## Diffusion Tensor Image processing

The basics





Do Tromp - 2012

# FROM TENSOR TO TRACTS Diffusion Tensor Imaging Basics



## **Diffusion Tensor Imaging Basics**





2. Brain diffusion



3. In Vivo White Matter

















### The tensor shape follows the water diffusion













## The Tensor









#### The relative degree of anisotropy

as measured by the weighted average – dominated by the largest component











Fractional Anisotropy



## Axial Diffusivity $\lambda_1$



Mean Diffusivity  $(\lambda_1 + \lambda_2 + \lambda_3)/3$ 



Radial Diffusivity  $(\lambda_2 + \lambda_3)/2$ 





## **DTI and Microstructure**

	FA	MD	AD	RD
		$(\lambda_1 + \lambda_2 + \lambda_3)/3$	$\lambda_1$	$(\lambda_2 + \lambda_3)/2$
Gray Matter	$\checkmark$	-	$\bullet$	<b>^</b>
White Matter	1	_	<b>^</b>	$\checkmark$
CSF	$\checkmark$	<b>^</b>	<b>^</b>	<b>^</b>
High myelination	1	$\checkmark$	—	$\checkmark$
Dense axonal packing	↑	↓	-	↓
WM Maturation	1	$\checkmark$	<b>^</b>	$\checkmark$
Axonal degeneration	¥	<b>^</b>	¥	<b>^</b>
Demyelination	$\mathbf{\bullet}$	<b>^</b>	—	<b>^</b>
Low SNR	$\mathbf{+}$	<b>^</b>	$\mathbf{+}$	_

Ref: Alexander et. al. (2012). Characterization of Cerebral White Matter Properties Using Quantitative Magnetic Resonance Imaging Stains. Brain Connectivity.





## **Fiber Tracking**









## **Processing Pipeline**

## FROM SCANNER TO STATISTICS

## 1. DICOM to NIFTI

#list scan dirs

ls /study/\$your\_study/raw\_data/\$subject\_nr/dicoms/

redwood:dicoms	tromp\$ ls						
cardiac/	s04 3dtof/	s1000 ADC/	s1100 ADC/	s1200 ADC/	s13 fse xl/	s15 3dtof/	s802 CMB/
s01 assetcal/	s07 <sup>2</sup> dfast/	s1001 FA/	s1101 FA/	s1201 FA/	s1400 COLLAPSE/	s400 COLLAPSE/	s900 ADC/
s02 bravo/	s08 dti/	s1002 CMB/	s1102 CMB/	s1202 CMB/	s14 3dtof/	s800 ADC/	s901 FA/
s03_fse_xl/	s09_dti/	s10_dti/	s11_dti/	s12_dti/	s1500_COLLAPSE/	s801_FA/	s902_CMB/

#### #convert from DICOM to NIfTI

convert\_file s08\_dti /\$output\_dir/\$subject\_nr\_s08\_dti nii





#### fslinfo subj\_s09\_dti.nii

data_type	INT16
dim1	256
dim2	256
dim3	67
dim4	49
datatype	4
pixdim1	1.00
pixdim2	1.00
pixdim3	2.00
pixdim4	1000.00
cal_max	0.0000
cal_min	0.0000
file_type	NIFTI-1-



## 2. Eddy Current Correction

#### Distortions





## d

#### Uncorrected



#### Registration



#### Corrected





## 3. Fieldmap (EPI) Distortion Correction





## 3. Fieldmap (EPI) Distortion Correction





## 4. Brain Extraction

- FSL tool brain extraction tool (bet)
- AFNI tool 3dSkullStrip
- Manual stripping fslview



Unfixed mask



#### Manual fixed mask



## **Tensor fitting**

#### 5. Produce SCHEME files

0.000000	0.000000	0.000000	0.000E00	
0.894652	-0.004314	-0.446744	1.000E09	LA CARA
-0.002455	-0.452065	-0.891982	1.000E09	
0.444643	-0.895686	0.006279	1.000E09	
0.891854	-0.452289	0.005567	1.000E09	Can
-0.000693	-0.897000	-0.442029	1.000E09	10000
0.452735	-0.007309	-0.891615	1.000E09	
0.894354	-0.006560	0.447313	1.000E09	
-0.000430	0.442349	-0.896843	1.000E09	NH 30 621
-0.449481	-0.893270	0.005917	1.000E09	「人」
0.896627	0.442770	-0.003869	1.000E09	
-0.000052	-0.891742	0.452544	1.000E09	ELX17
-0.447324	-0.004350	-0.894362	1.000E09	



## **Tensor fitting**

#### 5. Produce SCHEME files

- 6. Convert from NIfTI (.nii) to CAMINO (.Bfloat)
- 7. Run tensor model fit with CAMINO
- 8. Check the sanity of the fit
- 9. Convert from CAMINO to NIfTI

0.000000	0.000000	0.000000	0.000E00	State State
0.894652	-0.004314	-0.446744	1.000E09	
-0.002455	-0.452065	-0.891982	1.000E09	
0.444643	-0.895686	0.006279	1.000E09	
0.891854	-0.452289	0.005567	1.000E09	Par
-0.000693	-0.897000	-0.442029	1.000E09	600
0.452735	-0.007309	-0.891615	1.000E09	
0.894354	-0.006560	0.447313	1.000E09	
-0.000430	0.442349	-0.896843	1.000E09	NIN 35 45
-0.449481	-0.893270	0.005917	1.000E09	
0.896627	0.442770	-0.003869	1.000E09	
-0.000052	-0.891742	0.452544	1.000E09	El tra
-0.447324	-0.004350	-0.894362	1.000E09	1980

Camino





## **Tensor fitting**

- 5. Produce SCHEME files
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- 7. Run tensor model fit with CAMINO
- 8. Check the sanity of the fit
- 9. Convert from CAMINO to NIfTI



## 10. Produce Scalars (FA, MD, AD, RD)

TVtool -in tensor.nii.gz -fa -out tensor\_fa.nii.gz TVtool -in tensor.nii.gz -tr -out tensor\_md.nii.gz TVtool -in tensor.nii.gz -ad -out tensor\_ad.nii.gz TVtool -in tensor.nii.gz -rd -out tensor\_rd.nii.gz



## 11. Fiber Tracking

• Run fiber tractography on the tensor files



- Convert track files to Trackvis format (.trk)
- Open in Trackvis





## **11. Fiber Tracking**





## **11. Fiber Tracking**

## Tract-based analysis (TBA)

Testing a difference between the average FA (or MD, RD, AD) between groups for a specific WM pathway.





### **Voxel Based Analysis**



t-stat map of higher FA with age in genu of CC



t-stat map of Jacobian deformation with age



#### Cerebellum tracts showing t-stat coloring of FA change with age



## **Comparison VBA - TBA**

- Whole Brain (VBA) vs. Tract Specific (TBA)
- Same data different grouping
- VBA requires a large correction for multiple comparison since you are testing all the voxels in the brain. This can reduce the sensitivity
- TSA requires an a priori hypothesis on what brain regions and white matter tracts are of interest.



## **Normalization Tools**



ANTS is an excellent tool for scalar (e.g. FA, T1) based normalization, registration and atlas development



DTI-TK is a tensor based normalization tool, thus better capable of retaining the higher order information



## **Tensor Normalization with DTI-TK**

#### 1. Bootstrapping

TVMean -in \${subj\_list\_file}.txt -out mean\_initial.nii.gz TVResample -in mean\_initial.nii.gz -vsize 1.5 1.75 2.25 -size 128 128 64

#### 2. Rigid Alignment with Bootstrapped Template

sh dti\_rigid\_population mean\_initial.nii.gz \${subj\_list\_file}.txt EDS 3

**3. Affine Alignment with Final Refined Template Estimate from Rigid Alignment** sh dti\_affine\_population mean\_rigid3.nii.gz \${subj\_list\_file}.txt EDS 3

### 4. Deformable Alignment with the Final Refined Template Estimate from Affine Alignment

TVtool -tr -in mean\_affine3.nii.gz

BinaryThresholdImageFilter mean\_affine3\_tr.nii.gz mask.nii.gz 0 .01 100 1 0 sh dti diffeomorphic population mean affine3.nii.gz \${subj list file} aff.txt mask.nii.gz 0.002

