F.M. Kirby Research Center for Functional Brain Imaging

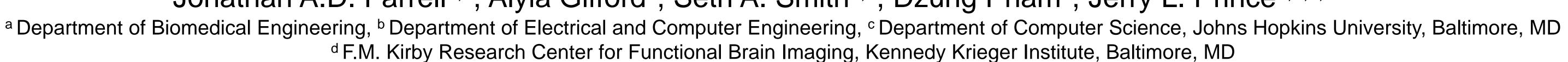


## CATNAP and JIST:

# DTI Processing Made Ridiculously Simple

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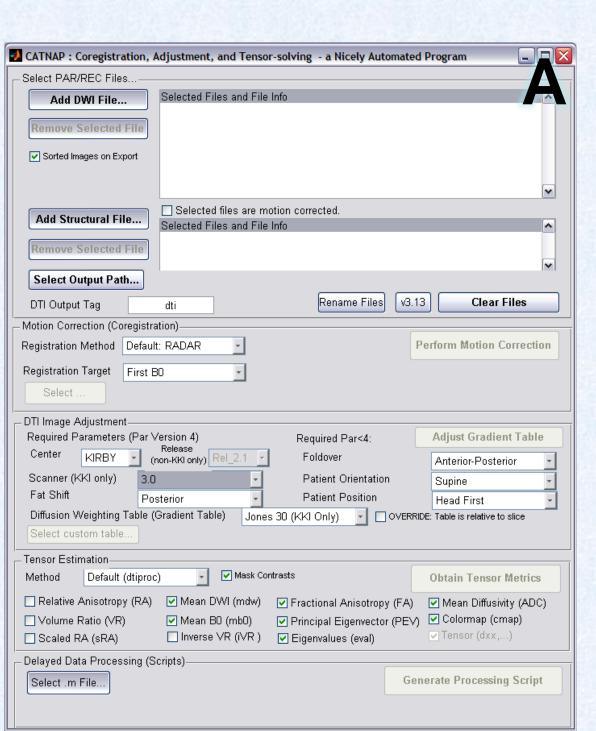
### INTRODUCTION

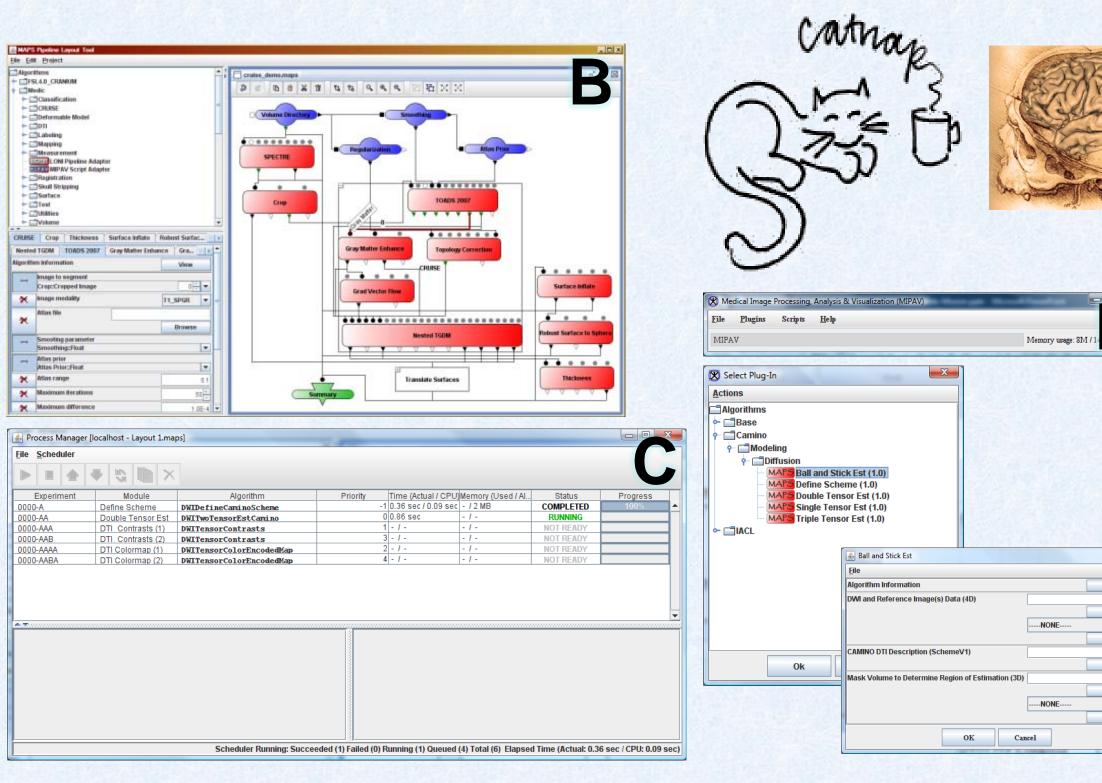
- Processing DTI data is not straightforward. Combining analyses of DTI and anatomical datasets can be cumbersome and time consuming, especially for large scale studies. These tasks include:
  - Co-registration of DTI and anatomical data.
  - Computation of diffusion tensors while taking into account the impacts of image registration.

We present a graphical user interface and control system to efficiently automate DTI and multi-modal MRI analyses.

- CATNAP (Coregistration And Tensor-solving a Nicely Automated Program) uses the Java Imaging Science Toolkit (JIST) to provide modular specification of analysis tasks and distributed computing capabilities. JIST builds upon the Medical Image Processing, Analysis, and Visualization (MIPAV) platform.
- CATNAP and JIST are available in open source under the Lesser GNU Public License through the Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC).

### SOFTWARE PACKAGES

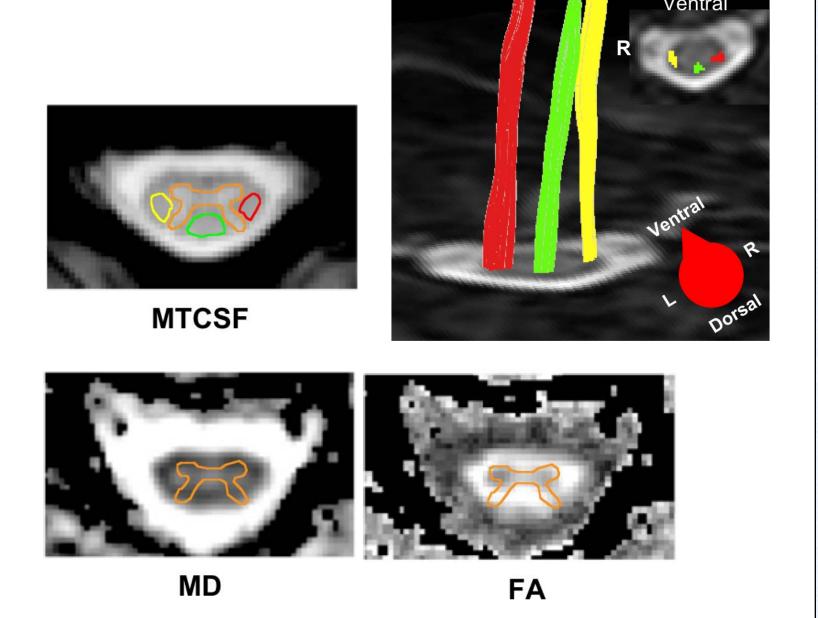




- Original CATNAP[1] software (left, A) was released as a Matlab package (The Mathworks, Natick, MA).
- CATNAP was ported to Java (Sun Microsystems, Menlo Park, CA) using the JIST framework (right). The new system includes a graphical layout tool (B) and a multi-threaded (grid engine aware) control package (C). Alternatively, steps may be run as MIPAV plugins (D).

### SPINAL CORD DTI ANALYSIS WITH CATNAP

- **Data:** Three repeated, multi-slice spin-echo DTI with single-shot EPI (TR/TE = 6300/63 ms, SENSE-factor = 2) were acquired with 1.5 (RL) x 1.25 (AP) mm resolution. 40 slices (3 mm slice thickness), FOV = 145 (RL) x 120 (AP) mm, 16 diffusion encoding directions, b = 500 s/mm². MT-weighted images were acquired using a 3D spoiled-gradient-echo sequence with multi-shot EPI readout (EPI factor = 3), TR/TE/a=110 ms/13 ms/9°, and SENSE-factor = 2.
- Analysis: MT and DTI data were coregistered and overlaid. Tensors were estimated using all available data. Regions of interest were defined to enable quantitative tract-based measures of the dorsal and lateral columns.
- Visualization: Processed data were manually examined in DTIStudio and MIPAV.



### Links to the Software and Source Code

CATNAP+JIST: <a href="http://www.nitrc.org/projects/maps4mipav/">http://www.nitrc.org/projects/maps4mipav/</a>

CRUISE: http://iacl.ece.jhu.edu/cgi-bin/download.scgi?sw=cruise

CATNAP (original Matlab): <a href="https://www.iacl.ece.jhu.edu/cgi-bin/download.scgi?sw=catnap">https://www.iacl.ece.jhu.edu/cgi-bin/download.scgi?sw=catnap</a>

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REFERENCES [1] Landman BA,et al. (2007) Neuroimage. [2] Carass, A., et al (2007) ISBI. [3] Bazin, P.-L. and Pham, D., (2007) IEEE Trans Med Imaging. [4] Han, X., et al., (2004) Neuroimage.

# BRAIN DTI ANALYSIS WITH CATNAP To the life of the lif

**Data:** Two repeated DWI acquisitions consisting of 30 directions with a 240mm x 240mm, matrix size 96x96 reconstructed to 256x256, 50 slices, and slice thickness of 2.5mm. The structural data input to this pipeline consisted of one MPRAGE acquisition with a field of view of 240mm x 240mm, matrix size 96x96 reconstructed to 256x256, 125 slices, and slice thickness of 1.5mm.

**DTI Processing (left):** The DTI data were processed with CATNAP[1] which co-registers the diffusion weighted volumes, adjusts the gradient tables, and performs log-linear minimum mean squared error tensor estimation. The tensor contrasts, FA, MD and principal eigenvectors were also computed. Geometry correction was performed with a deformable registration to the MPRAGE. Fiber tracts were reconstructed with a line-tracing technique with an FA threshold of 0.2 and an angle threshold of 40 degrees. All of the above were implemented in the MAPS framework and were computed entirely automatically.

Cortical Surface Processing (right): The structural MPRAGE was processed with SPECTRE[2], a skull-stripping algorithm, TOADS[3], which classifies gray matter, white matter, and subcortical structures, and CRUISE[4], a cortical surface reconstruction algorithm. Thickness measurements (not shown) and gyral labels (below) were estimated on the surfaces.

Visualization: Processed data were visualized and rendered in MIPAV, DTIStudio, and Paraview.

### **RESULTS**

