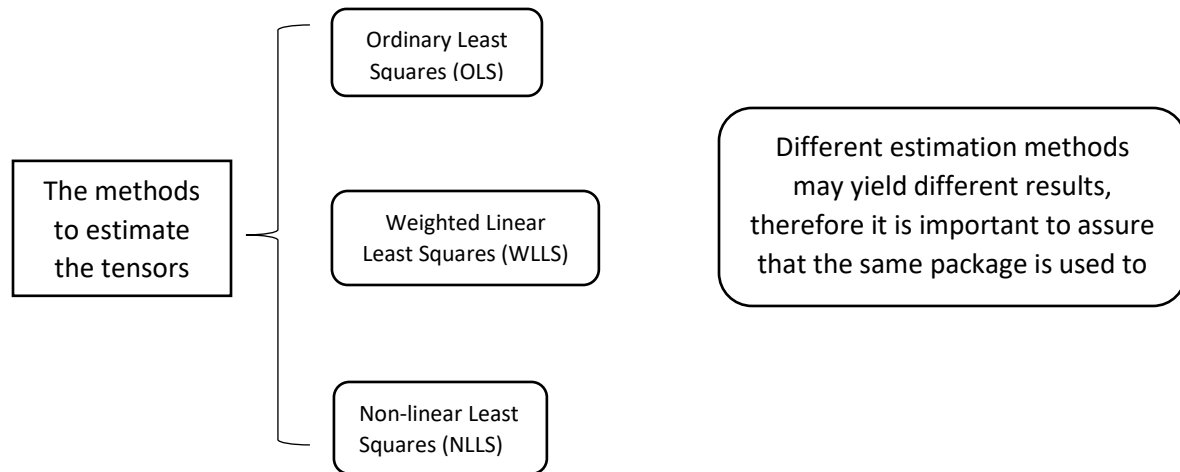# Summary

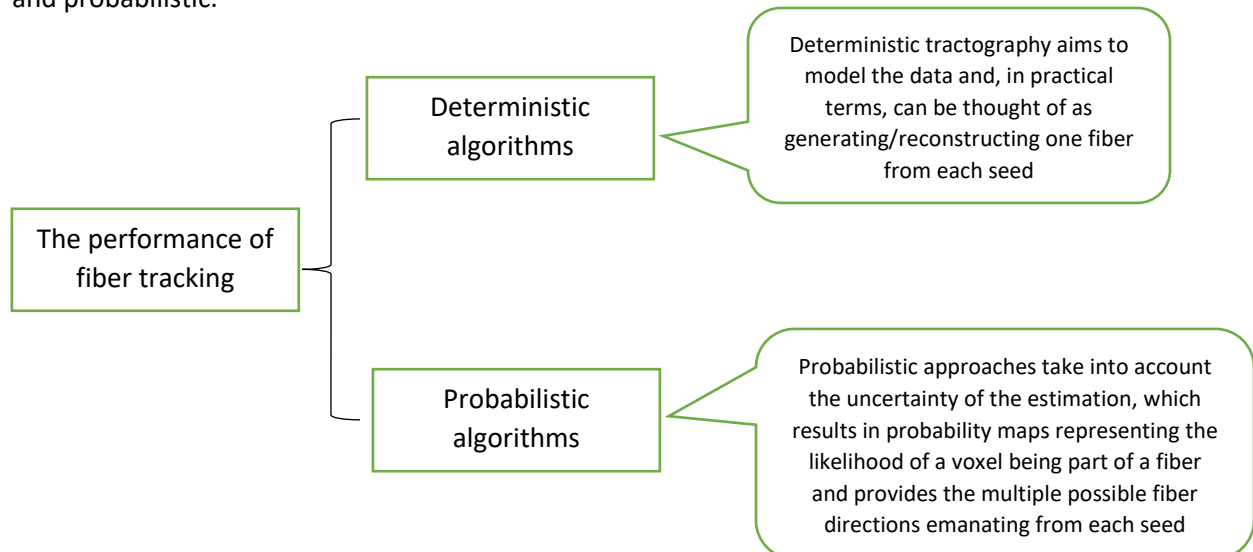## 1. Processing and Visualization

Comprises tensor estimation

1, three main methods to estimate the tensors: Ordinary Least Squares (OLS), Weighted Linear Least Squares (WLLS) and Non-linear Least Squares(NLLS)

The methods to estimate the tensors

- Ordinary Least Squares (OLS)
- Weighted Linear Least Squares (WLLS)
- Non-linear Least Squares (NLLS)

Different estimation methods may yield different results, therefore it is important to assure that the same package is used to

The biggest challenges in DTI is to visualize and present the tensor information in an intuitive and easily understandable way. But the data is high dimensional and the diffusion tensor domain is complex association.

If we use 2D visualization of scalar maps due to its simplicity and instant visualization. But this approach has limitations in the quantity of information presented.

Fiber tracking can be performed with different algorithms divided in two main categories: deterministic and probabilistic.

The performance of fiber tracking

Deterministic algorithms

Deterministic tractography aims to model the data and, in practical terms, can be thought of as generating/reconstructing one fiber from each seed

Probabilistic algorithms

Probabilistic approaches take into account the uncertainty of the estimation, which results in probability maps representing the likelihood of a voxel being part of a fiber and provides the multiple possible fiber directions emanating from each seed

2. Quantitative analysis

Extract summary measures from either specific anatomical regions or whole brain

ROIs

ROI analysis is based on manual delineation of a priori specific regions of the brain or on automated parcellations. ROI analyses are time-consuming, require anatomical knowledge and are applied to quantify diffusion parameters (mainly MD and FA) within those areas. The main problems of ROI analyses include: the influence of the image intensity on ROI boundaries by direct segmentations on the map of interest (typically FA or MD); the difficulty to co-register diffusion with typical anatomical images (T1 or T2 weighted) when using anatomical ROIs; performing analysis in smaller/thinner tracts; and difficult application in longitudinal studies. Of note, ROI analysis can be performed with the main tensor estimation and visualization software, such as Slicer, TrackVis, MedINRIA, and ExploreDTI.

histogram

The histogram of each diffusion parameter presents the mean, the peak height and location, values that can be used to compare groups through statistical tests. Histograms allow analysis of whole brain in an automated way, without any a priori specified ROI; however, such an approach requires the removal of the tissue of no interest (typically CSF), does not retain any information about the location of abnormalities and is sensitive to partial volume effect from atrophy. For such approach, tools such as TrackVis or MedINRIA can be used.

Voxel-based

Voxel Based Analysis (VBA) involves registration of diffusion maps into a standard space (a process known as normalization) to achieve correspondences between subjects across voxels and consequently anatomical structures. This enables the comparison of diffusion parameters between groups and correlations with covariates of interest (e.g., age). This approach allows spatially specific (as ROIs) and unbiased (as histogram) analysis and does not require previous ROI definition. The main problem is the accuracy of registration algorithms using tensor datasets. VBA can be carried out with SPM or Brain Voyager QX, with SPM as the most widely used software tool for this kind of analysis.

Tract-based spatial statistics (TBSS)

A recent method designed to overcome the problems with registration algorithms and arbitrariness of spatial smoothing is TBSS. TBSS is an automated method for detecting group voxel-wise changes in whole brain, based on the skeletonization of group registered FA maps (Figure1O). TBSS removes the need to perform spatial smoothing, increases the statistical power (reducing number of total voxels tested). On the other hand, the skeletonization of FA images may be inaccurate in images with large anatomical shifts or WM lesions and registration errors are difficult to identify visually in the skeleton. Back projection to native space is also an issue since the skeletonization process aligns local maxima, which may not necessarily correspond to the same anatomical location across all subjects. This method is part of the FSL distribution.