



NA-MIC

National Alliance for Medical Image Computing

<http://www.na-mic.org>

Driving Biological Problem Huntington's Disease



THE UNIVERSITY
OF IOWA

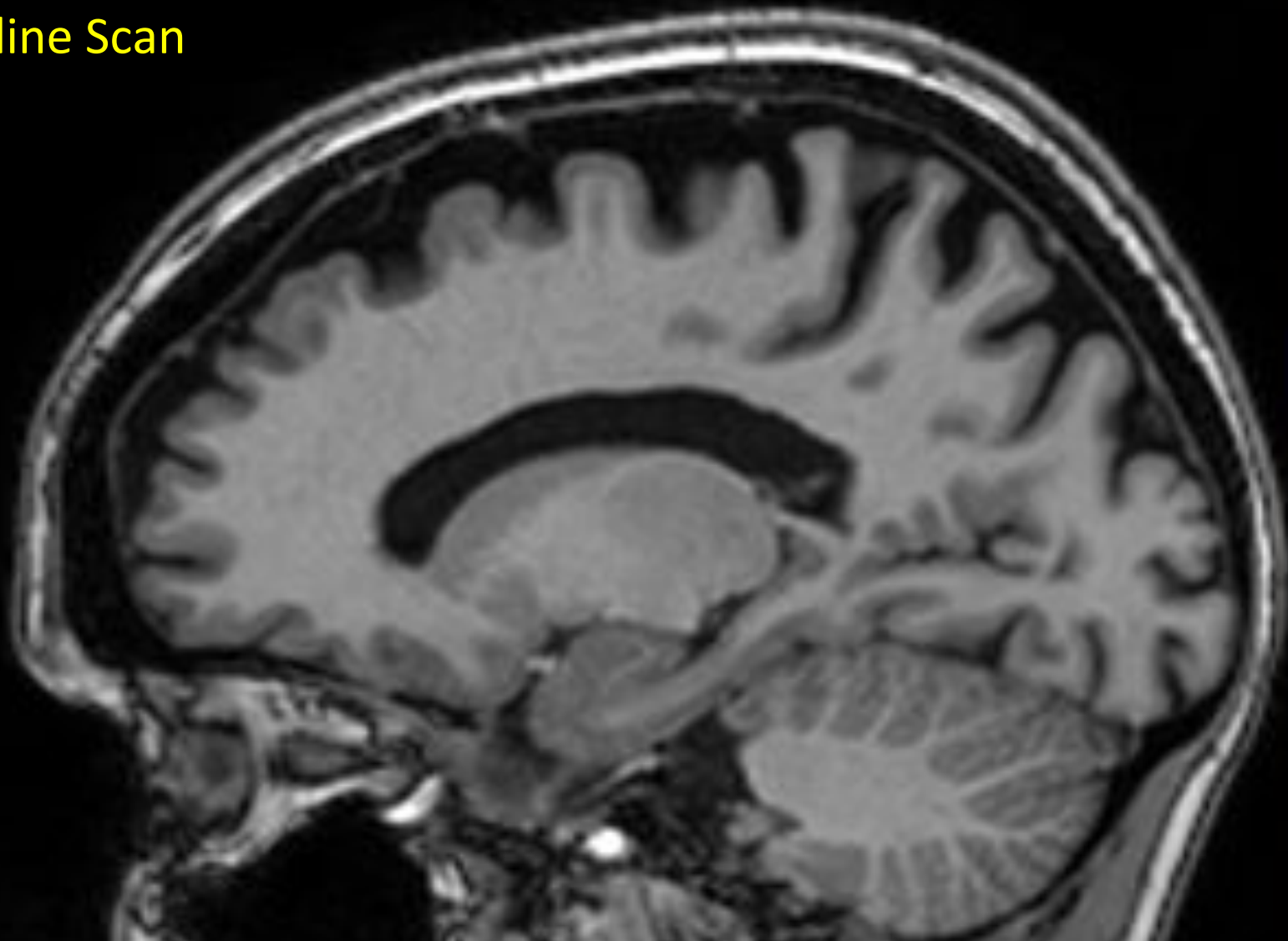


Builds on PREDICT-HD

- The NIH-funded project “Neurobiological Predictors of Huntington’s Disease” (PREDICT-HD) studies Huntington’s disease (HD), a neurodegenerative genetic disorder that affects muscle coordination, behavior, and cognitive function, and causes severe debilitating symptoms by middle age.

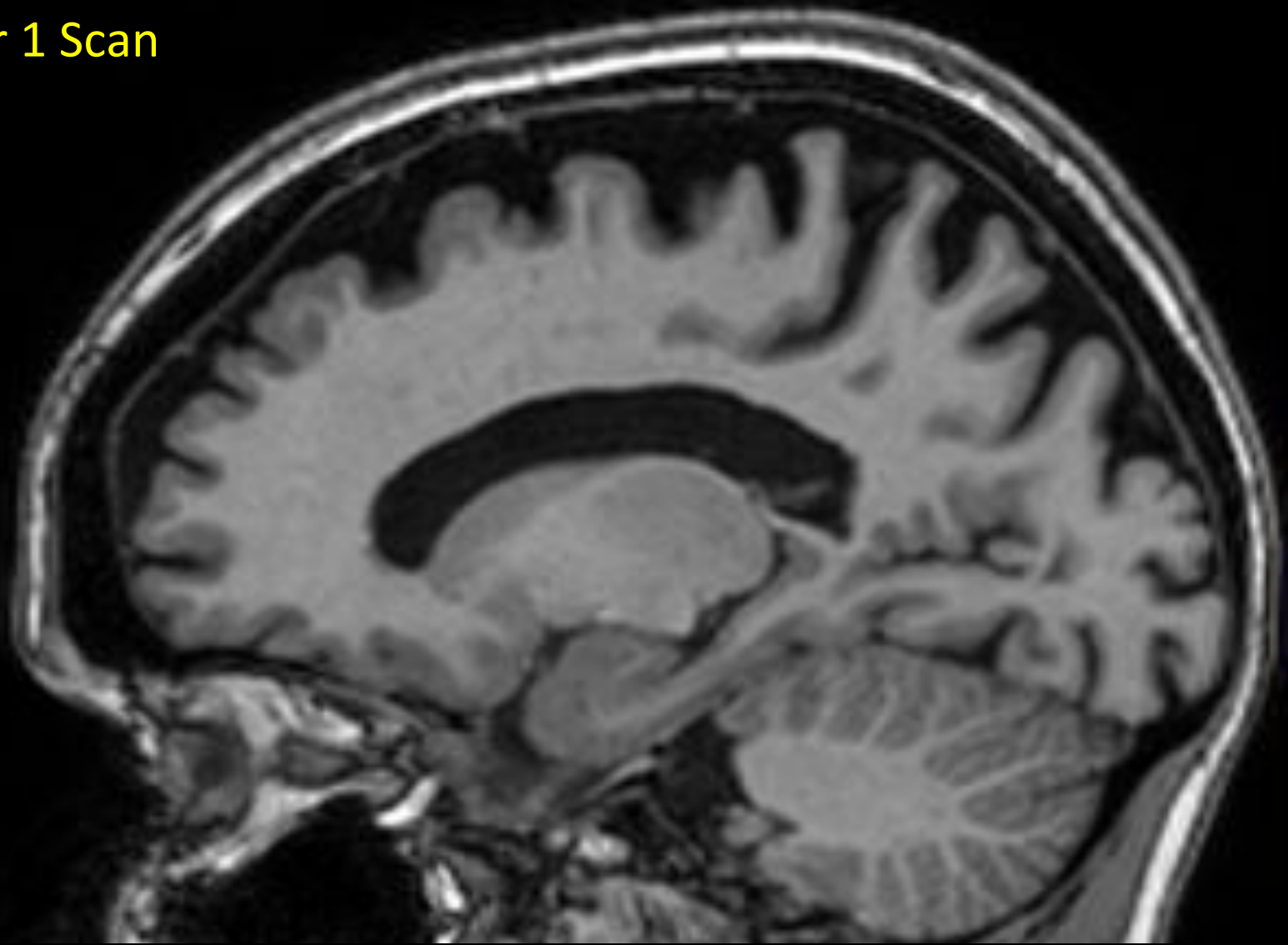
TRACK-HD Stage 1 HD Subject

Baseline Scan



TRACK-HD Stage 1 HD Subject

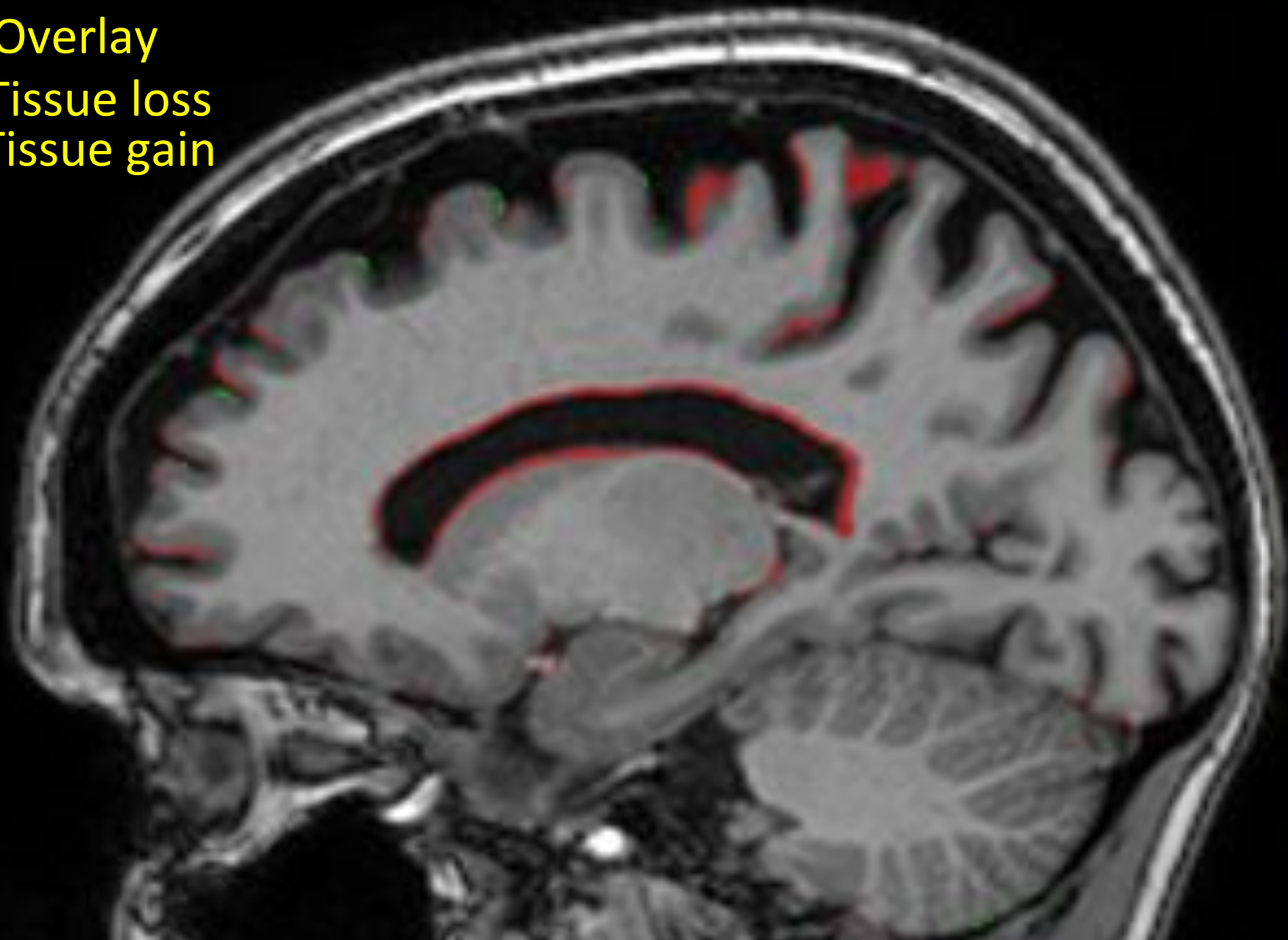
Year 1 Scan



TRACK-HD Stage 1 HD Subject

BSI Overlay

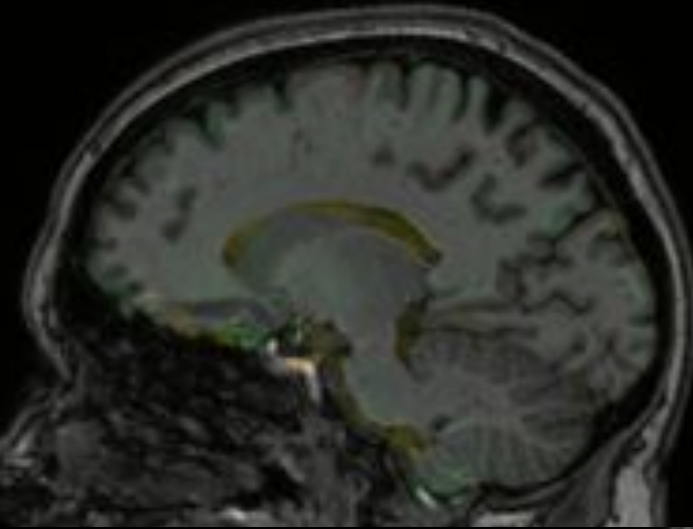
- Tissue loss
- Tissue gain



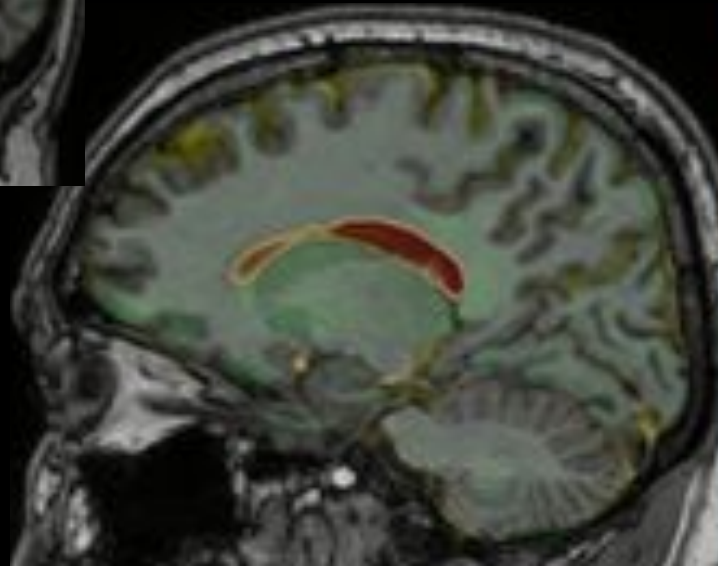
Atrophy Rate: 1.9% Premanifest Rate: 0.7% Control Rate: 0.2%

24-month voxel-compression mapping

Control



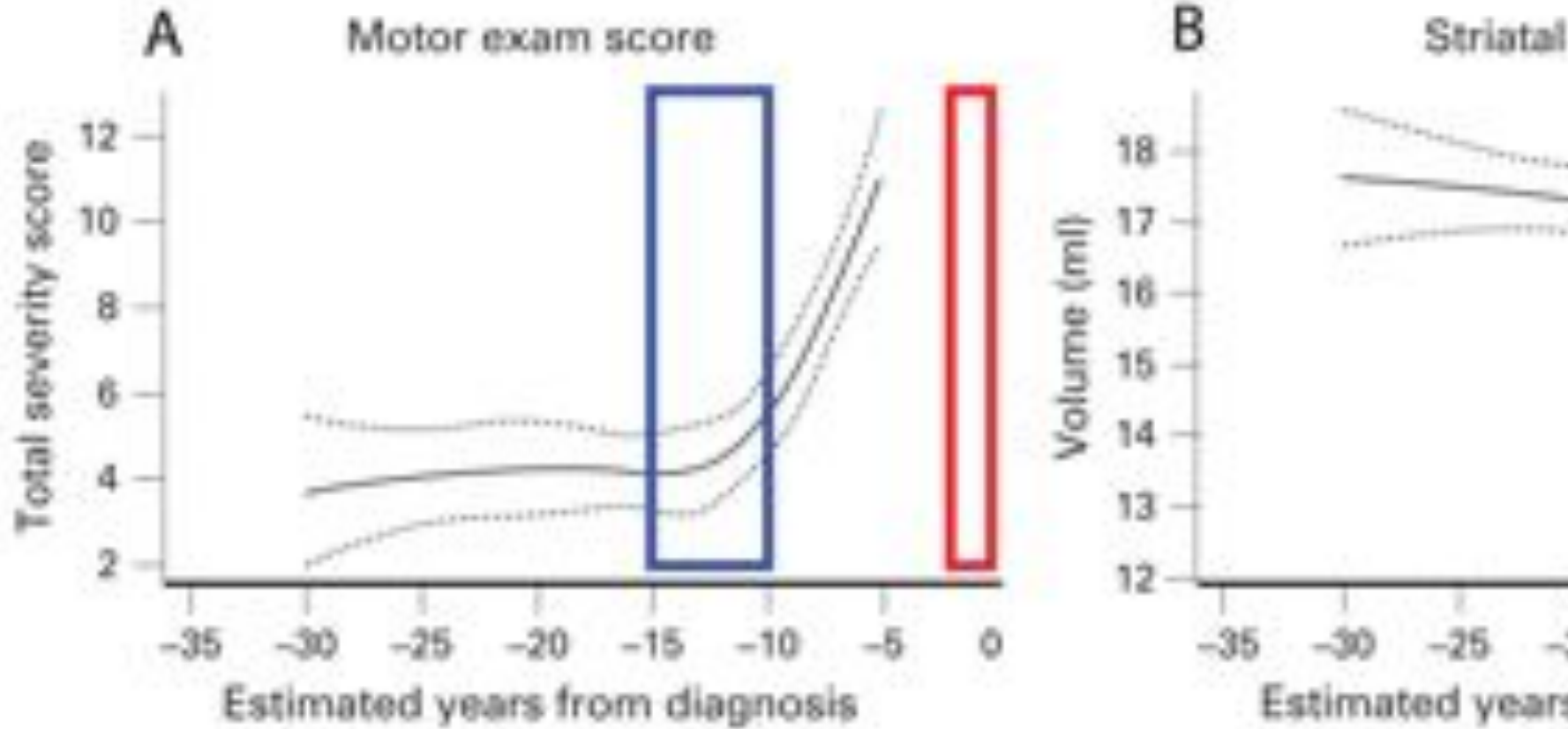
PreA



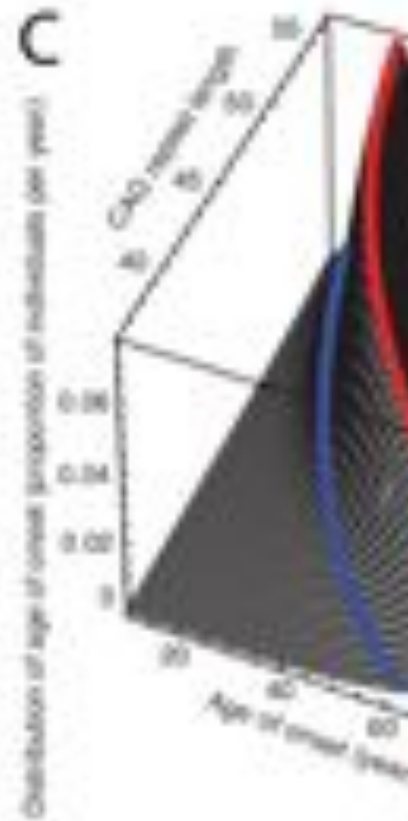
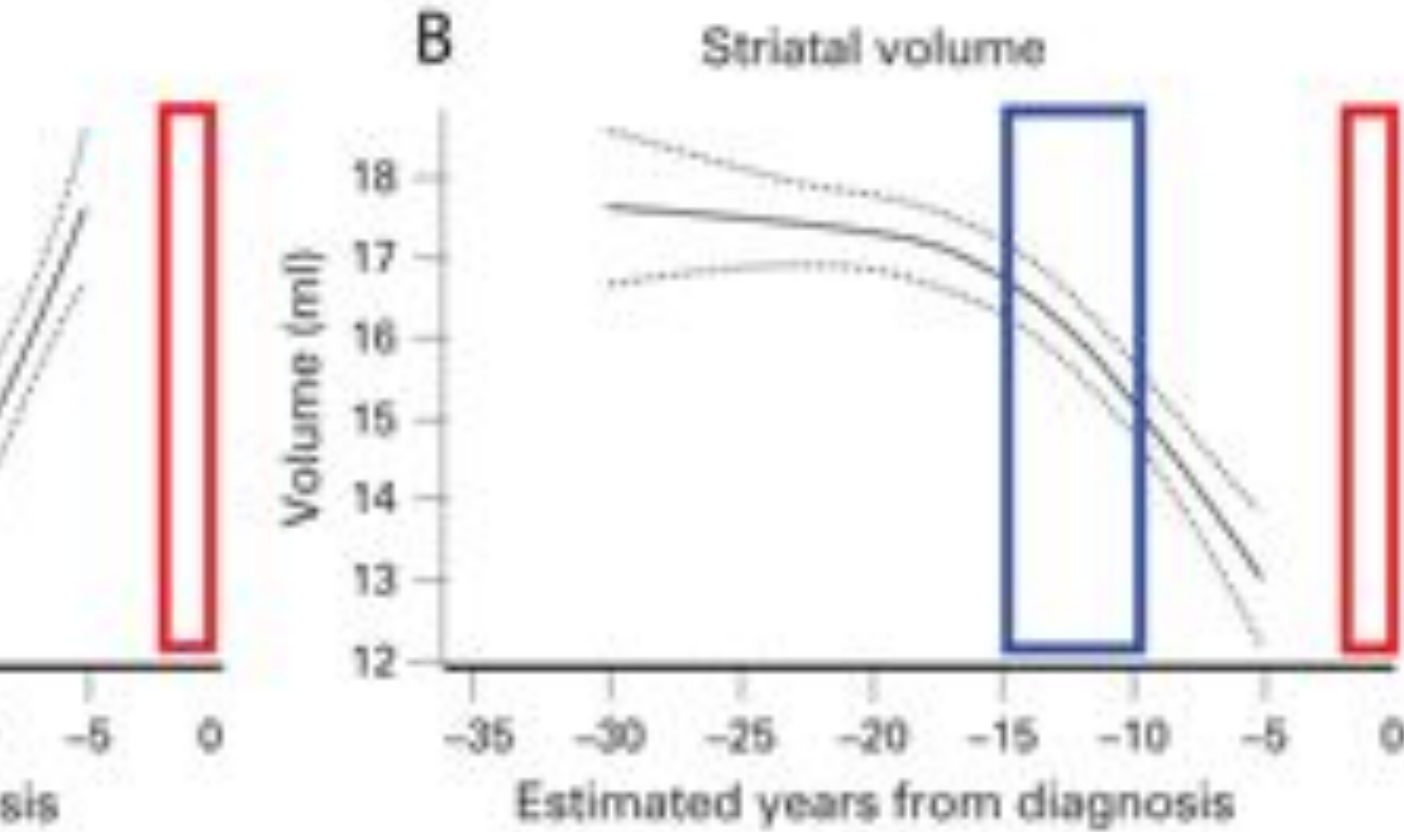
HD2



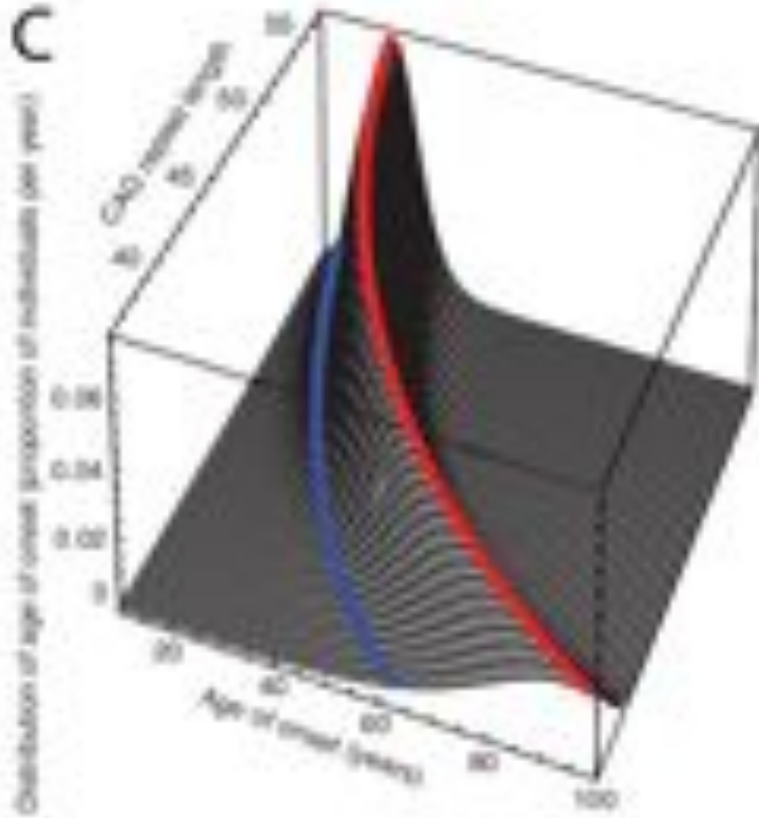
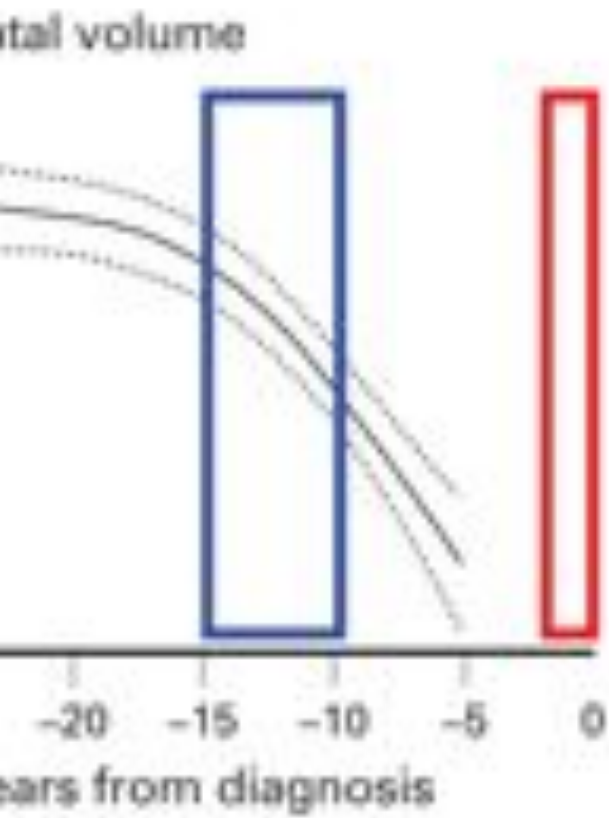
HD Background



HD Background



HD Background





Specific Aims

- Perform individualized longitudinal shape change quantification from multi-modal data.
- Complete full brain Diffusion Tensor Imaging tractography analysis.
- Deploy extensible tools for sharing source data, derived data, algorithms and methods to multi-site analysis teams.



Sharing HD Data

http://www.na-mic.org/Wiki/index.php/2011_Summer_Project_Week

User:

Home New ▾ Upload ▾ Administer ▾ Tools ▾

Launch Uploader

Search
PREDICTHD currently contains: 48 Projects, 1920 Subjects, and 4556 Imaging Sessions.

Projects Subjects MR PET CT

Projects
+ Recent



Sharing HD Data

http://www.na-mic.org/Wiki/index.php/2011_Summer_Project_Week

User:

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Launch Uploader

Search
PREDICTHD currently contains 48 Projects, 1920 Subjects, and 4556 Imaging Sessions.

Projects Subjects MR PET CT

TrackOnHD

Home New Upload Administer Tools

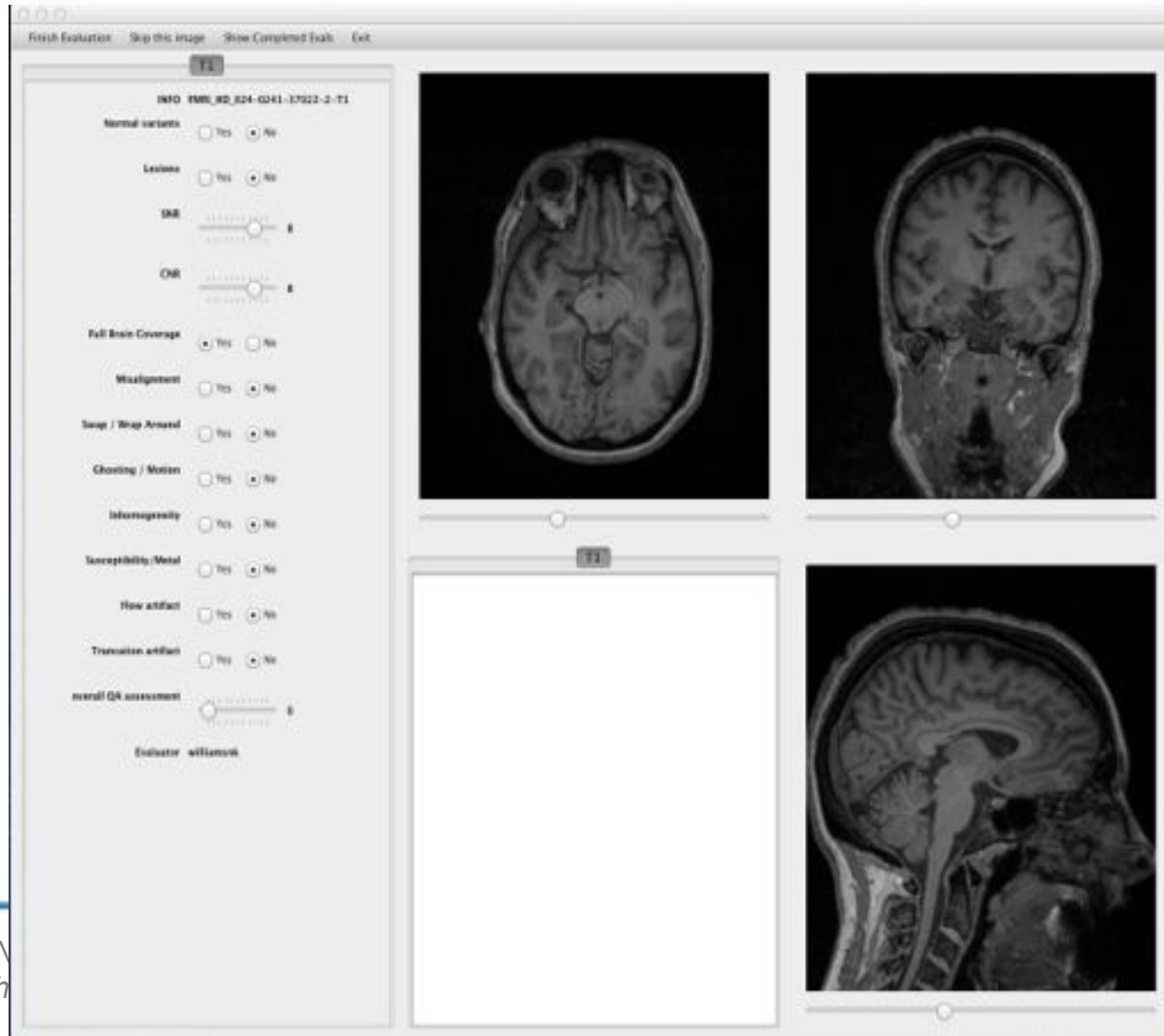
Launch Uploader

HDNI currently contains 4 projects, 454 subjects, and 1703 imaging sessions.

Projects Subjects MR PET CT

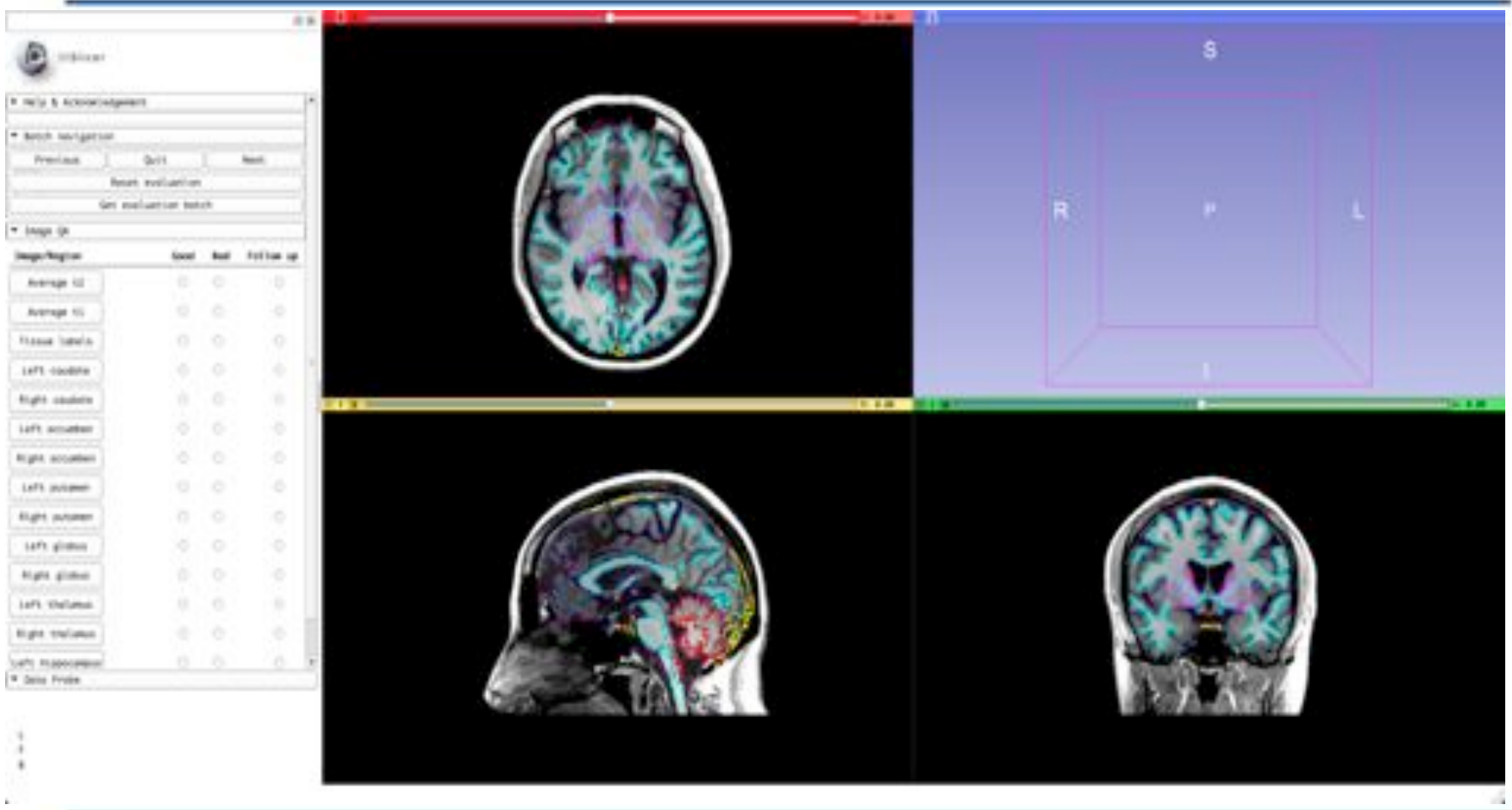


Quality Assurance tools





Quality Assurance tools





Quality Assurance tools

The screenshot displays the 3DSlicer software interface. On the left, the 'Image QA' panel is visible, containing the following sections:

- Image/Region:** A dropdown menu set to 'DWI'.
- Artifacts:**
 - Susceptibility:** Frontal, Temporal, Parietal, Occipital, Cerebellum (all unchecked).
 - Cropping:** Frontal, Temporal, Parietal, Occipital, Cerebellum (all unchecked).
 - Dropout/Vibration:** Frontal, Temporal, Parietal, Occipital, Cerebellum (all unchecked).
- Check here if the image is interleaved:** Interleave (unchecked).
- Missing Data:** A text input field for a comma-separated list of DWI components.
- Enter a comment: (optional):** A text input field.
- Buttons:** 'Get next DWI'.

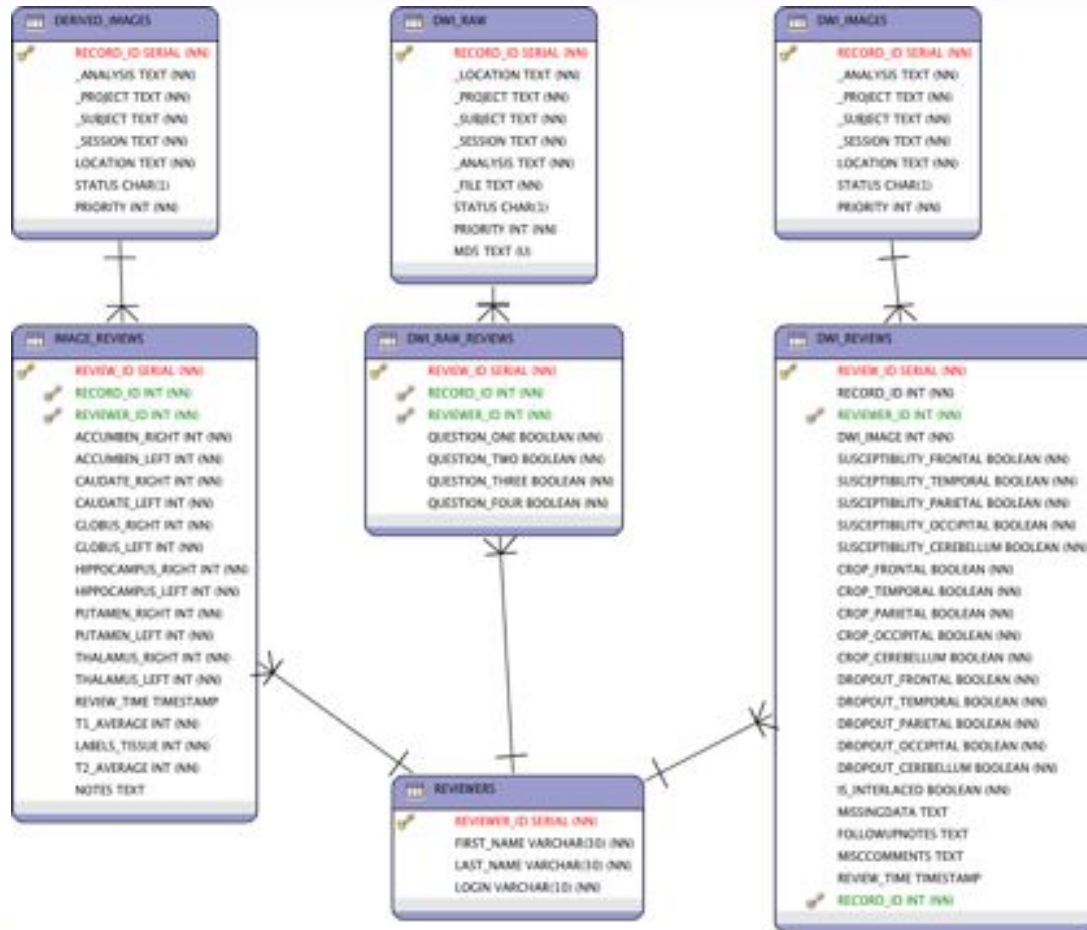
The central 3D view shows a brain slice with a 'Data Probe' window overlaid, displaying a list of coordinates:

```
0000 -0 0 0
0001 -0.20 -0.51 -0.83
0002 -0.19 -0.51 0.83
0003 -0.40 -0.17 0.83
0004 -0.40 -0.73 -0.54
0005 -0.20 -0.94 -0.20
0006 -0.83 -0.51 -0.83
0007 -0.73 -0.51 -0.83
0008 -0.40 -0.17 -0.83
0009 -0.73 -0.17 -0.83
0010 -0.65 -0.73 0.20
0011 -0.51 -0.94 0.20
0012 -0.20 0.17 -0.73 0.20
```

The right side of the interface shows a 3D view of a brain slice with a purple bounding box and axes labeled S (Superior), I (Inferior), R (Right), and L (Left).



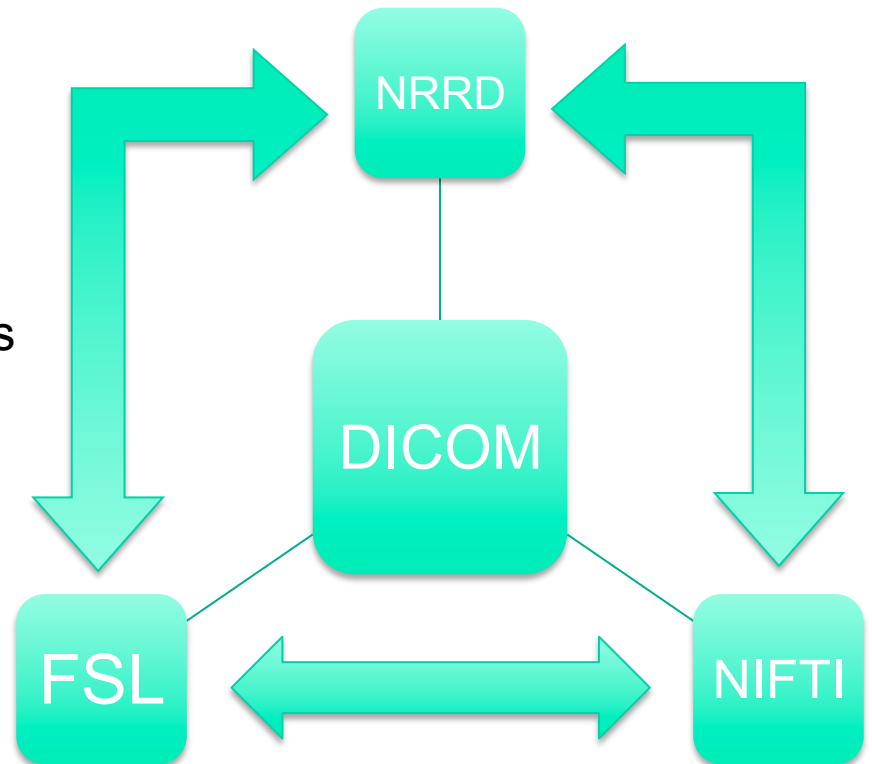
Quality Assurance tools





DWIConvert

- Replacement for DicomToNrrdConverter
- ~4 months of effort
 - Help from NAMIC Team
 - Help from Scanner Manufactures
 - Help from MR Physicist
- Built on ITKv4
- Depends on DCMTK
 - Removed GDCM





Improve DICOM conversion

How we improved conversion from DICOM

- Found **differences in DICOM metadata** for different data types in THP data
- Expanded compatibility of program **DicomToNrrdConverter** to correctly convert 42 varieties of DICOM data to NRRD file format
 - Still some data could not be converted
- **COMPLETELY REWROTE TO DWIConvert**
 - 2012 Revealed 2 new incarnations of diffusion data from DICOM
 - DWIConvert is more modular and easier to incorporate new rules
 - DWIConvert is built against ITKv4 and DCMTK allowing the reading of multiframe data
 - DCMTK support is not also part of ITKv4
 - Public and private element tag metadata compatibility
 - Devised a method to calculate missing diffusion gradient direction coordinates from private data in some scanners



Improve DICOM conversion

Traveling Human Phantom (THP) Data Set

(Shared With NAMIC, 17 external groups using it)

- Designed to overcome compatibility issues with multi-site data
- 5 healthy subjects
- Each subject imaged at 8 sites in 1 month
 - 5 Siemens scanners, 3 Philips scanners
 - 4 different scanner software versions
- T1- and T2-weighted images
- Diffusion-weighted images
 - 30/32 direction scan (4 repeats per site)
 - 71 direction scan (2 repeats per site)



MultiCenter Reliability of Diffusion Tensor Imaging

Vincent A. Magnotta, Joy T. Matsui, Dawei Liu, Hans J. Johnson, Jeffrey D. Long, Bradley D. Bolster, Jr., Bryon A. Mueller, Kelvin Lim, Susumu Mori, Karl G. Helmer, Jessica A. Turner, Sarah Reading, Mark J. Lowe, Elizabeth Aylward, Laura A. Flashman, Greg Bonett, and Jane S. Paulsen

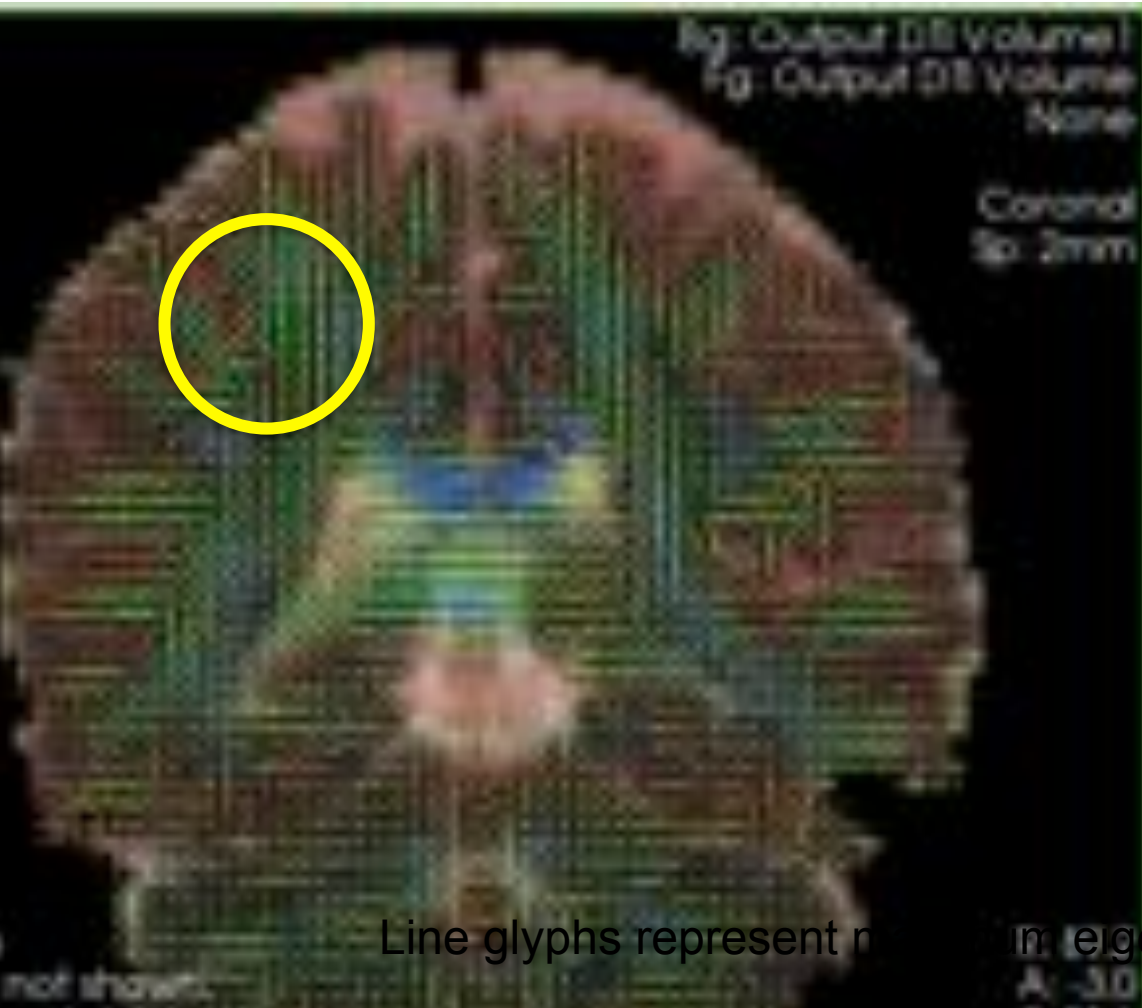
Brain Connectivity. December 2012, Vol. 2, No. 6: 345-355



Improve DICOM conversion

Incorrect

Correct



Line glyphs represent normal in eigenvector orientation



Improve DICOM conversion

Many different locations (element tags) of metadata important to DWI data analysis

Element tag	GE (Signa)	Siemens (Trio Tim)	Siemens (Verio)	Philips (Achieva)
B value	0043,1039	0029,1010	0029,1010	2001,1003
Gradient vector coordinates	0019,10BB (<i>x</i>) 0019,10BC (<i>y</i>) 0019,10BD (<i>z</i>)	0029,100E	0029,100E	2001,1004
Mosaic size parameters		0051,100B 0029,100A	0051,100B 0051,100B	
Measurement frame		0020,0032	0020,0032	0020,0032
B matrix		0019,100E		

Software revision used to determine when estimation from B matrix is needed



Improve DICOM conversion

Calculate missing (or incorrect) diffusion gradient direction coordinates by using **b** matrix coordinates in private element tag

Missing gradient direction coordinates

$$\mathbf{g} = \mathbf{G}_n \mathbf{G}_n^T = \begin{pmatrix} g_x \\ g_y \\ g_z \end{pmatrix} \begin{pmatrix} g_x & g_y & g_z \end{pmatrix} = \begin{pmatrix} g_x^2 & g_x g_y & g_x g_z \\ g_y g_x & g_y^2 & g_y g_z \\ g_z g_x & g_z g_y & g_z^2 \end{pmatrix}$$

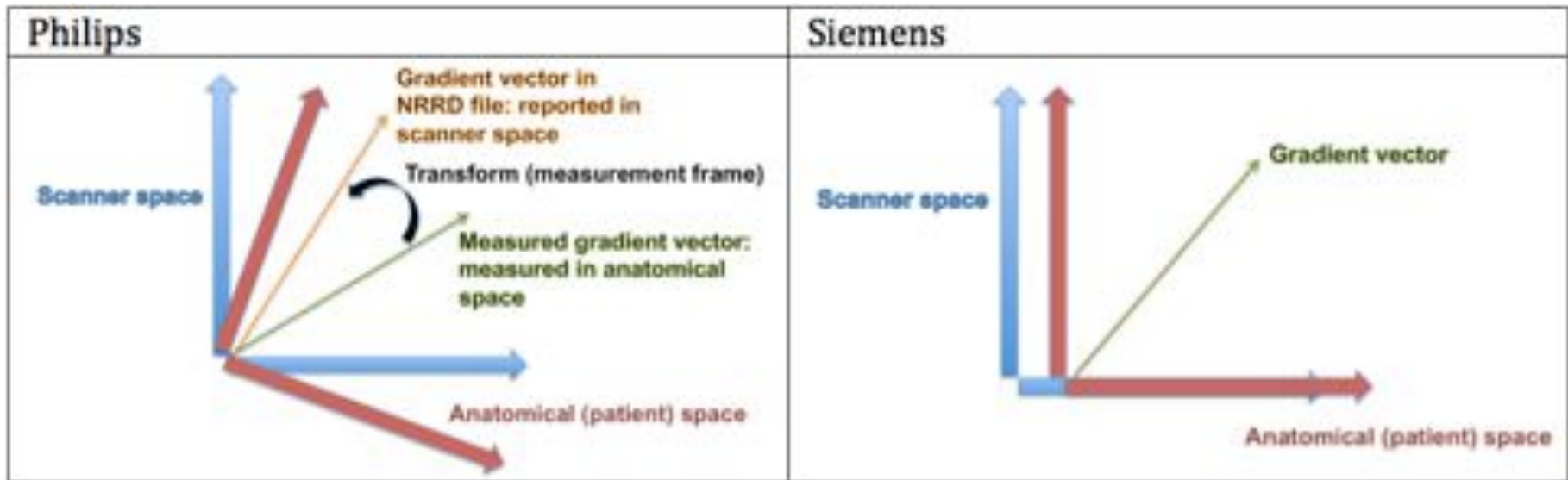
$\mathbf{b} = b\mathbf{g}$

6 elements of symmetric matrix
given in private element tag

→ SVD → b-value for gradient



Improve DICOM conversion





Contribute to many NA-MIC family tools

- ITKv4 Contributions
- Many contributions to Slicer to prepare for ITKv4 update, add new modules, improve end-user experience, replace legacy/broken modules with compliant functionality
- Wrap tools needed for processing in Slicer Execution Model(SEM)
- Developed converter for SEM to nipyen for automatic wrapping
- Updated tools to ITKv4
- Updated tools to consistent “SuperBuild”
- Many, many contributions to the “Advanced Normalization Toolkit (ANTS)” (Wrap in nipyen, ITKv4 compliant, SuperBuild, Testing Suite)

ANTS Dashboard

No file changed since Wednesday, January 09, 2013 - 19:00 CST View Auto-refresh Help

Site	Build Name	Update			Configure			Build			Test			Build Time
		Files	Error	Warn	Error	Warn	Not Run	Fail	Pass					
neuron.uiowa.edu	Darwin-clang31-64bits-QT4.8.2-ITK4-Debug	0	0	0	0	1	0	54	526	10 hours ago				
neuron.uiowa.edu	Darwin-clang31-64bits-QT4.8.2-ITK4-Release	0	0	0	0	1	0	0	580	11 hours ago				

National Alliance for Medical Image Computing

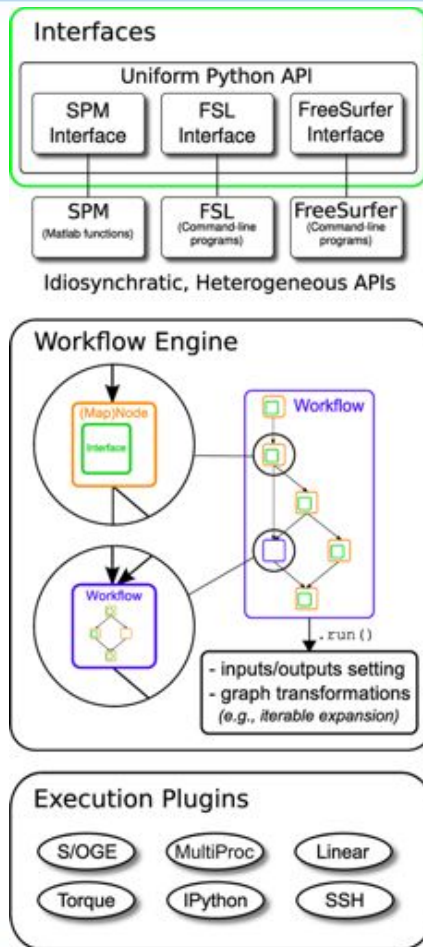


Improving shared derived data processing

- Convert brains2 internal tools auto workup into fully NA-MIC compliant tool suite
 - **(DONE)** Convert major applications to SEM compliance (Decouple SEM from Slicer)
 - **(DONE)** Use SimpleITK to replace brains2 basic image processing building blocks
 - **(In Progress)** Transition Slicer to ITKv4
 - **(DONE)** Define workflows in NiPype (Thanks Satra Ghosh)



NiType: Large catalog of tools with a uniform interface



- **Batch processing**
 - Distributed processing plugins
 - Reruns affect updated/edited node connections ONLY!
- **Uniform node creation**
 - Stable and consistent API
 - Nipype's Function node allows easy integration of CLI tools
- **Pipeline complexity**
 - Iterables, MapNodes
 - Nested workflows

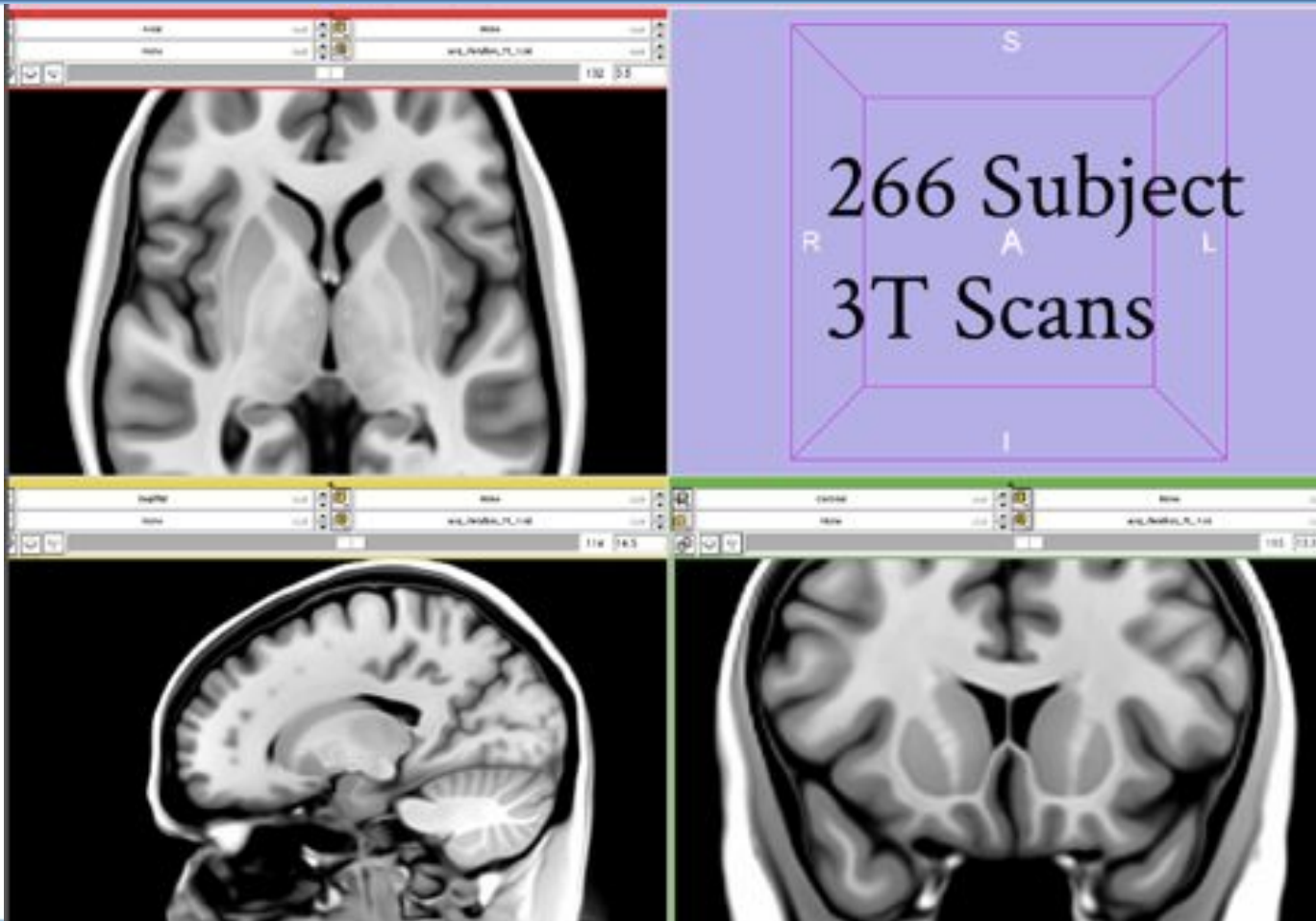


Diagram of Longitudinal Processing Pipeline



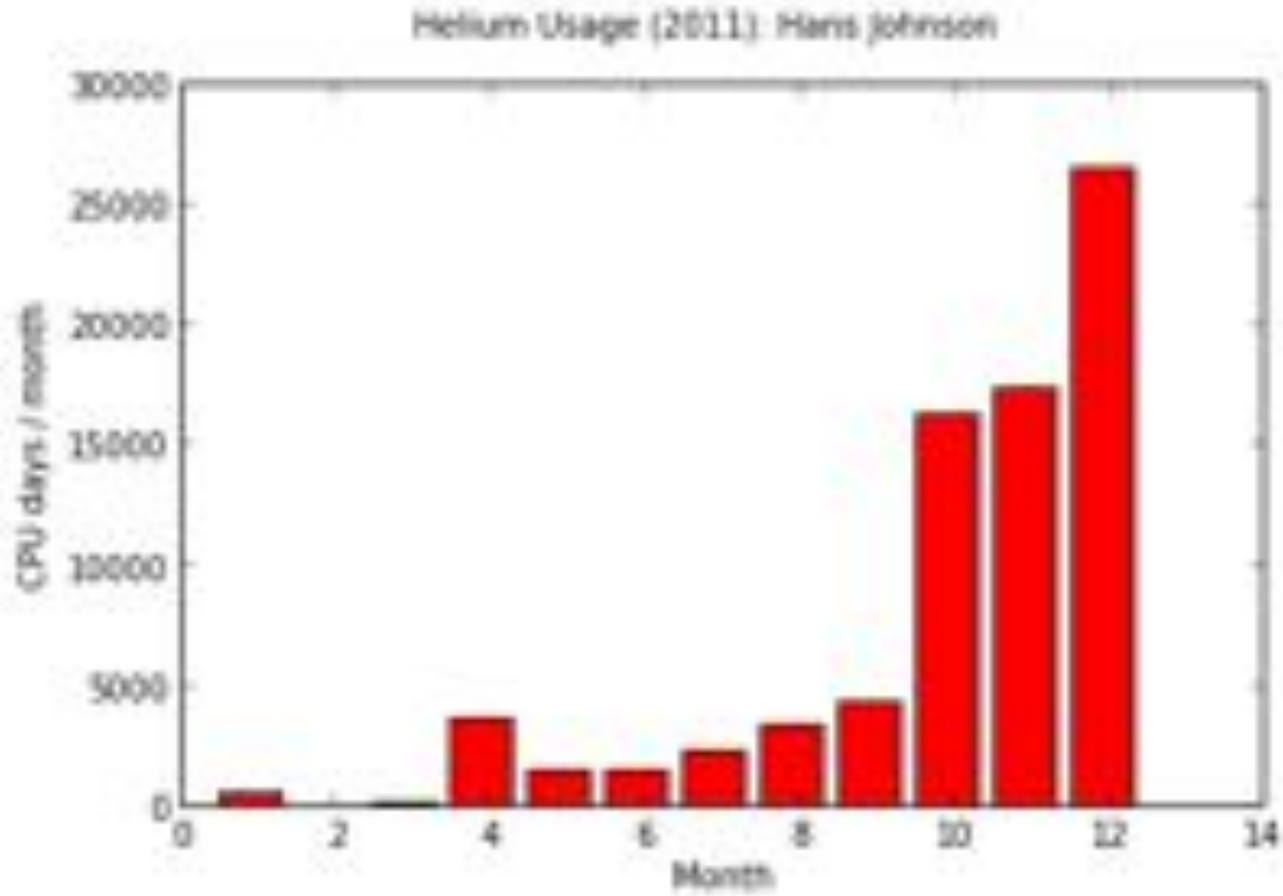


Improved Template Building with ANTS





Cost of Longitudinal Analysis





Brain Sub-Cortical Structures: BRAINSCut (Longitudinal estimation)

Developed

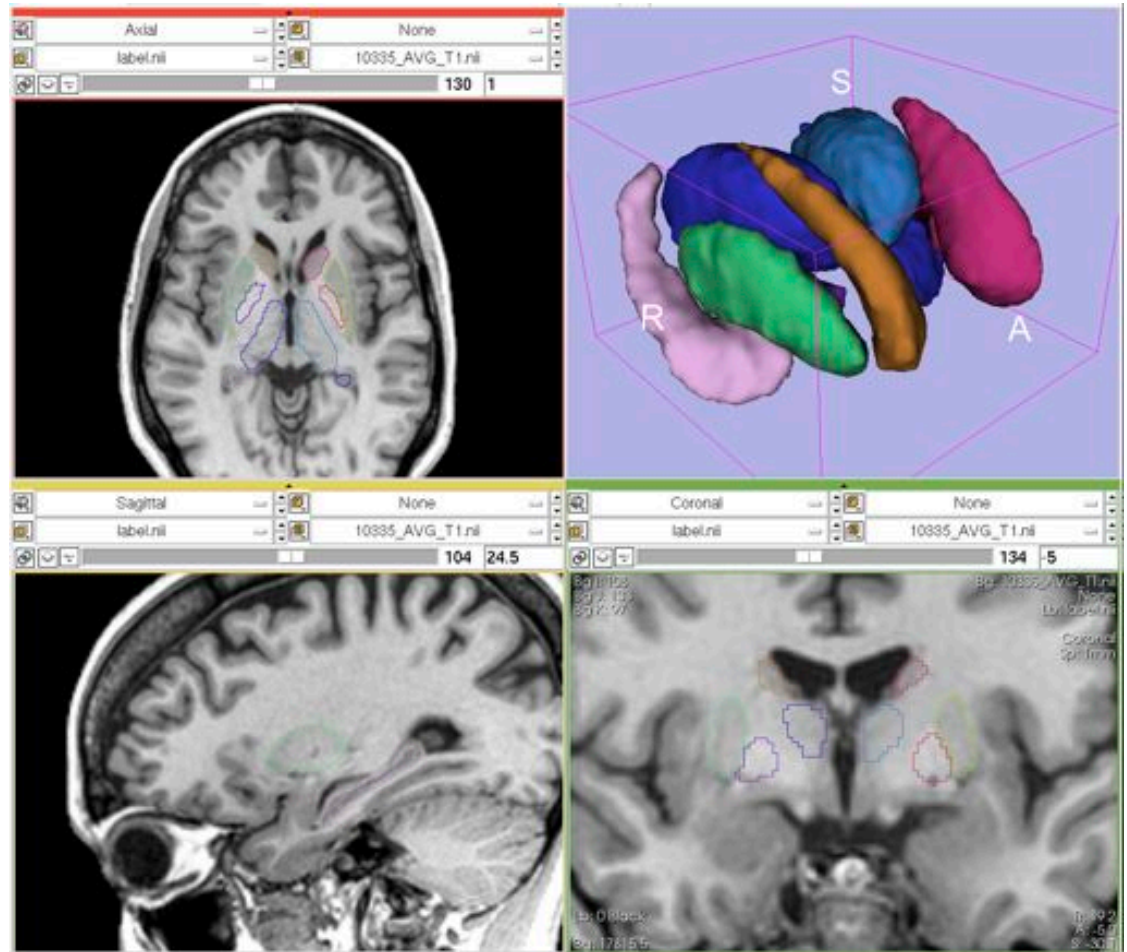
- Caudate
- Putamen
- Thalamus

New structure

- Hippocampus

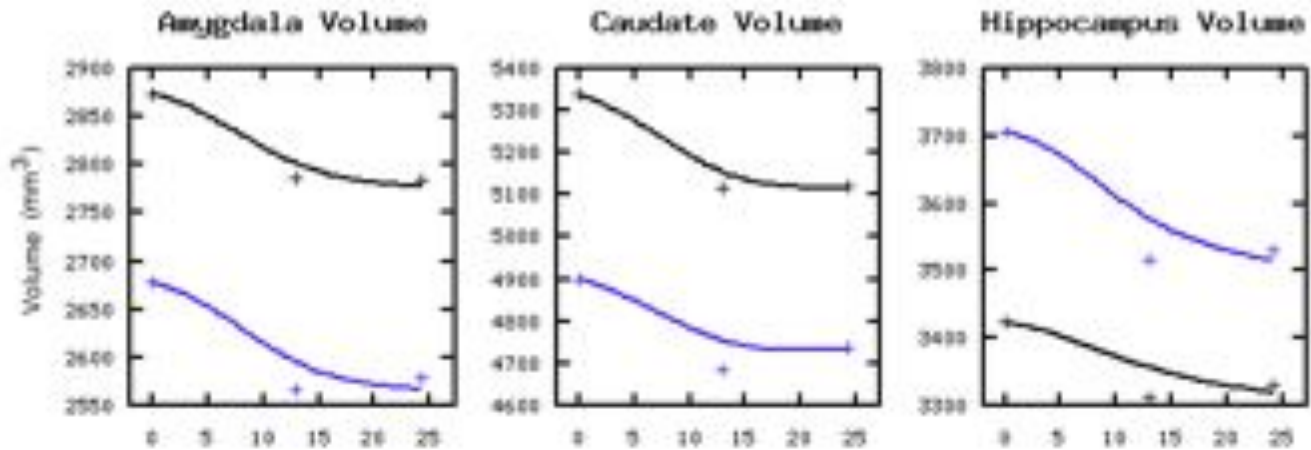
On going

- Globus
- Accumbens
- And more...





Longitudinal Shape





MICCAI 2012

- Joy Matsui & Regina Kim participated in the DTI Challenge
- Joy participated in poster session

Derivation of fiber tracts representing the corticospinal tract using anatomical landmarks

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¹University of Iowa, Department of Psychiatry, Iowa City, IA, USA

²University of Hawaii, John A. Burns School of Medicine, Honolulu, HI, USA

³University of Iowa, Department of Radiology, Iowa City, IA, USA

joy-matsui, eunyoung.kim, vincent-magnotta, hans-johnson@iowa.edu

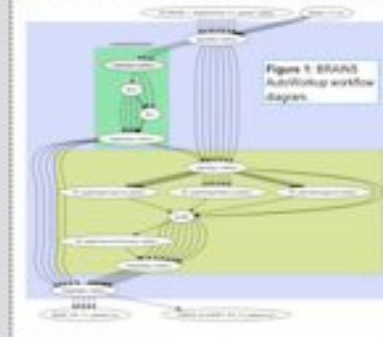
Abstract

White matter fiber tractography holds the promise of contributing to the precision and improving the outcomes of neurosurgical procedures by characterizing underlying anatomy before, after, and during surgery. Traditional methods of tractography often require seed regions to provide starting and stopping points for the tractography algorithm. In a neurosurgical setting, brain anatomy can be altered significantly by preoperative pathology. Segmentation tools or labor intensive weeping that could provide seed regions may not work optimally in this setting because these techniques are based on relatively normal brain anatomy. Therefore, the methods presented here for reconstructing the corticospinal tract attempt to bypass the need to delineate all structures in the brain for successful tractography by instead deriving seed regions from anatomical landmarks. In addition, a multi-tensor tractography algorithm is used to better estimate crossing fibers, along with several other tools developed by the National Alliance for Medical Computing (NAMIC) community.

Methods

1) Structural data processing

Rare T1- and T2-weighted images were processed by a derivative of the fully-automated BRANS AutoWorkflow pipeline [1]. The BRANS AutoWorkflow pipeline for this study (Figure 1) isolated anterior commissure-posterior commissure (AC-PC) alignment of the T1- and T2-weighted images, detection of anatomical landmarks via a correlation-detection algorithm, bias field correction, and segmentation of whole brain tissue (white matter, gray matter, and cerebrospinal fluid) and subcortical structures (thalamus, globus, putamen, and substantia) [1].



2) Regions of interest derivation

Five white matter regions of interest (ROIs) in each hemisphere were derived using the outputs of the BRANS AutoWorkflow pipeline: medulla, pons, midbrain, posterior limb of the internal capsule (PLIC), and precentral gyrus. The medulla, pons, midbrain (Figure 2) and precentral gyrus ROIs (Figure 3) were derived from custom filters that selected voxels from the whole brain white matter mask based on location relative to designated landmarks. Left or right hemisphere designation for the pons, midbrain, and precentral gyrus ROIs was determined by lateral location relative to the anterior commissure (AC) landmark. Each ROI was resampled into the diffusion-weighted image space with BRANStoolsample [2], using a B-spline transformation between the diffusion-weighted T1-weighted and T2-weighted image derived from BRANSPFT [2].



Figure 2: Anatomical landmark examples.

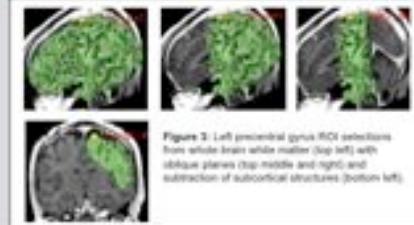


Figure 3: Left precentral gyrus ROI selections from whole brain white matter (top left) with oblique planes (top middle and right) and subtraction of subcortical structures (bottom left).

3) Tractography and further tract selection

Tractography was performed with an algorithm using an unoriented Riemann fiber (URF) [4] in a loop that estimated the fiber model at the current position, moved one step in the most consistent direction, and then reestimated the fiber model again. At each voxel, the diffusion pattern was modeled as a mixture of three equally weighted Gaussian tensors [5]. Precentral gyrus ROIs were used to derive a set of seeds for each hemisphere with the three-tensor method, two seeds per voxel, and a step-length of 0.2 mm in the most consistent direction during each iteration of tractography. Seed points whose fractional anisotropy (FA) was less than 0.7 were excluded from tractography. Tractography stopping criteria included a minimum generated anisotropy of 0.05 and maximum FA of 0.1.

4) Further tract selection

Selection of relevant fibers was done for each hemisphere in Tractography Desktop, a Slicer module for including and/or excluding tracts (<http://www.slicer.org/software/index.php/Documentation/Modules/TractographyDesktop>). Positive selection boxes were placed in relevant regions of the pons and midbrain ROIs to select tracts passing through the corticospinal tract areas (Figure 4).

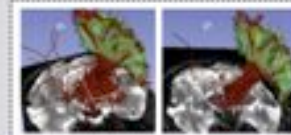


Figure 4: Further tract selection.

Results, Discussion, and Conclusions

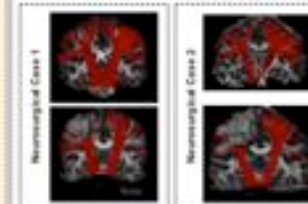


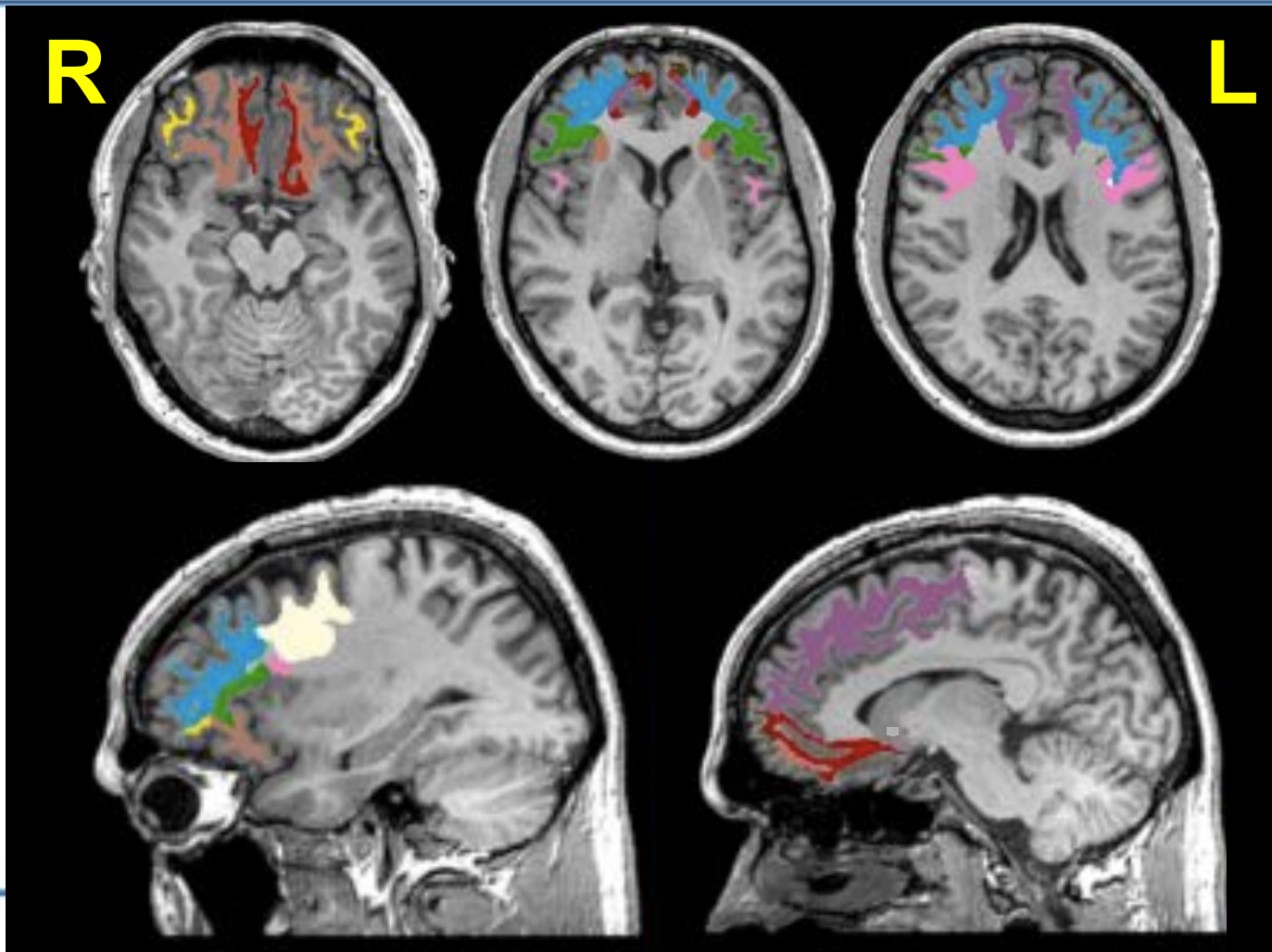
Figure 5: Corticospinal tracts for two neurosurgical cases displayed in radiologic convention with (below) and without (above) right hemisphere tumors.

Figure 5 displays the results of the fiber tracking and selection methods for two neurosurgical cases, each with a tumor in the right hemisphere. The main limitation of this study was the lack of automation in the final selection of tracts. Future versions of BRANS AutoWorkflow could provide surface-based options to automatically define ROIs like the precentral gyrus. The methods presented here were specifically designed to delineate the corticospinal tract via information from anatomical landmarks and feature several tools developed by NAMIC.



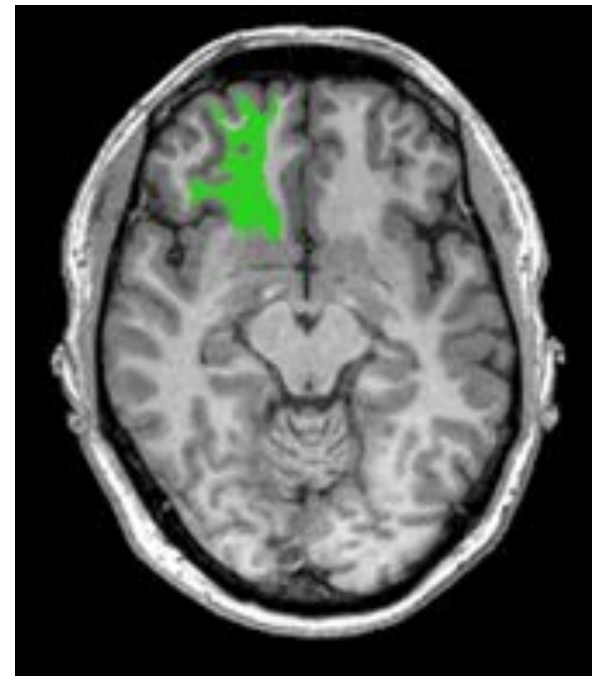
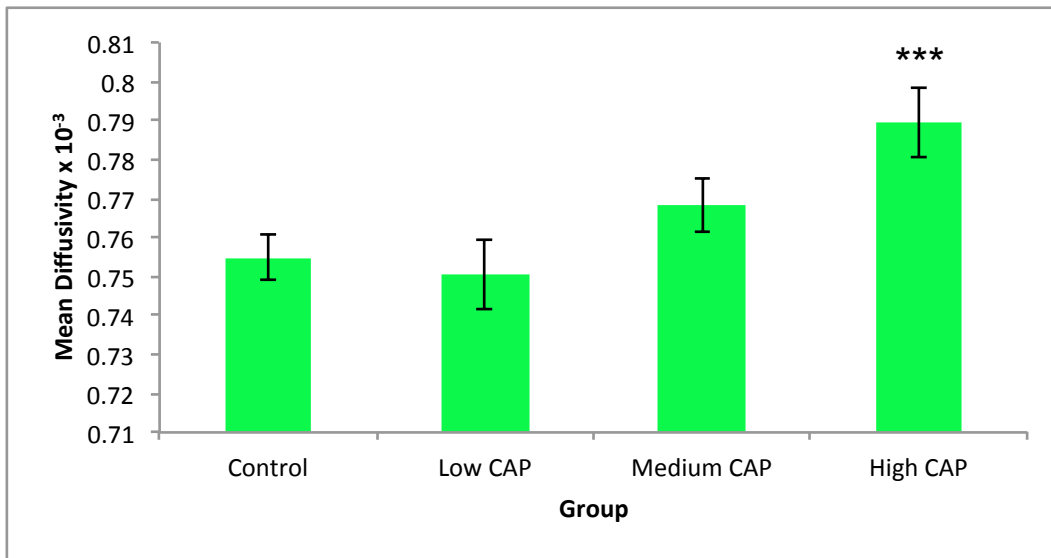
Diffusion weighted imaging of prefrontal cortex in prodromal Huntington's disease

[Submitted Human Brain Mapping Oct 2012]



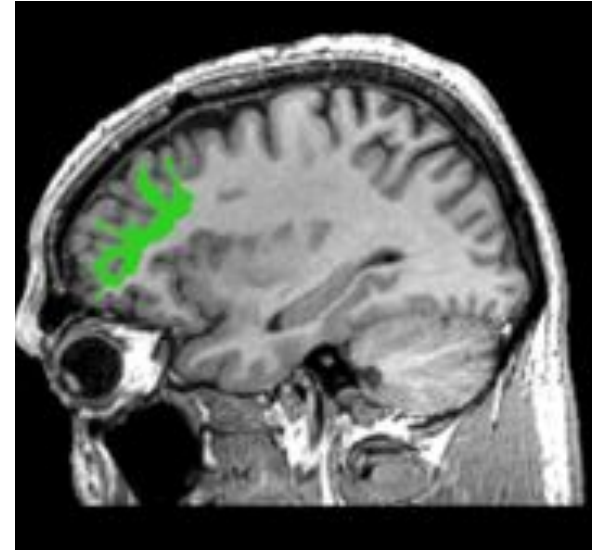
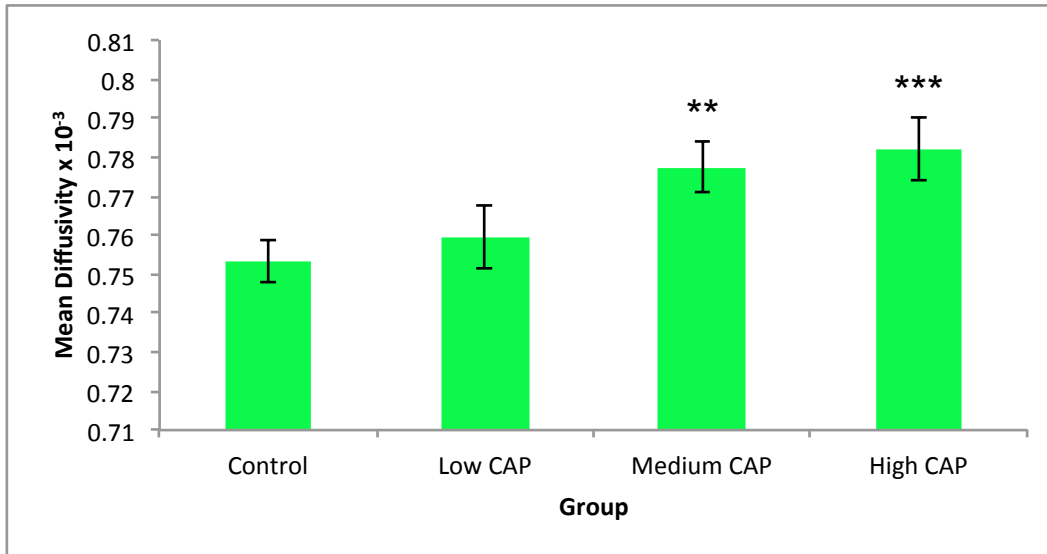


Mean Diffusivity in the Right Lateral Orbitofrontal Region by Group



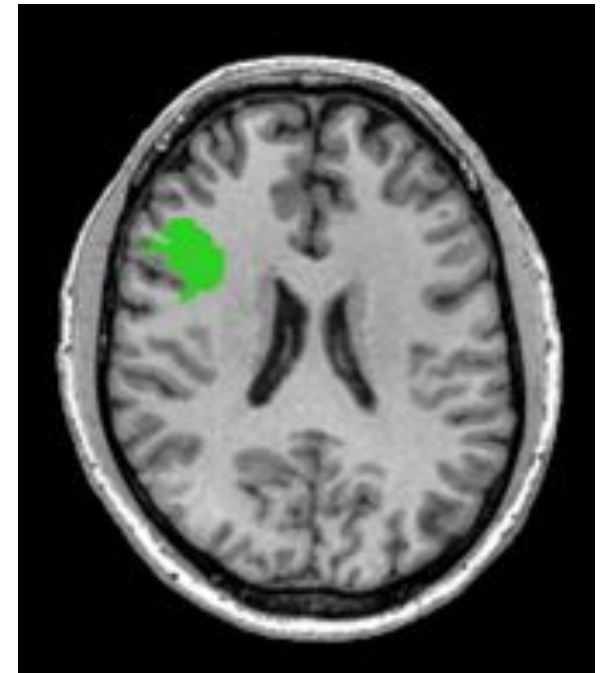
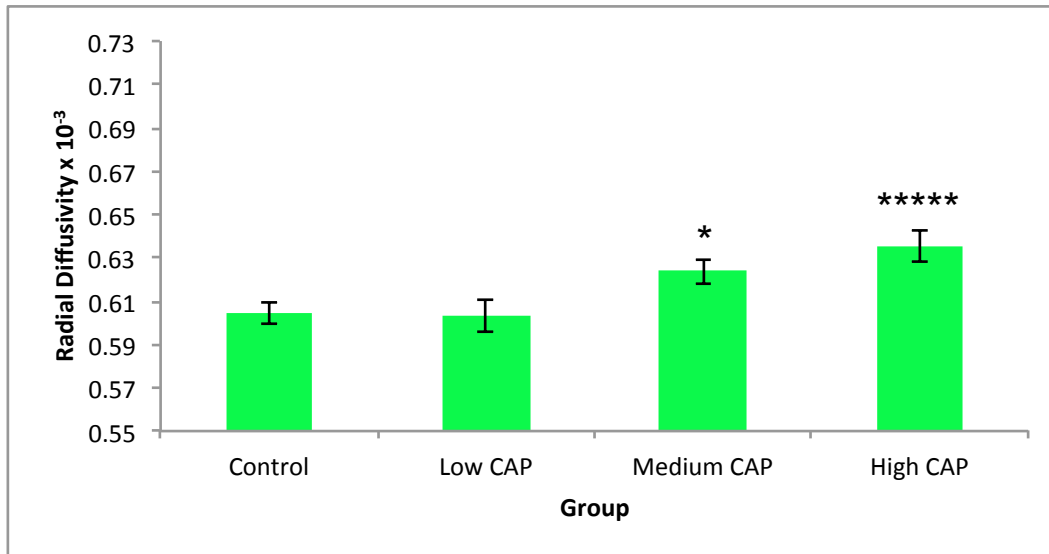


Mean Diffusivity in the Left Rostral Middle Frontal Region by Group



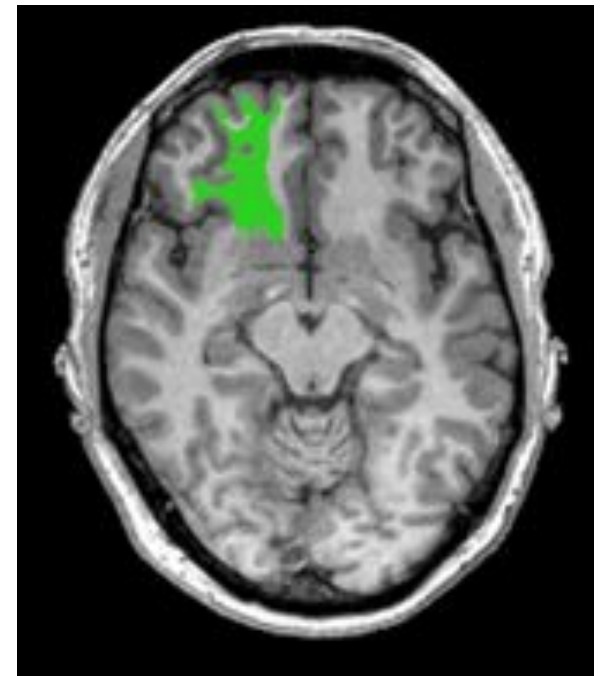
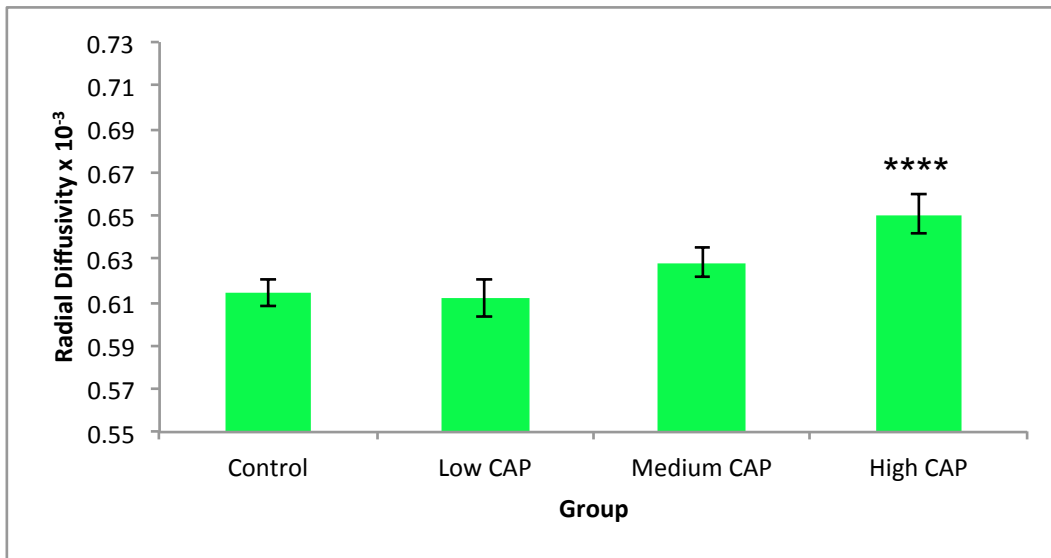


Radial Diffusivity in the Right Pars Opercularis Region by Group



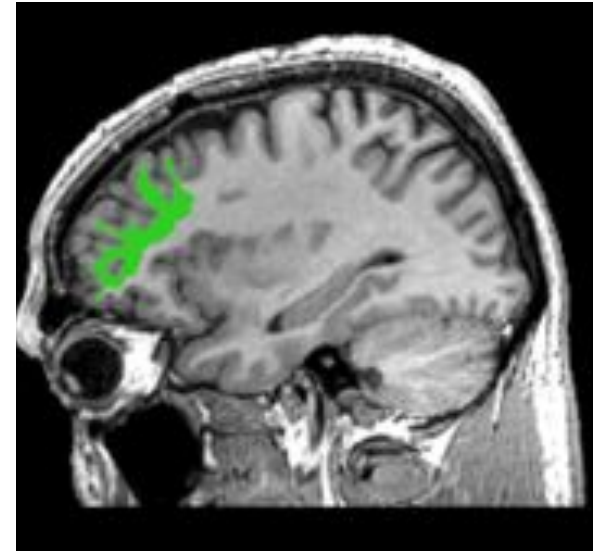
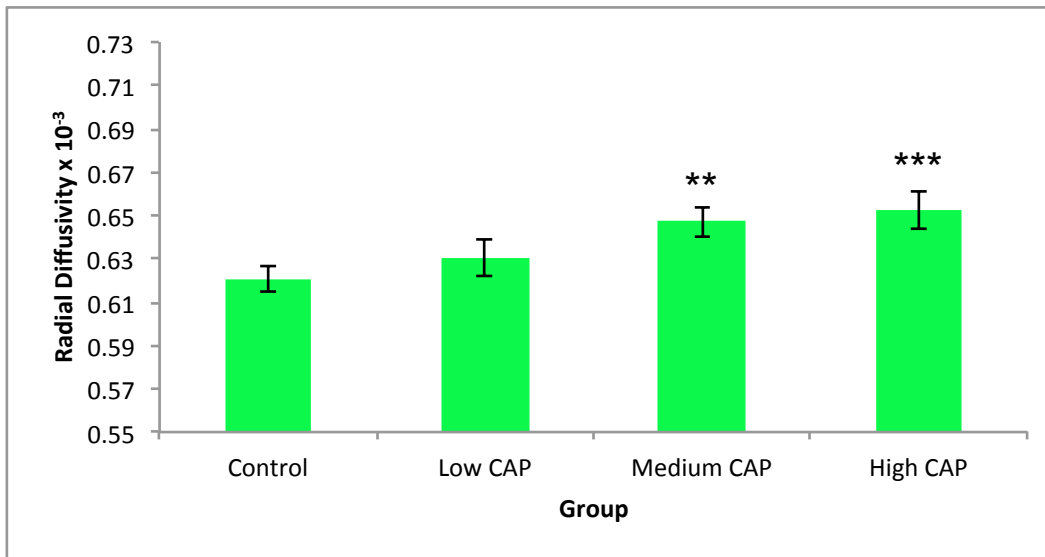


Radial Diffusivity in the Right Lateral Orbitofrontal Region by Group



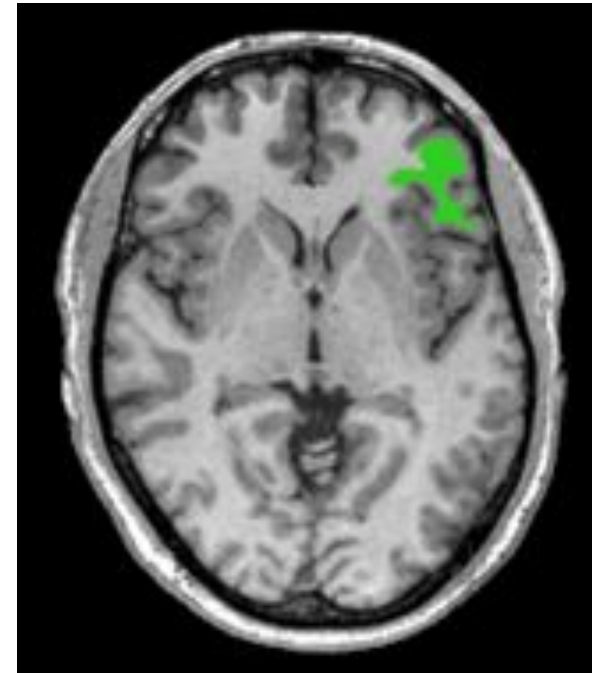
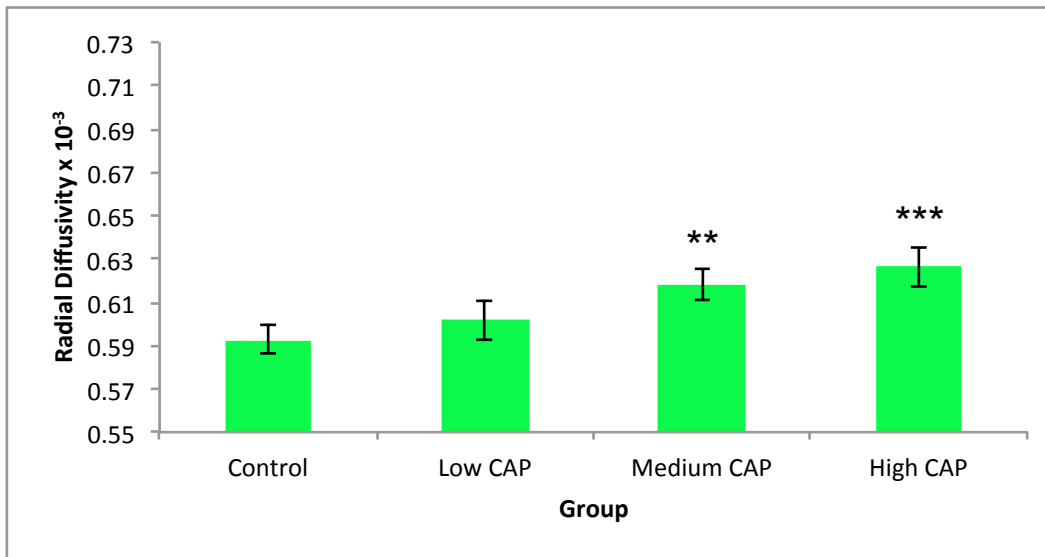


Radial Diffusivity in the Left Rostral Middle Frontal Region by Group



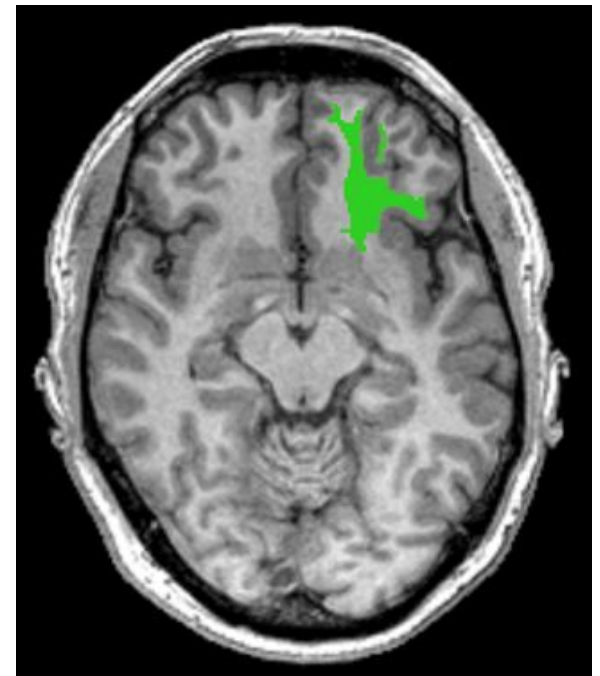
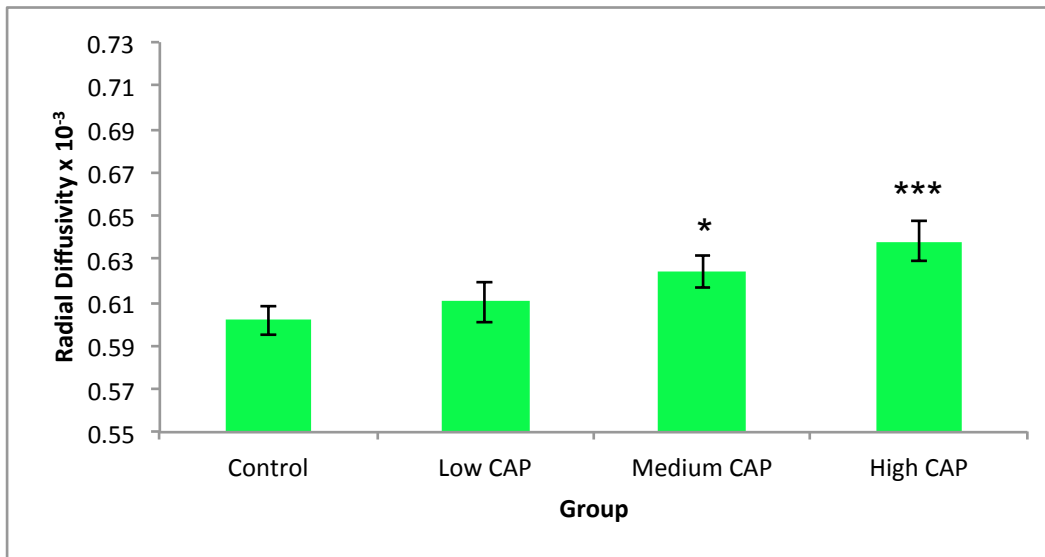


Radial Diffusivity in the Left Pars Triangularis by Group



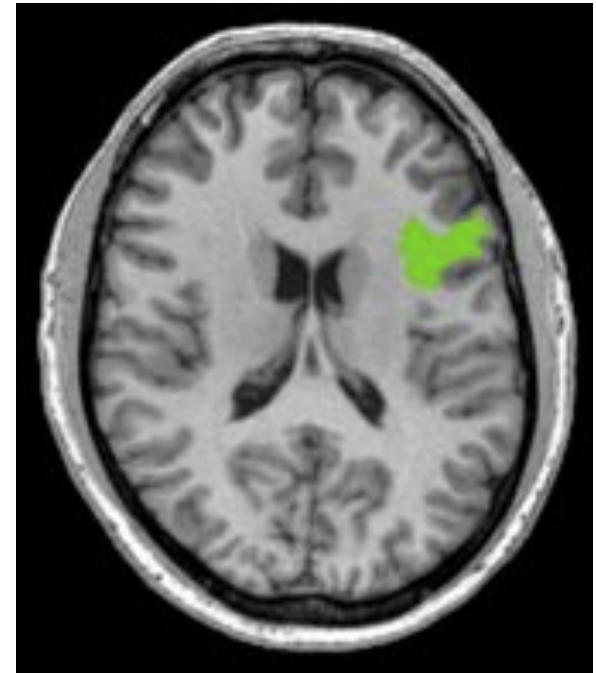
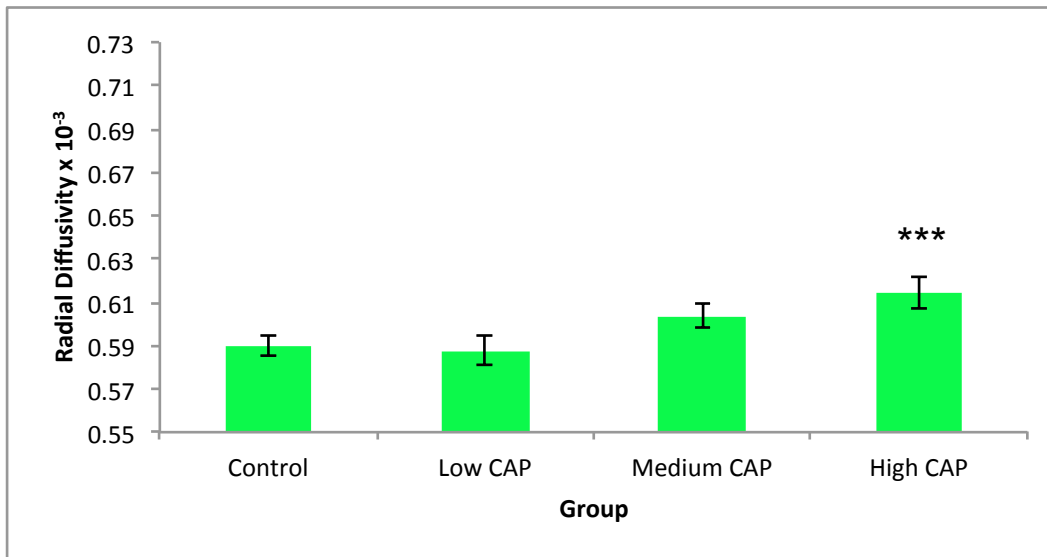


Radial Diffusivity in the Left Lateral Orbitofrontal Region by Group



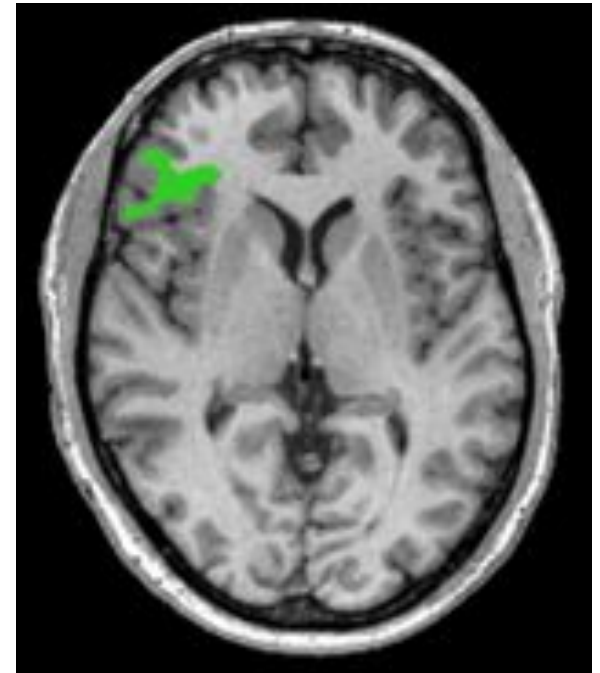
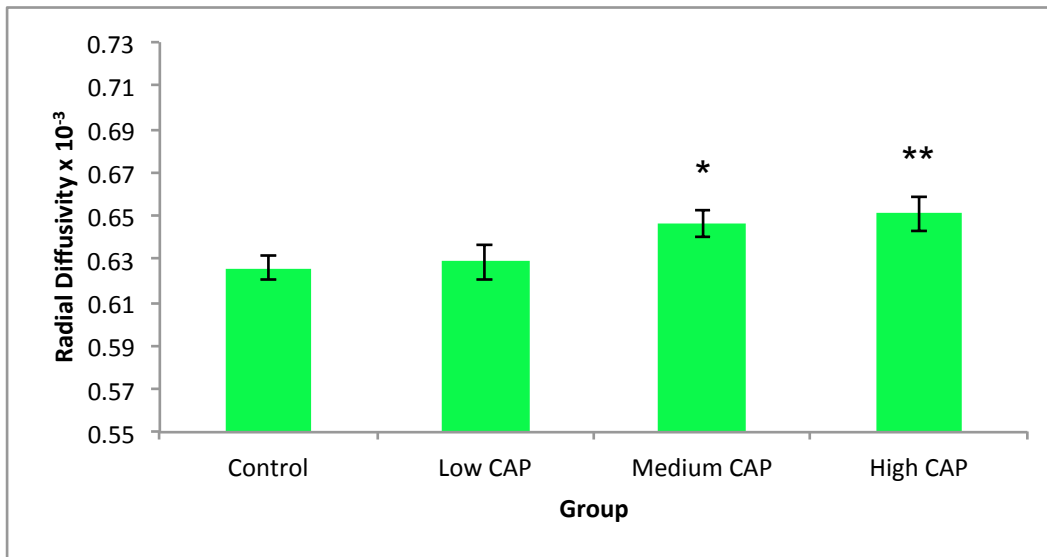


Radial Diffusivity in the Left Pars Opercularis by Group



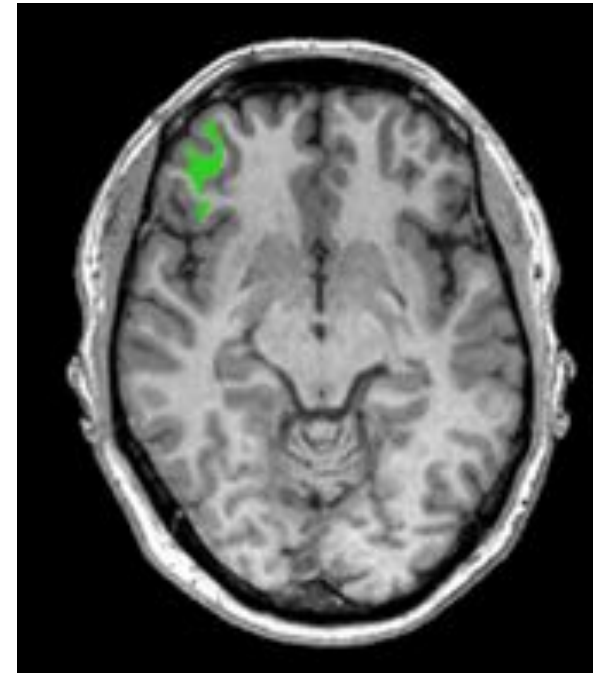
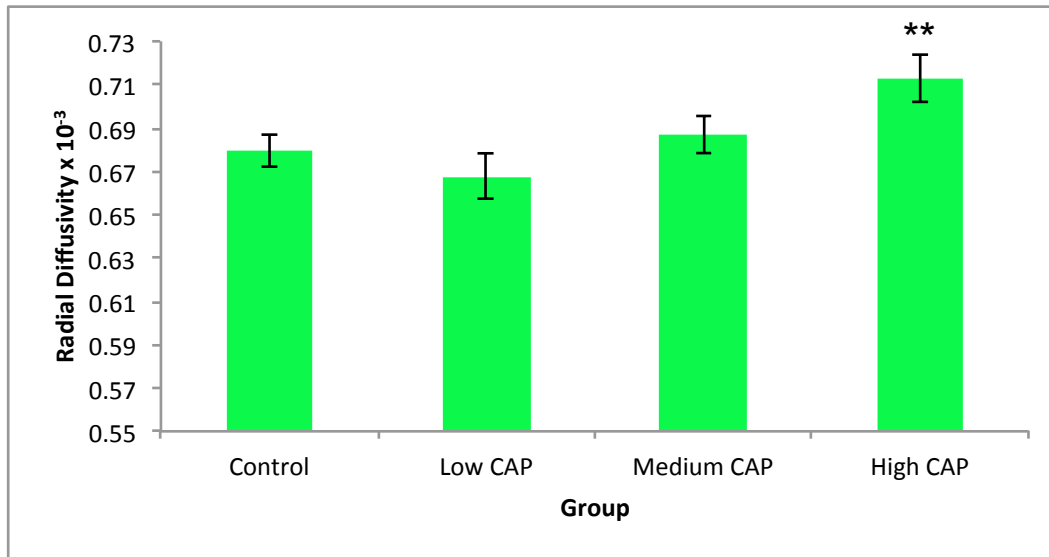


Radial Diffusivity in the Right Pars Triangularis by Group





Radial Diffusivity in the Right Pars Orbitalis by Group





Future

- Seminar Series Spring 2013
- BRAINSCamp 2013
- EHDN DWI Imaging Meeting (Sept 2013)
- Continue Integration of UNC/Utah/MGH in processing tools as they mature
- Deploy on 1000's of data sets
- Export QC Review Tools for closer Slicer Integration



Thank You!

- Questions?