Using MRI to link Microstructure and Macrostructure

Bruce Fischl

MGH ATHINOULA A. MARTINOS CENTER Harvard Medical School

MIT CSAIL/HST

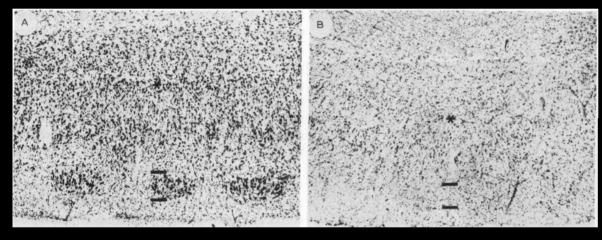


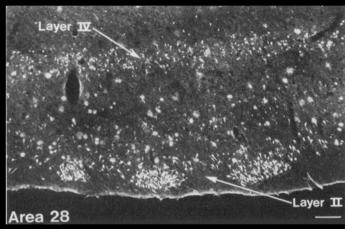
Histology in Alzheimer's Disease

(entorhinal cortex=BA28)

CONTROL

AD





Nissl Stain

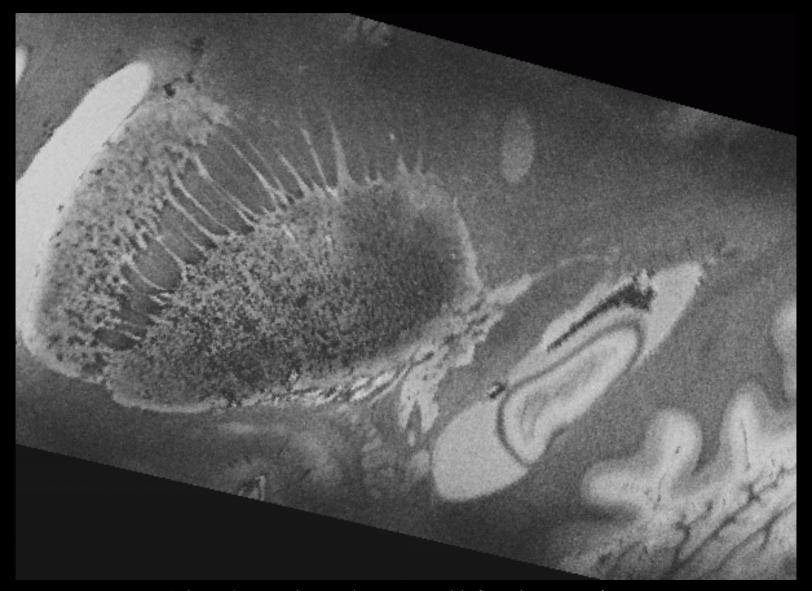
thioflavin S (neurofibrillary tangles and neuritic plaques)

Thanks to Brad Hyman and Jean Augustinack for this slide.

Why Image ex vivo brains?

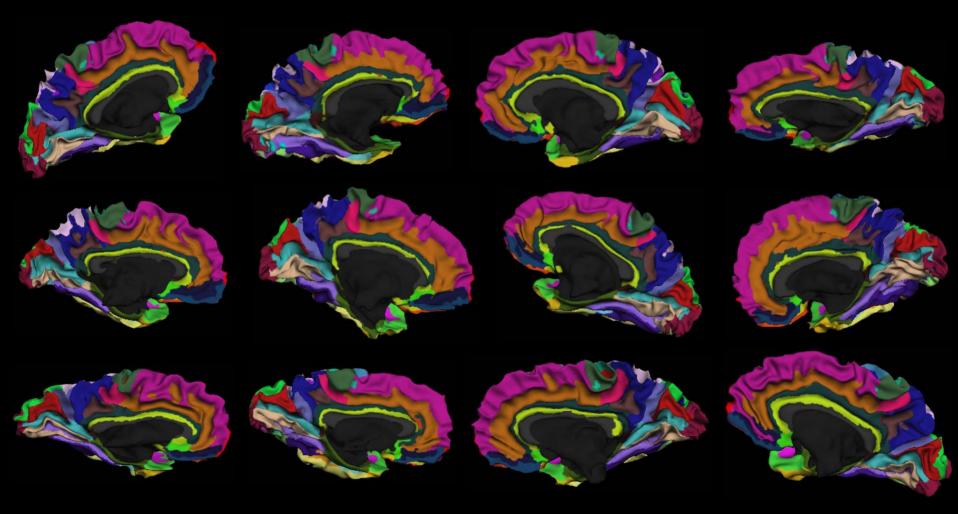
Can obtain orders of magnitude more SNR than *in vivo*, allowing the direct visualization of otherwise (almost) undetectable histological properties.

Imaging Cytoarchitecture (150µm)



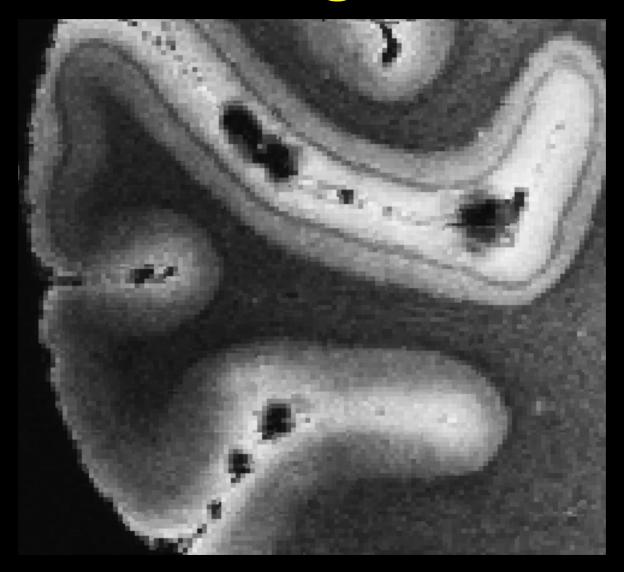
(that's why they call it the striatum)

Automatic Parcellation of ex vivo Hemispheres



Thanks to Brian T Quinn for helping generate these results

Delineating Area 17



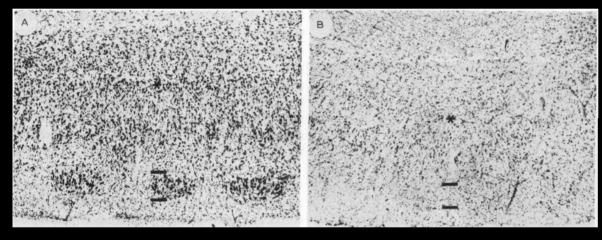
7T, 160 μ m isotropic, NEX=2, 4 echos, TR=55 ms, esp 13ms, α =10°

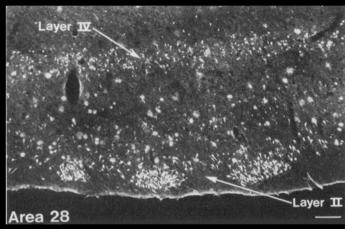
Histology in Alzheimer's Disease

(entorhinal cortex=BA28)

CONTROL

AD



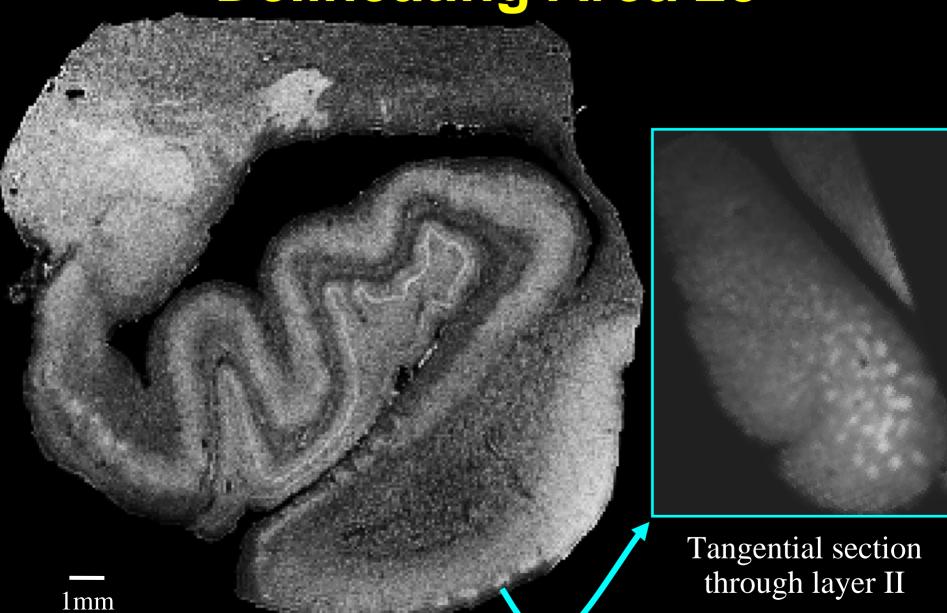


Nissl Stain

thioflavin S (neurofibrillary tangles and neuritic plaques)

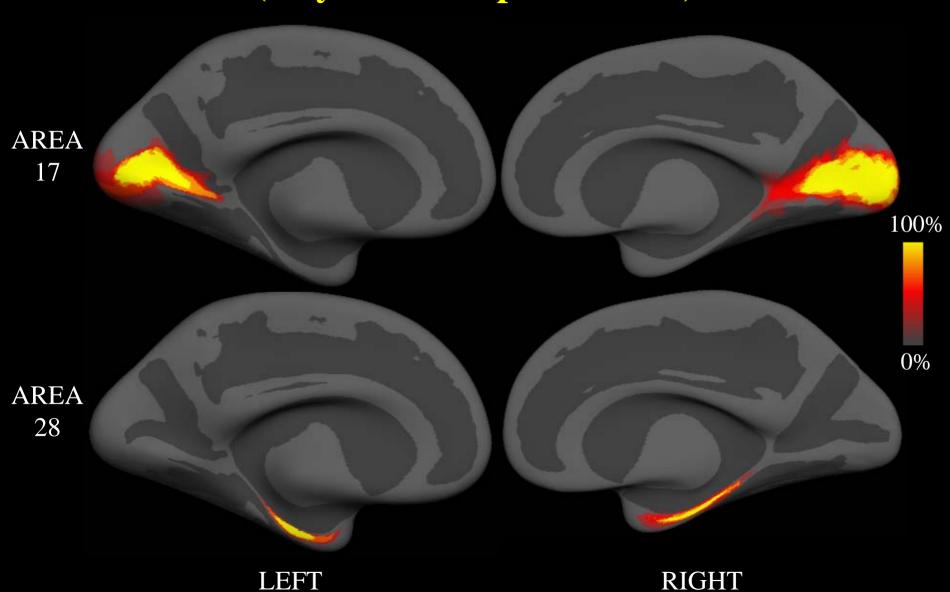
Thanks to Brad Hyman and Jean Augustinack for this slide.

Delineating Area 28

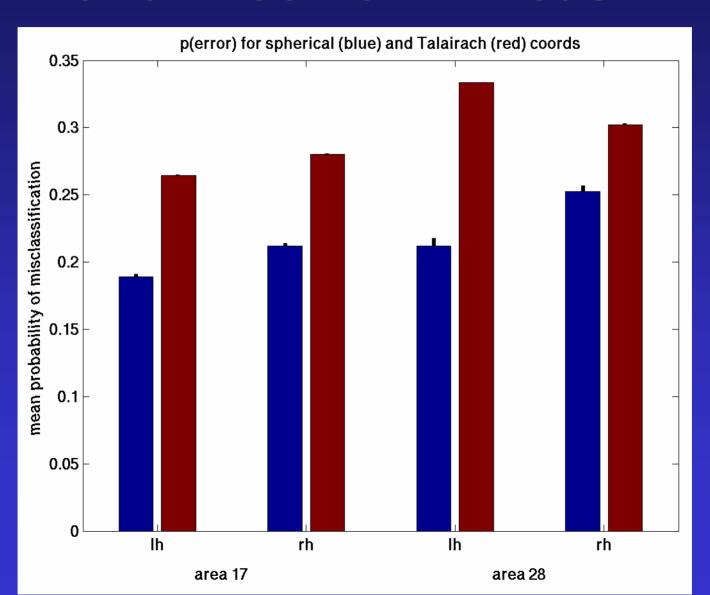


Predicting Brodmann Areas from MRI

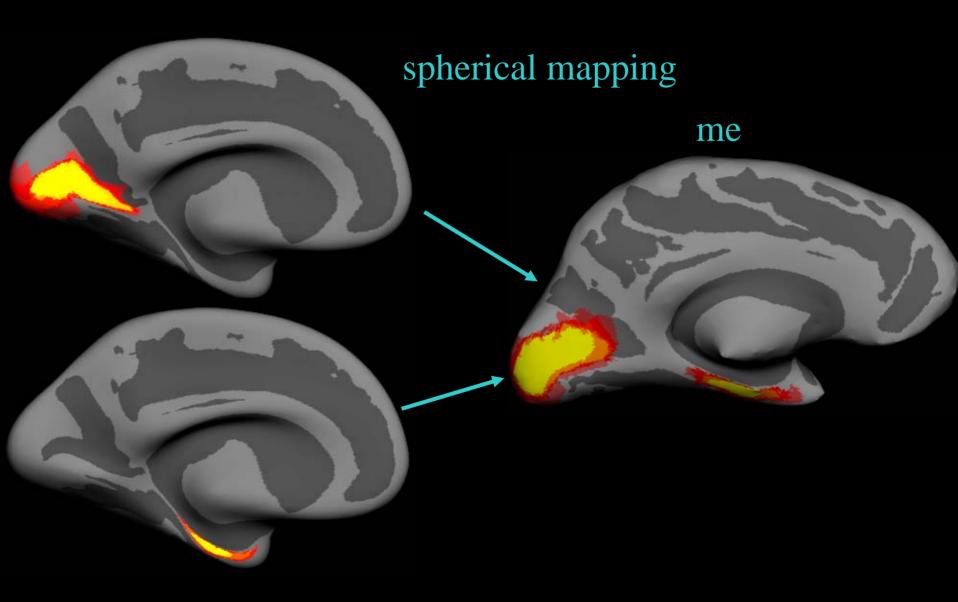
(only 5-6 hemispheres/area)



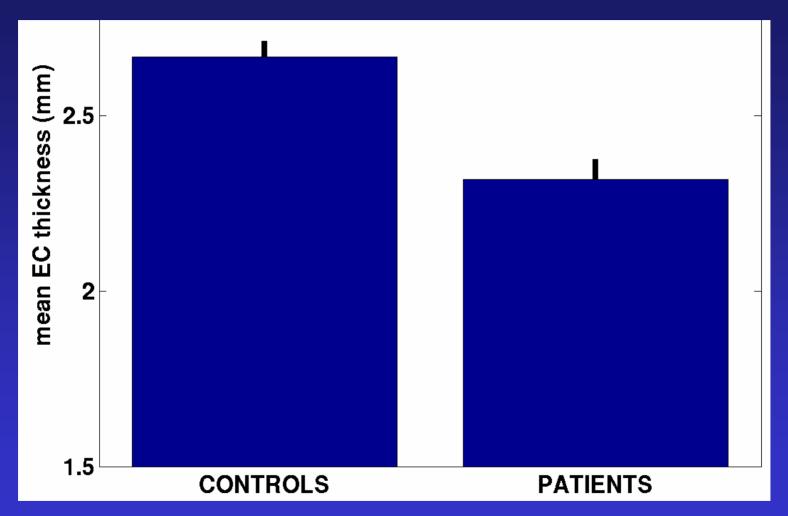
Comparing Coordinate Systems and Brodmann Areas



Making in vivo Predictions



Assessing Degeneration in AD

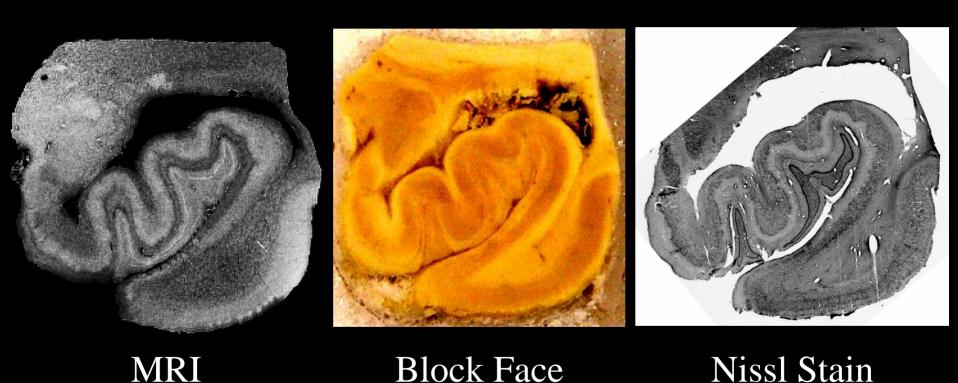


Thickness difference in cytoarchitecturally defined entorhinal cortex between 57 patients (22 CDR 1, 35 0.5) and 58 controls (p<10⁻⁵).

How to visualize additional areas/borders?

- 1. Increase SNR by building phased arrays (in collaboration with Larry Wald, Graham Wiggins and Siemens).
- 2. Determine borders with standard histology, and align histological images with MR (in collaboration with Gheorghe Postelnicu and Jean Augustinack).
- 3. MR Histology make histological stains MR visible (in collaboration with Christian Farrar, Megan Blackwell, Jean Augustinack and Bruce Rosen).

Transferring Histological Information to MRI



Joint work with Jean Augustinack, Matt Frosch, Gheorghe Postelnicu and Andre van der Kouwe

Entropy-based Rigid Registration

ML (Leventon and Grimson, 1998) similarity metric drawback:

- -The model is specified by a pair of manually aligned images → all histograms should coincide
- -The metric is sensitive to the overlapping area of the 2 images

Entropy
$$H(X) = \sum_x p_X(x) \log_2(p_X(x))$$
 Joint Entropy
$$H(X,Y) = \sum_x p(x,y) \log_2(p(x,y))$$
 Mutual Information
$$MI(X,Y) = H(X) + H(Y) - H(X,Y)$$

Use Mutual Information (MI) or Joint Entropy (JE) as similarity metric:

- -No need to use prior manually aligned pair;
- -Robust to change in direction of contrast

Drawbacks:

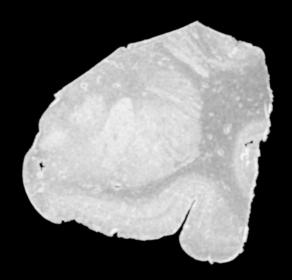
-Does not take spatial correlations in the image into account.

Proposed Solution

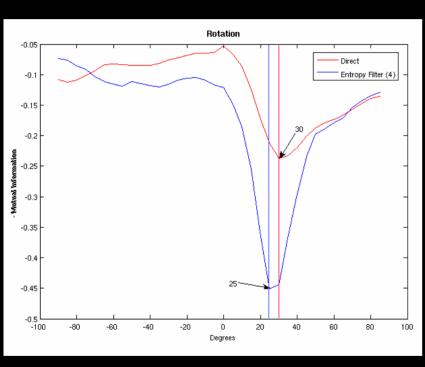
• Use MI or JE and consider a texture filter instead of the noisy histology slice

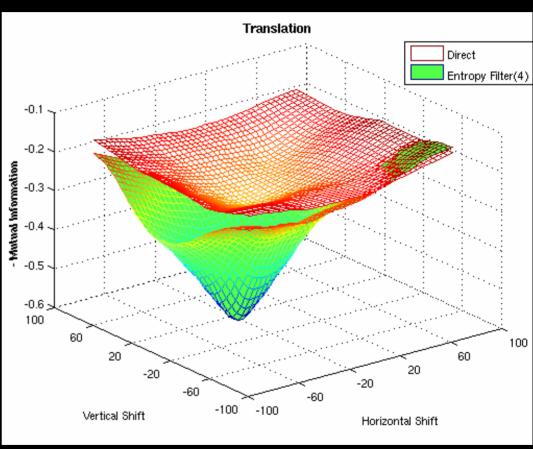
Entropy filter size r

$$EF_r(i,j) = H\left(I(i \pm r, j \pm r)\right)$$

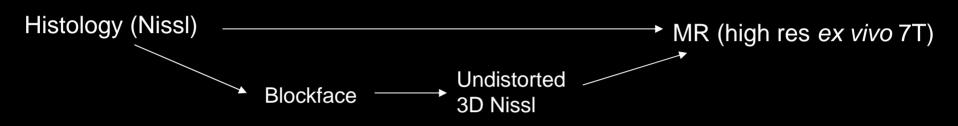


Probing Capture Regions (Mutual Information)





Histology Volume Reconstruction and Registration with MR data



Steps:

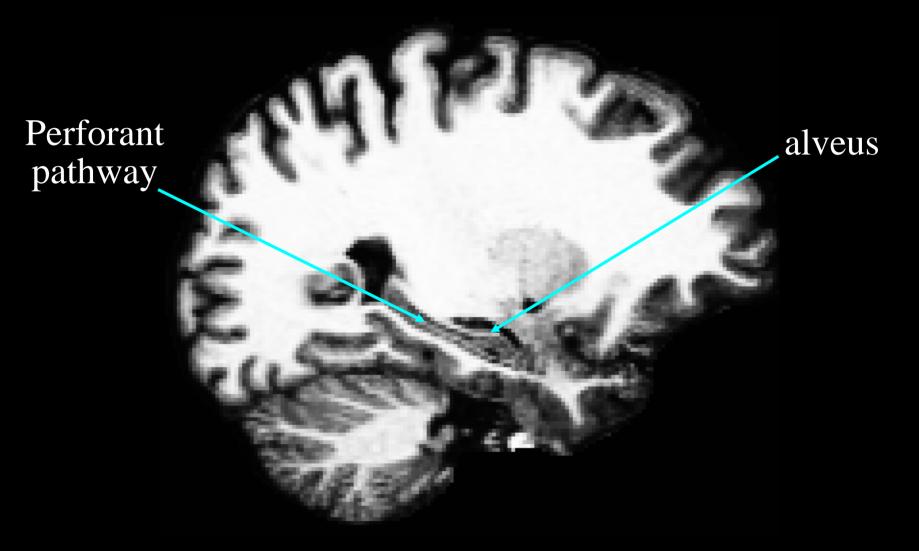
- 1. Reconstruct a 3D volume from the histology slices
 - Automatic rigid registration with the blockface pictures;
 - Correct mounting distortions (elastic warping)
- 2. Align histology volume to the MR
 - Rigid registration (3D)
 - In this case → also non-rigid (tubing problems and MR distortions)

Joint work with Jean Augustinack and Gheorghe Postelnicu

Overview of the MR->Histology Rigid Nissl Registration

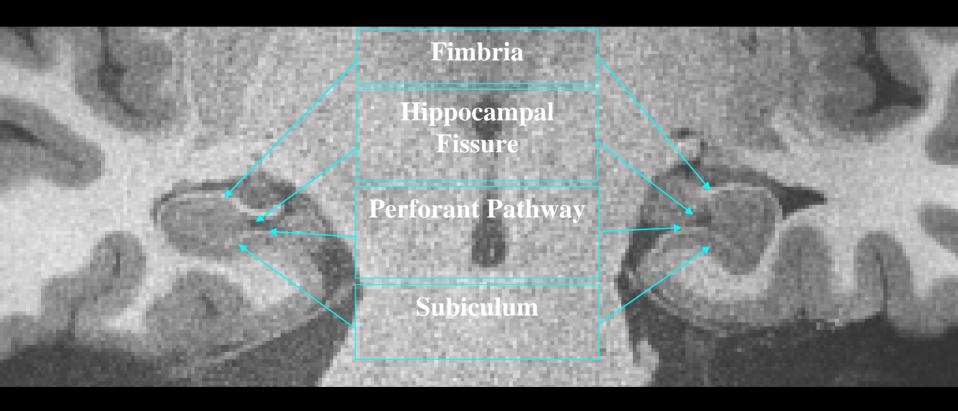
Blockface Unwarped Nissl Rigid MR Warped MR

High Resolution Hippocampal Modeling



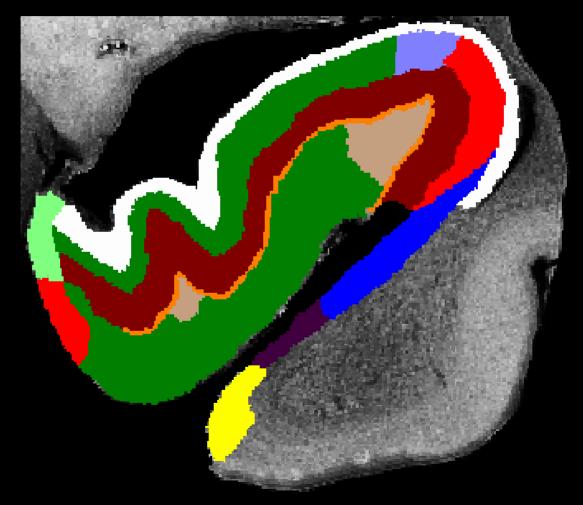
Even in standard 1mm MP-RAGE can discern hippocampal substructures (e.g. alveus, perforant pathway)

High Resolution in vivo Hippocampal Imaging



3T MP-RAGE, $400\mu m$ isotropic, 8 channel phased-array, TE=4.54msec, TI=1sec, α =12°, NEX=4 (12.5 minutes/scan)

High Resolution Hippocampal Modeling



Joint work with Jean Augustinack, David Salat and Andre van der Kouwe

Inferring in vivo Structure

1. Compute linear transform that maximizes overlap with *in vivo* segmentation (Dice coefficient).

$$I = \arg \max \frac{\Gamma}{\iiint_{\mathbf{r}} I(\mathbf{r}) \wedge H(L\mathbf{r})}$$

2. Compute nonlinear transform that maximizes overlap while minimizing metric distortion.

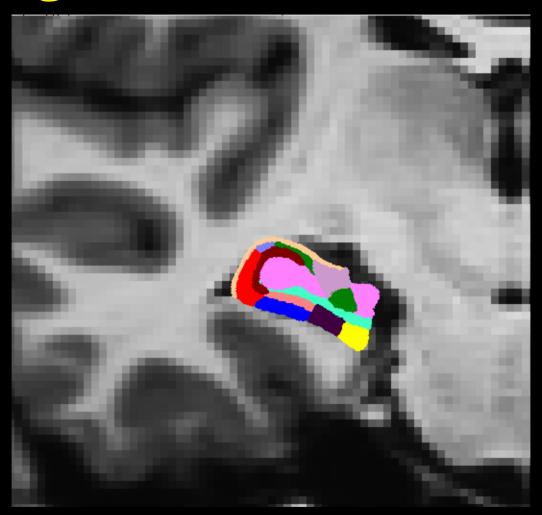
$$J = \lambda_d J_d + \lambda_P J_P + \lambda_B J_B + J_S$$



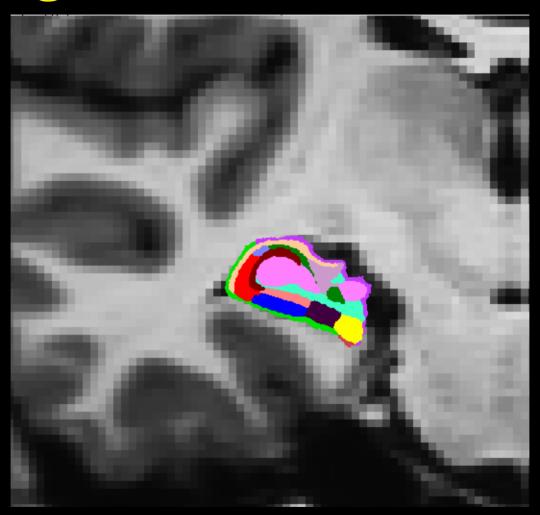
1mm MP-RAGE



Whole-Brain Segmentation

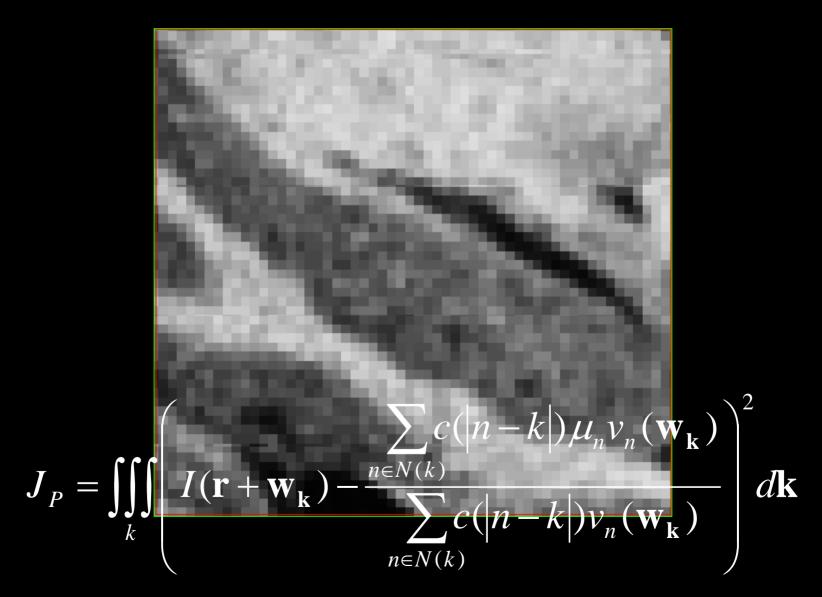


Linear Registration



Nonlinear Registration

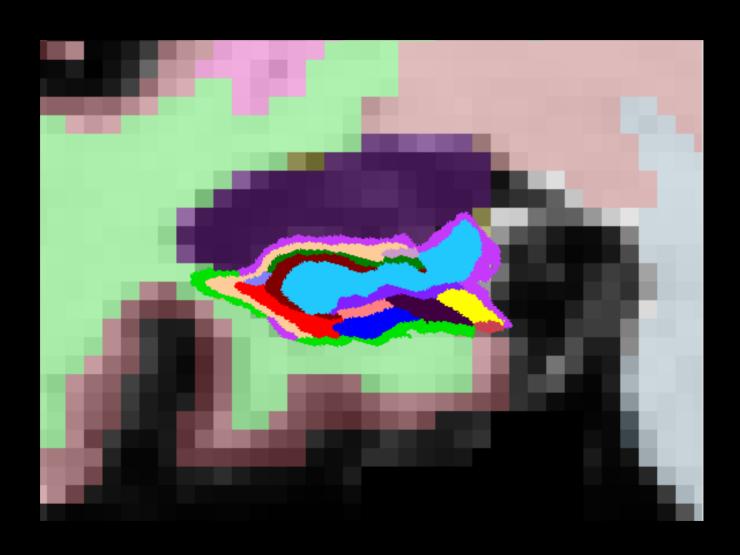
Using Intensity Information



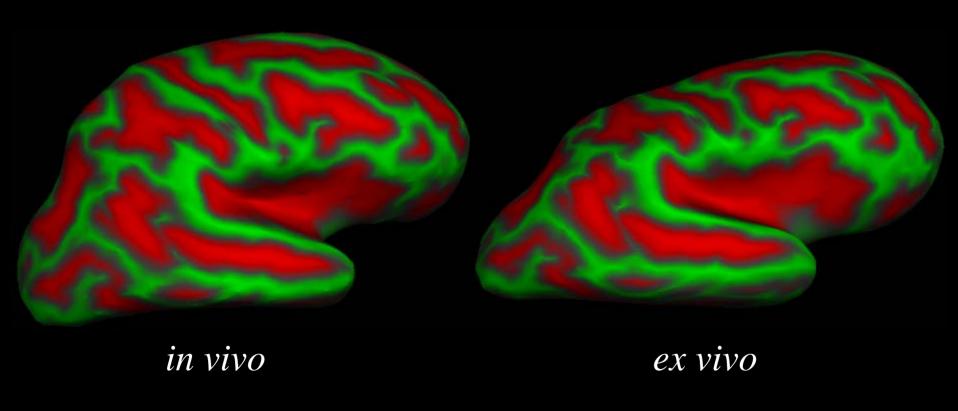
Preliminary Results: Initial



Preliminary Results: Deformed



Direct Validation: in vivo and ex vivo scans of same subject



Thanks to Xiao Han for helping generate these results

Hippocampal Labeling: Direct Validation



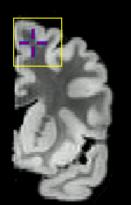
Outline of subiculum

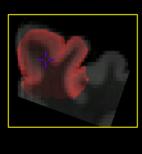
Thanks to Xiao Han for helping generate these results

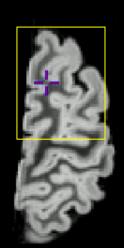
Ex vivo DTI studies in human cortex

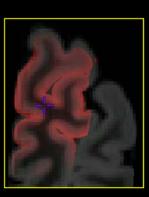


- Normal adult male premotor cortex
- Cut from an entire fixed hemisphere
- 225μm isotropic resolution
- $b=4,000 \text{ smm}^{-2}$







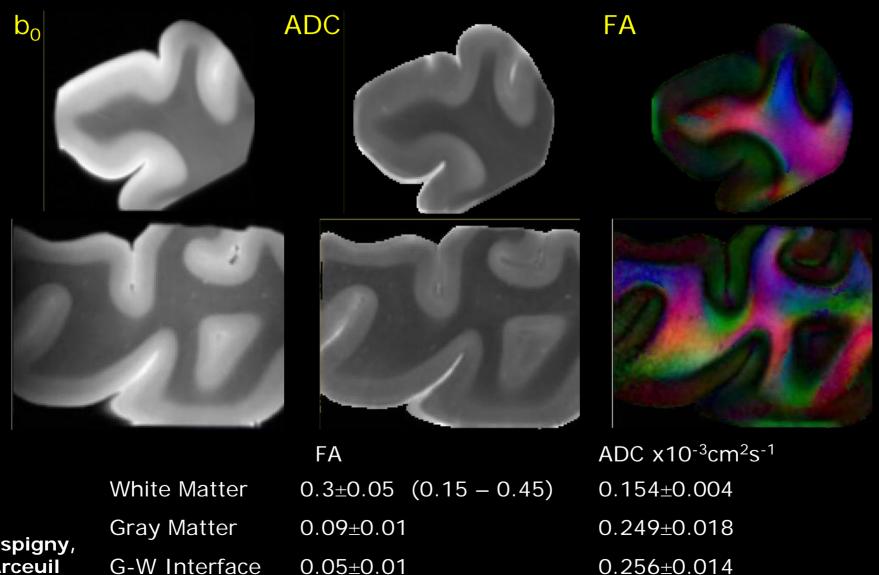






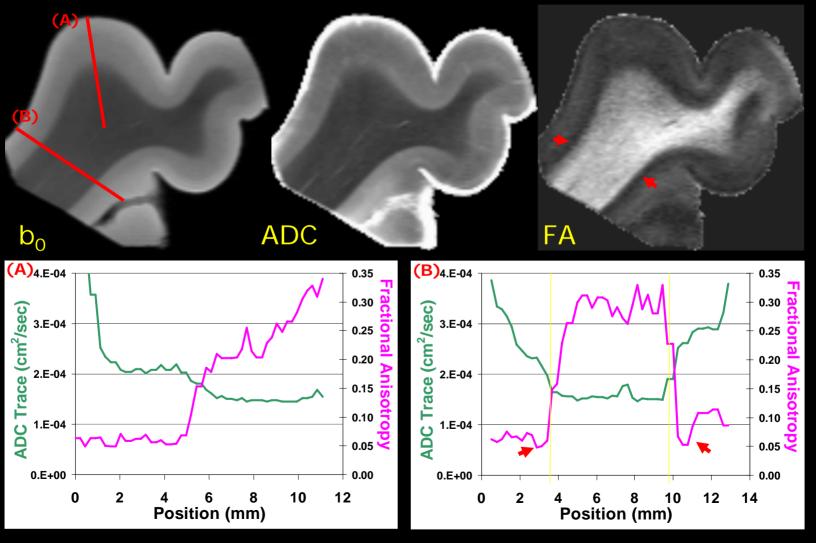
de Crespigny, D'Arceuil, MGH

Ex vivo normal human cortex



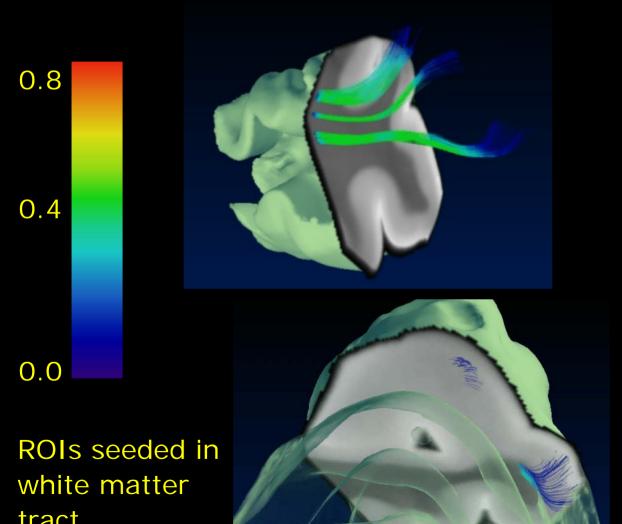
de Crespigny, D'Arceuil MGH, 2005

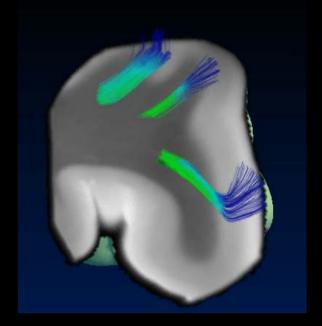
Ex vivo normal human cortex



de Crespigny, D'Arceuil MGH

DTI Tractography in the cortex (250um isotropic)



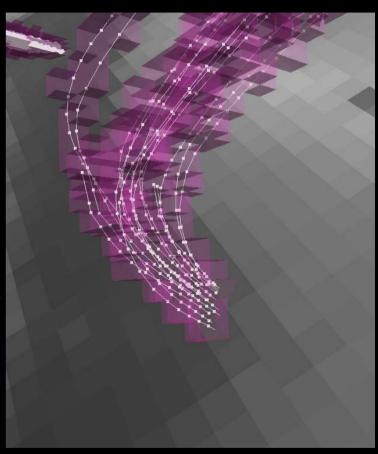


tract

de Crespigny, D'Arceuil, Concha **MGH**

DTI Tractography in the cortex

ROIs seeded in cortical GM



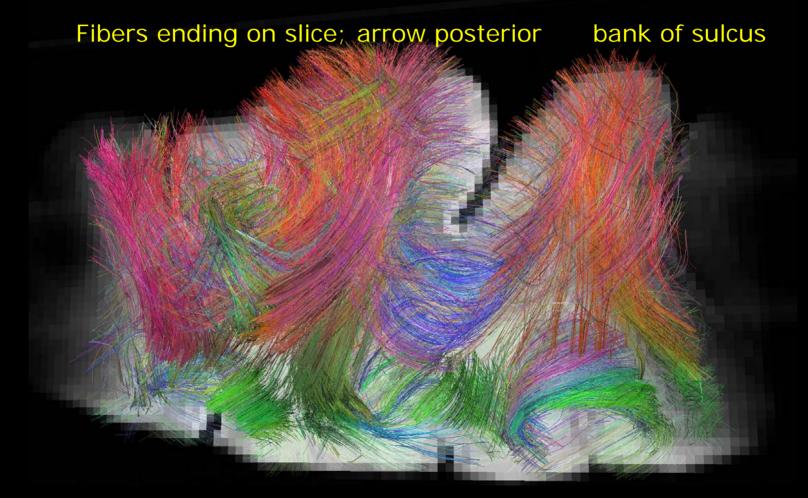
Short association fibers?
Sharp 90° bend?

Turn into the cortex is smooth, FA is low here

de Crespigny, D'Arceuil, Concha MGH

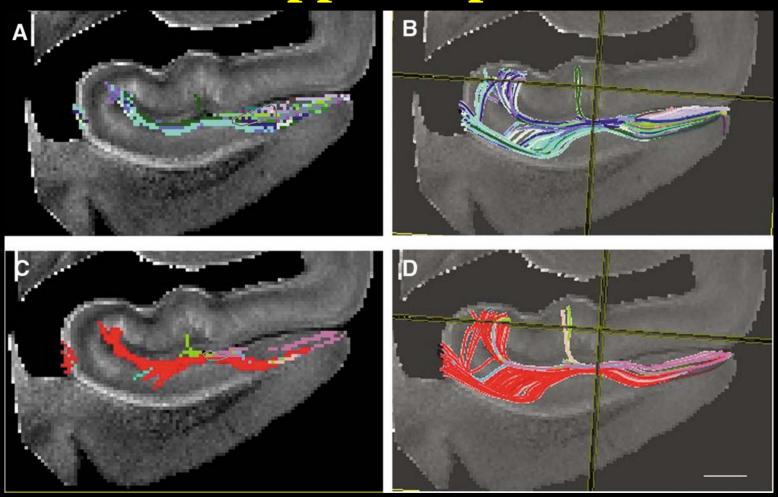
DSI Tractography in human cortex

DSI in fixed cortex: 4.7T, 3D EPI, $450\mu m$, 1 NEX, 9 hours, b=40,000, 514drns, (truncated 11^3 cube)



de Crespigny, D'Arceuil, Wang, Wedeen, MGH

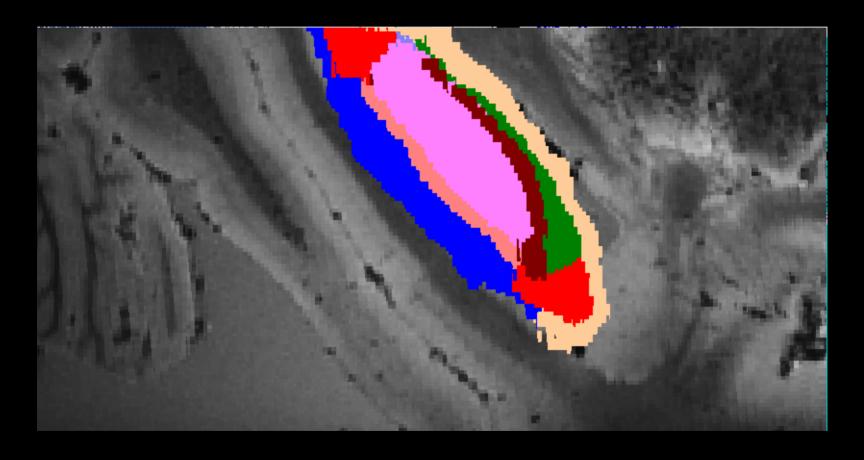
Modeling Fiber Tracts in the Hippocampus



Priors for Tractography?

Joint work with Jean Augustinack and Alex de Crespigny

Hippocampal Labeling: Direct Validation



In vivo labeling mapped to ex vivo scan (200μm)

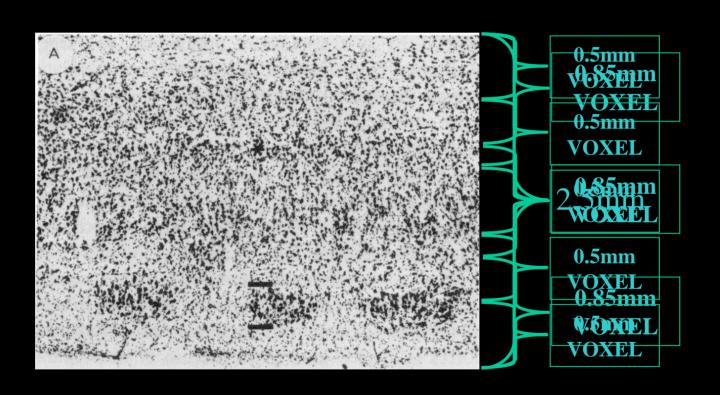
Thanks to Xiao Han for helping generate these results

in vivo Imaging of Laminar Structure

Can we detect laminar structure in the distribution of intensities across the cortical ribbon?

Imaging Markers of the Underlying Meyelo- and Cytoarchitecture

Entorhinal Cortex

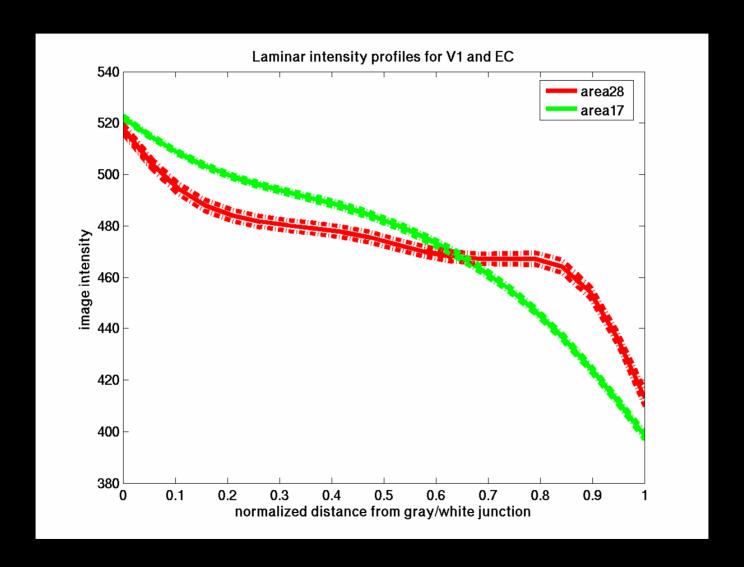


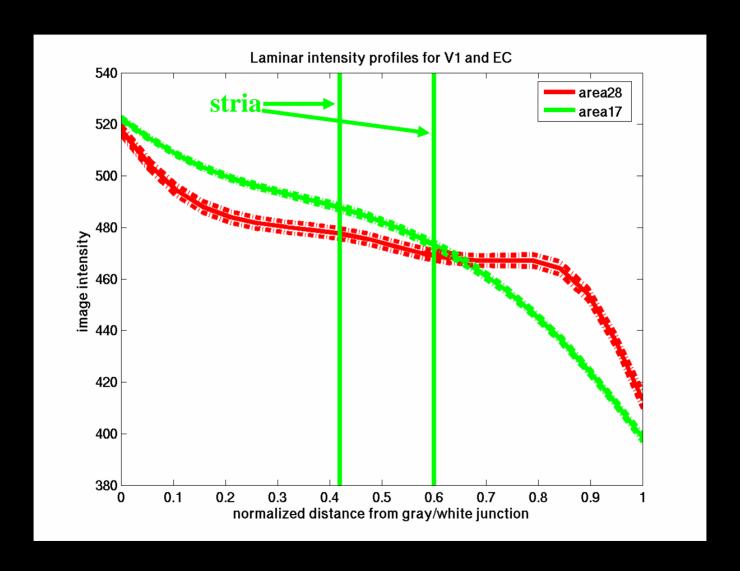
The laminar distribution of cell types and degree of myelin should be detectible *in vivo*!

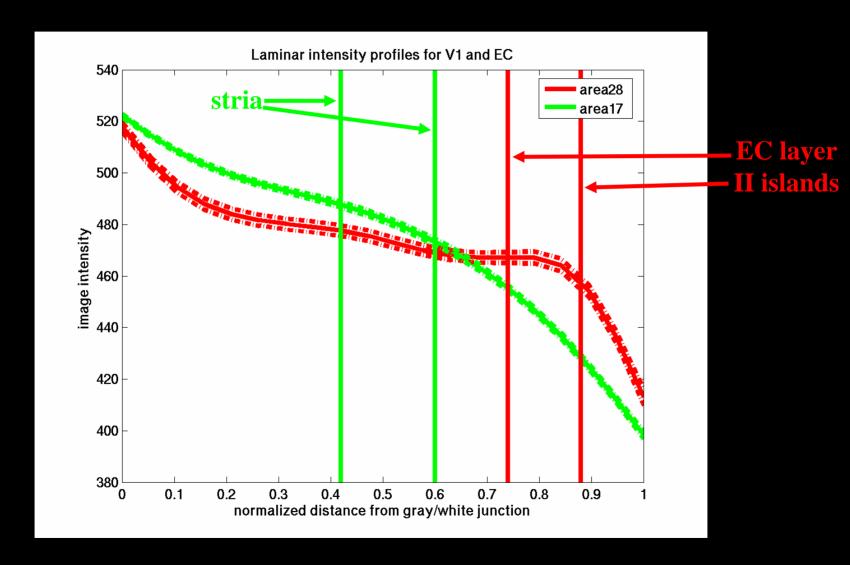
Imaging Temporal Visual Cortex

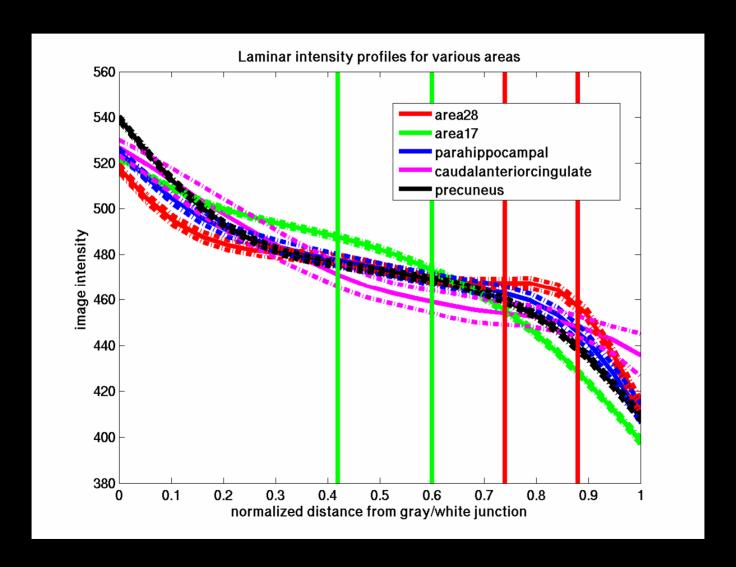
Are there structural differences between functionally defined regions and the surrounding cortex?

Specifically, can we use signal intensity and/or T1 as a surrogate marker for degree of myelination?

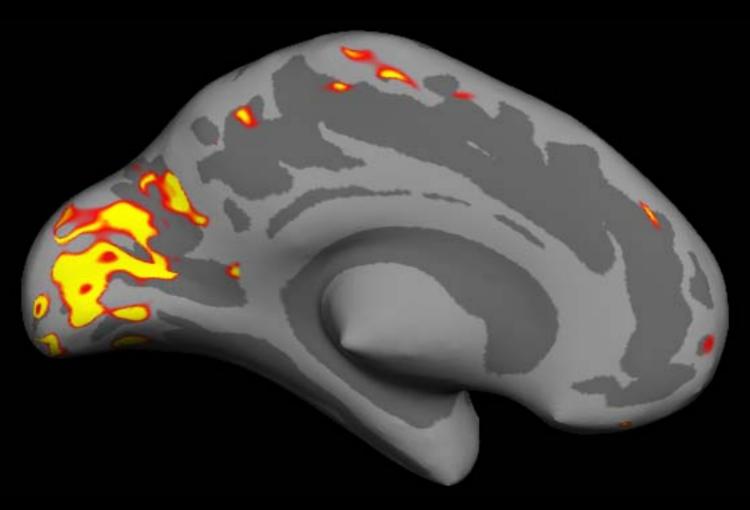






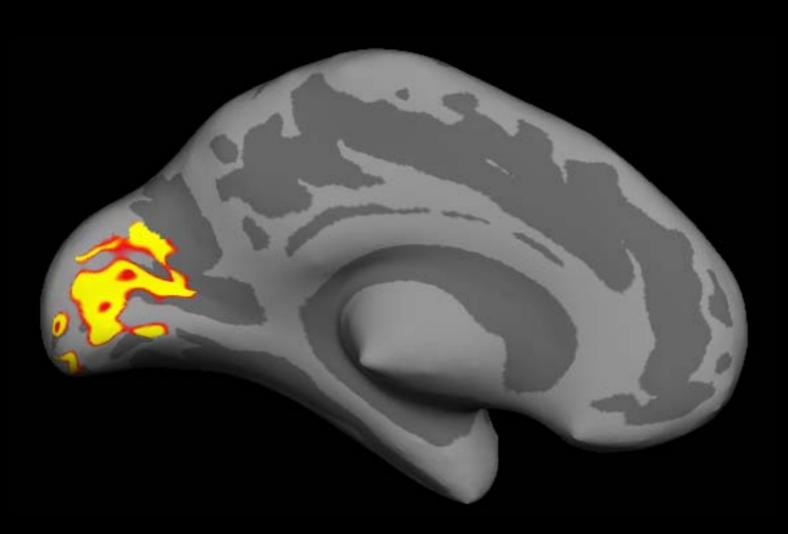


Finding V1 (BA 17)

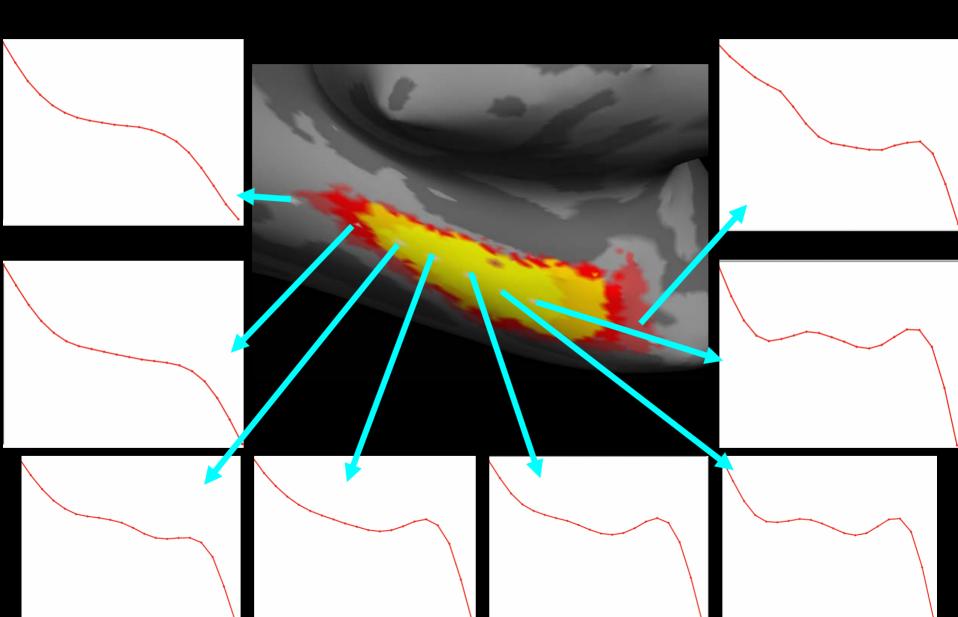


Likelihood

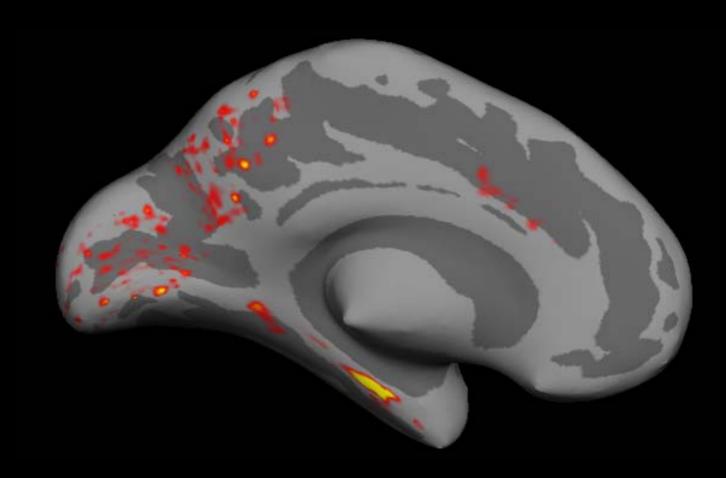
Finding V1 (BA 17)



How Selective are Profiles?

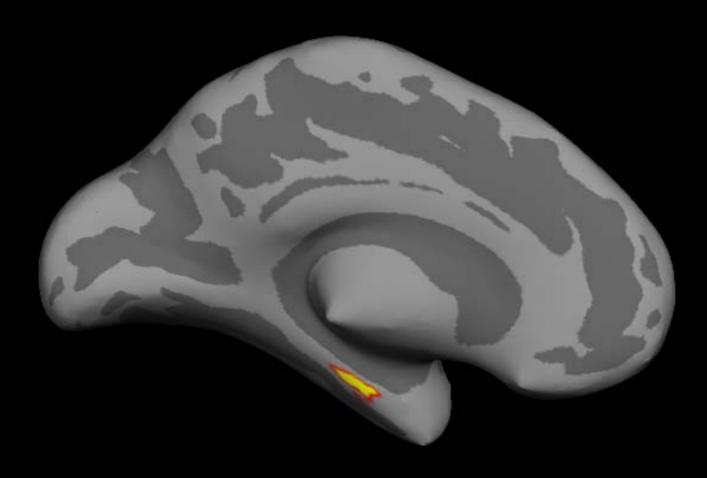


Finding Entorhinal Cortex (BA 28)



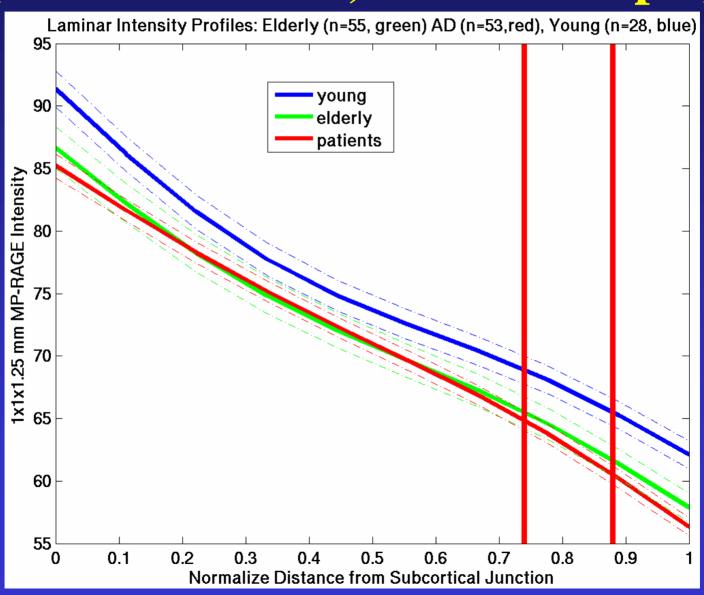
Correlation of EC intensity profile across a different hemisphere

Finding Entorhinal Cortex (BA 28)



Posterior density of EC (product with prior)

Young, Elderly and AD EC Profiles (not normalized, 1mm isotropic)



Acknowledgements

MGH

Andre van der Kouwe
Doug Greve
David Salat
Jean Augustinack
Evelina Busa
Jenni Pacheco
Niranjini Rajendran
Brad Dickerson
Gheorghe Postelnicu
Brian T Quinn

Oxford University
Mark Jenkinson
Siemens
Andreas Potthast

MGH

Bruce Rosen
Diana Rosas
Larry Wald
Graham Wiggins
Chris Wiggins
Megan Blackwell
Xiao Han
Christian Farrar
Alex de Crespigny
Matthew Frosch
Brad Hyman

Boston Univeristy

Jon Polimeni
Oliver Hinds
UC San Diego

Anders Dale

Marty Sereno MIT

John Fisher
Nancy Kanwiser
Becca Schwarzlose
Polina Golland
Peng Yu
Florent Ségonne
HMS/MEEI
Jennifer Melcher

Irina Sigalovsky



