

Medical Image Processing and Analysis

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25 June 2018

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Medical Imaging and Image Analysis

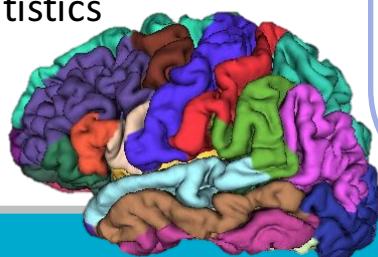
What we do

- Develop and apply advanced computational tools to turn individual (and populations of) images into information (imaging biomarkers).
 - Accurate and reliable automated image analysis (reduces costs and may improve care),
 - provide new insights (Validity, reproducibility and predictive value),
 - enables new and improved diagnostics, screening and treatments.

Medical Images

Image analysis team

- image processing
- registration
- segmentation
- pattern recognition
- machine learning
- statistics

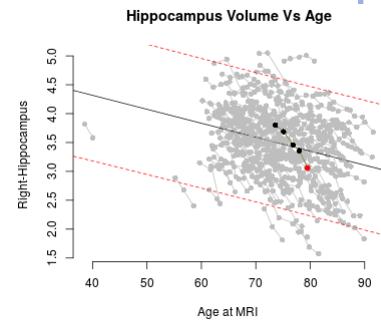


Personalized medicine

- Monitor individuals changes.
- Patient specific treatments
- Characterize phenotype variability of disease.

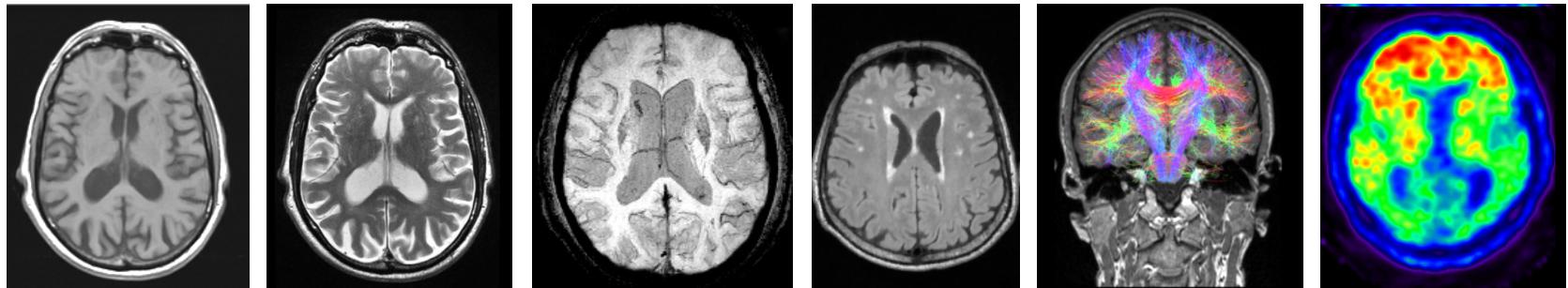
Preventing diseases

- Population studies
- Early detection/screening
- Diagnosis tools



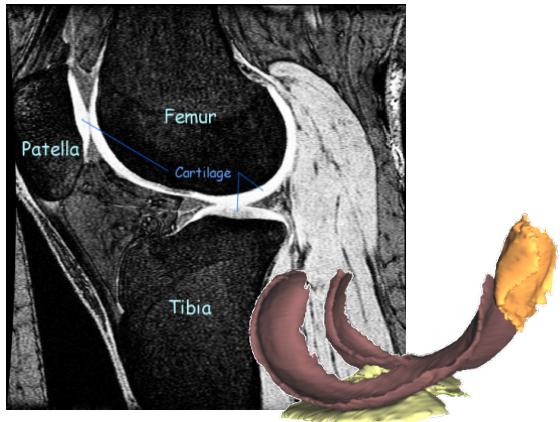
Quantitative Image Analysis

Overview of Neuroimaging Biomarkers we extract

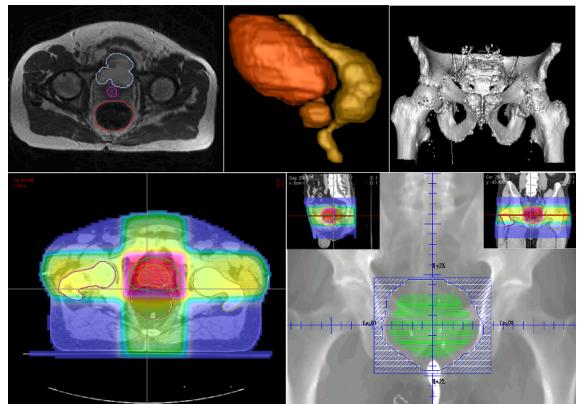


T1W	T2W	SWI	FLAIR	DWI	PET
Anatomy	CSF and structures	Venous tree	White matter lesions	White matter connections	Amyloid beta load Glucose metabolism
Tissue atrophy		Microbleeds	White matter lesions	Connectivity strength	Neocortical uptake
Cortical thickness		Iron deposit		Axonal integrity	Patten of uptake
Hippocampus volume					
Atrophy patterns					
Tissue contrast					

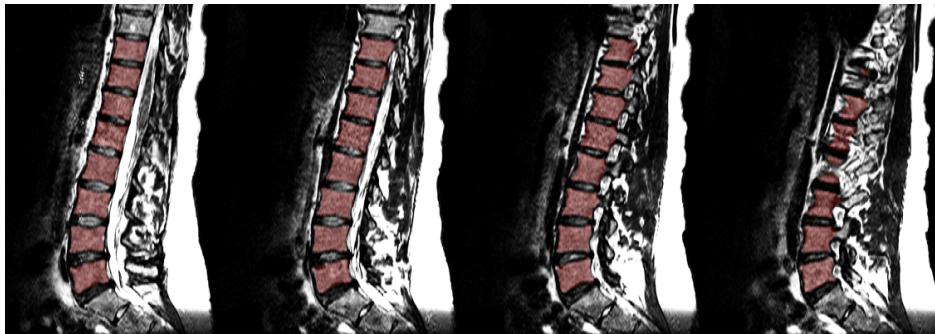
Quantitative Image Analysis



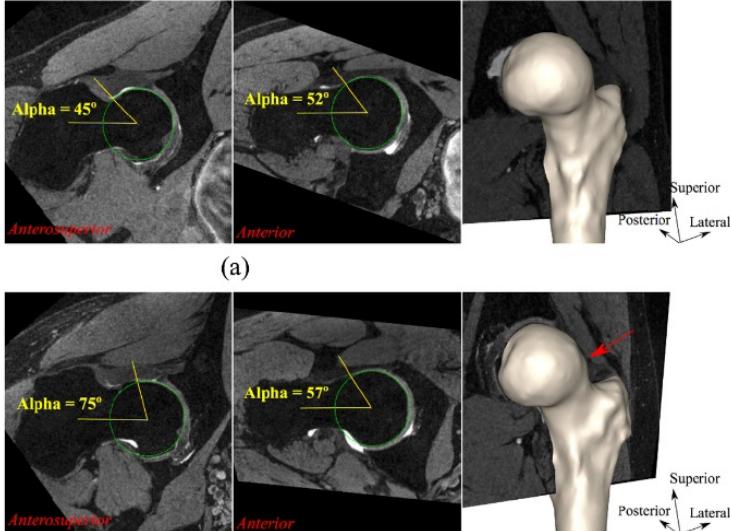
Knee



Prostate radiotherapy
planning with MRI



Vertebrae



Hip

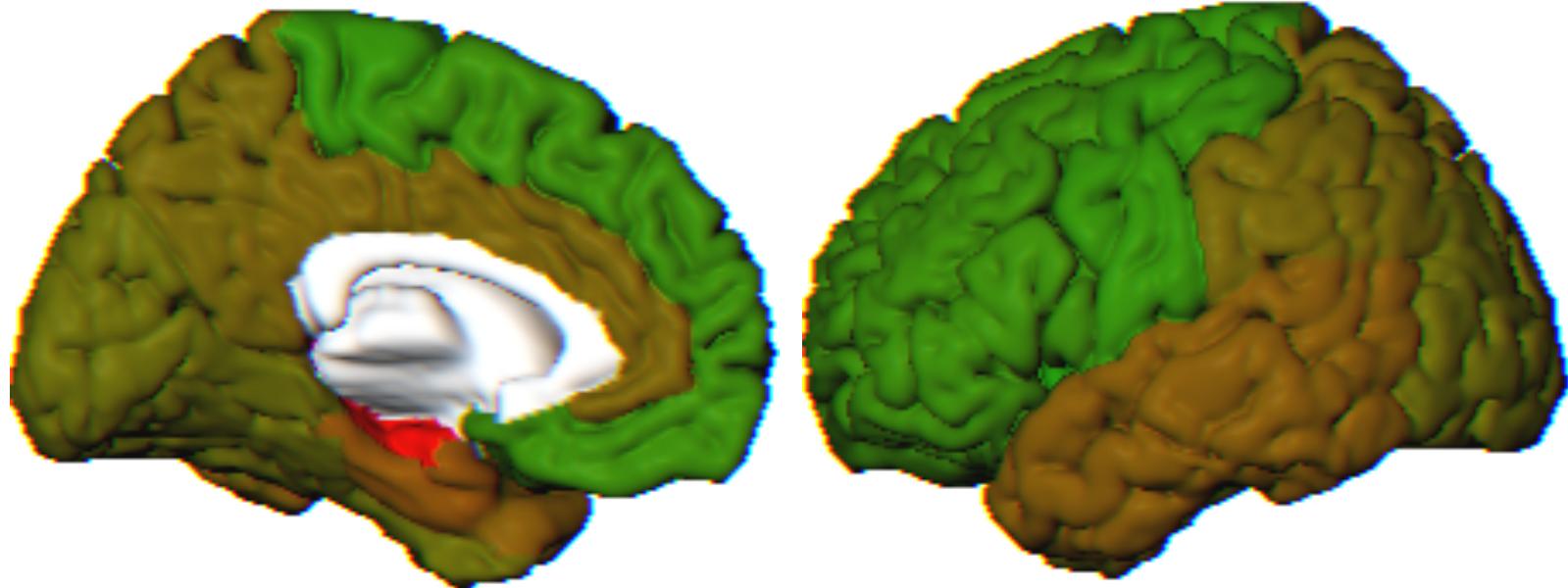
Structural MRI: structural changes in neurodegenerative diseases



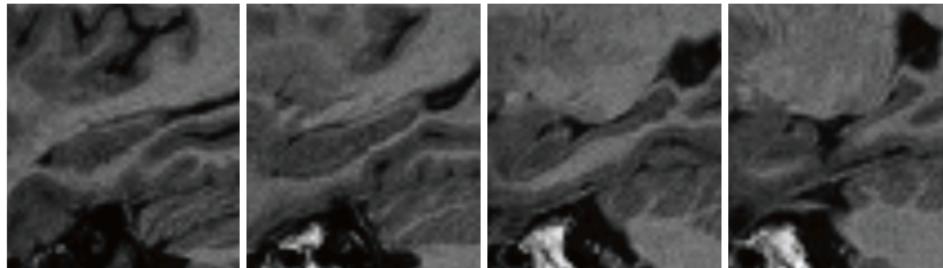
Normal

Alzheimer's

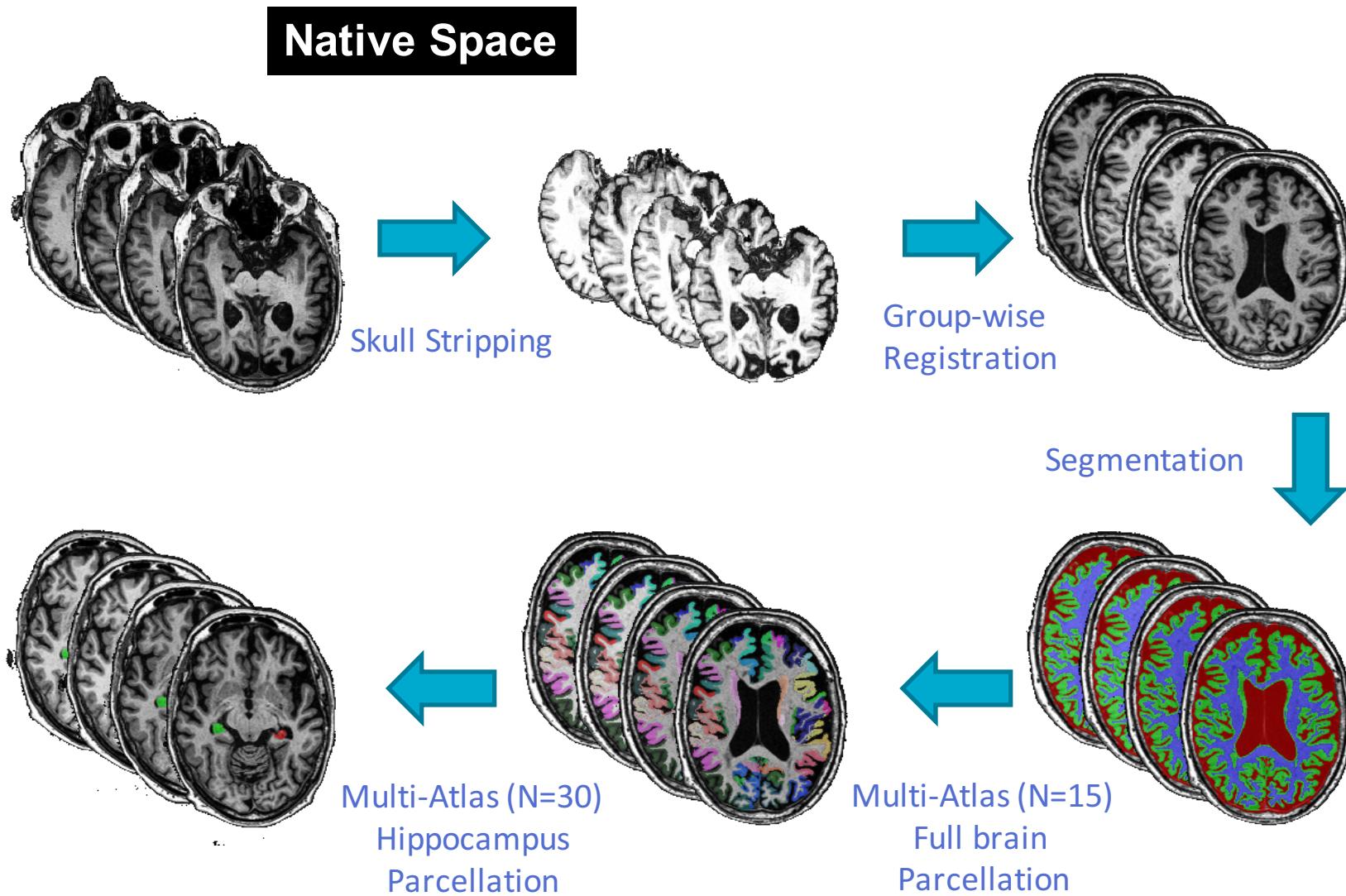
Structural MRI: structural changes in neurodegenerative diseases



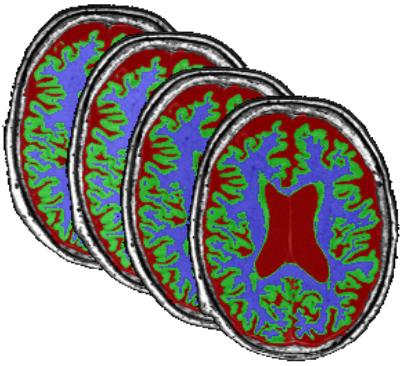
Atrophy compared to Healthy control in early Alzheimer's disease



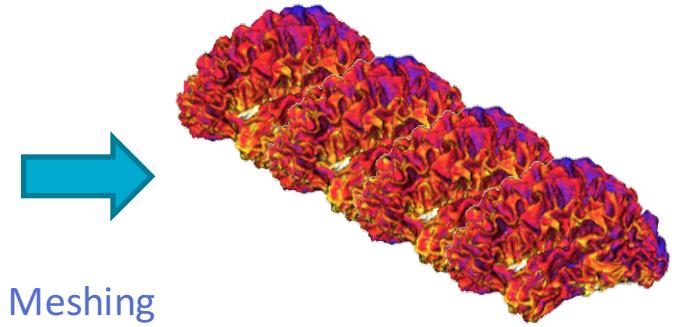
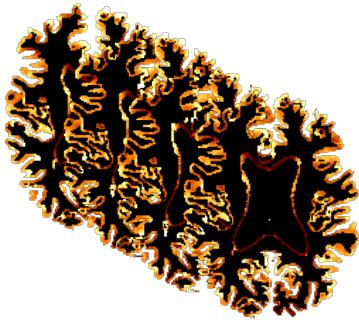
Structural MRI: Volumetric Analysis



Structural MRI: Cortical thickness

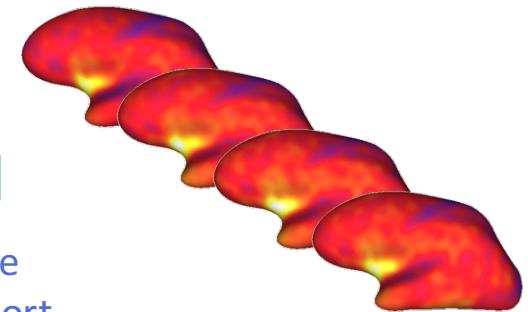


Cortical
Thickness

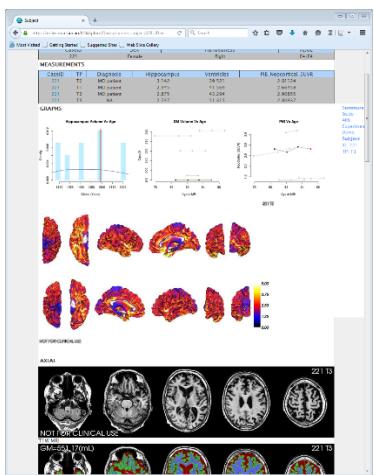


Meshing

Smoothing
and registration
to template

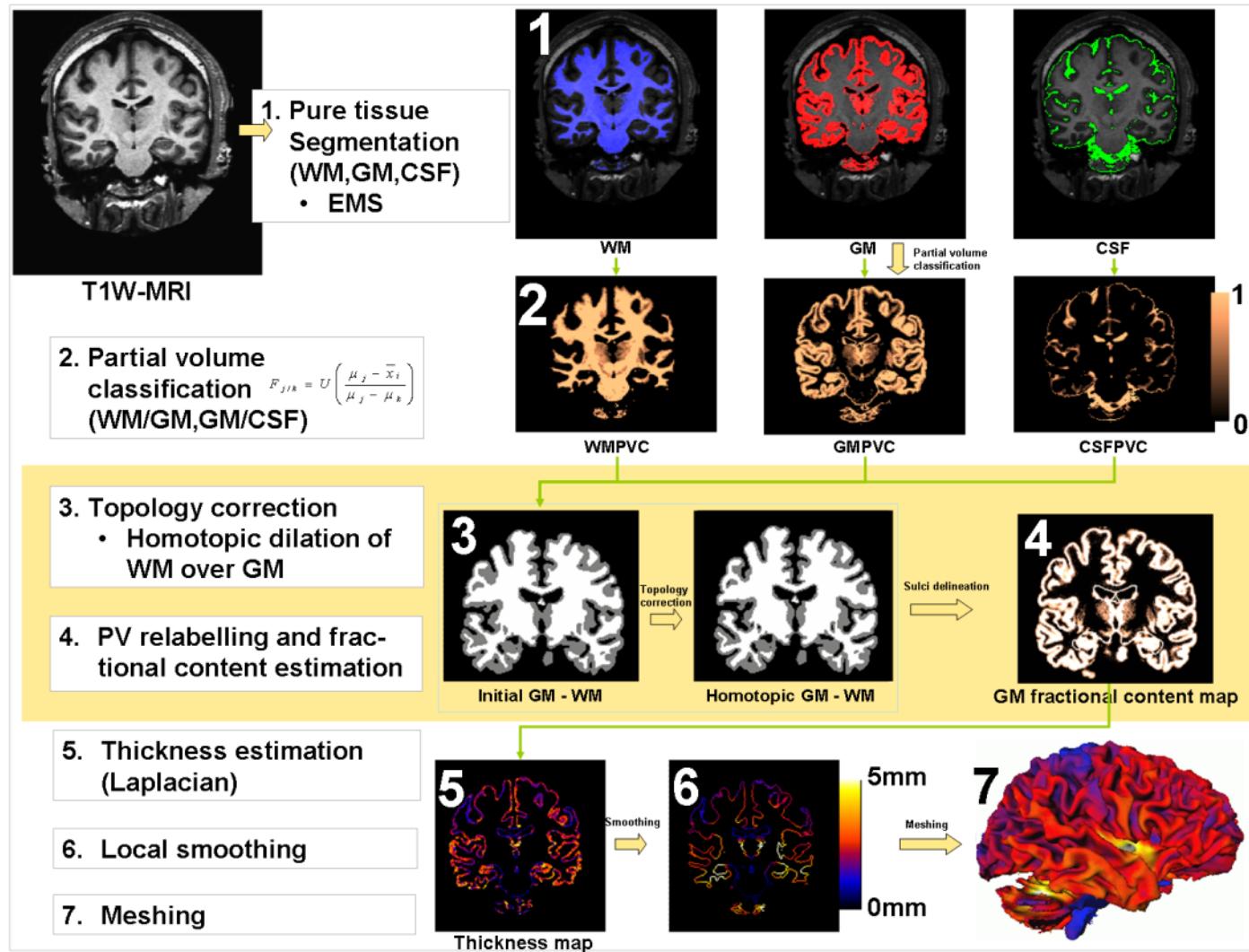


Z-score
and report



Web interface

Structural MRI (cont.)



CurAIBL: MR Assessment of Neurodegeneration

<https://milxcloud.csiro.au>

NOT FOR CLINICAL USE

MR Quantification Report

SUBJECT: HC Anon
AGE: 71.28

REPORT DATE: Thursday 19th March,

Cortical thickness Z-Score map

Z-score was computed using a population of 100 healthy controls (MMSE>28,CRD=0,A β =negative) low cardiovascular risk from the AIBL cohort and was adjusted for age

GM volume (mL) Vs Age

Hippocampus volume (mL) Vs Age

Lateral Ventricular volume (mL) Vs Age

Green region represents the 25%-75% normative percentile. Gray region represents the 5%-95% normative percentile

	Gray Matter	Hippocampus	Lateral Ventricles
Volume (mL)*	604.9	7.7	13.6
[5% - 95%] normal range	[539.1 - 636.6]	[6.2 - 8.4]	[13.0 - 57.9]
Left/Right Asymmetry**	-1.6%	-1.5%	7.5%

aibl The Australian Imaging, Biomarker and Lifestyle Imaging Study of Ageing

Austin Health

For evaluation purposes only. See <https://curailb-milxcloud.csiro.au> for conditions of use. Software version 1.0.

* Volume is ICV adjusted based on the mean AIBL cohort intracranial volume

** Asymmetry is defined as the difference between the left and right uptake divided by their average

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MR Quantification Report

SUBJECT: AD Anon
AGE: 63.50

REPORT DATE: Thursday 19th March, 2015

Cortical thickness Z-Score map

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Lateral Ventricle volume (mL) Vs Age

Green region represents the 25%-75% normative percentile. Gray region represents the 5%-95% normative percentile

	Gray Matter	Hippocampus	Lateral Ventriles
Volume (mL)*	506.8	6.2	31.2
[5% - 95%] normal range	[562.6 - 658.5]	[6.6 - 8.6]	[10.3 - 47.7]
Left/Right Asymmetry**	-0.1%	0.1%	-2.0%

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Cursor Inspector



Cursor position (x,y,z):

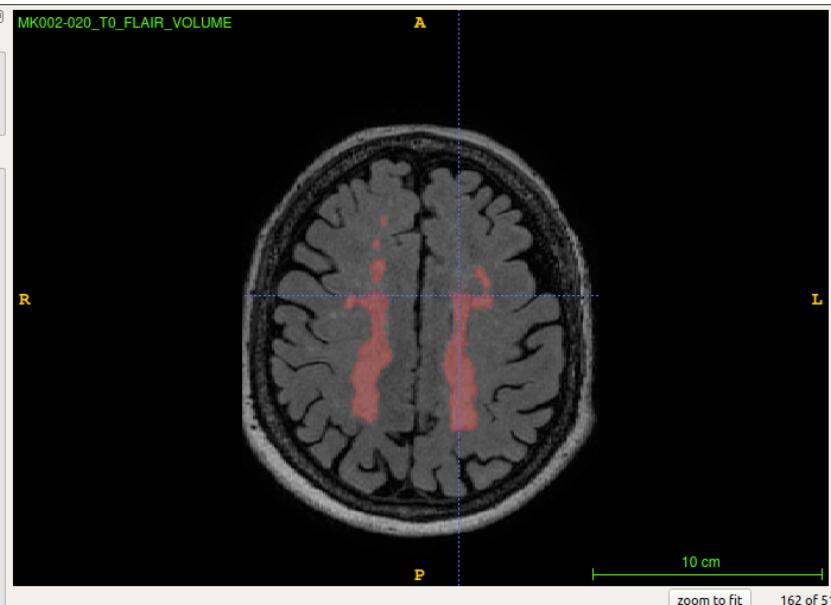
254 162 68

Intensity under cursor:

Layer	Intensity
MK002-020_T0...	167.7

Label under cursor:

1 Label 1

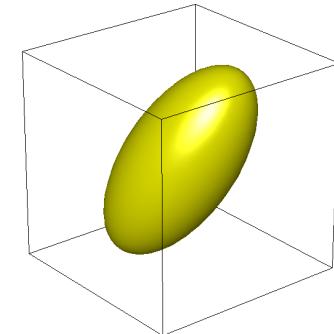
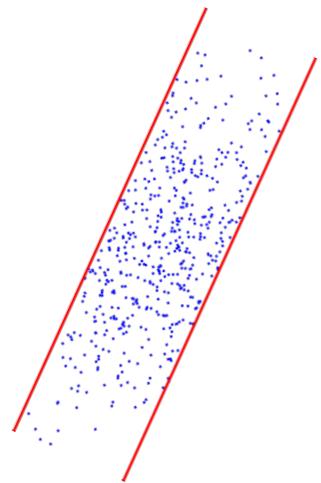
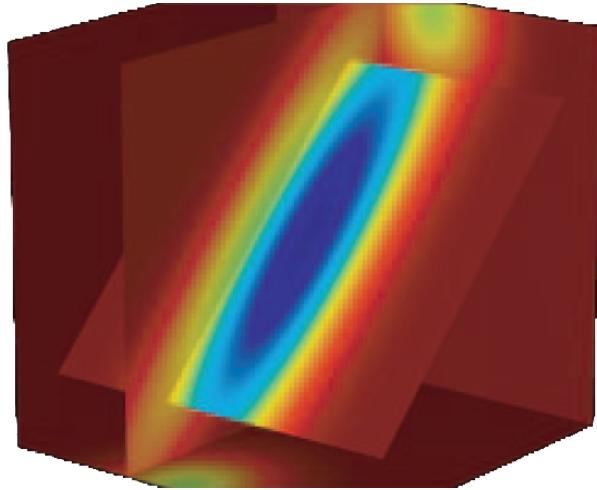
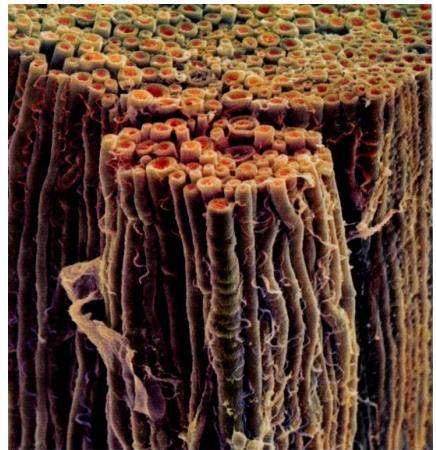
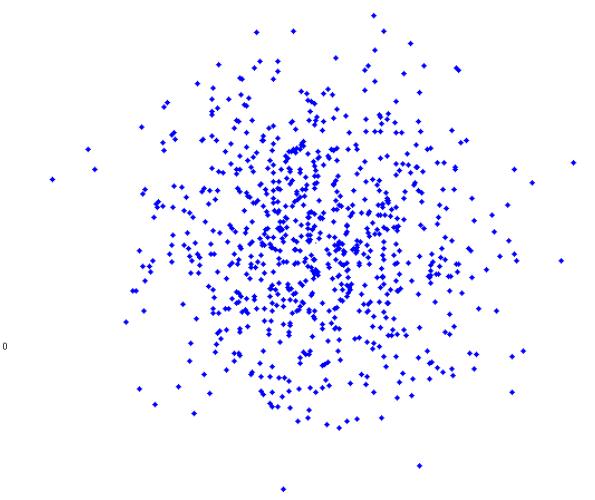
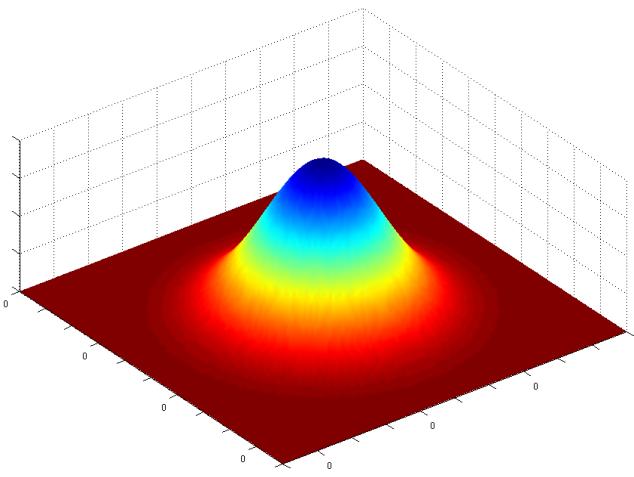


FLAIR WM
lesion segmentation



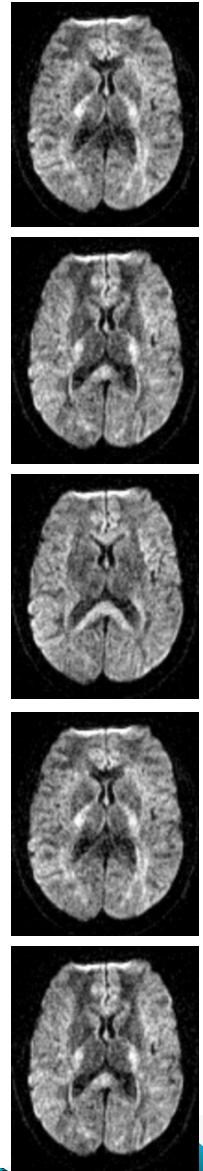
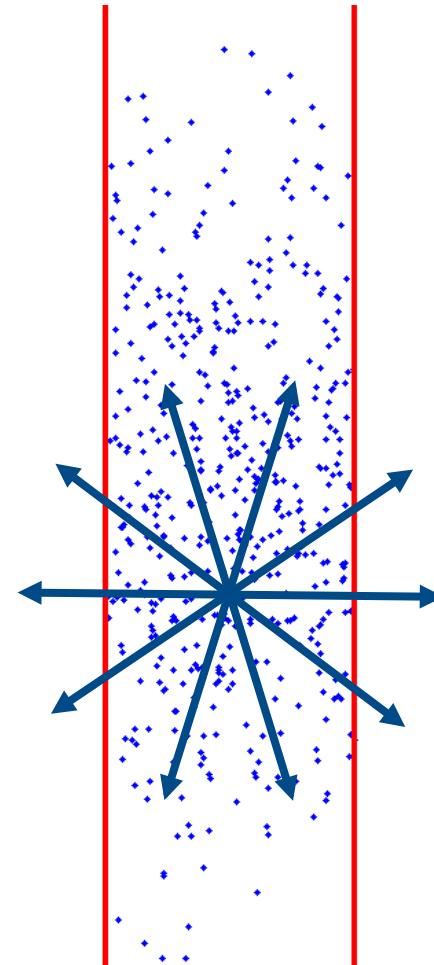
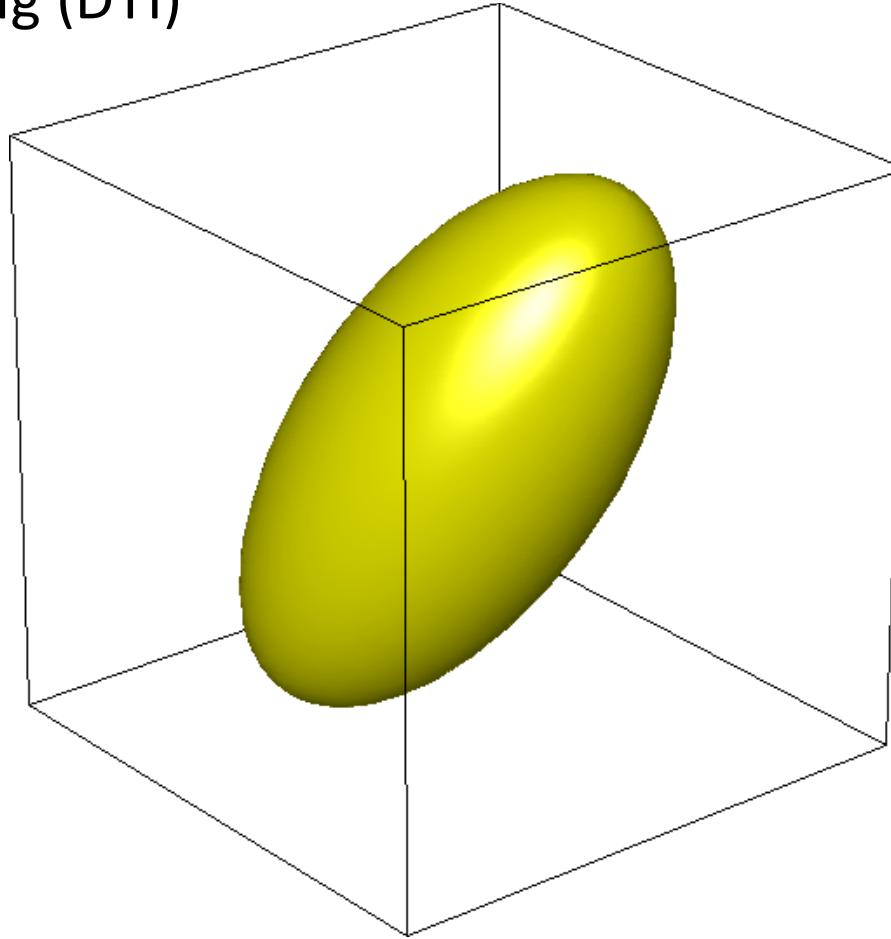
Diffusion MRI: Background

Unrestricted diffusion
Brownian motion



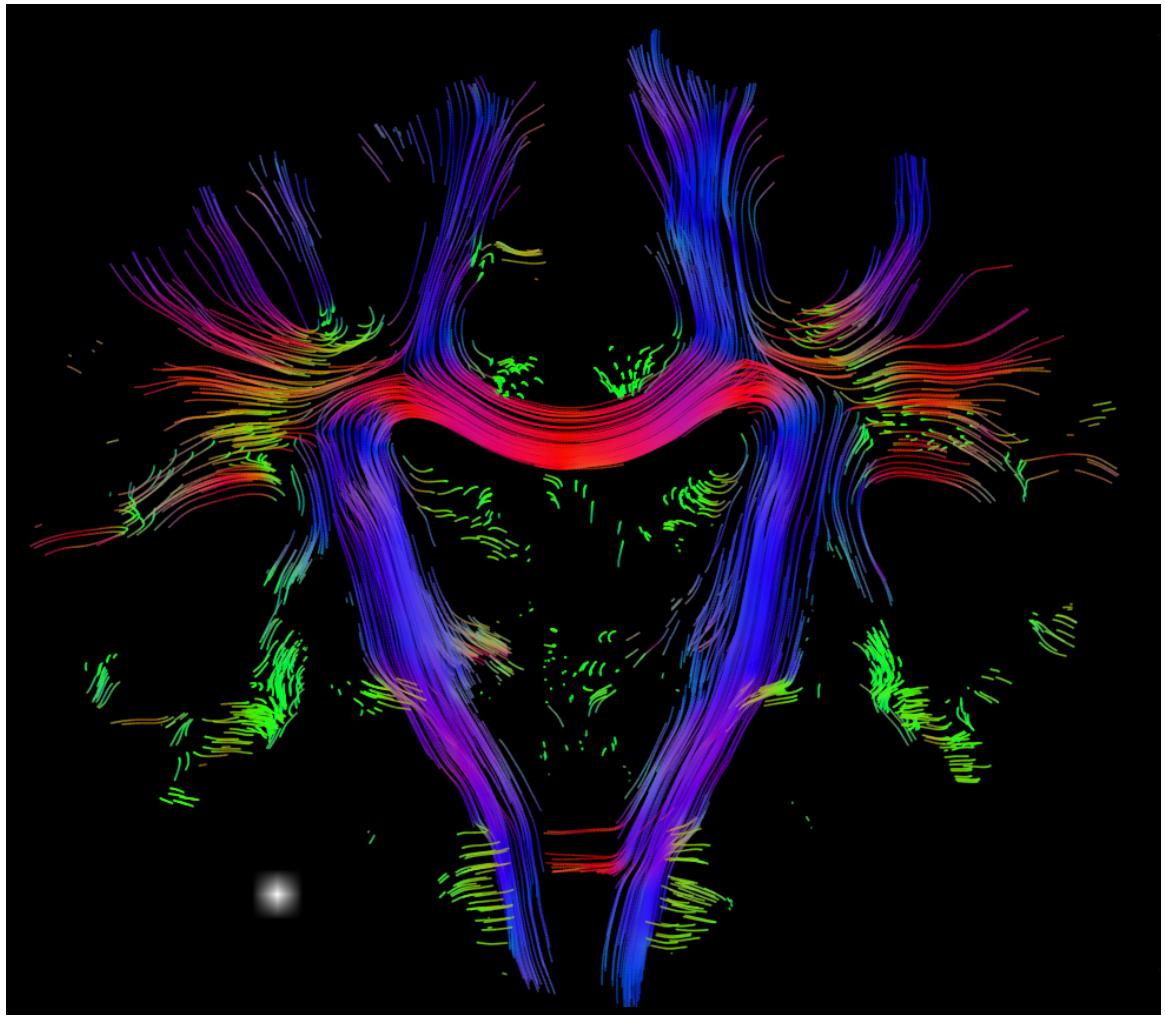
Diffusion MRI: Background

Diffusion Tensor
Imaging (DTI)

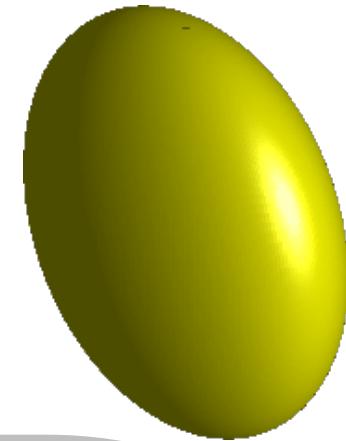
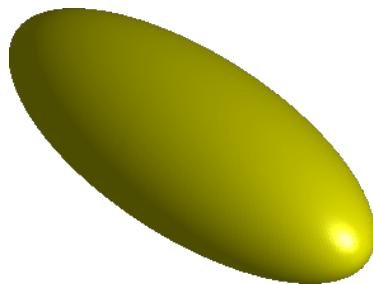
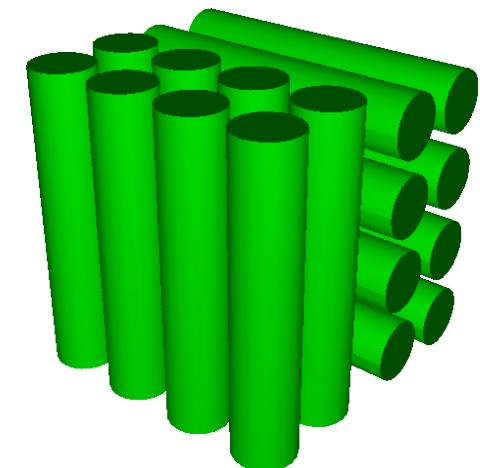
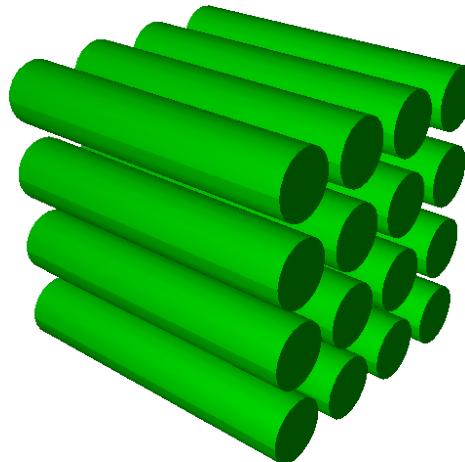
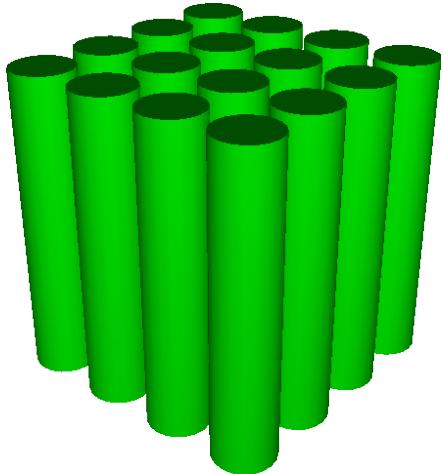


Diffusion MRI: Background

Colour codes
for orientation

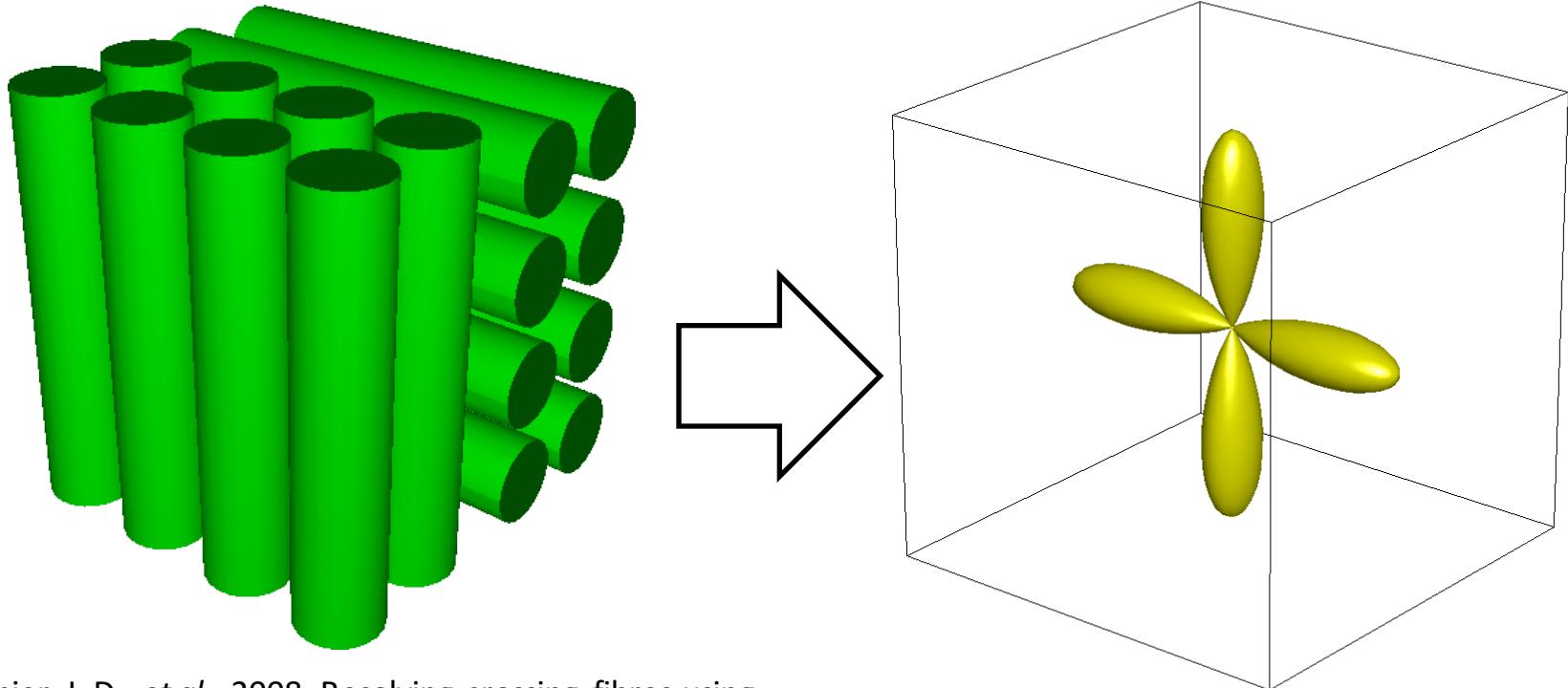


Diffusion MRI: Background



Diffusion MRI: Background

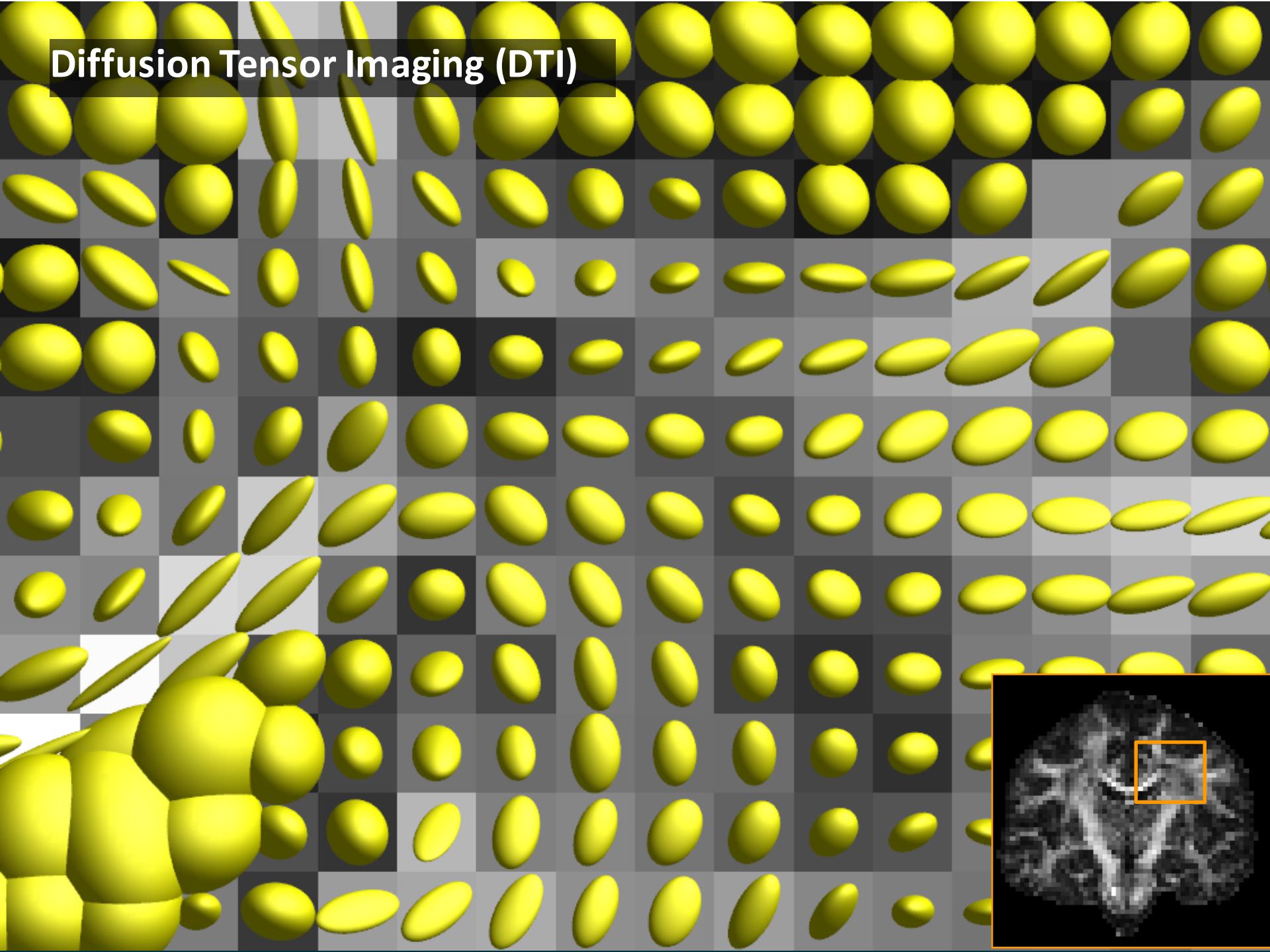
- Fibre Orientation Distribution (FOD)
 - Constrained spherical deconvolution (Tournier *et al.*, 2008)



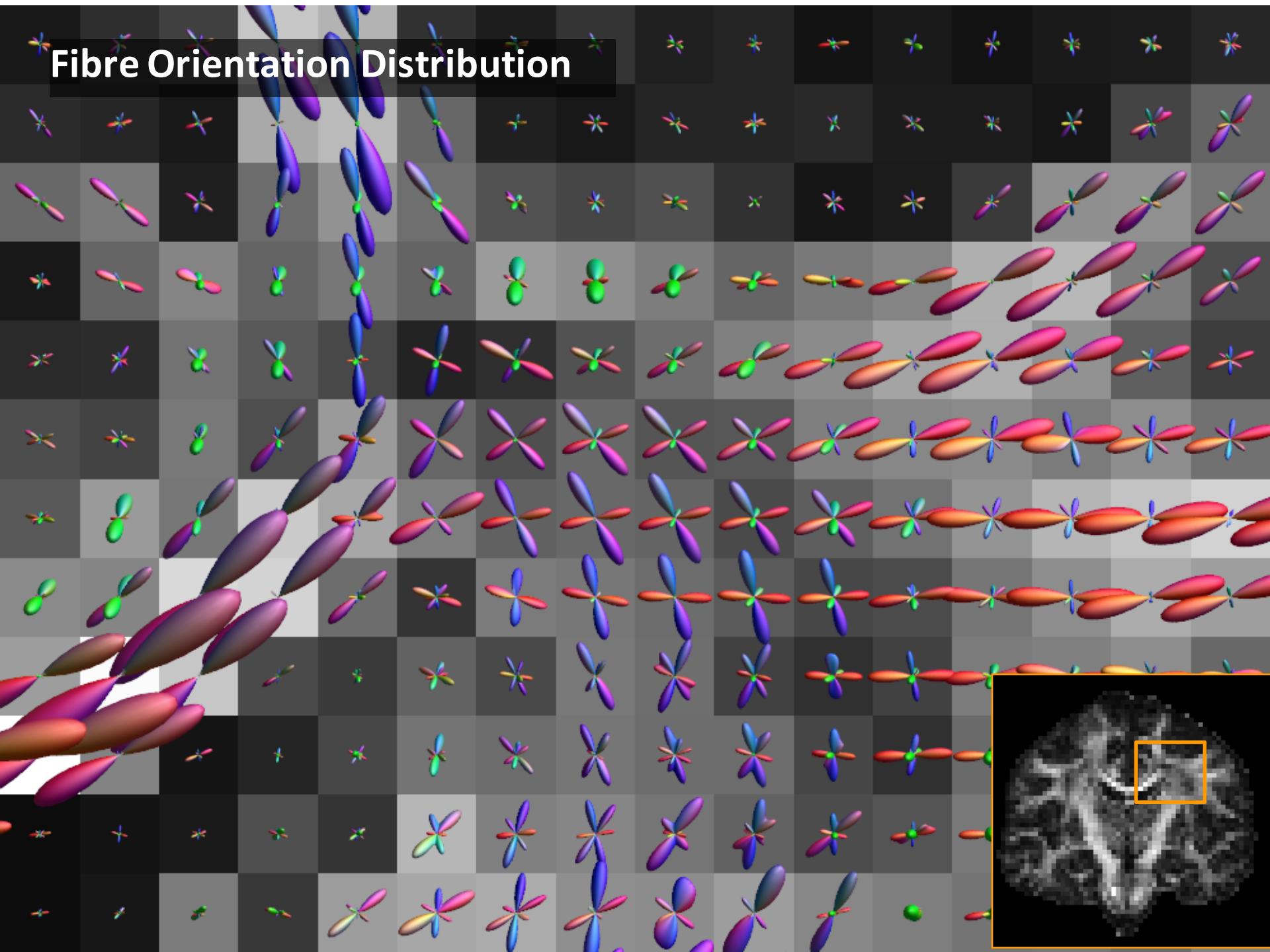
Tournier, J.-D., *et al.*, 2008. Resolving crossing fibres using constrained spherical deconvolution: Validation using diffusion-weighted imaging phantom data. *NeuroImage* 42, 617–625.

Fibre Orientation Distribution
(FOD)

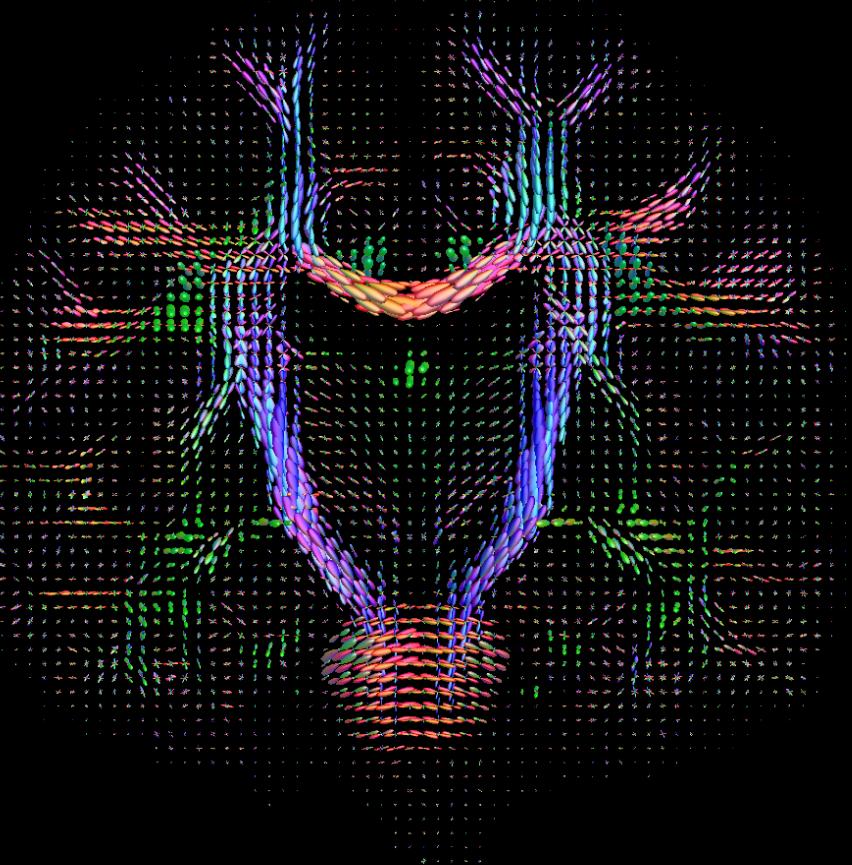
Diffusion Tensor Imaging (DTI)



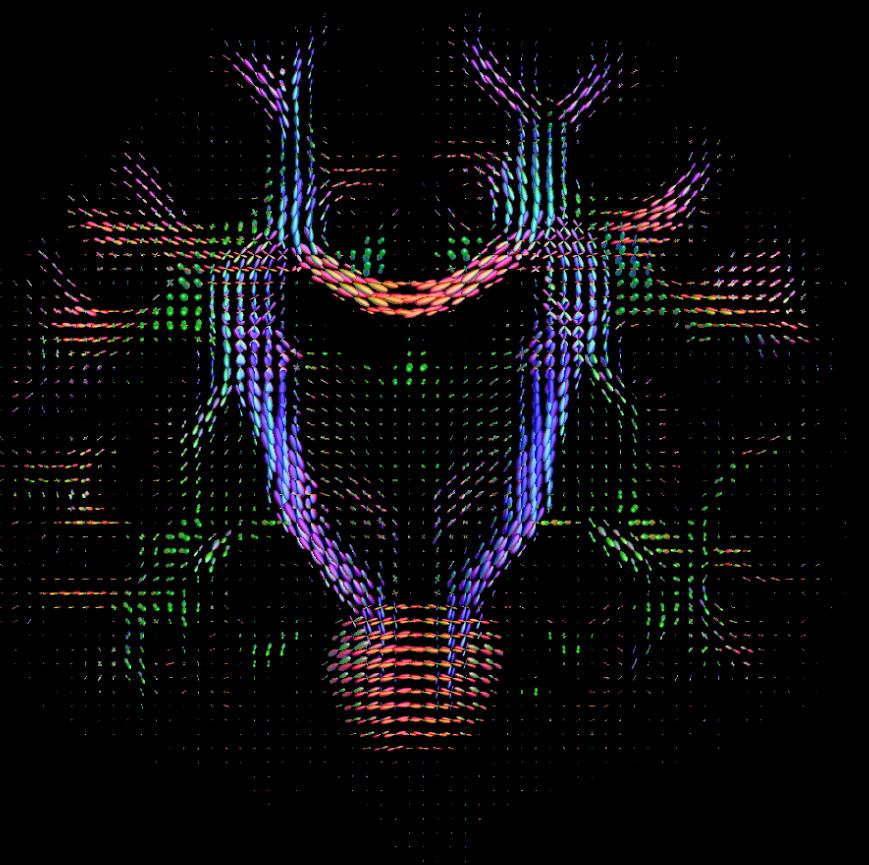
Fibre Orientation Distribution



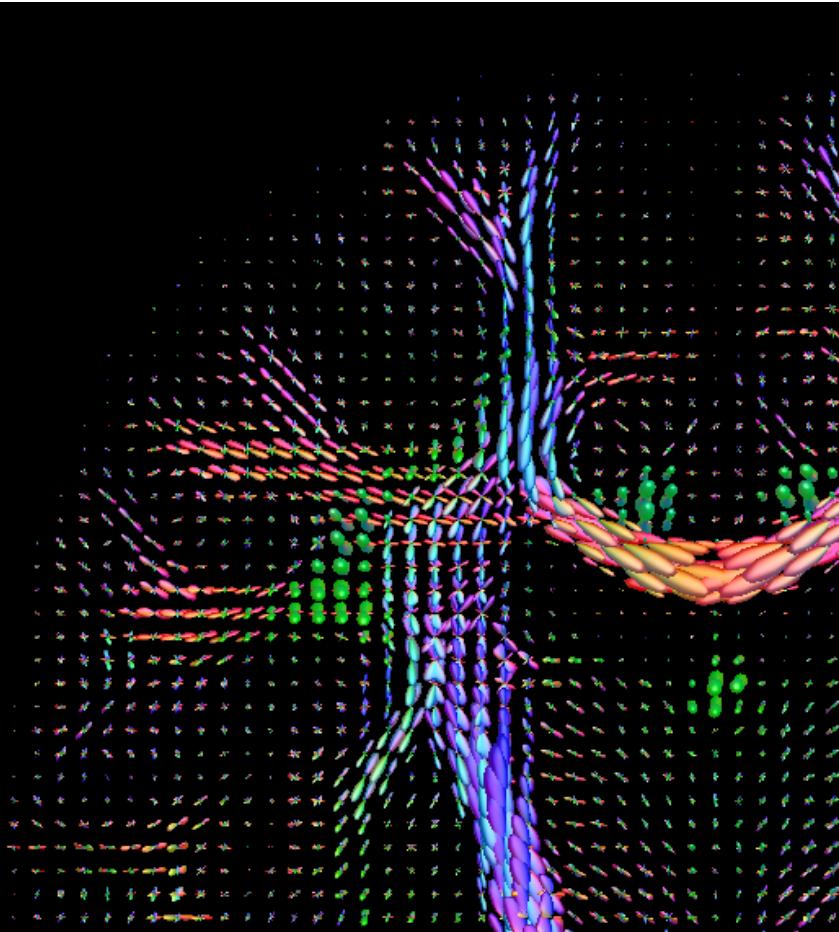
single-shell single-tissue FOD ($b = 3000 \text{ s/mm}^2$)



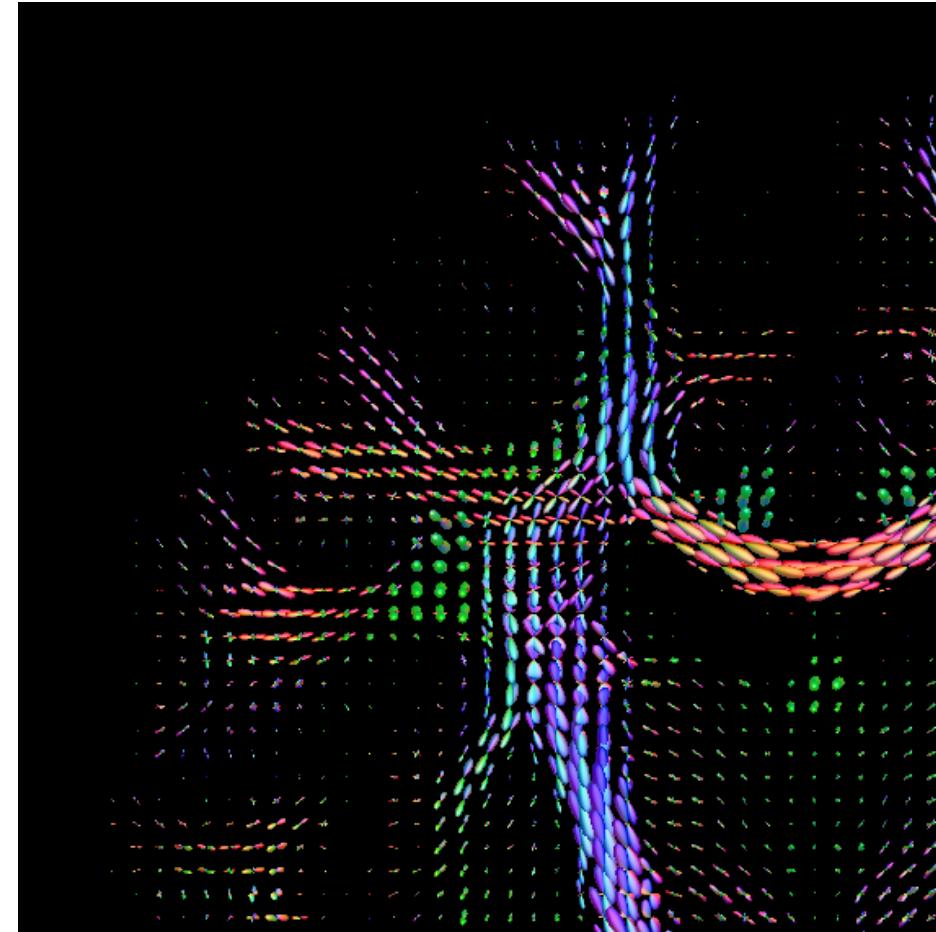
multi-shell multi-tissue FOD



FOD @ $b = 3000 \text{ s/mm}^2$

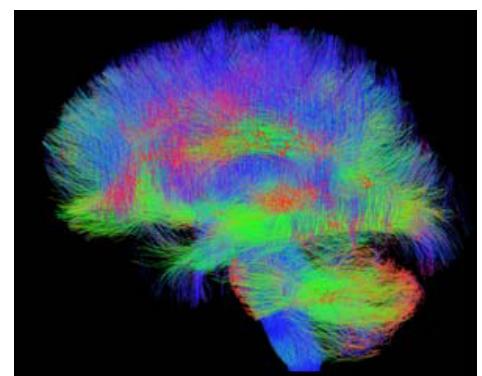
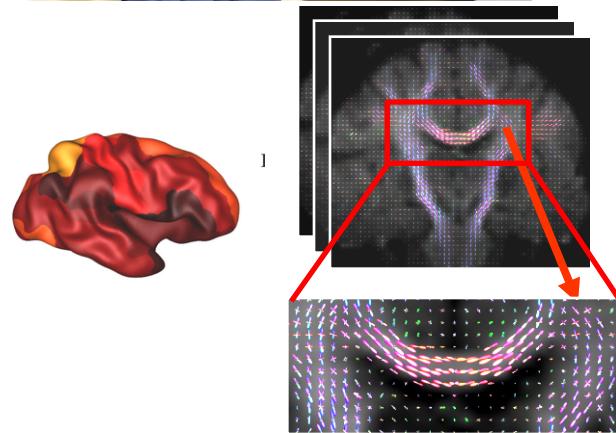


multi-shell multi-tissue FOD



Genetic influence on connectivity

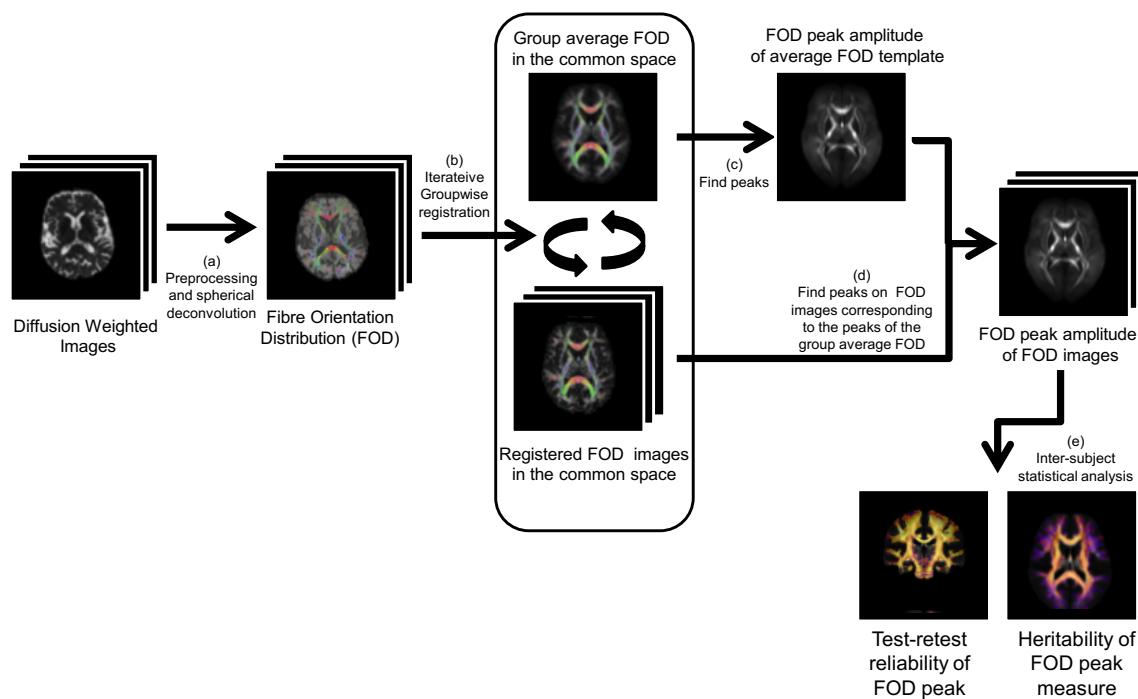
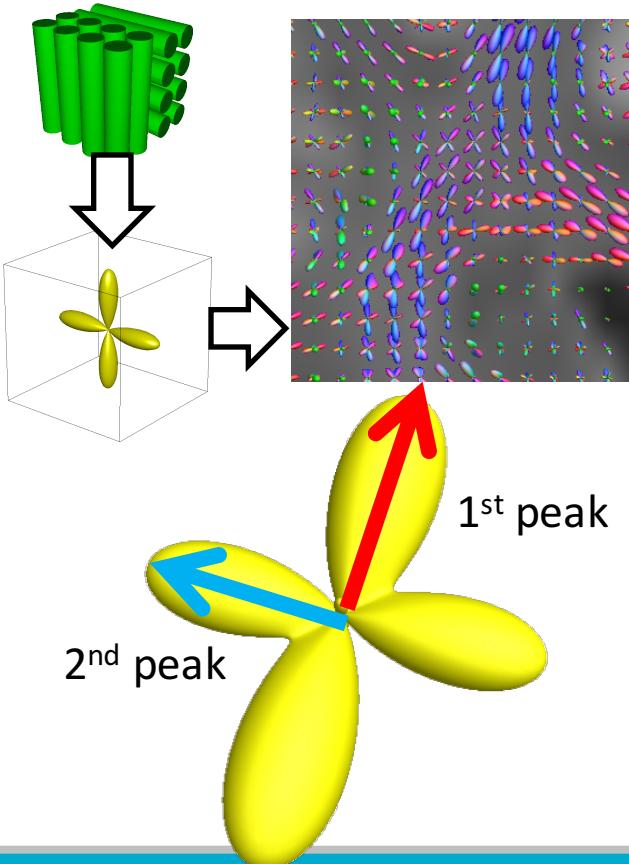
- Aims
 - To develop new insights into brain development
 - To understand how our brains work in health, illness, youth, and old age
 - To study the cerebral cortex and the underlying neural connectivity, from the structural and diffusion MR images
 - To investigate the influence of genes by imaging monozygotic (MZ) and dizygotic (DZ) twins
- Twin Study
 - Queensland Twin IMaging study (QTIM)
 - CSIRO and Queensland Institute of Medical Research (QIMR)



de Zubicaray, G.I., Chiang, M.C., McMahon, K.L., Shattuck, D.W., Toga, A.W., Martin, N.G., Wright, M.J., Thompson, P.M., 2008. Meeting the challenges of neuroimaging genetics. *Brain Imaging Behav.* 2, 258–263.

Genetic influence on connectivity: Methods

- Measure the FODs
 - Peak amplitude
- Processing/Analysis framework
 - Raffelt *et al.*, 2012



Raffelt, D., *et al.*, 2012. Apparent Fibre Density: A novel measure for the analysis of diffusion-weighted magnetic resonance images. *NeuroImage* 59, 3976–3994.

Genetic influence on connectivity: Methods

- Diffusion MR: 94 gradient directions at $b = 1159 \text{ s/mm}^2$
- Twin cohort
 - $N=328$ subjects (118M, 210F), age 22.7(2.3)
 - 71 pairs ($N=142$, 48M, 94F) of monozygotic twins (MZ) + 90 pairs ($N=180$, 69M, 111F) of dizygotic twins (DZ)
- Heritability
 - ACE model: Additive genetics + Common environment + unique Environment

$$\text{FOD} = A + C + E$$

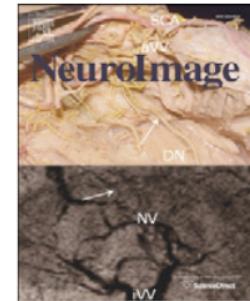
- Heritability

$$h^2 = \frac{\text{Var}(A)}{\text{Var}(A) + \text{Var}(C) + \text{Var}(E)}$$

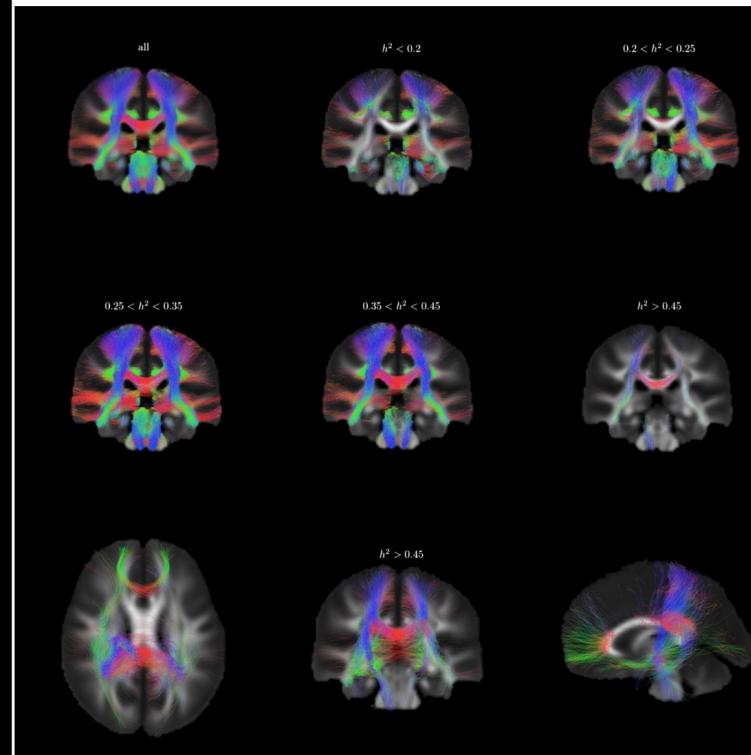
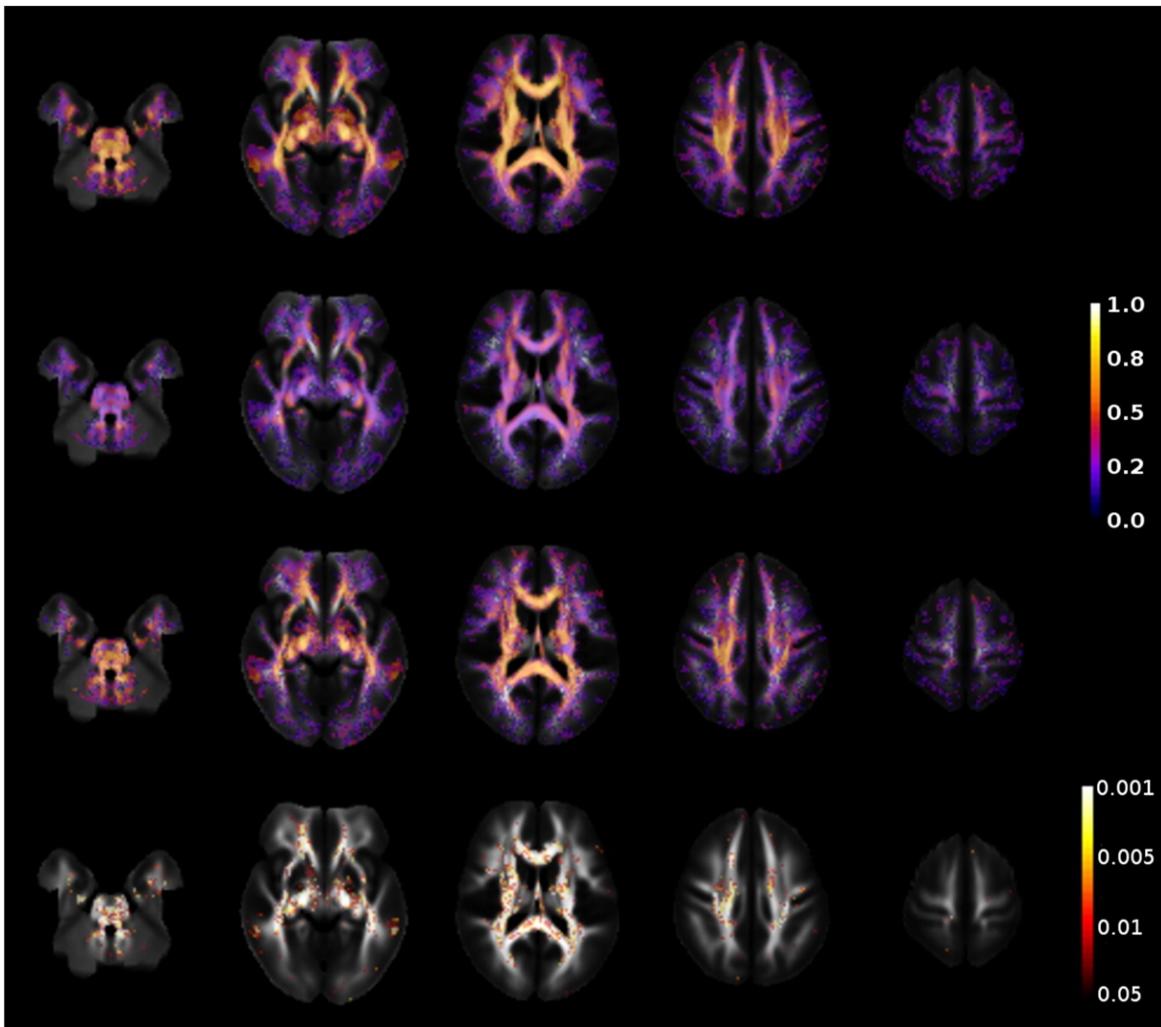
Falconer's formula

$$h^2 = 2(r_{\text{MZ}} - r_{\text{DZ}})$$

Investigating brain connectivity heritability in a twin study using diffusion imaging data

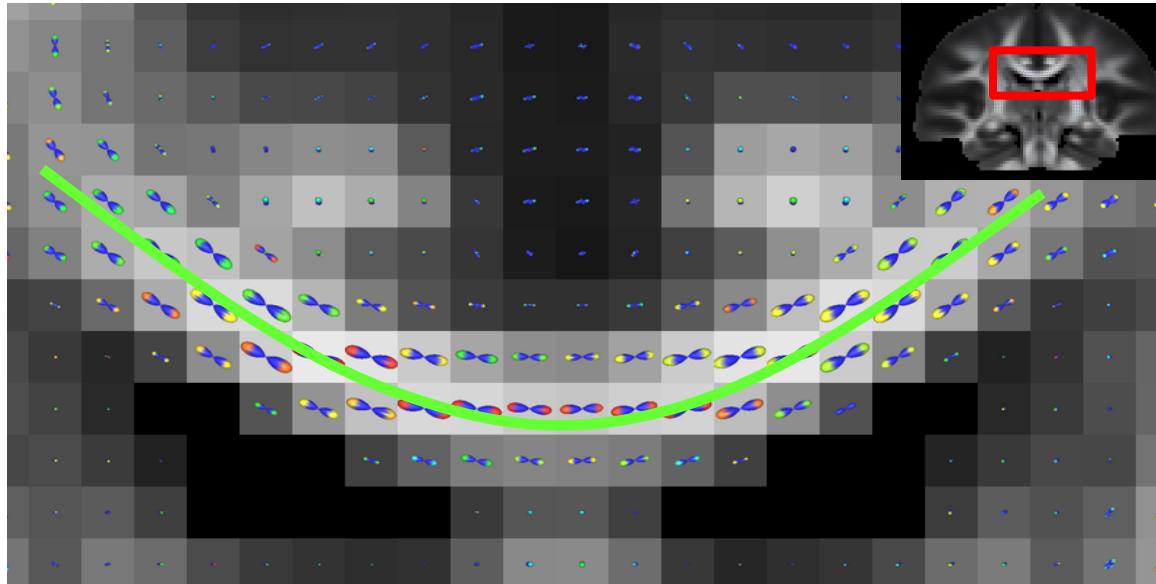


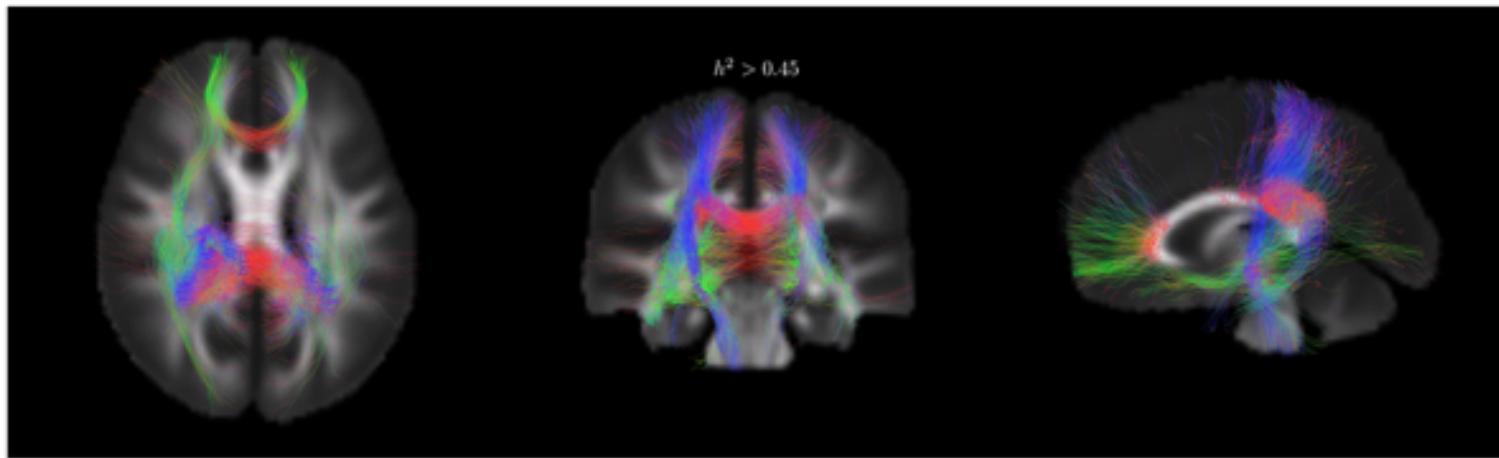
Kai-Kai Shen ^a, Stephen Rose ^a, Jurgen Fripp ^a, Katie L. McMahon ^b, Greig I. de Zubicaray ^c, Nicholas G. Martin ^d, Paul M. Thompson ^e, Margaret J. Wright ^d, Olivier Salvado ^a



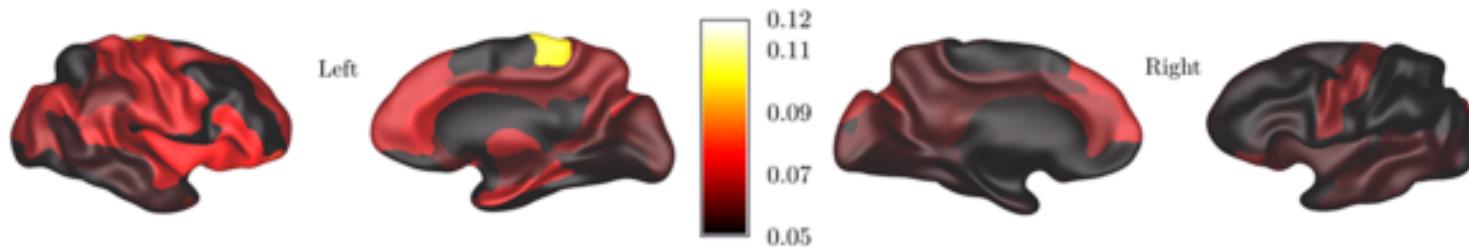
Genetic influence on connectivity: Methods

- Tractography
 - Whole brain, probabilistic using FOD
- Tract-wise heritability
 - Interpolation of heritabilities of nearest peaks
 - Tract average heritability





(a) A tractogram of fiber tracts with average $h^2 > 0.45$.

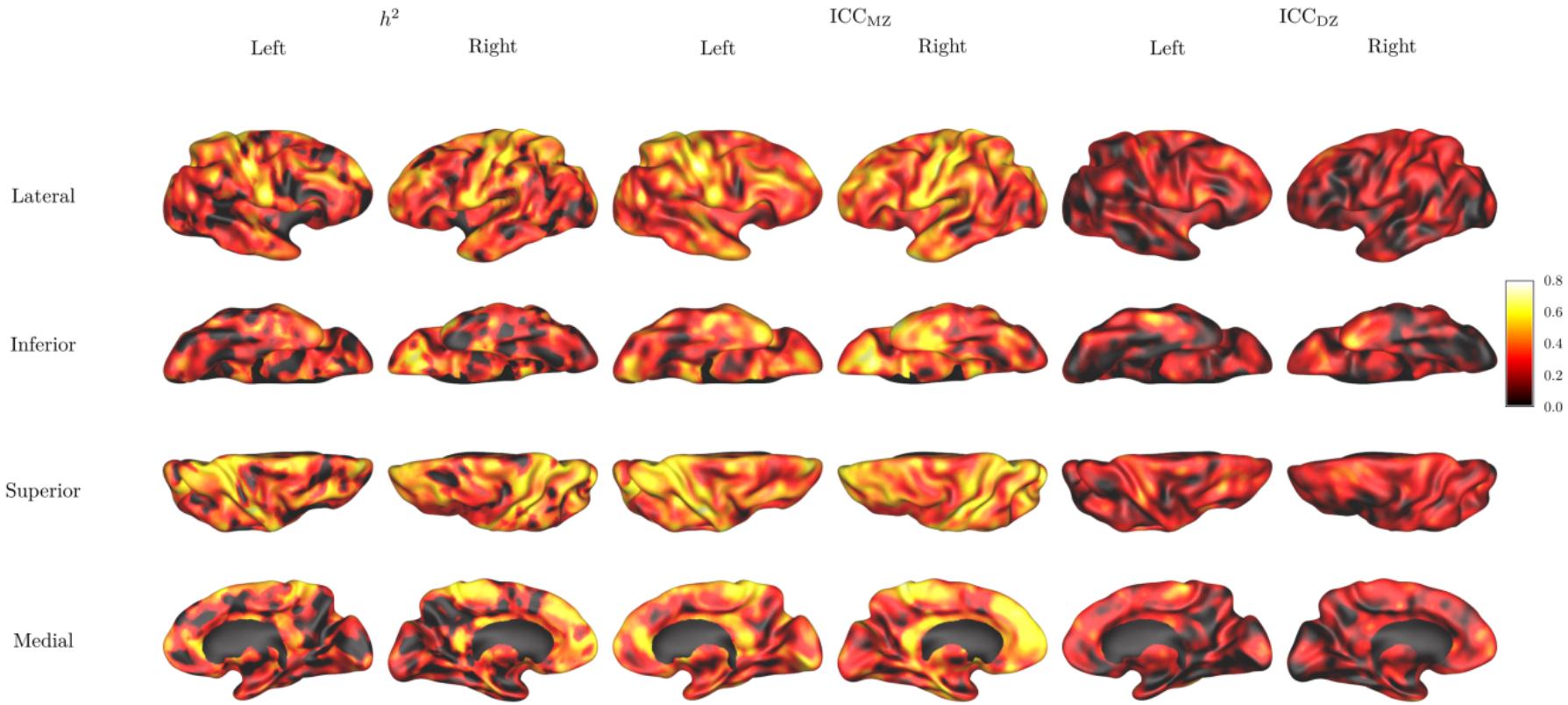


(b) mean h^2 of fiber tracts connected to each cortical region

Human Brain Mapping

Volume 37, Issue 6, pages 2331-2347, 23 MAR 2016 DOI: 10.1002/hbm.23177

<http://onlinelibrary.wiley.com/doi/10.1002/hbm.23177/full#hbm23177-fig-0004>

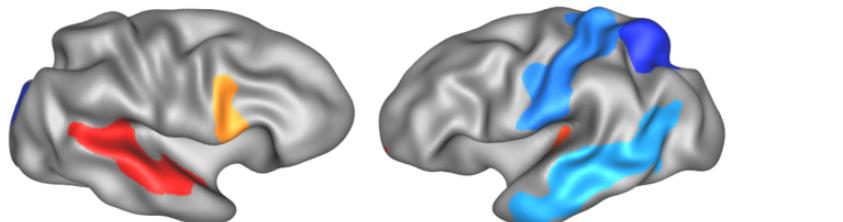


Heritability maps of cortical thickness. From left to right: heritability index h^2 , intraclass correlation between monozygotic twins ICC_{MZ} , intraclass correlation between dizygotic twins ICC_{DZ} .

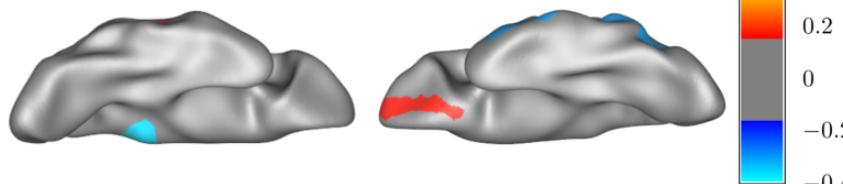
Left

Right

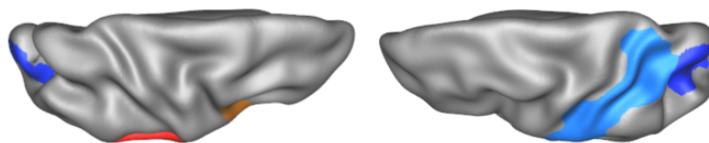
Lateral



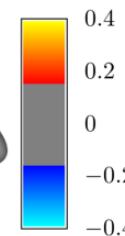
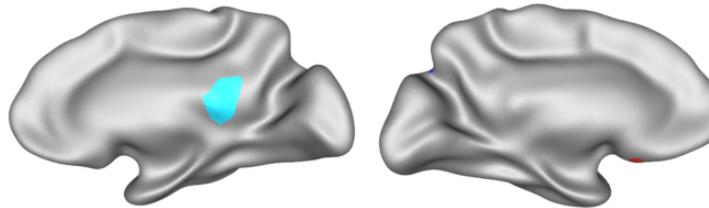
Inferior



Superior



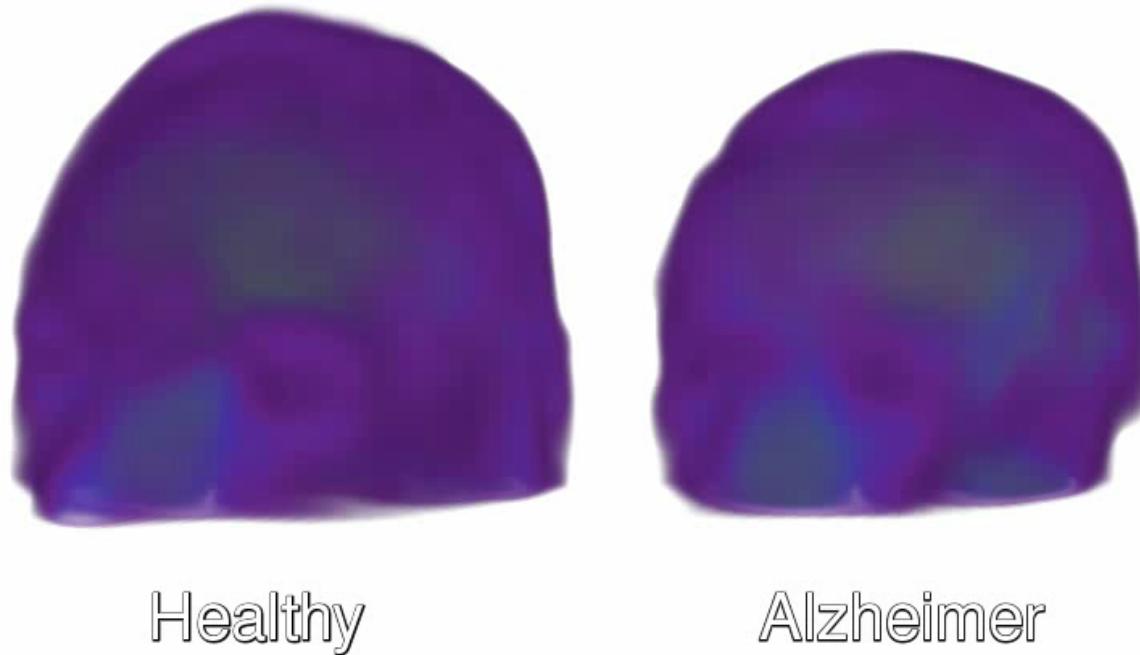
Medial



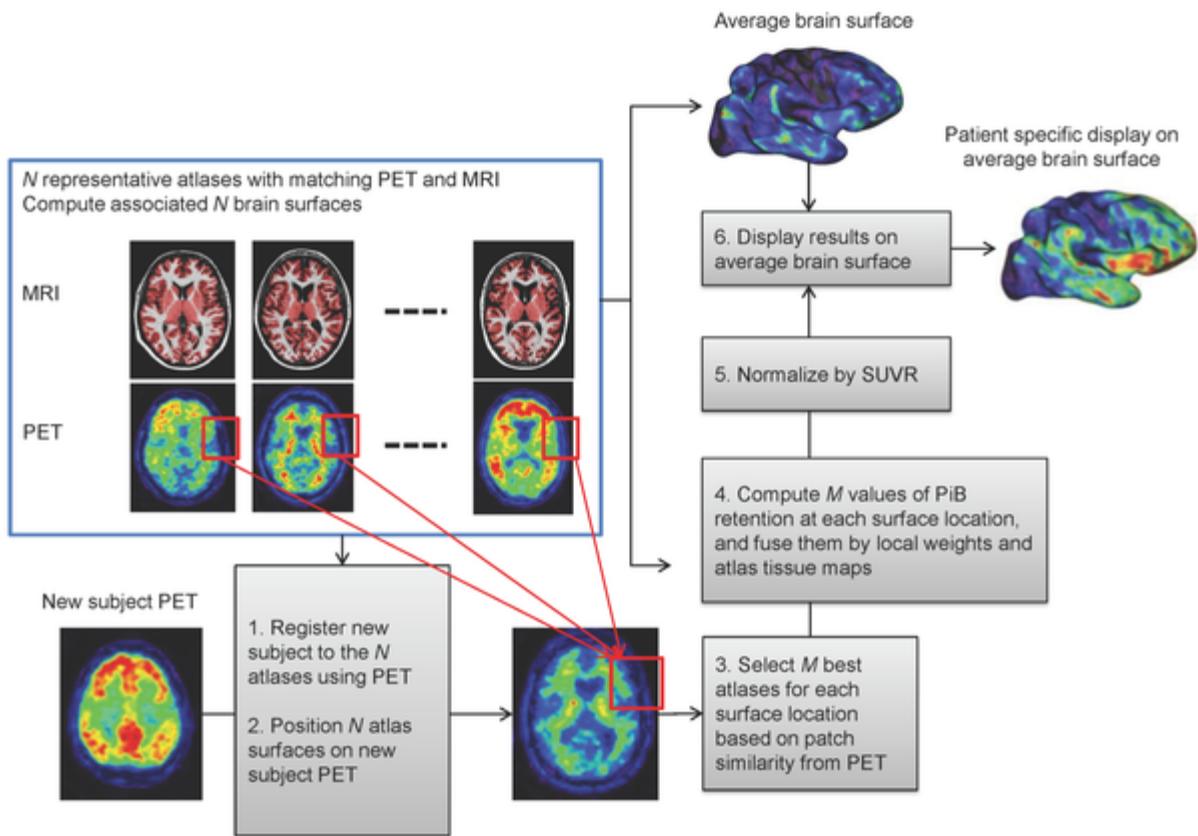
The genetic correlation r_g between the cortical thickness and white matter connectivity measured for each cortical region.

Positron Emission Tomography (PET)

- β -amyloid plaque in Alzheimer's disease
- PET ^{11}C -PiB has been used as the tracer in many clinical studies since 2006

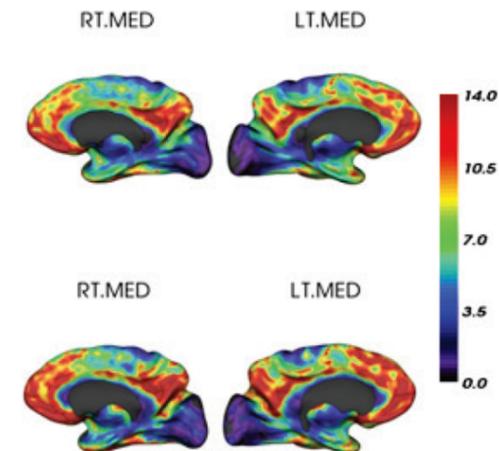


PET: Quantification



Multi-atlas

- Local Patch based selection.
- Bayesian Fusion
- Estimated GM



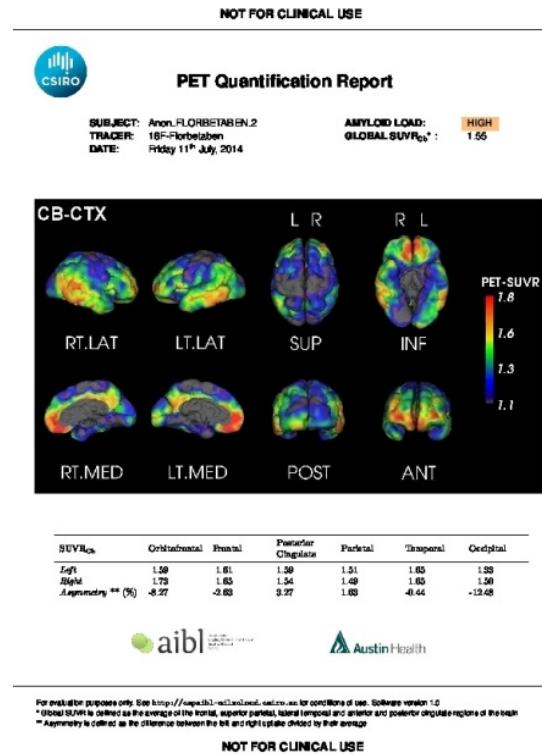
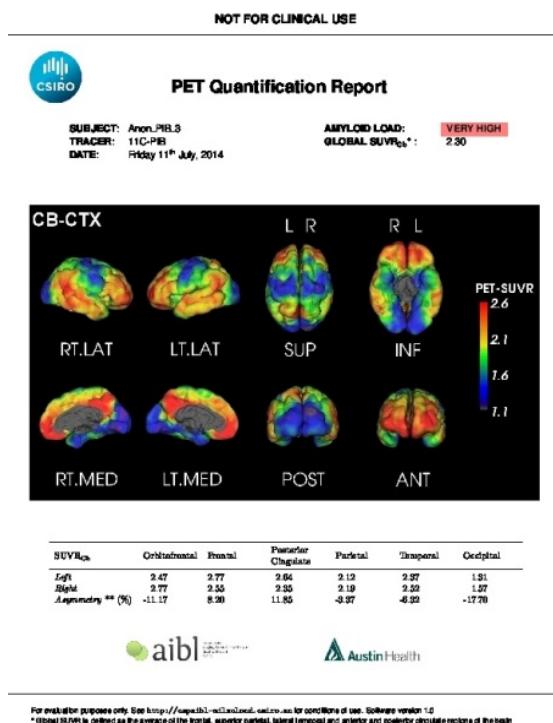
Results:

MR based top
PET only bottom

CapAIBL: PET Assessment of Neurodegeneration

MILXCloud: <https://milxcloud.csiro.au/>

- CapAIBL: PET quantification
- CurAIBL: MRI



Acknowledgement

Olivier Salvado
Jurgen Fripp
(CSIRO)

Pierrick Bourgeat
Shekhar Chandra
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Thank you

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