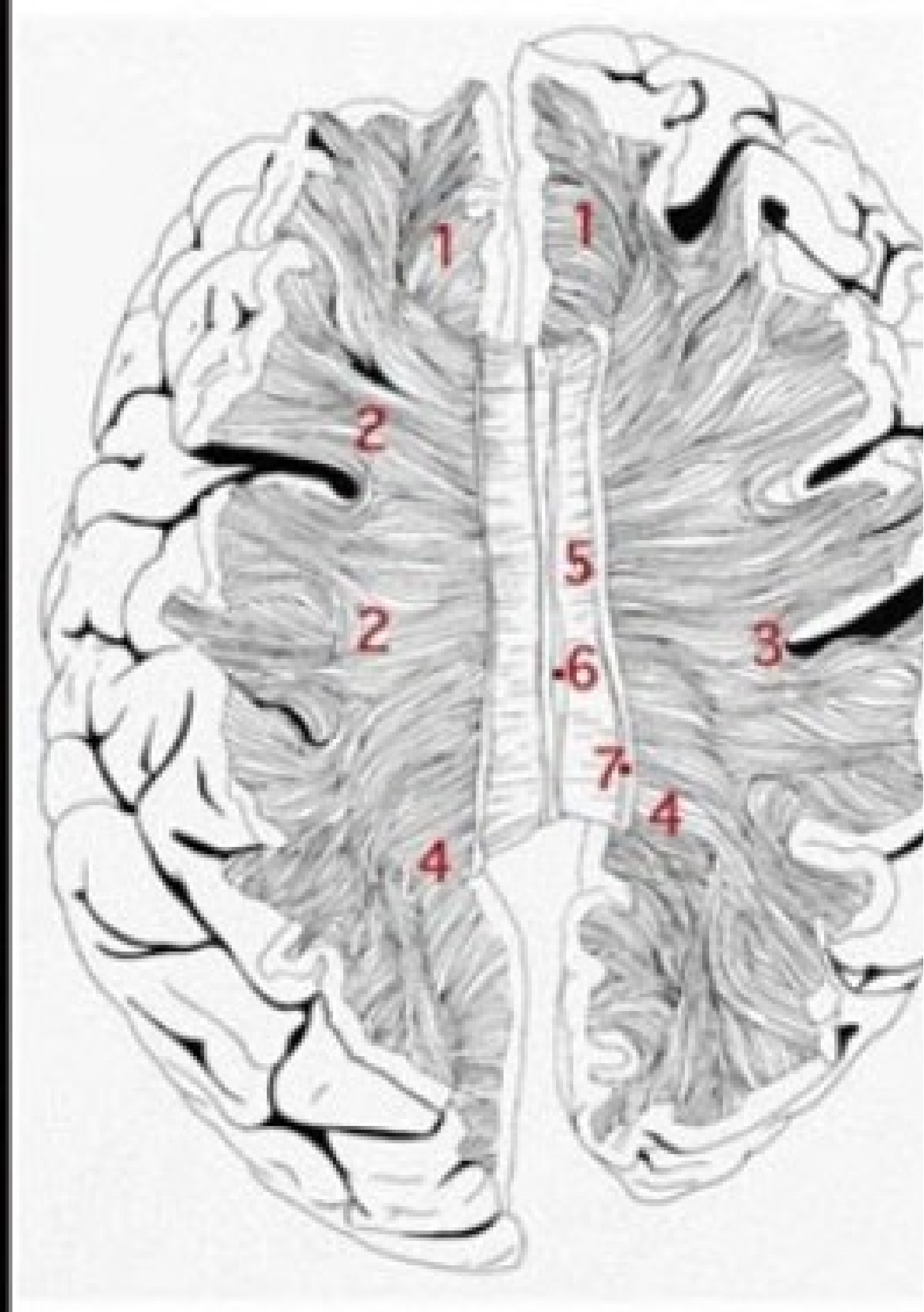
Tractography tutorial



Dr. Alessandro Crimi

Overview


Fractional Anisotropy
Tensors
Fiber tracking
White matter delineation



1
1
2
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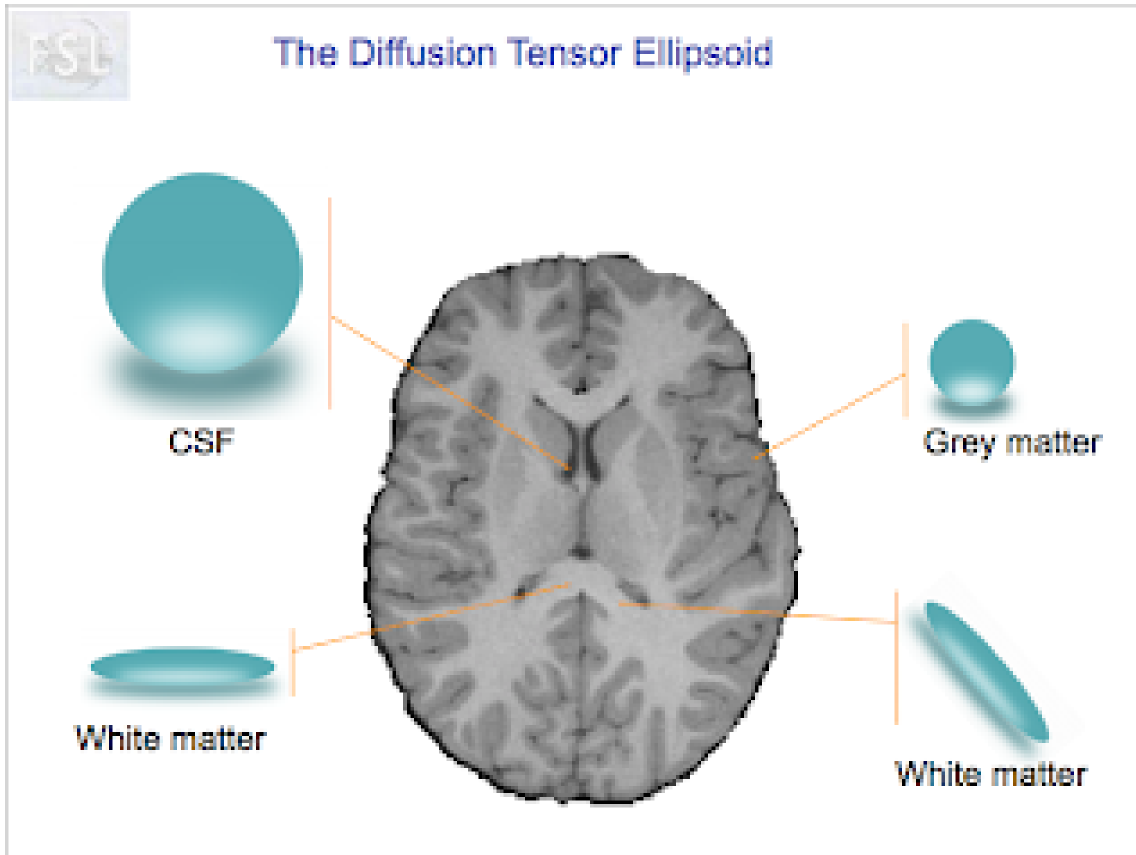
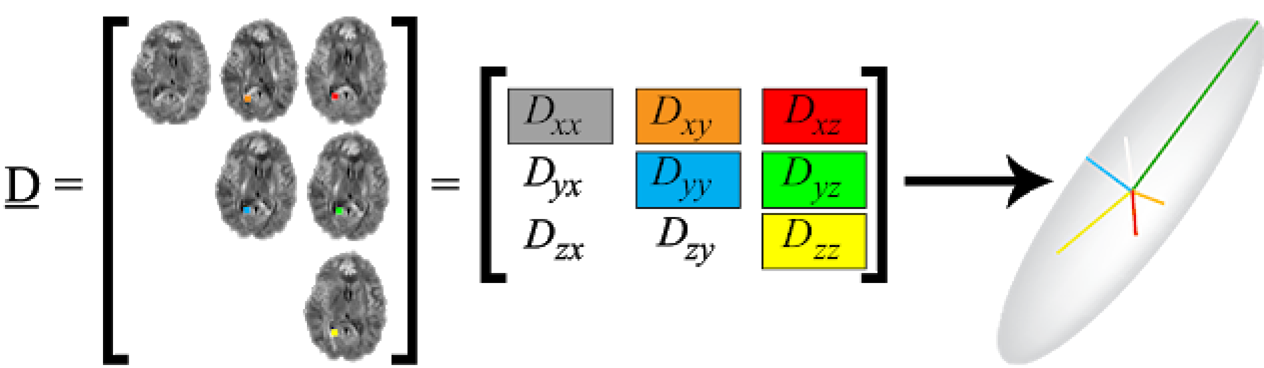
2
3
6
7
4
4

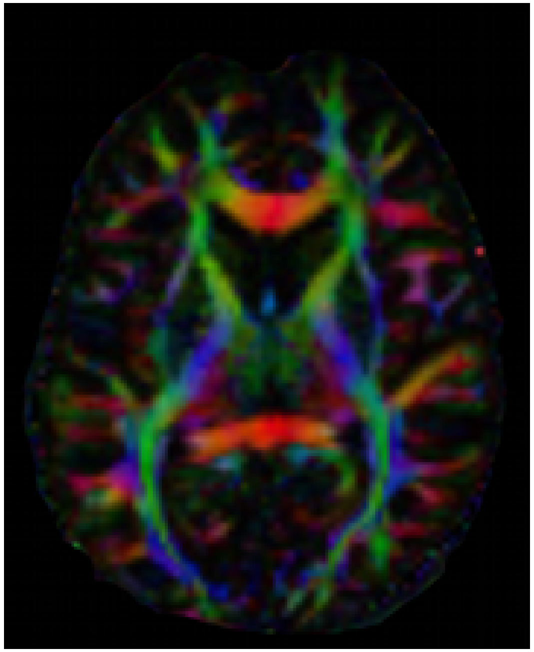
Axons are what we want





Diffusion files

1) A dwi data file.
2) A bvals files contains a scalar value for each applied gradient, corresponding to the respective b-value.
3) A bvecs contains a 3x1 vector for each gradient, indicating the gradient direction. The entries in bvals and bvecs are as many as the number of volumes in the dwidata file. The ith volume in the data corresponds to a measurement obtained after applying a diffusion-sensitising gradient with a b-value given by the ith entry in bvals and a gradient direction given by the ith vector in bvecs.



Jupiter Notebooks

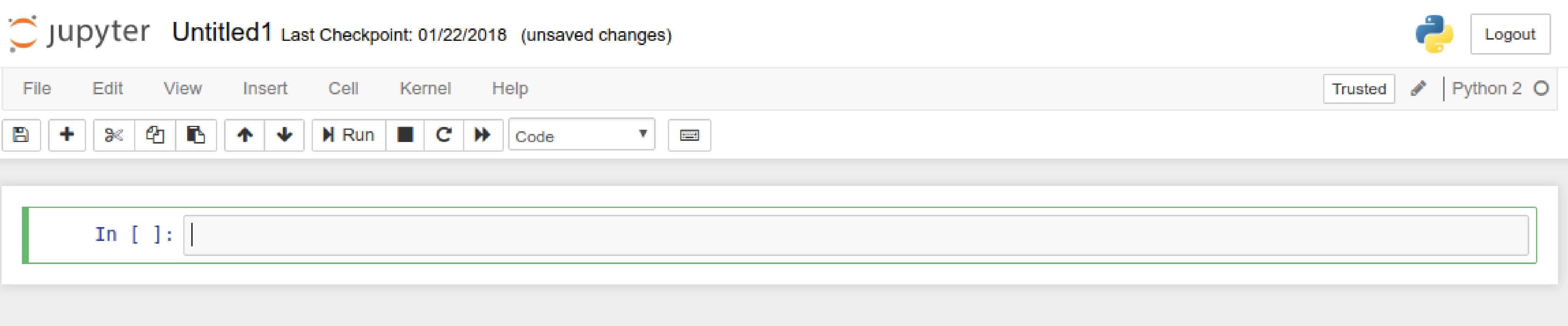
First, install Ipython:
sudo apt-get -y install ipython ipython-notebook

Now we can move on to installing Jupyter Notebook:

sudo -H pip install jupyter

Running Jupyter Notebook

jupyter notebook



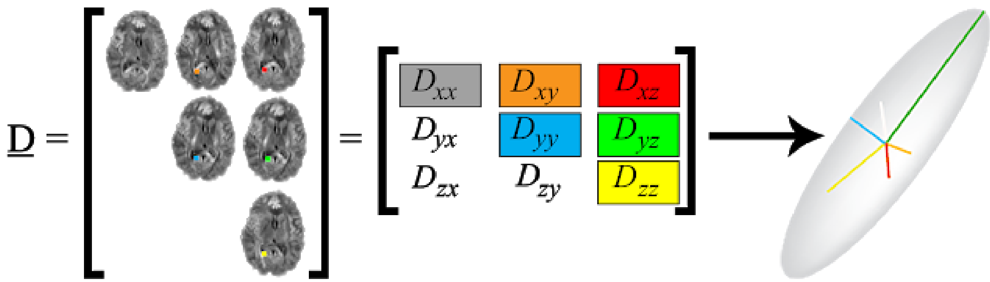
Load data

```
import dipy
import numpy as np
import nibabel as nib

fimg = "dti_fm_bet.nii.gz"
img = nib.load(fimg)
data = img.get_data()
affine = img.get_affine()
header = img.get_header()
voxel_size = header.get_zooms()[:3]
mask, S0_mask = median_otsu(data[:, :, :, 0])
fbval = "../../../../bvals"
fbvec = "../../../../bvecs"

bvals, bvecs = read_bvals_bvecs(fbval, fbvec)
gtab = gradient_table(bvals, bvecs)
```

We use the fractional anisotropy (FA) of the DTI model to build a tissue classifier.



$$FA = \sqrt{\frac{1}{2}}\frac{\sqrt{(\lambda_1-\lambda_2)^2+(\lambda_2-\lambda_3)^2+(\lambda_3-\lambda_1)^2}}{\sqrt{\lambda_1^2+\lambda_2^2+\lambda_3^2}}$$

```
from nibabel import trackvis as tv
from dipy.tracking.streamline import
set_number_of_points
from dipy.segment.mask import median_otsu
from dipy.io import read_bvals_bvecs
from dipy.core.gradients import gradient_table
from dipy.reconst.dti import TensorModel
from dipy.reconst.dti import fractional_anisotropy
from dipy.reconst.dti import color_fa
from dipy.reconst.shm import CsaOdfModel
from dipy.data import get_sphere
from dipy.reconst.peaks import peaks_from_model
from dipy.tracking.eudx import EuDX
from dipy.tracking.utils import density_map
from dipy.tracking import utils
```

```
ten_model = TensorModel(gtab)
ten_fit = ten_model.fit(data, mask)
```

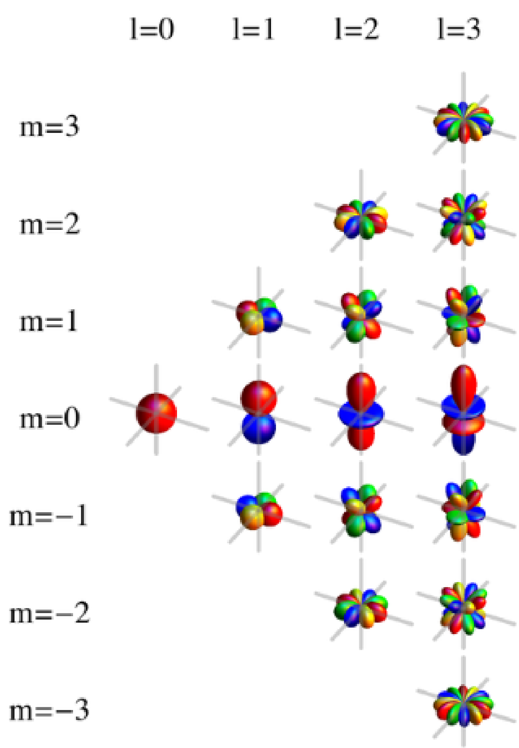
```
fa = fractional_anisotropy(ten_fit.evals)
cfa = color_fa(fa, ten_fit.evecs)
```

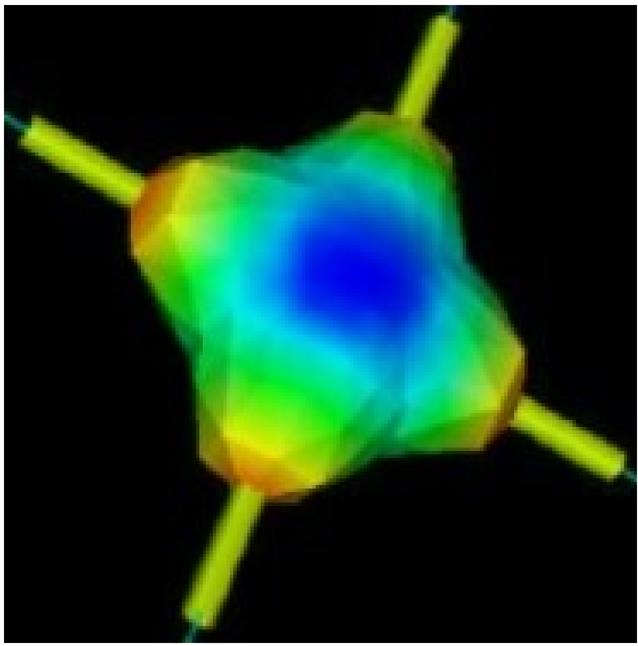
Constant Solid Angle

- The DTI model is limited by the “Gaussian assumption” → We use spherical harmonics and Orientation Distribution Functions (ODF).
- So, in order to get the main direction of diffusion we fit the data to a Constant Solid Angle ODF Model. The peaks of an ODF are good estimates for the orientation of tract segments at a point in the image:

```
csamodel = CsaOdfModel(gtab, 6)
sphere = get_sphere('symmetric724')
sphere = get_sphere('symmetric724')

pmd = peaks_from_model(model=csamodel,
                       data=data,
                       sphere=sphere,
                       relative_peak_threshold=.5,
                       min_separation_angle=25,
                       mask=mask,
                       return_odf=False)
```

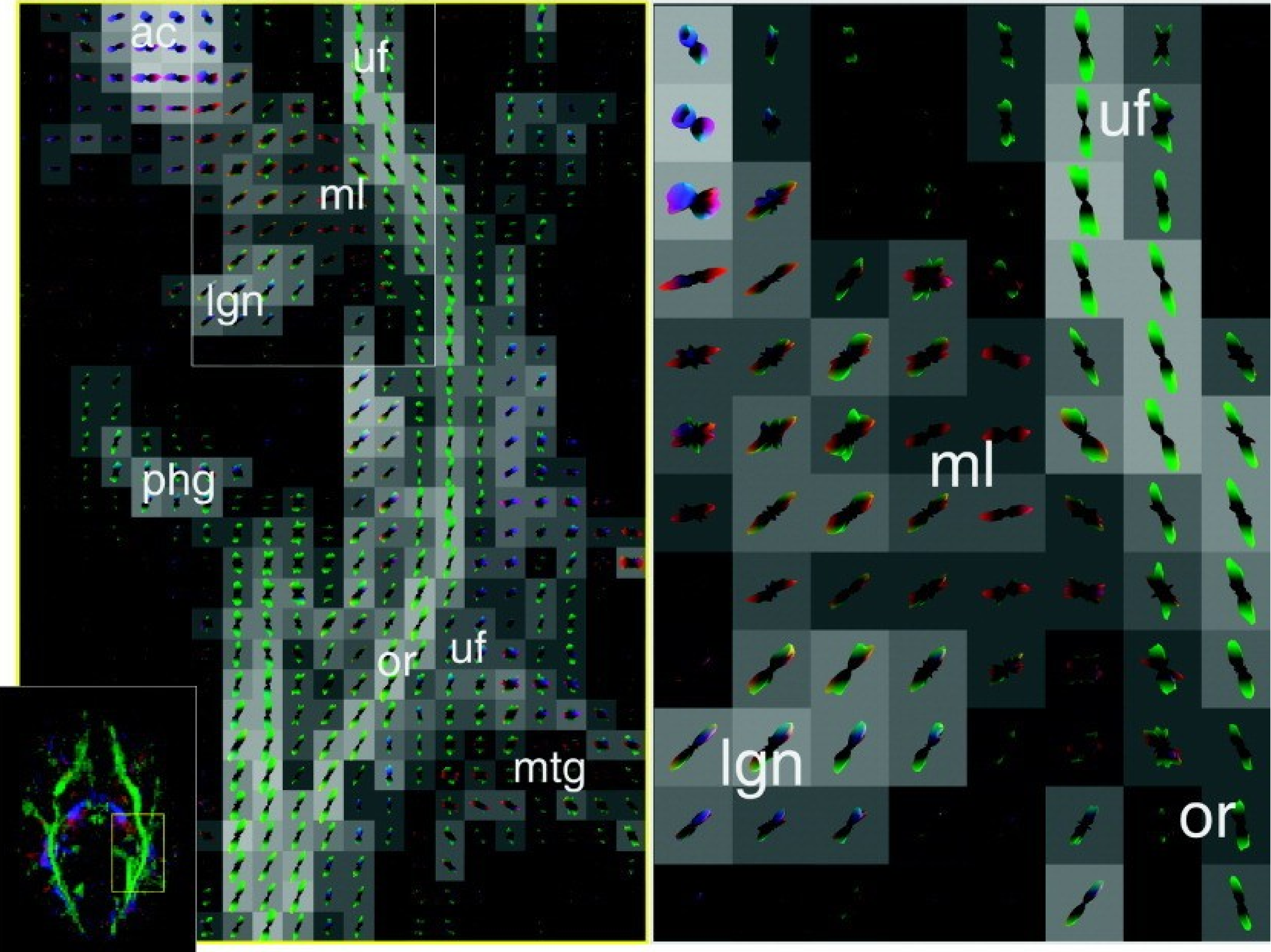




For further reading:

J. Cohen-Adad, et al. (2008). "Detection of multiple pathways in the spinal cord using q-ball imaging". NeuroImage, 42, 739-74

D. Tuch (2004) Q-ball imaging, MRM 52.



ac
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ml
lgn
phg
or
uf
mtg
uf
ml
lgn
or

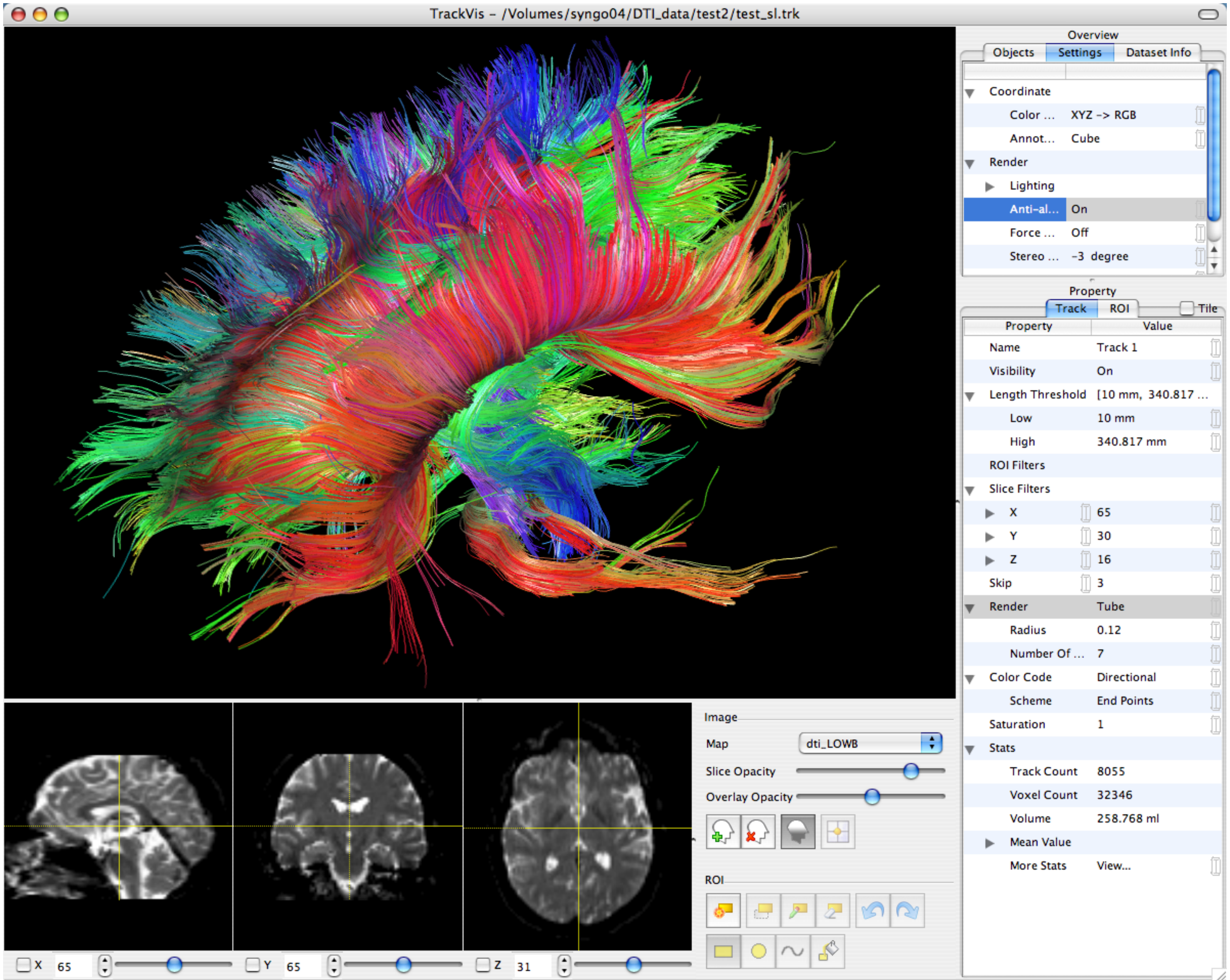
Perform Tractography

```
#Deterministic tractography

eu = EuDX(a=fa, ind=pmd.peak_indices[..., 0],
seeds=2000000, odf_vertices=sphere.vertices, a_low=0.01)

affine = eu.affine

csd_streamlines= list(eu)


#Remove tracts shorter than 30mm

from dipy.tracking.utils import length

csd_streamlines=[t for t in csd_streamlines if length(t)>30]
```

Save as a trackvis file

```
#Trackvis
hdr = nib.trackvis.empty_header()
hdr['voxel_size'] = img.get_header().get_zooms()[:3]
hdr['voxel_order'] = 'LAS'
hdr['dim'] = fa.shape
tensor_streamlines_trk = ((sl, None, None) for sl in csd_streamlines)
ten_sl_fname = 'tensor_streamlines.trk'
nib.trackvis.write(ten_sl_fname, tensor_streamlines_trk, hdr, points_space='voxel')
```

Now open Trackvis



Thank you for your attention

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