

MINC meeting 2003

Pipelines: analyzing structural MR data

Jason Lerch
<jason@bic.mni.mcgill.ca>



Whither this talk?

- **Provide a brief overview of what we can do with anatomical MRI (aMRI)**
- **Describe the procedure, including the necessary commands, for running Voxel Based Morphometry (VBM)**
- **Give a quick overview of our visualization tools.**
- **Outline other analysis possibilities**

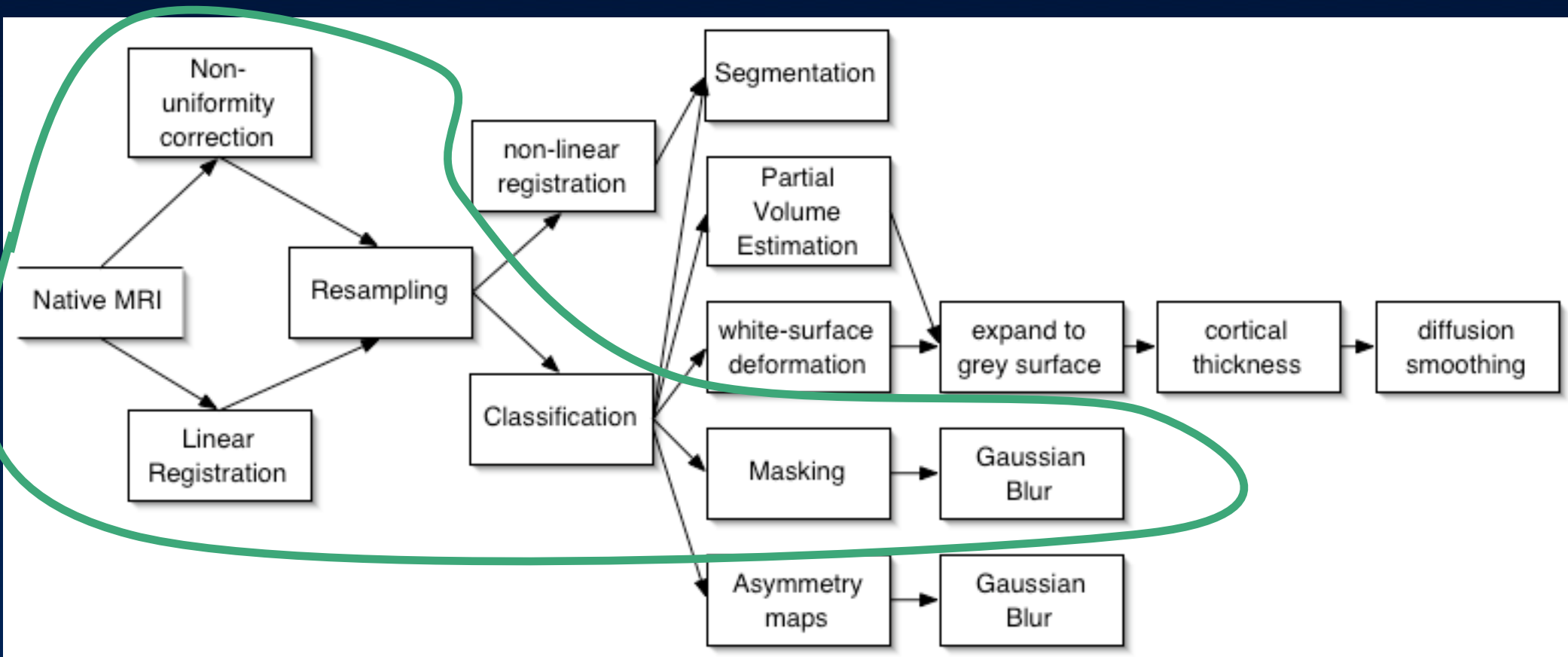
A plug for aMRI

- **Clinical:**
 - how is the patients' anatomy different from controls
 - use of anatomical information to diagnose disorders
- **Anatomy - identification of macroscopic features.**
- **Psychology: does anatomy change with behavioural function?**
 - ex: right hippocampus bigger in London taxi drivers

Population Analyses

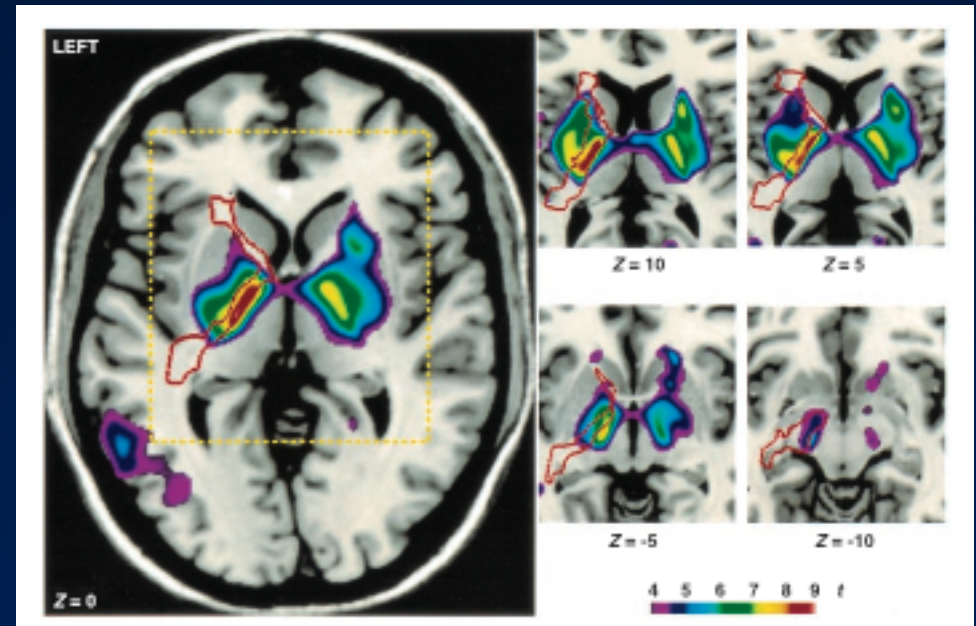
Voxel Based Morphometry	Tissue densities at every voxels
Asymmetry Analysis	Tissue asymmetry at every voxel
Comparison of Volumes	Whole brain, tissue type, or structure volumes
Cortical Thickness Analysis	Thickness at every vertex
Deformation Analysis	Deformation difference in registration towards model

The image processing pipeline



Voxel Based Morphometry (VBM)

- Looks at changes in tissue concentration.
- Fully automatic.
- Useable for all tissue types.
- Fairly simple procedure.
- Widely used.

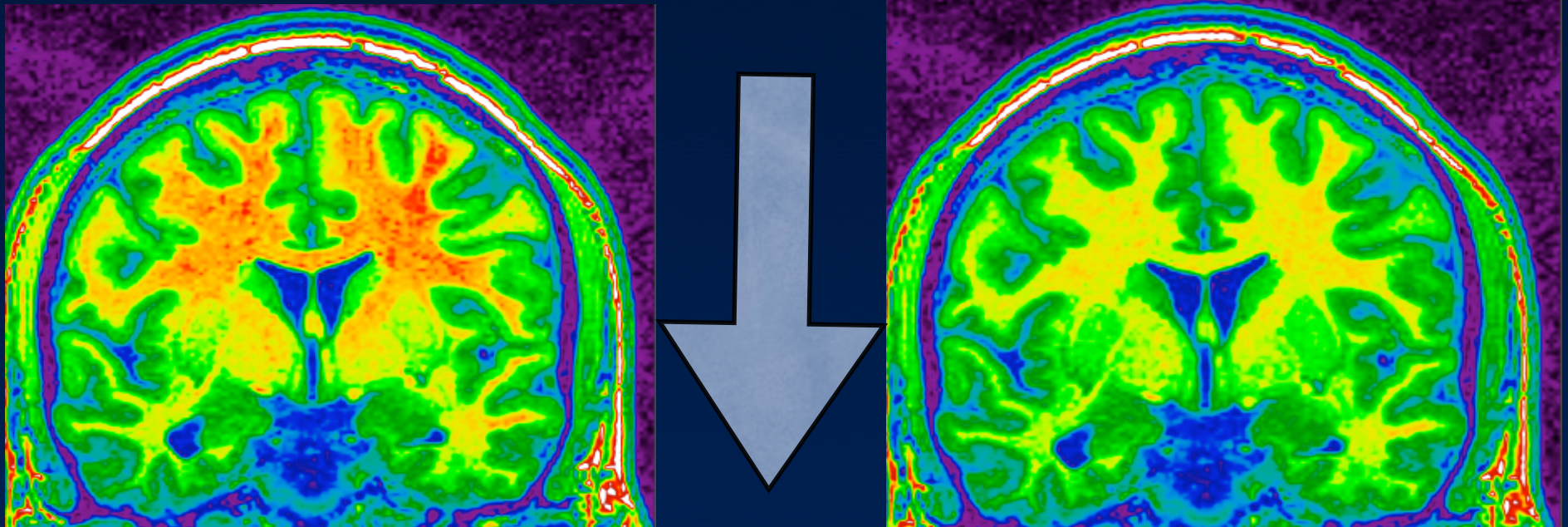


From Paus et al, Science, 1999

Non-uniformity correction

Native

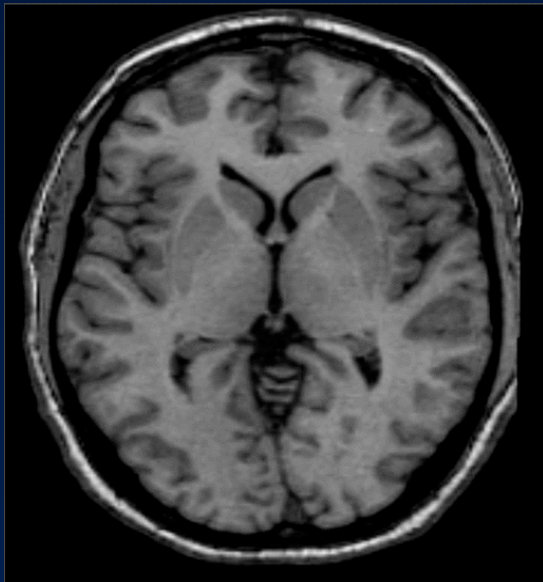
Corrected



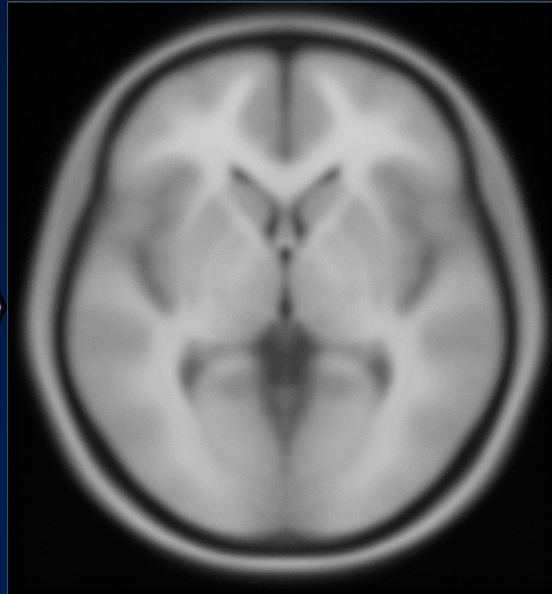
nu_correct native.mnc corrected.mnc

Registration

Subject



Model



Transform

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

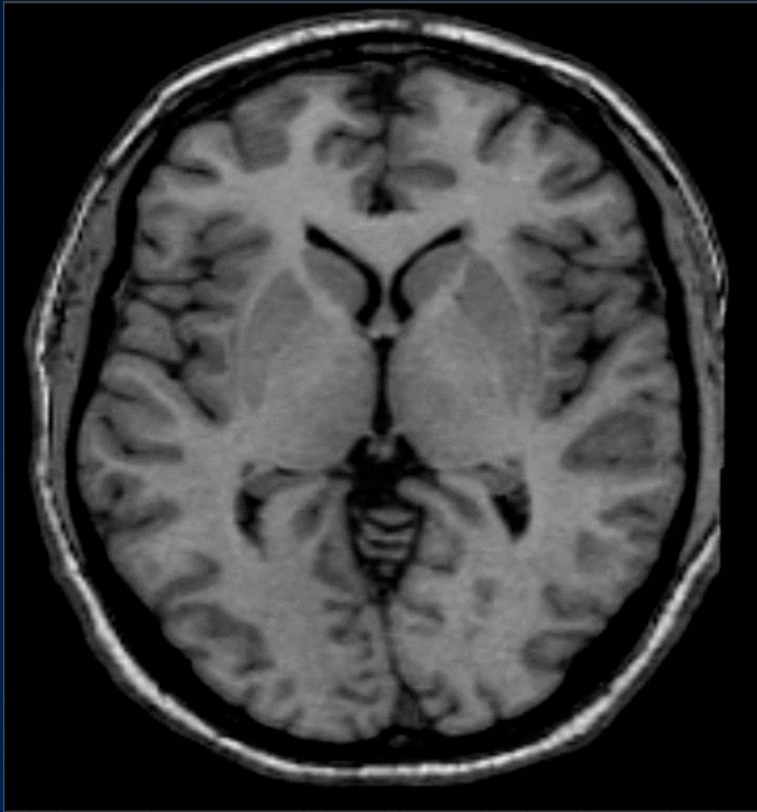
`mritotal native.mnc to-tal.xfm`

Resampling

- **Creates a volume that is:**
 - Non-uniformity corrected using the output of nu_correct.
 - Transformed using the output of mritotal.
 - Given the same sampling as a model.

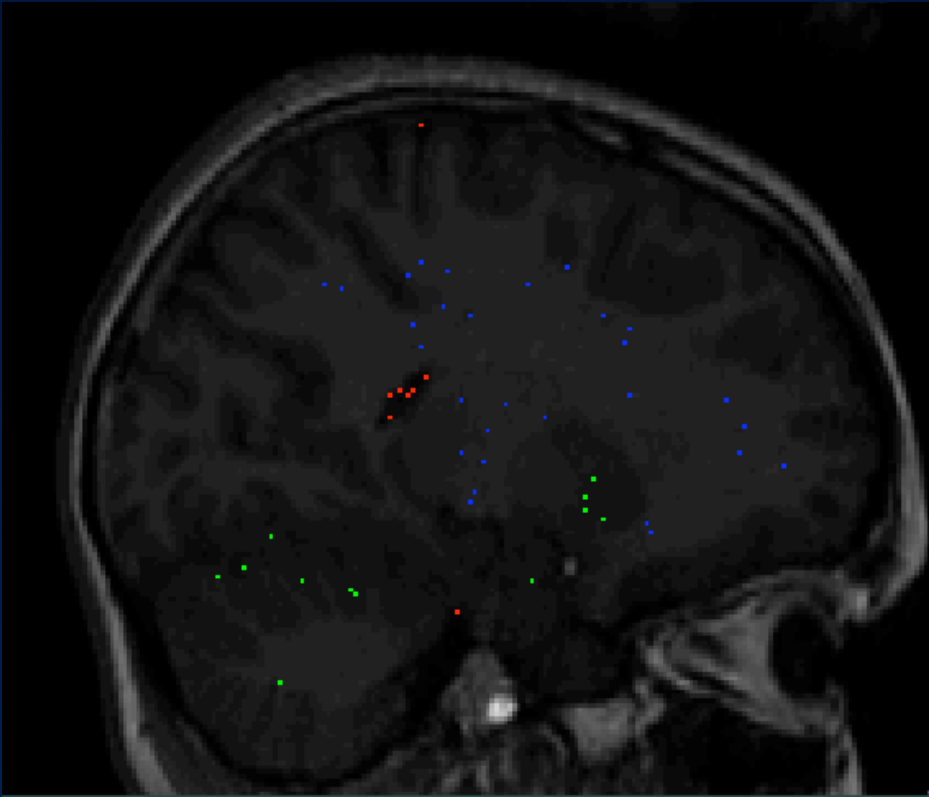
```
mincresample -like model.mnc -transform  
to-tal.xfm corrected.mnc final.mnc
```

Classification



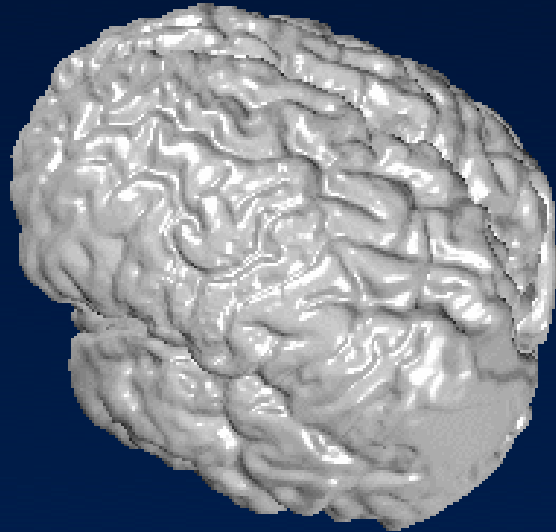
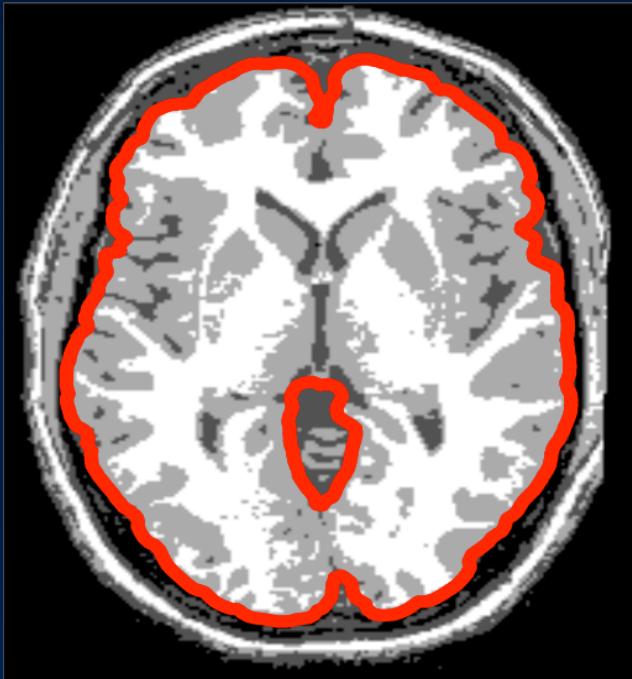
classify_clean final.mnc classified.mnc

Classification explained



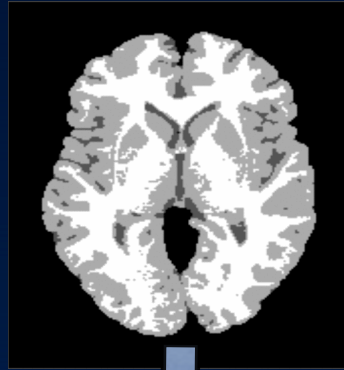
- **Set of spatial priors:**
 - Based on talairach space.
 - Generated from tissue probability maps.
 - Used to train classifier for each individual subject.
- **Can handle multiple inputs (t1, t2, PD).**
- **Multiple outputs**
 - GM, WM, CSF
 - Lesions.

Masking

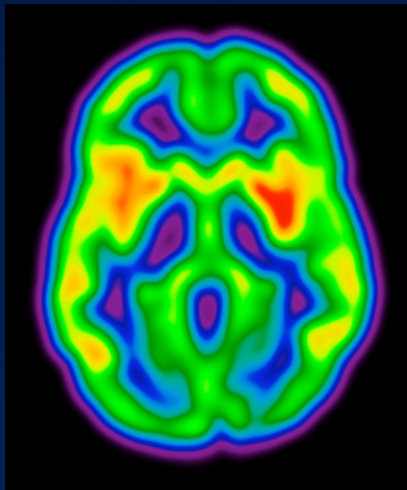


cortical_surface classified.mnc mask.obj 1.5
surface_mask2 classified.mnc mask.obj masked.mnc

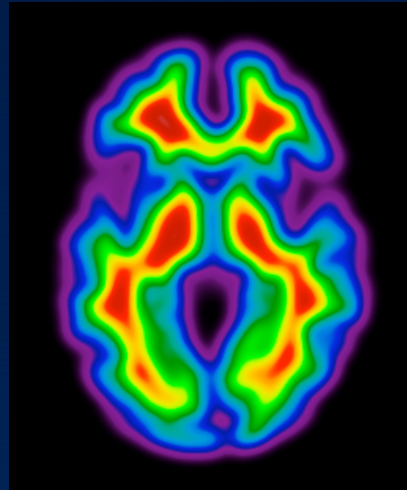
Tissue Maps



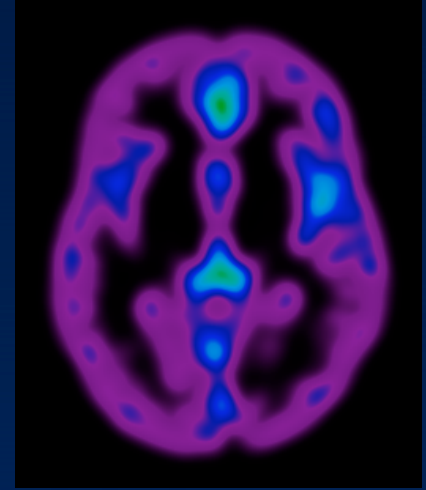
Grey Matter



White Matter



CSF

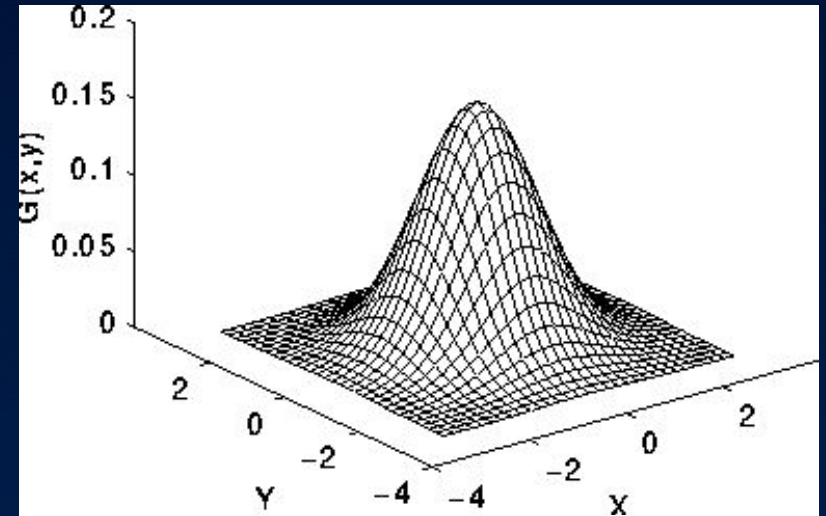


`smooth_mask -binvalue x -fwhm x masked_cls.mnc map.mnc`

Tissue Density Explained

- **Tissue Density:**

- Neighbourhood average of one tissue type.
- Size of neighbourhood can be specified.
- Resulting voxels have values between 0 (no voxels of that tissue type in that neighbourhood) and 1 (all voxels in neighbourhood of that tissue type).



$$\frac{1}{273}$$

1	4	7	4	1
4	16	26	16	4
7	26	41	26	7
4	16	26	16	4
1	4	7	4	1

Statistical Modelling

Linear Model $y = X\beta + \varepsilon$

y = tissue density map

X = matrix of predictors

β = slope of predictors

ε = random variance

F = significance of whole model

t = significance of term within model


The GLIM file

Filename corresponding to
tissue density file of each
subject

Intercept - always 1

Predictor

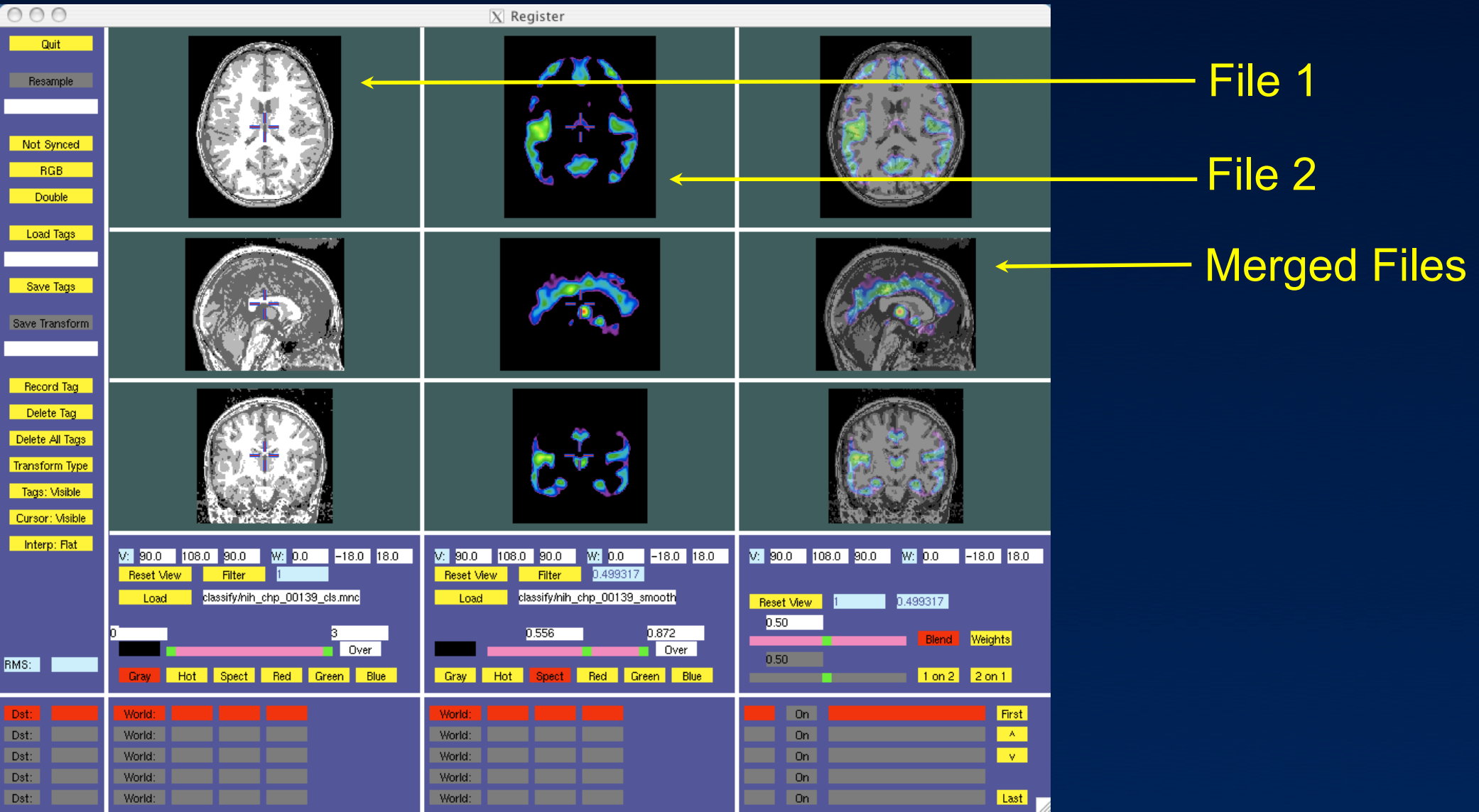
Text file



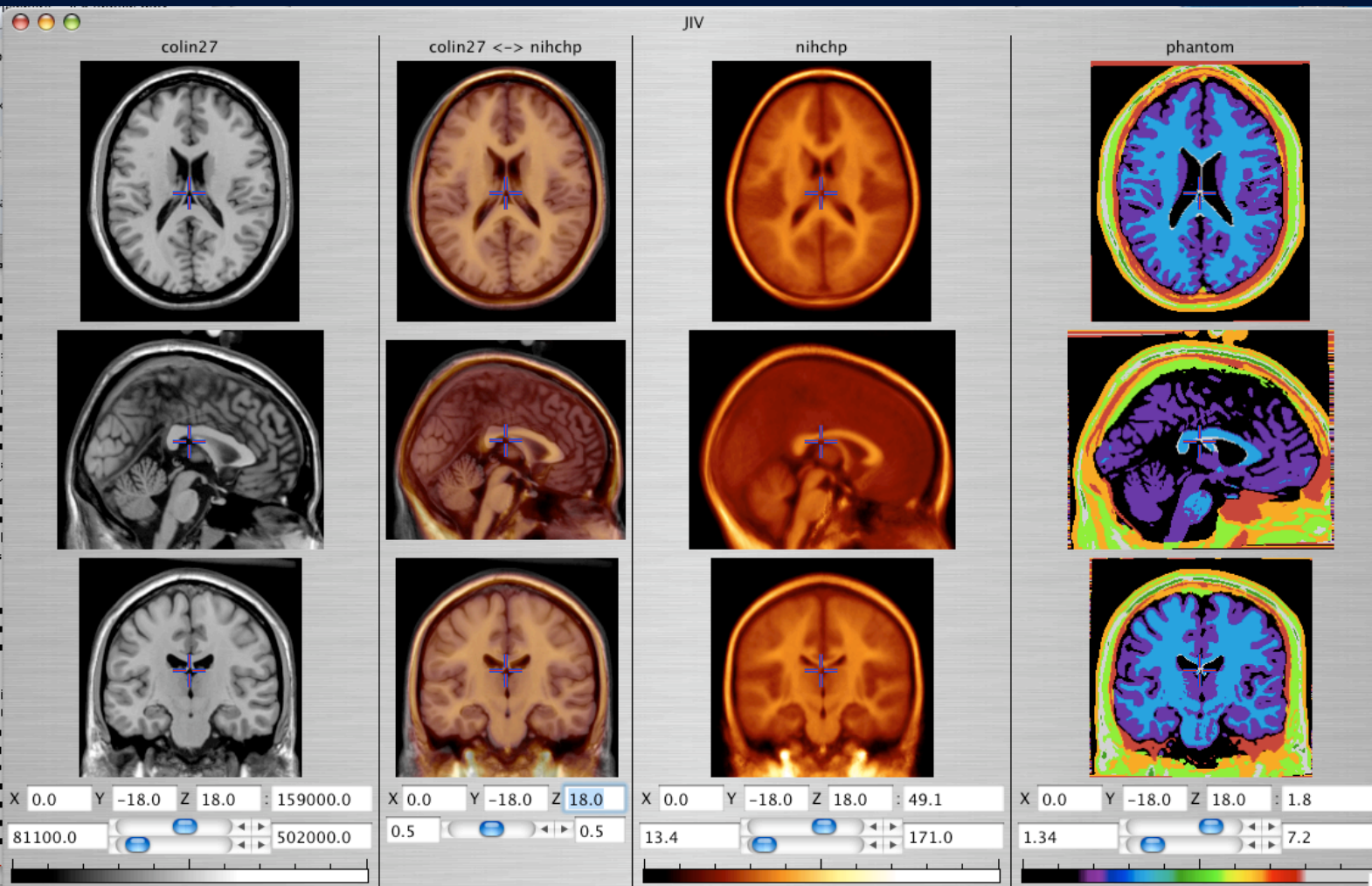
Subject_001_smooth_gm.mnc 1 25
Subject_002_smooth_gm.mnc 1 32
Subject_005_smooth_gm.mnc 1 38
Subject_013_smooth_gm.mnc 1 15

`glim_image -t_stat output.mnc t_stat voxel column 2 matrix.glim`

An aside on visualization



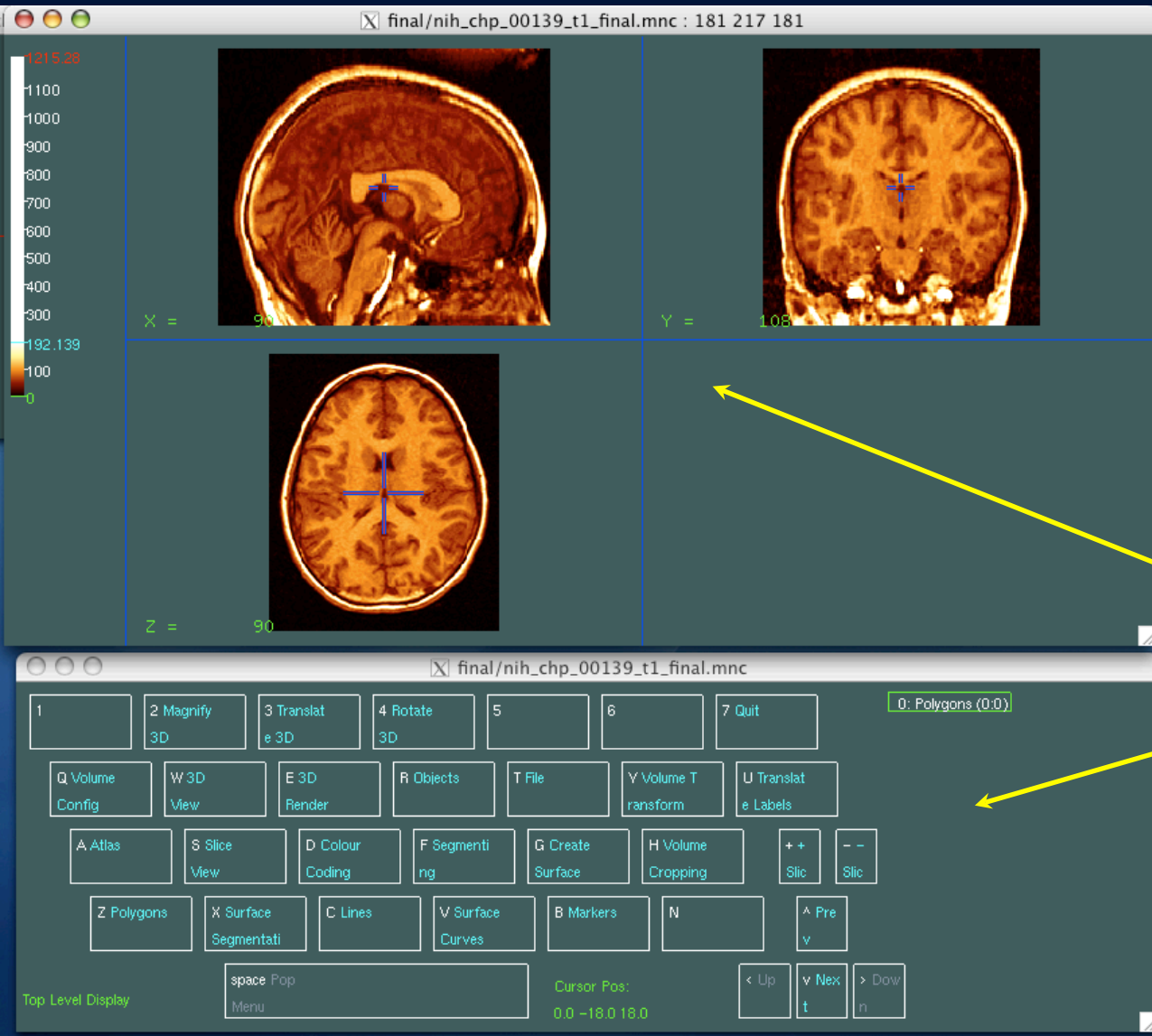
Visualization 2: JIV



- **JIV**

- Java: runs over the internet.
- Great for sharing data with others.
- Able to show multiple volumes.

Visualization 3: Display



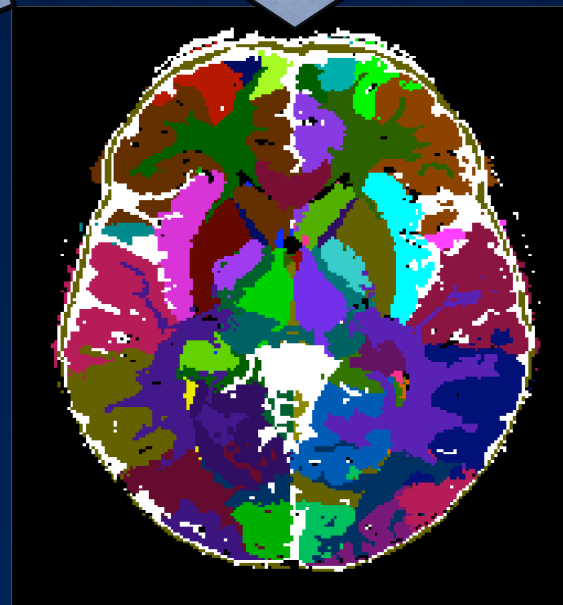
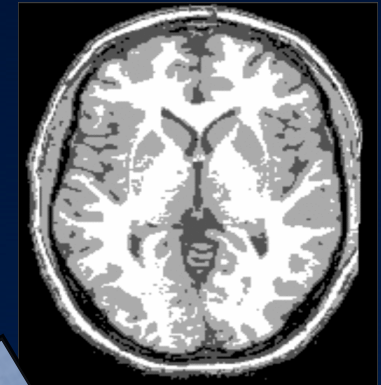
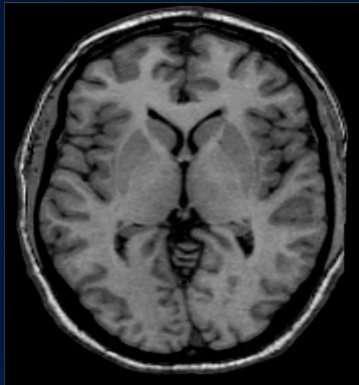
- **Display:**

- Brain painting.
- Viewing object files.
- Placing tags.
- Basic visualization

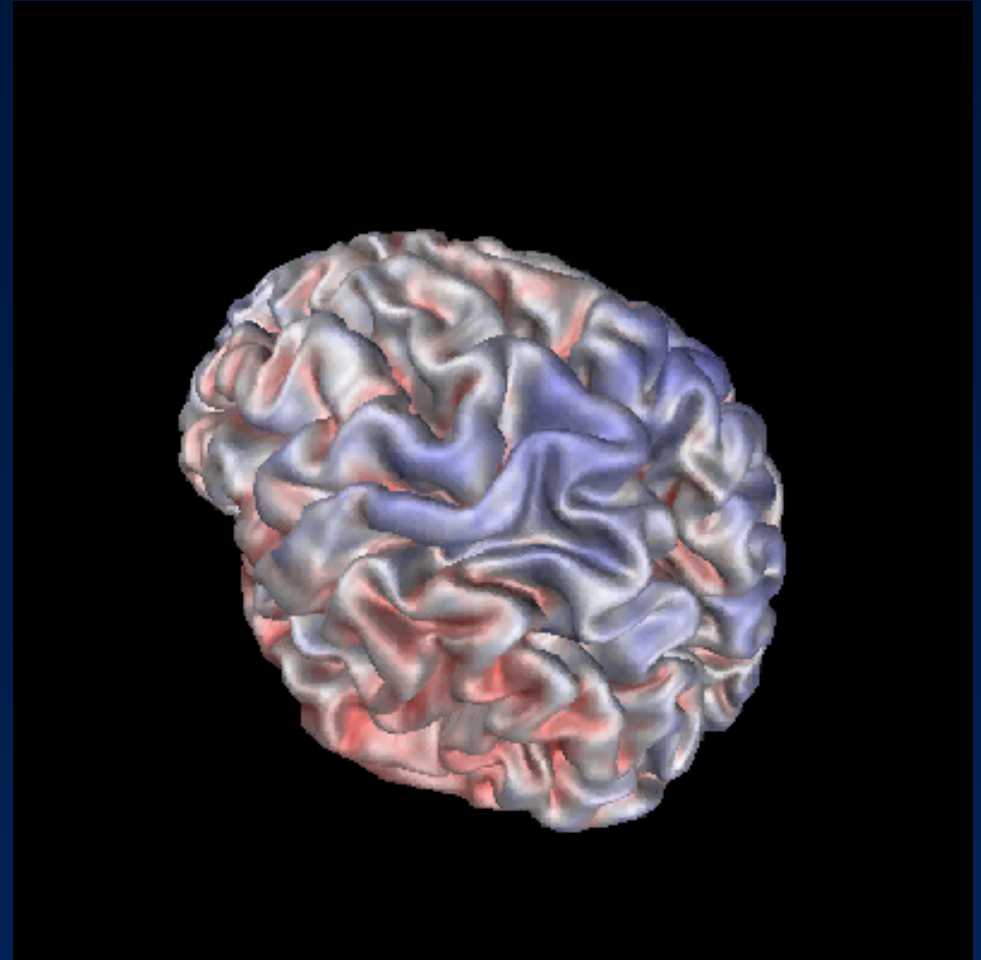
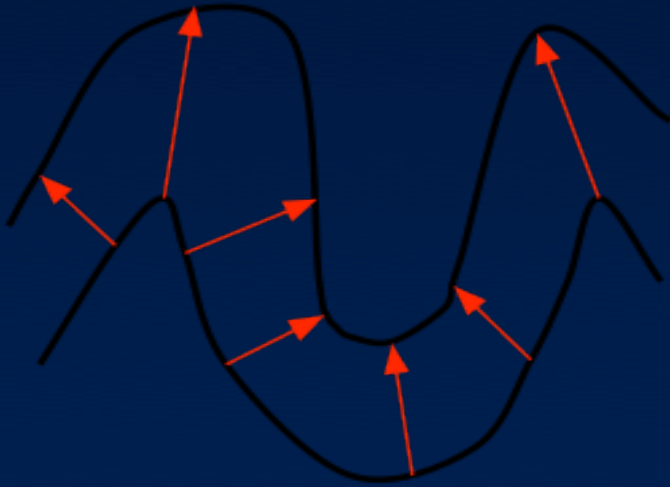
Volume Window

Menu Window

Segmentation



Cortical Thickness estimation



Conclusions

- **More questions?**
 - Sign up to the minc-users listserv!!
 - Email me at jason@bic.mni.mcgill.ca