

United Diffusion Kurtosis Imaging (UDKI) toolbox

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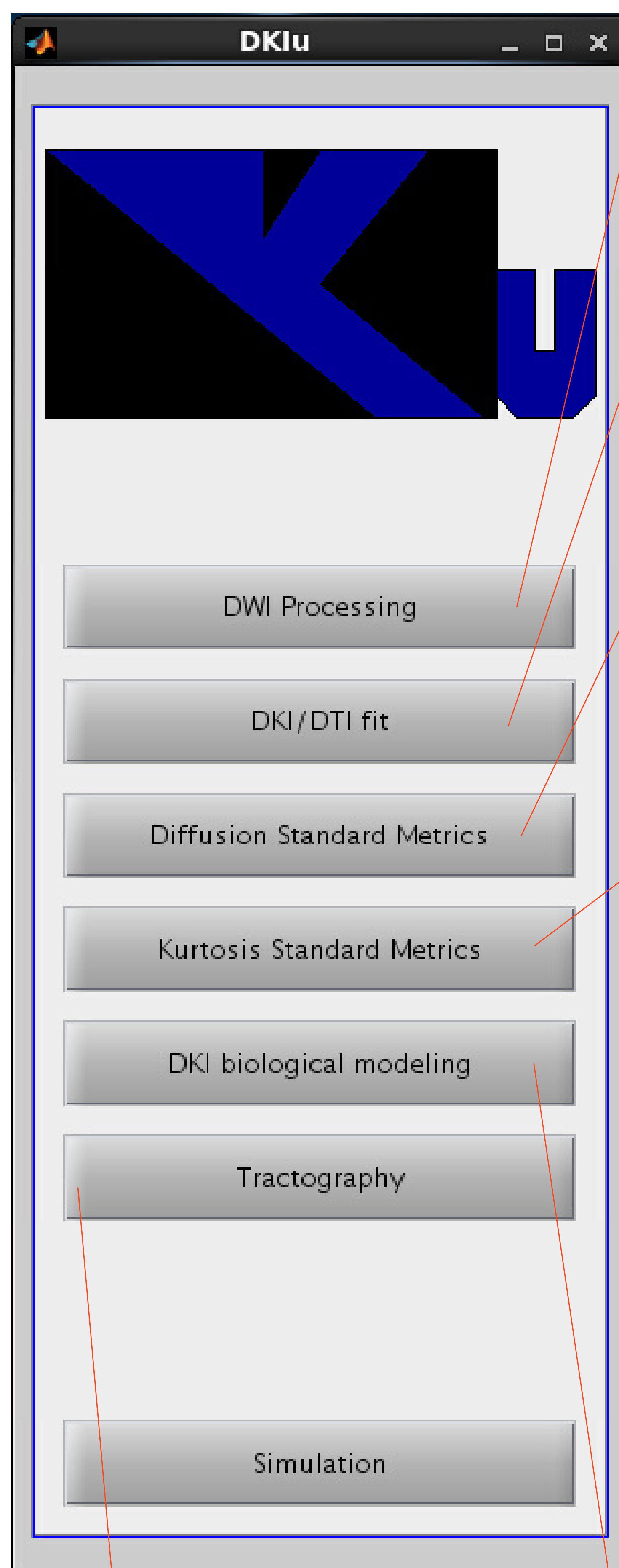
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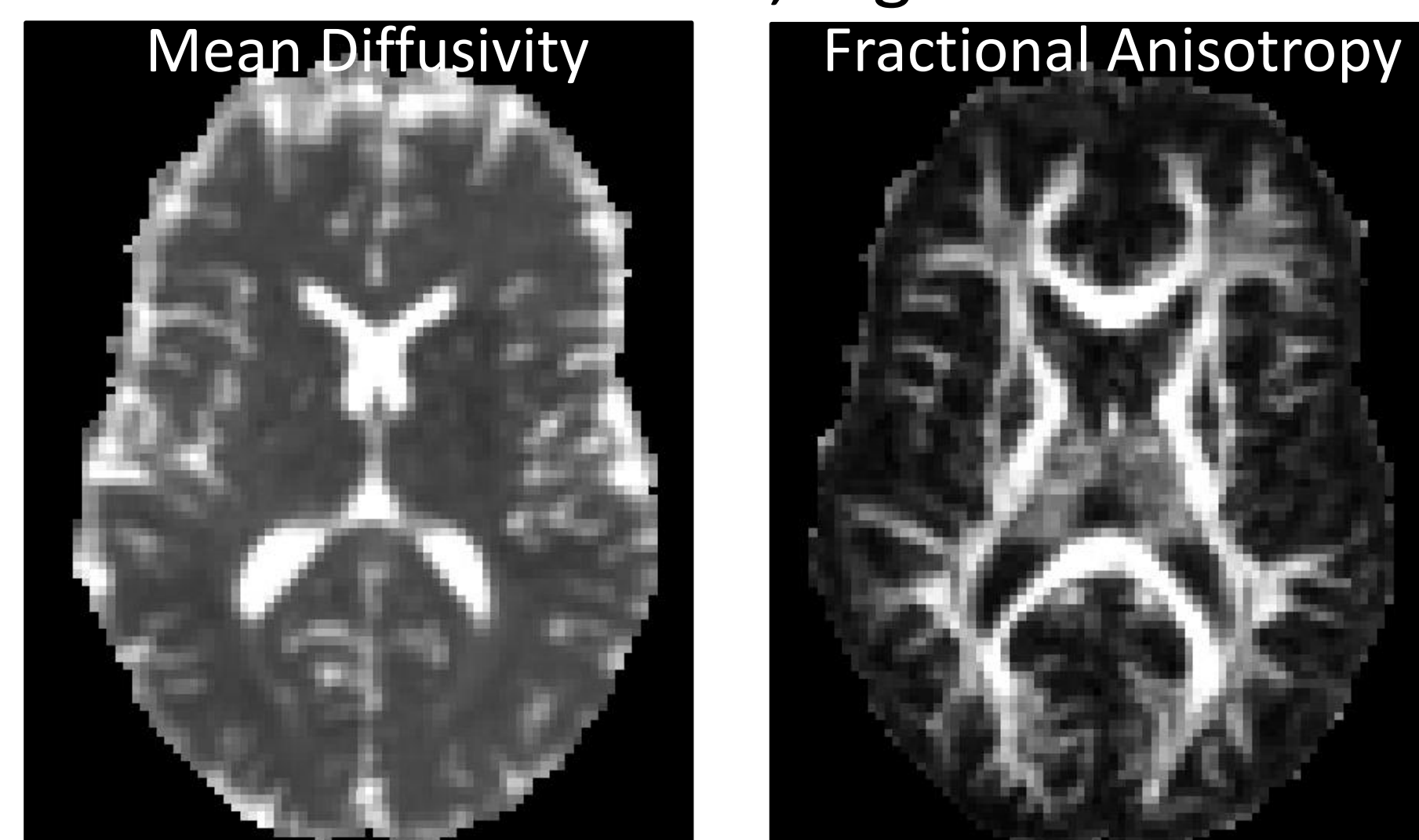
United Diffusion Kurtosis Imaging toolbox (UDKI) is a toolbox for Diffusion Kurtosis Imaging (DKI) that brings together several well established DKI processing algorithms and the latest advances of DKI analysis.

UDKI functionalities are grouped in six modules which can be called from UDKI's main graphical user interface:

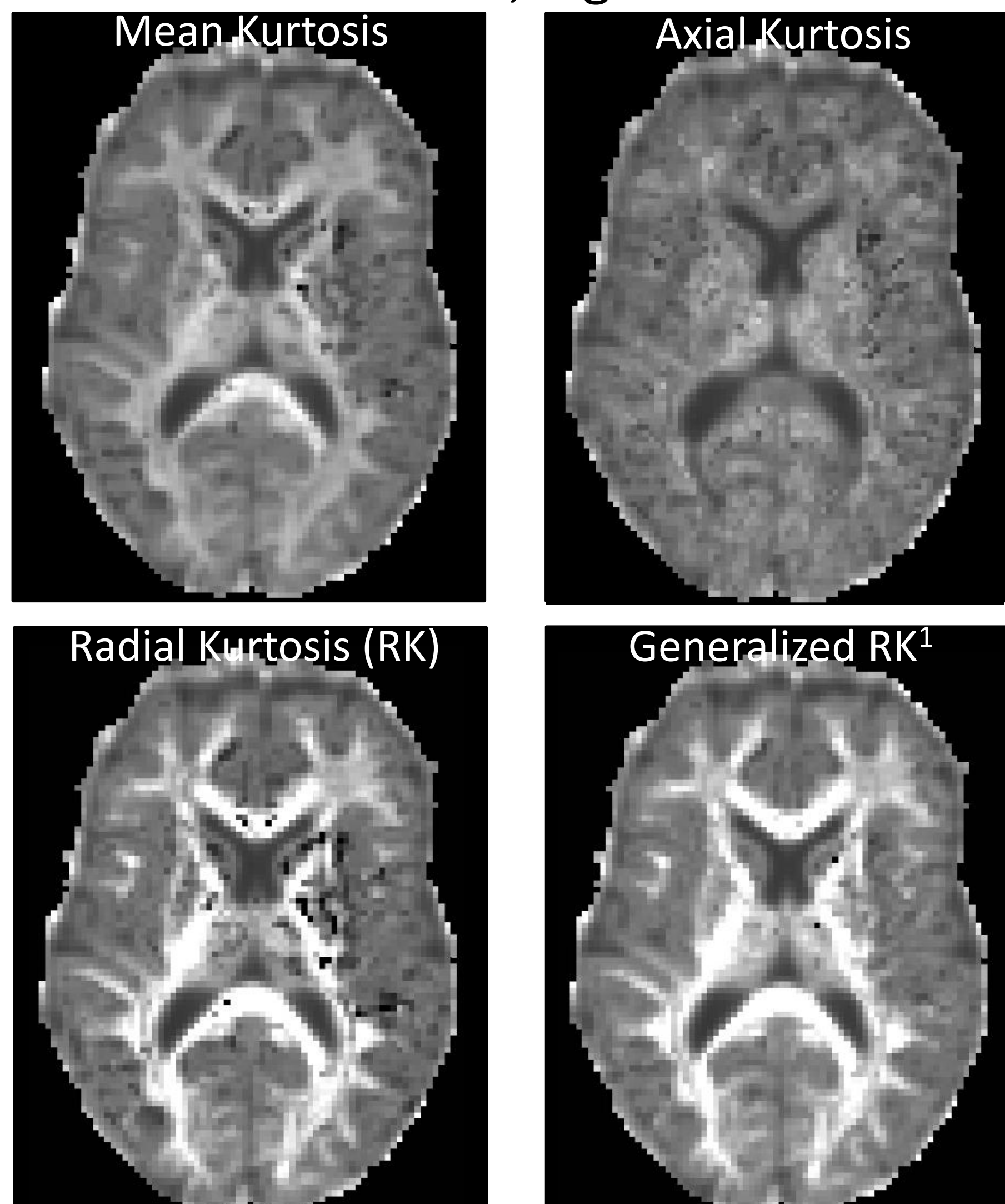


- Methods for brain extraction, Gaussian smoothing and Image downsampling
- DTI linear and non-linear least squares fit.
- DKI unconstrained and constrained linear least squares fit²

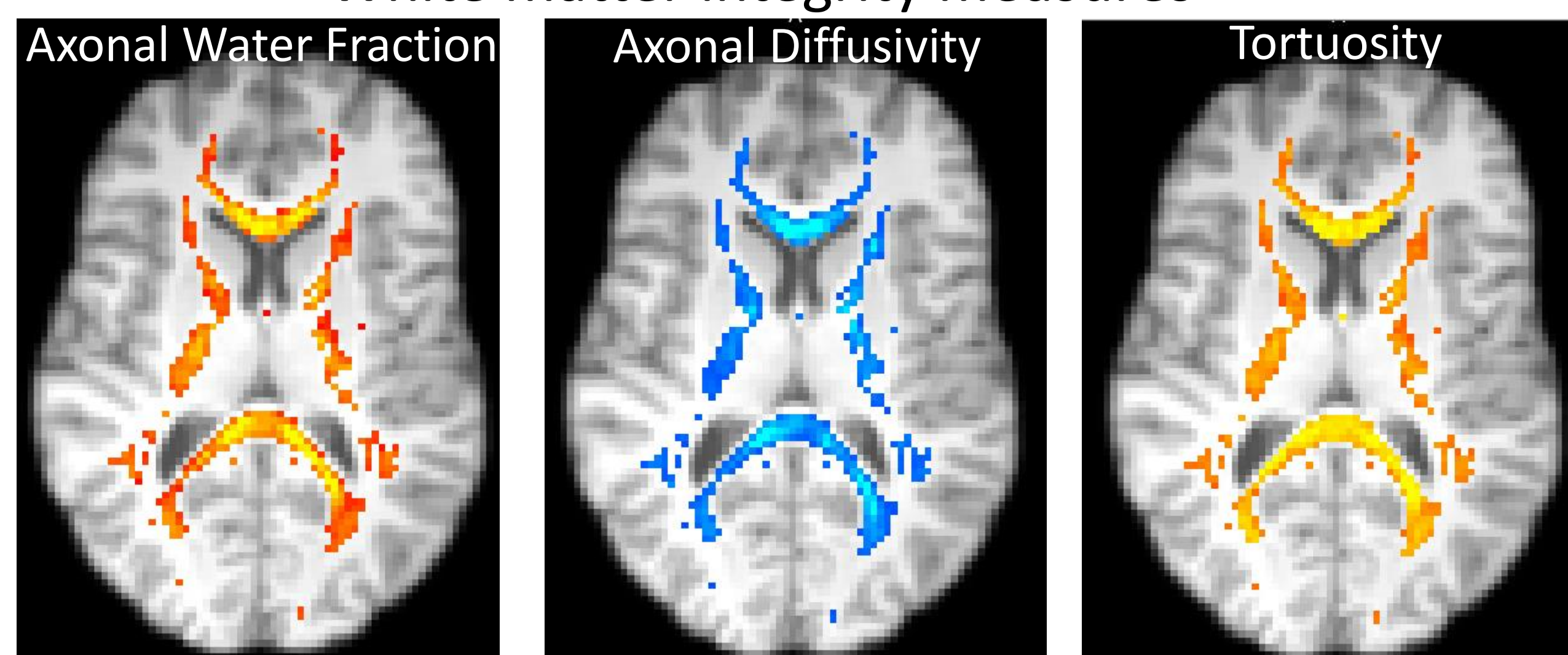
- Diffusion measures⁵, e.g.:



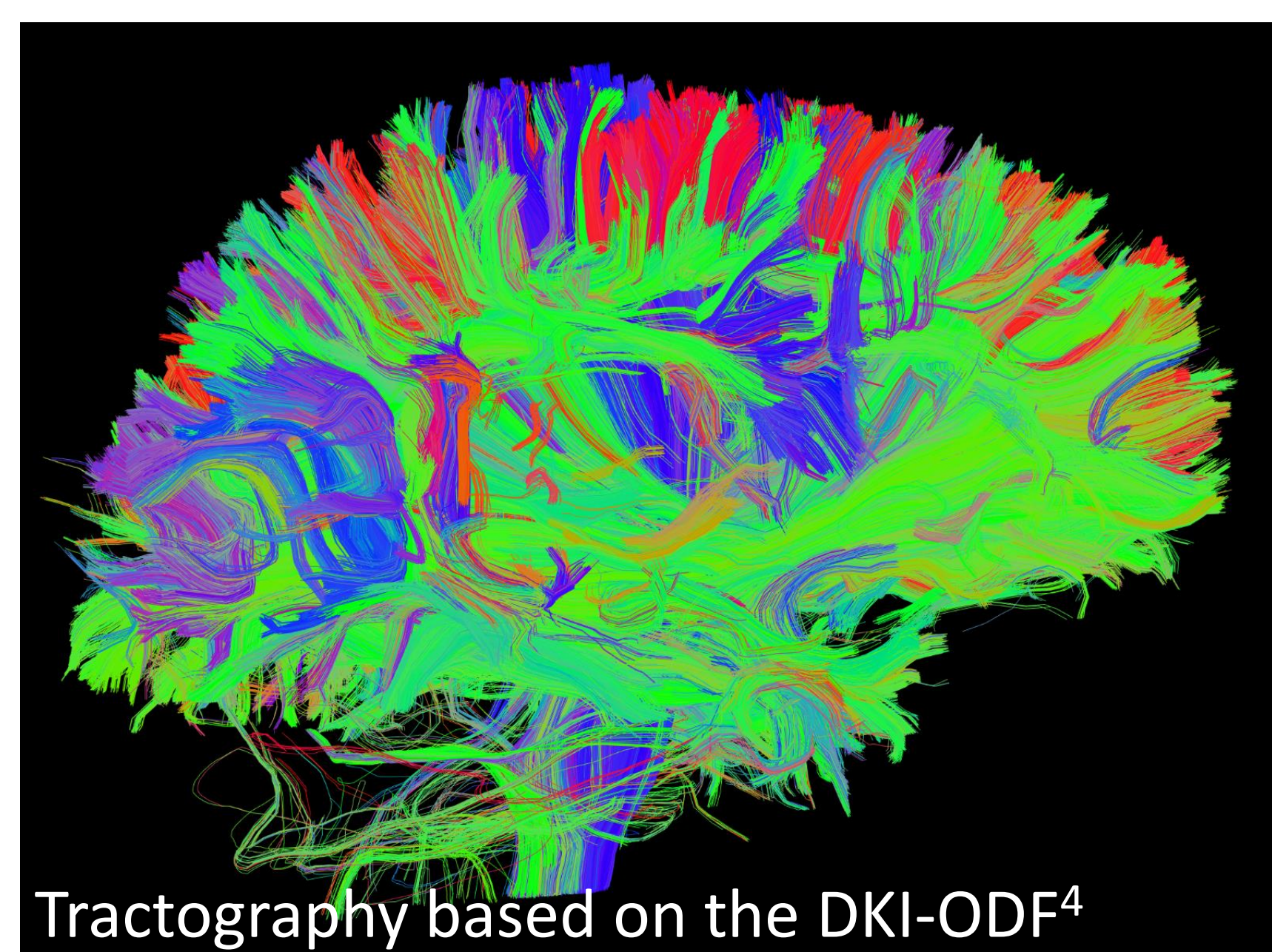
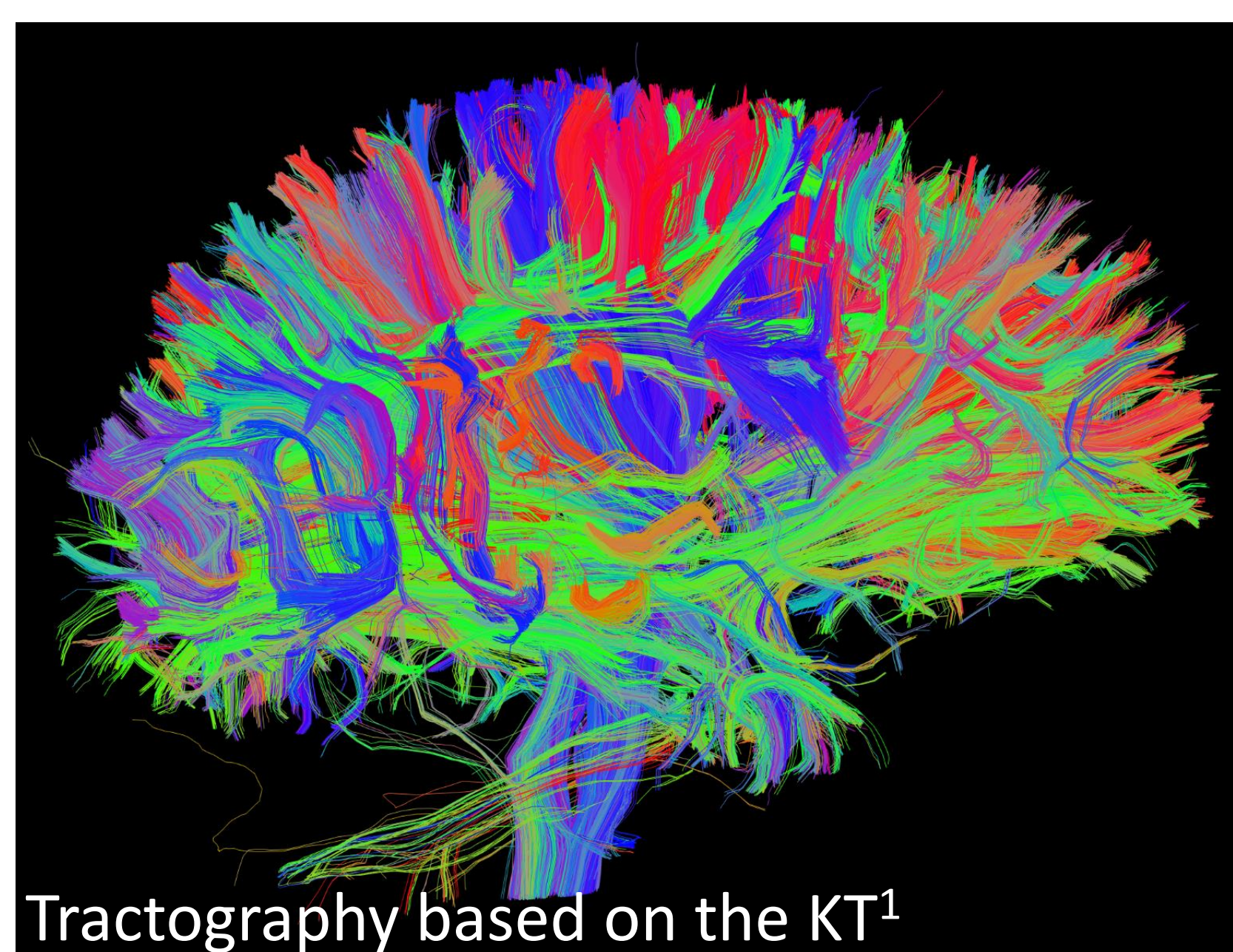
- Kurtosis measures², e.g.:



- White matter integrity measures³



- DKI-based tractography procedures^{1,4}



Why Diffusion Kurtosis Imaging?

- Diffusion kurtosis imaging (DKI) is a diffusion MRI modality that overcomes the major problems of the widely used diffusion tensor imaging (DTI)¹.
- In addition to the standard diffusion measures, DKI estimates the diffusion kurtosis tensor (KT) which can be used as a measure of microstructural heterogeneity².
- DKI can provide estimates of biophysical properties such as the water axonal volume fraction and diffusion tortuosity³.
- DKI can be used to resolve crossing fibers for tractography approaches^{1,2} and generalize diffusion based metrics to cases not limited to well-aligned white matter fibers¹.

System requirements

UDKI is fully implemented in MATLAB and it is compatible with any operating system (Window, Linux or Mac OS X) with a base installation of MATLAB (version 7.8 onwards)

Future steps

UDKI is continuously being updated to keep up with the new advances on DKI processing and analysis reported in the literature. Below are some of the techniques that will be incorporated in UDKI in the near future:

- DKI weighted linear least squares fit⁶
- Metrics of diffusional kurtosis anisotropy⁷

A version of UDKI's functions is currently being implemented in python and incorporated in the huge collaborative free and open source project (<http://nipy.org/dipy/>).

References

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- [7] Glenn et al., 2015. NMR Biomed. 28(4): 448-59.

Acknowledgments

This project was funded by Fundação para a Ciência e Tecnologia FCT/MCE (PIDDAC) under grants:

- SFRH/BD/89114/2012
- PTDC/SAU-ENB/120718/2010

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