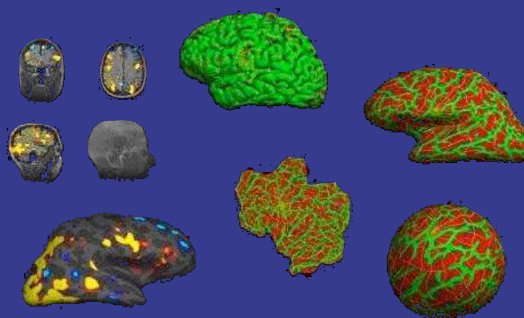


**FreeSurfer**



# **FREESURFER HANDS-ON WORKSHOP**

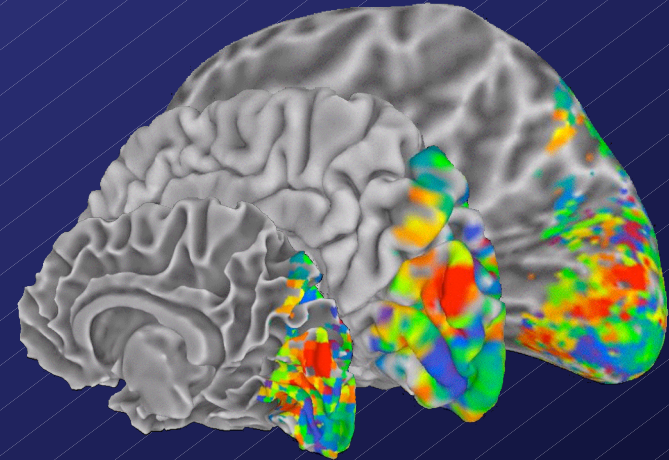
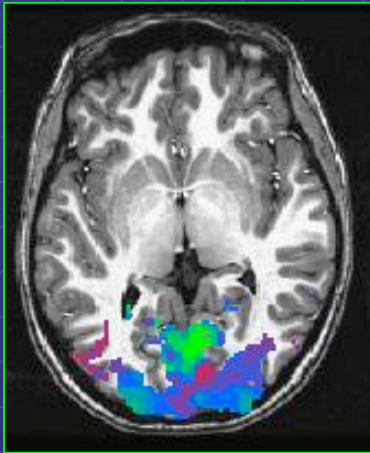
Peggy Christidis

November 8, 2005

National Institutes of Health

## GOAL OF WORKSHOP

Learn to create surfaces using FreeSurfer



- Start with several anatomical scans (MPRAGE)
- Create surfaces using FreeSurfer
- Overlay functional data on surface using SUMA  
(*Hands-On class for SUMA on 11-9-2005*)

# Agenda

- *FreeSurfer Overview*
- *Hands-On*
  - *Volume Preprocessing*
  - *Segmentation*
  - *Tessellation/Inflation*
  - *Manual Editing/Re-inflation*
- *Lunch Break*
- *Hands-Off*
  - *Fix Topology*
  - *Final Surface*
  - *Cut and Flatten*

## About FreeSurfer

- FreeSurfer is a set of tools for analysis and visualization of structural and functional brain imaging data.
- FreeSurfer provides many anatomical tools such as:
  1. Representation of the cortical surface between gray and white matter -- known as the 'white matter surface'.
  2. Representation of the cortical surface between the gray matter and the Cerebral Spinal Fluid (CSF) -- known as the 'pial surface'.
  3. Segmentation of white matter from the rest of the brain.
  4. Skull stripping

## About FreeSurfer

5. B1 bias field correction (a.k.a. ‘intensity normalization’ or ‘non-uniformity correction’).
6. Nonlinear registration of the cortical surface of an individual with a stereotaxic atlas.
7. Labeling of regions of the cortical surface -- Parcellation.
8. Statistical analysis of group morphometry differences -- cortical thickness.
9. Labeling of subcortical brain structures (*new!* Command line mode only).

# About FreeSurfer

- FreeSurfer runs in **TWO** modes:
  1. Graphical User Interface mode
    - ❖ The majority of this workshop will focus on the FreeSurfer GUI, since it's a good place to begin for a FreeSurfer novice.
  2. Command Line mode
    - ❖ For those more familiar with FreeSurfer.

# About FreeSurfer

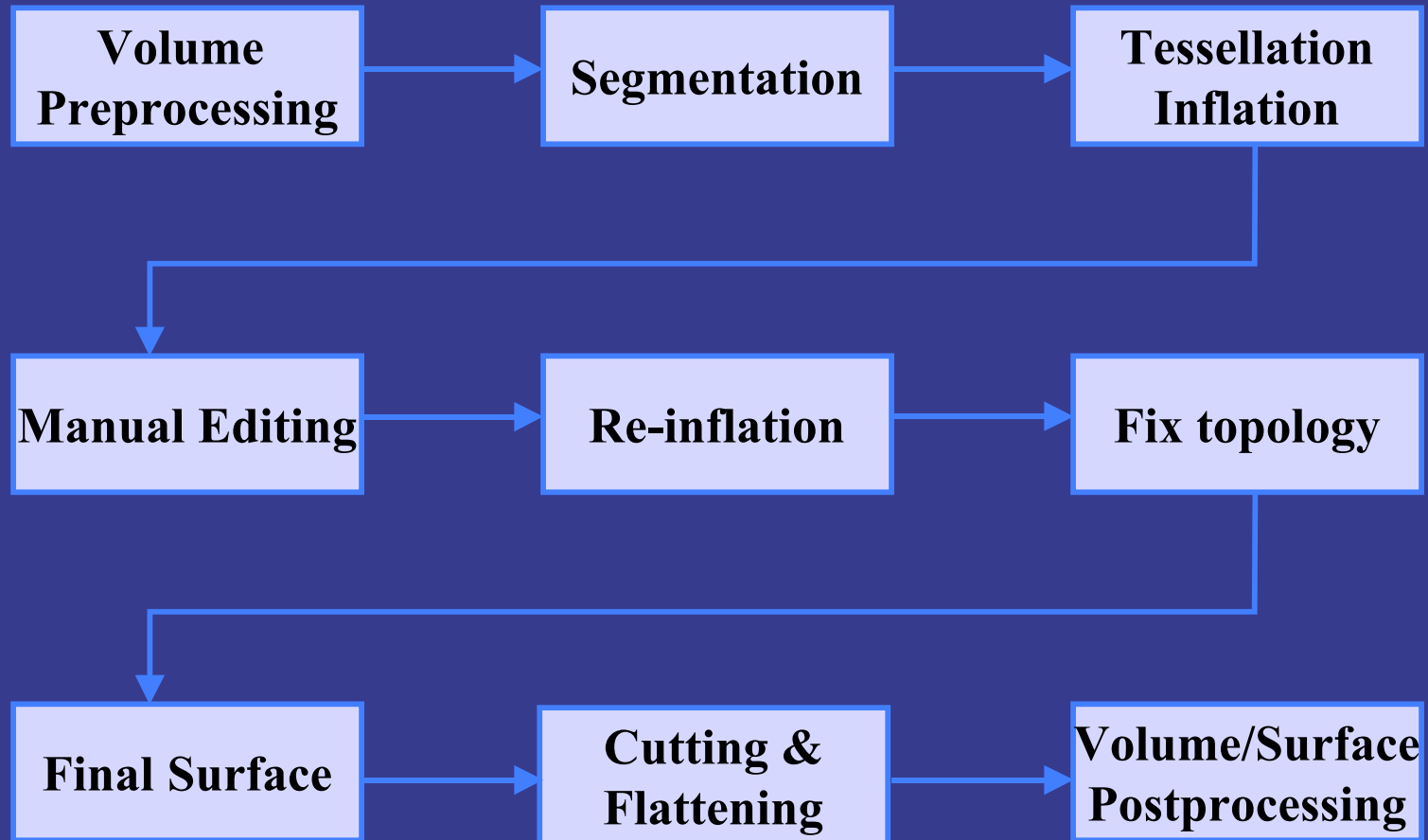
- Major changes have been made to FreeSurfer within the last year.
- However, these changes have been applied only to the *command line* mode of FreeSurfer.
  - ❖ Biggest change has to do with the manual editing tool.
    - In the past, users had to manually correct topological defects that appeared on the first-pass surface.
    - These defects showed up as “holes” and “handles” on the surface.
  - ❖ Now, if you use the command line mode, the program attempts to automatically fix most of these topological defects.
    - This is done by segmenting the sub-cortical features of the brain, thus locating those “problem” areas that cause the holes and handles, such as the basal ganglia, lateral ventricles, and fornix.
  - ❖ Note: You may still have to manually edit other defects that the automated topology fixer didn't catch.

## About FreeSurfer

- The recent changes in FreeSurfer have not been applied to the FreeSurfer GUI mode.
- If you've started creating surfaces on a sample of subjects using the GUI mode, remain consistent and continue using the GUI mode.
- Why bother using the GUI mode, which still requires users to go through the laborious process of manual editing, when you can use the command line mode and have the software fix the defect automatically?
  - ❖ Because the user must understand WHAT structures need to be edited, WHY they need to be edited, and HOW they need to be edited.
  - ❖ This way, you'll be able to check if the automated editor did the editing correctly.



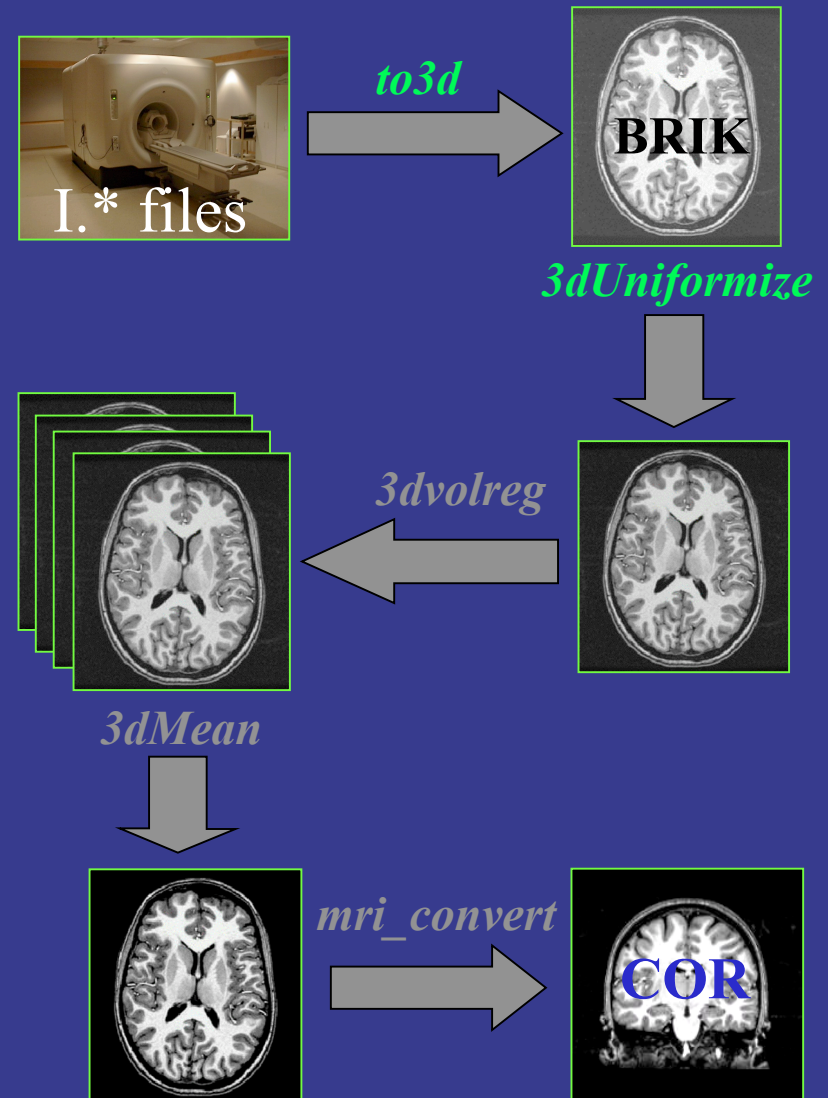
# FreeSurfer Flowchart for Graphical Interface Mode





# 1. Volume Preprocessing

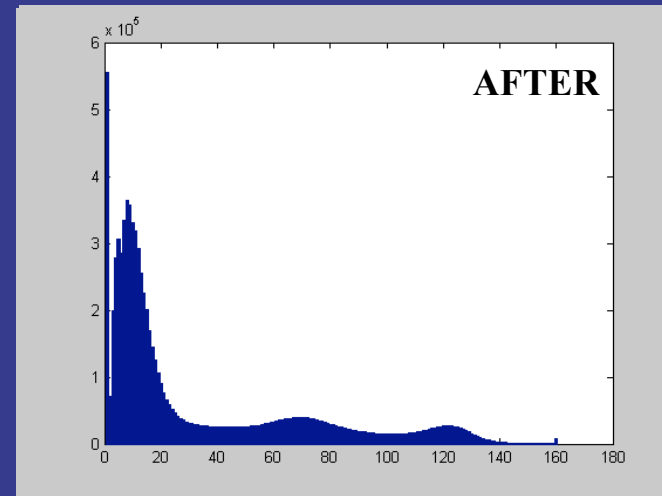
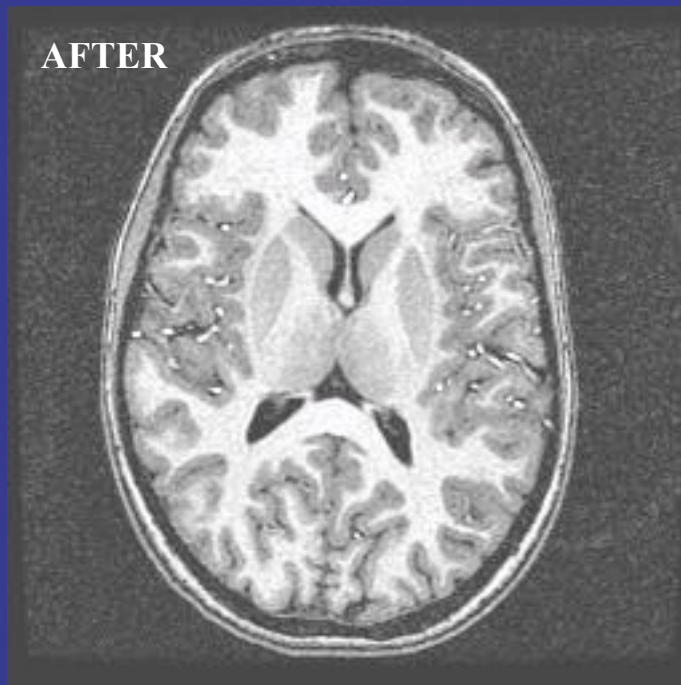
- Convert *I.\* files* to *BRIK* using AFNI *to3d*
- Perform intensity normalization using AFNI *3dUniformize*
- Register multiple volumes using AFNI *3dvolreg*
- Average the registered volumes using AFNI *3dMean*
- Convert to FreeSurfer format using FreeSurfer *mri\_convert*



# 1. Volume Preprocessing

## Intensity normalization – critical for segmentation

- Inhomogeneities in scanner fields cause gray and white matter intensities to vary as a function of their spatial location.
- Removes residual non-uniformities in gray and white matter intensity values.

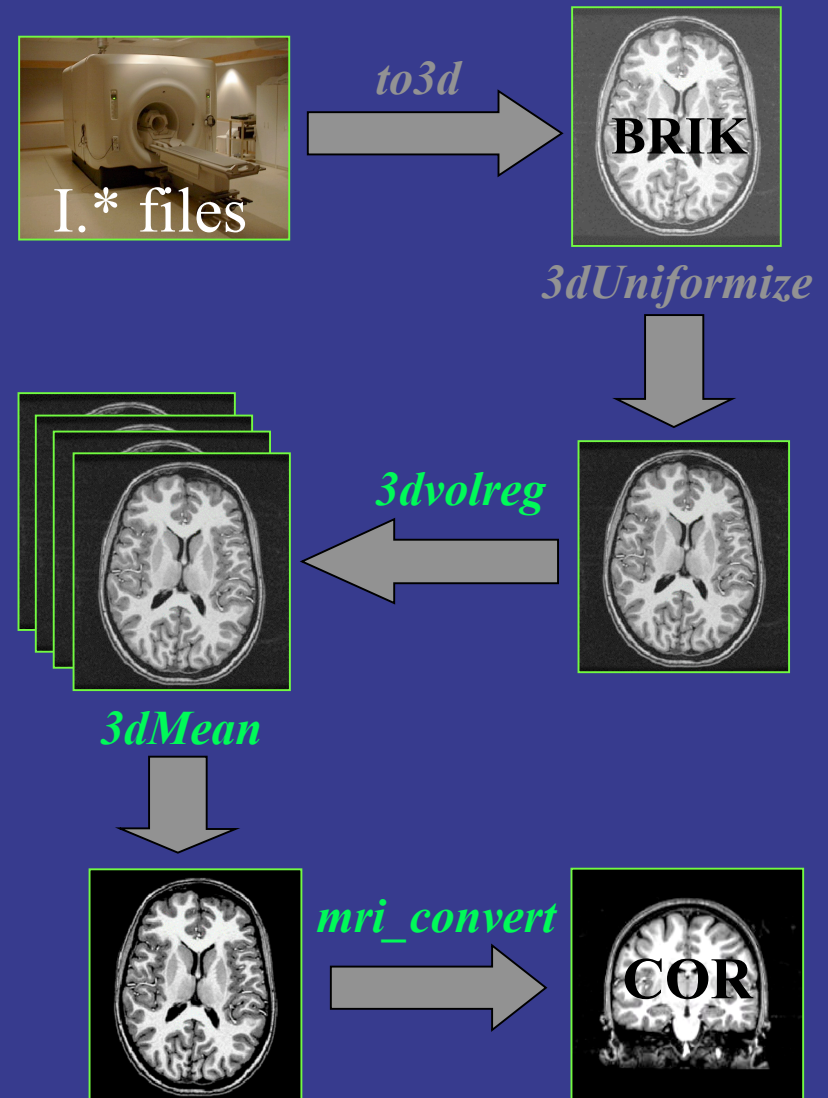


- Increases gray and white matter contrast.
- Sharpens the peaks of the two tissue classes.
- Makes the intensity distribution of gray and white matter spatially uniform.



# 1. Volume Preprocessing

- Convert I.\* files to BRIK using AFNI *to3d*
- Perform intensity normalization using AFNI *3dUniformize*
- *Register multiple volumes using AFNI 3dvolreg*
- *Average the registered volumes using AFNI 3dMean*
- *Convert to FreeSurfer format using FreeSurfer mri\_convert*





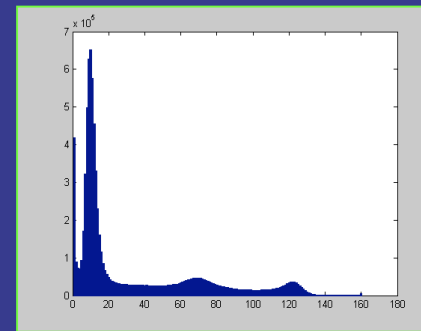
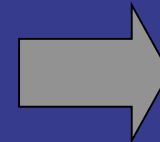
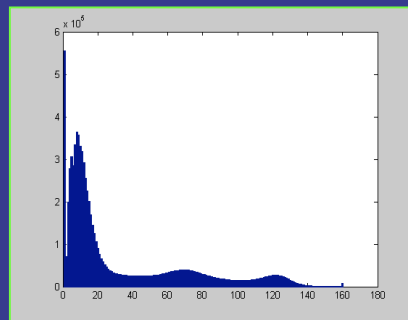
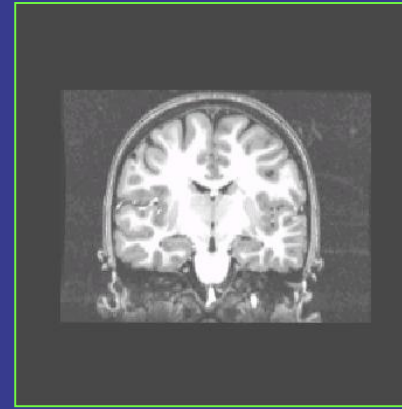
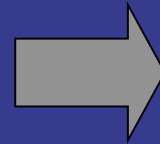
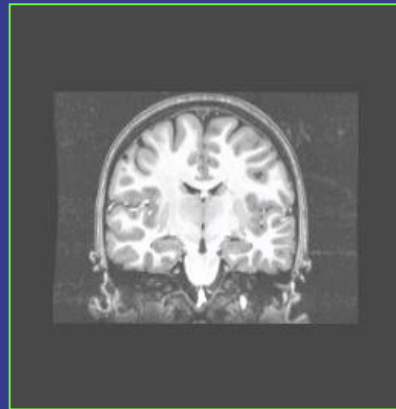
## 2. Segmentation

- Intensity normalization
- Skull stripping
- White matter labeling

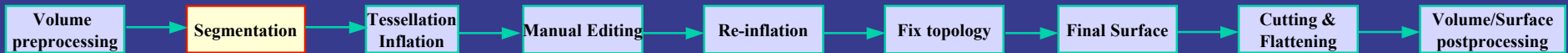


## 2. Segmentation

- Intensity normalization



- Skull stripping
- White matter labeling

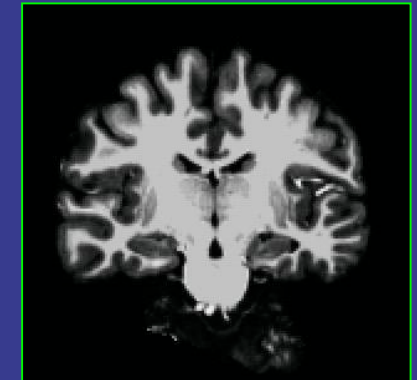


## 2. Segmentation

- Intensity normalization
- Skull stripping
  - Shrink-wrap algorithm
  - Start with ellipsoidal template
  - Minimize brain penetration and curvature



*Skull stripping*



- White matter labeling

## Skull Stripping



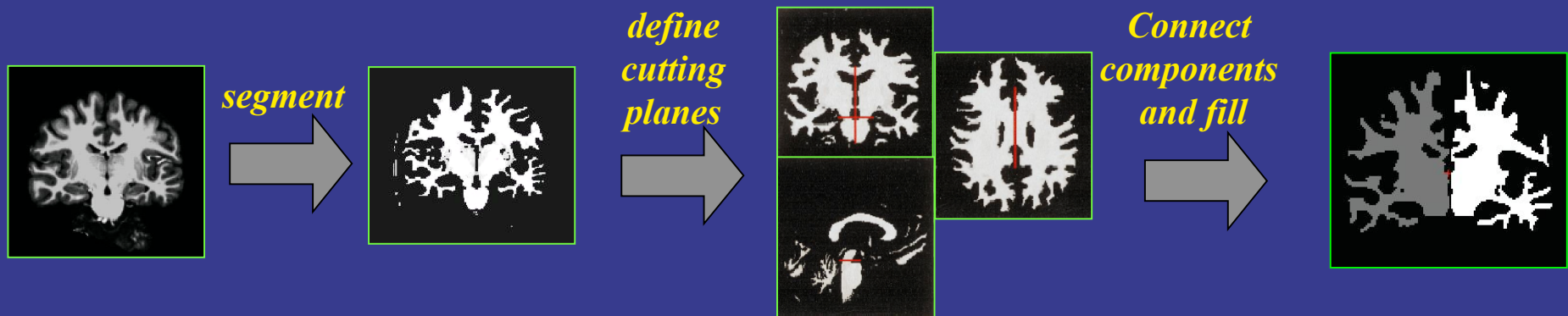
*Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>*





## 2. Segmentation

- Intensity normalization
- Skull stripping
- White Matter labeling
  - Preliminary classification solely intensity based
  - Relabeling of mislabeled voxels based on neighborhood information
  - Define cutting planes
  - Find connected components and fill





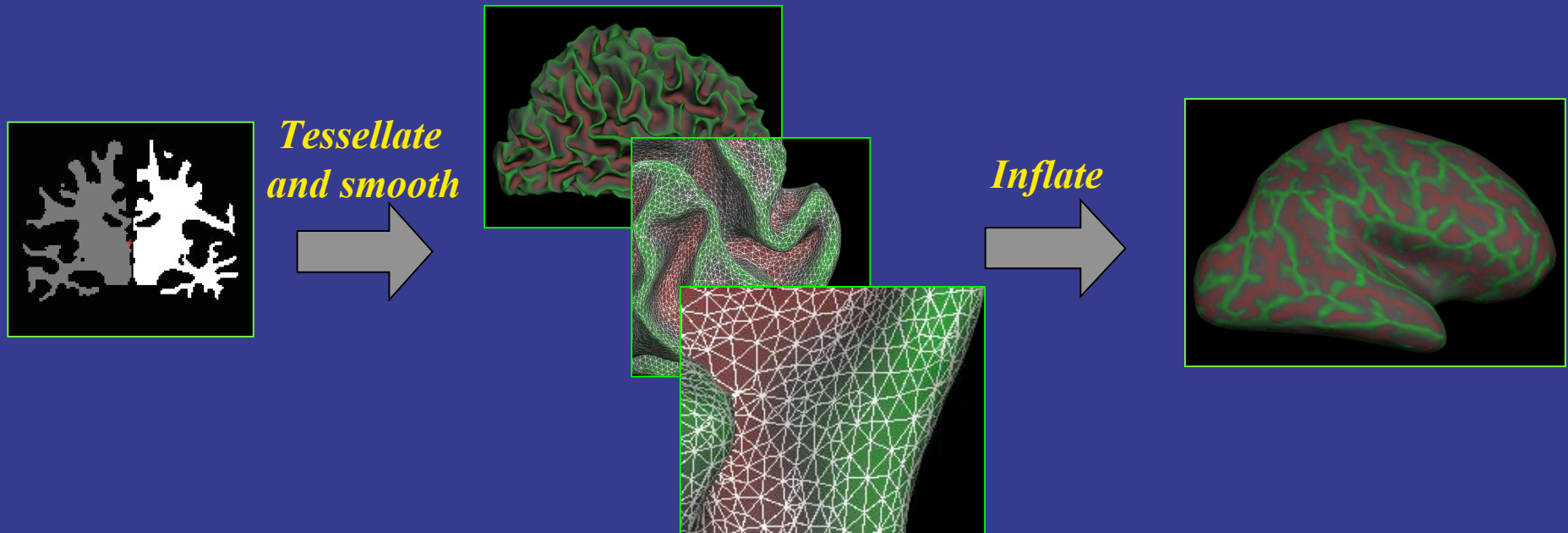
## 3. Tessellation and Inflation

- **Surface Tessellation**

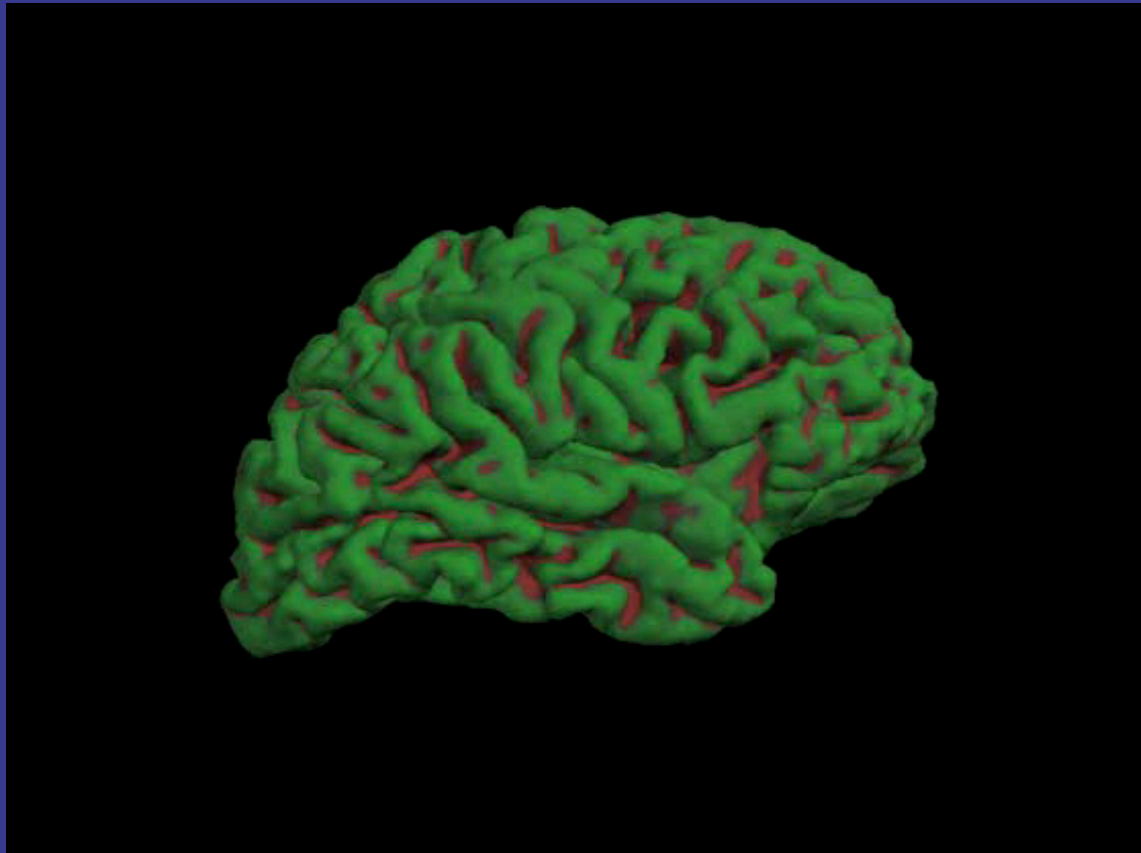
- ❖ Use two triangles to represent each face separating white matter voxels from other voxels
- ❖ Smooth initial tessellation with a deformable surface algorithm

- **Surface Inflation**

- ❖ Retain shape and metrics while making the interior of sulci visible



# Inflation

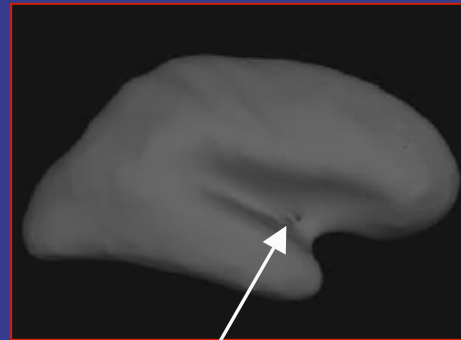


*Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>*

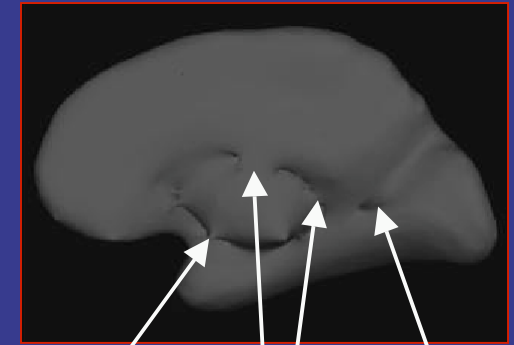


## 4. Manual editing

- Examine surface for defects
  - ❖ manually reclassify voxels in the following areas:
    - Lateral ventricle
    - Fornix
    - Optic nerve
    - Basal ganglia
    - Other defect areas

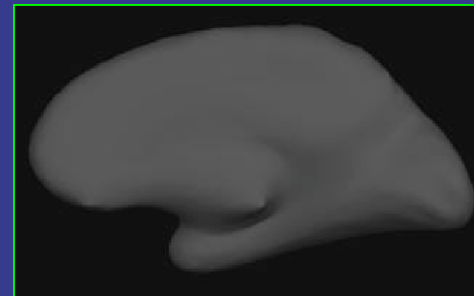


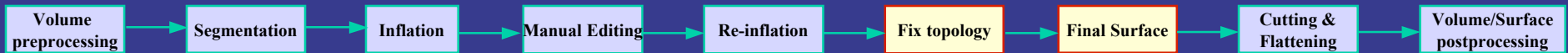
*Basal  
Ganglia*



*Optic  
Nerve*      *Fornix*      *Lateral  
Ventricle*

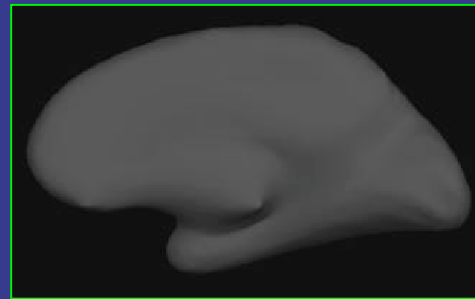
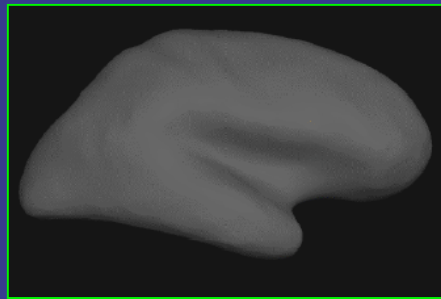
## 5. Re-inflation





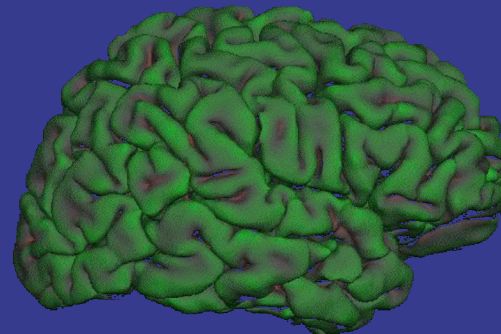
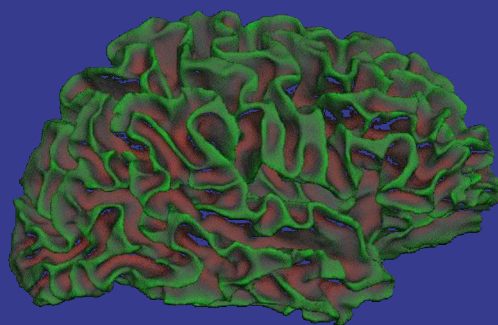
## 6. Fix topology

- Automatic defect removal algorithm that removes minor defects ensuring that the surface is topologically correct.



## 7. Make final surface

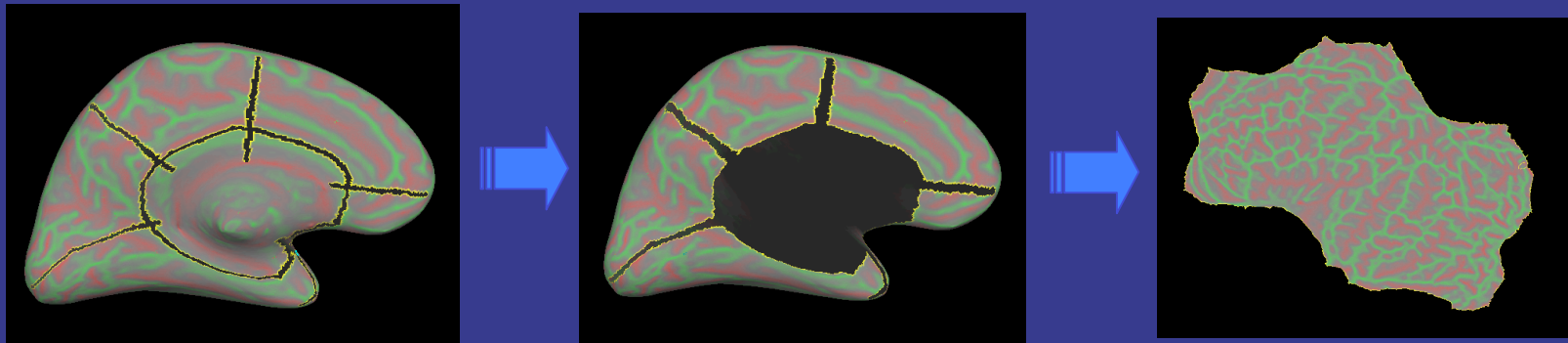
- Final gray/white boundary (white)
- Final gray/csf boundary (pial)



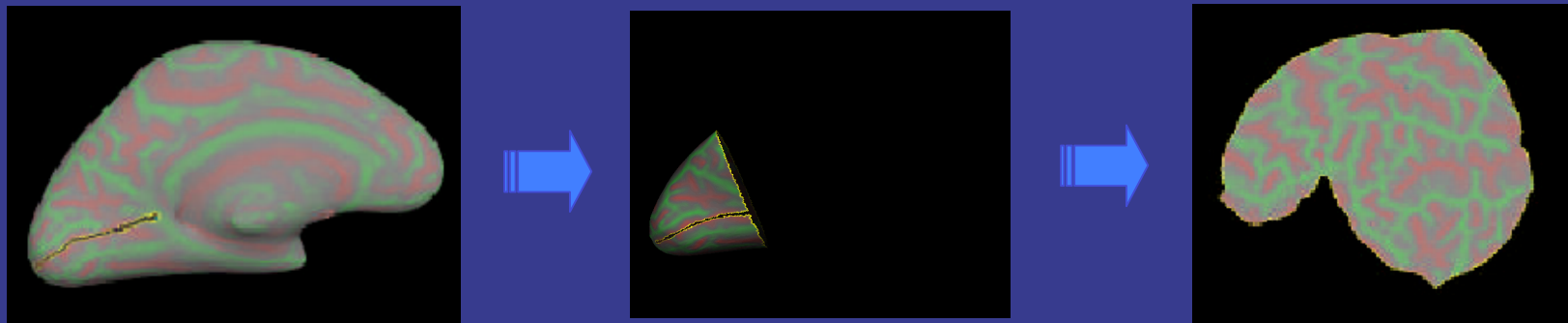


## 8. Cutting and flattening

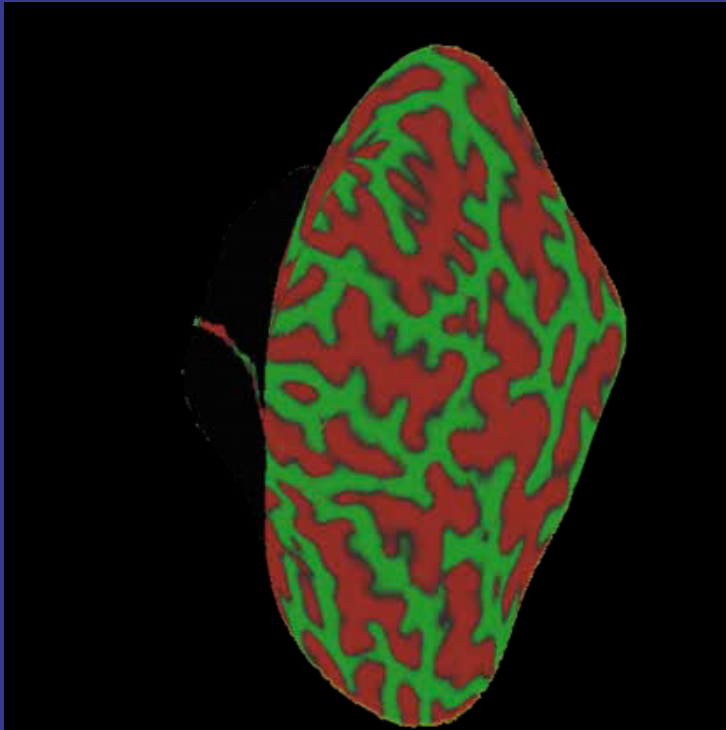
- For a full surface patch



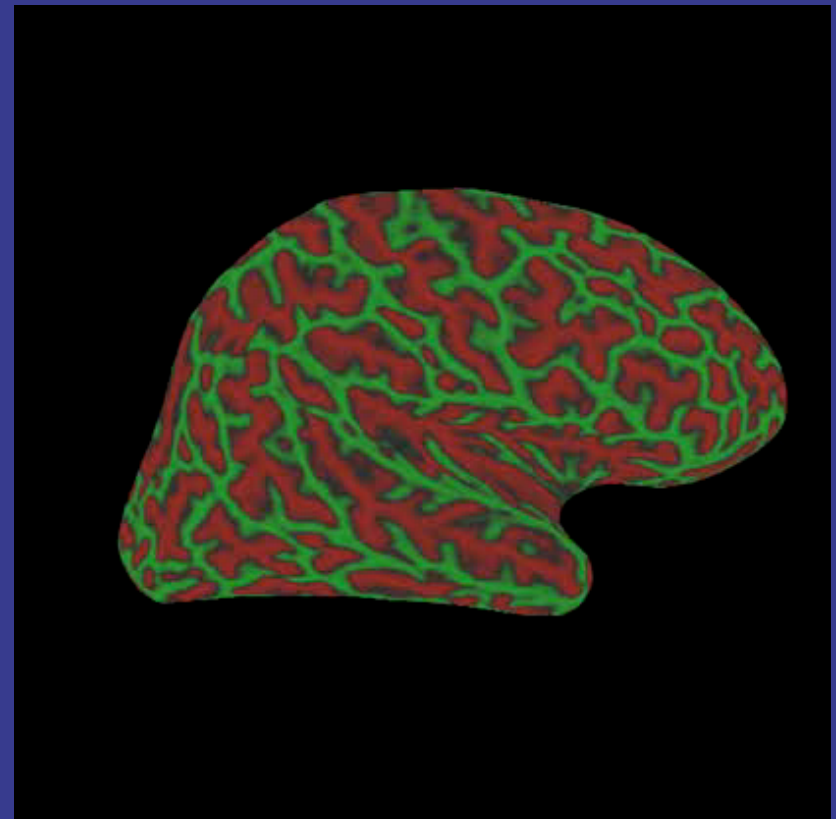
- For occipital patch



## Flattening of occipital patch



## Flattening of full surface



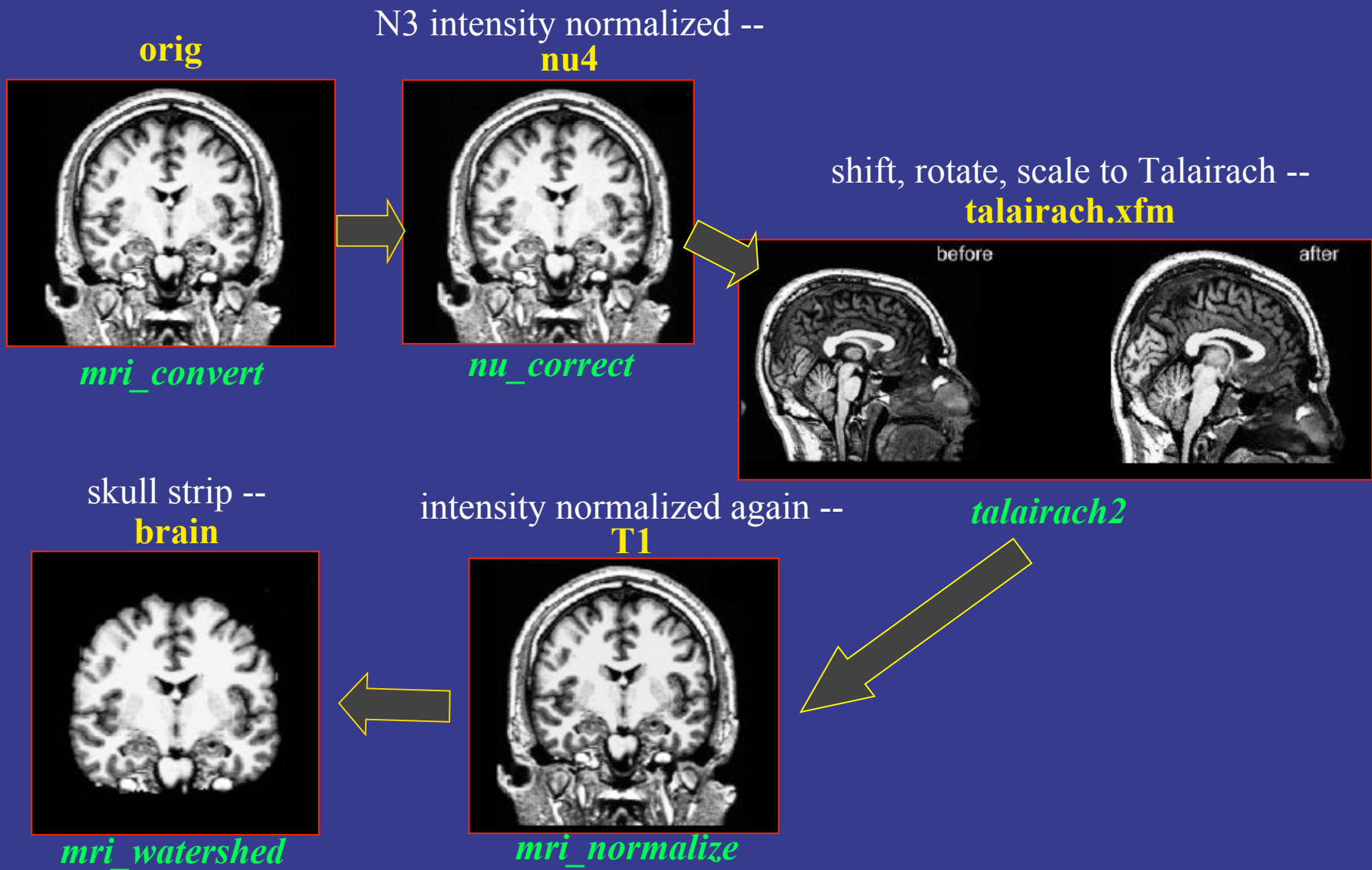
Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>

# Using FreeSurfer in Command Line Mode

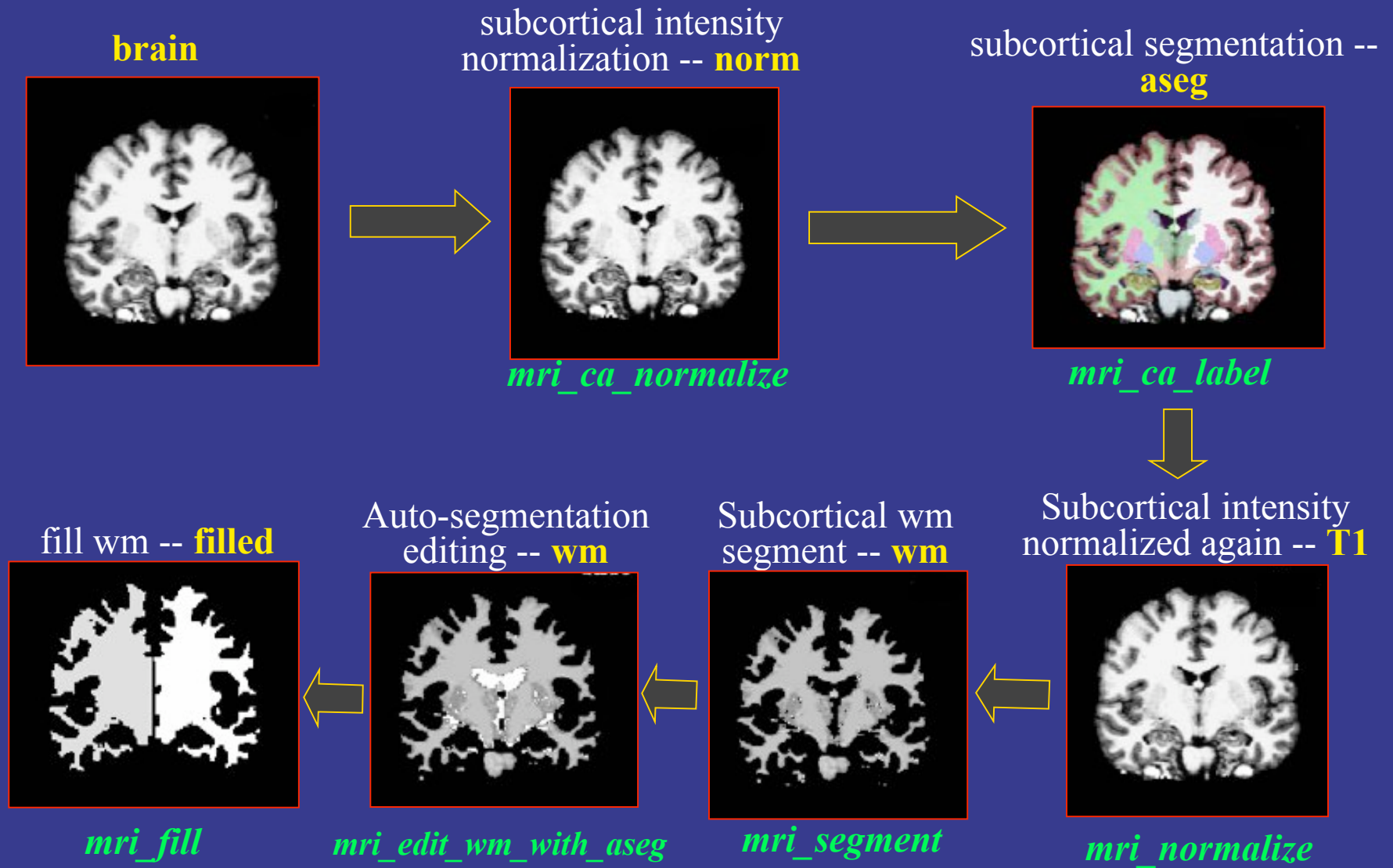
- Three different “families” of command line programs:
  1. Legacy Clustered Directives
    - old commands, similar to GUI mode
    - still work great
    - E.g., *segment\_subject*, *inflate\_subject*, *fix\_subject*
  2. Deprecated Clustered Directives
    - *recon-all -stage1,2,3,4a,4b*
  - new** → 3. Manual-Intervention Workflow Directives
    - *recon-all -autorecon 1,2,3* (or *autorecon-all*, fully automated)
- There are also individual FS commands for volume or surface processing
  - ❖ For the FreeSurfer aficionado
  - ❖ E.g., run *mri\_watershed* to strip skull



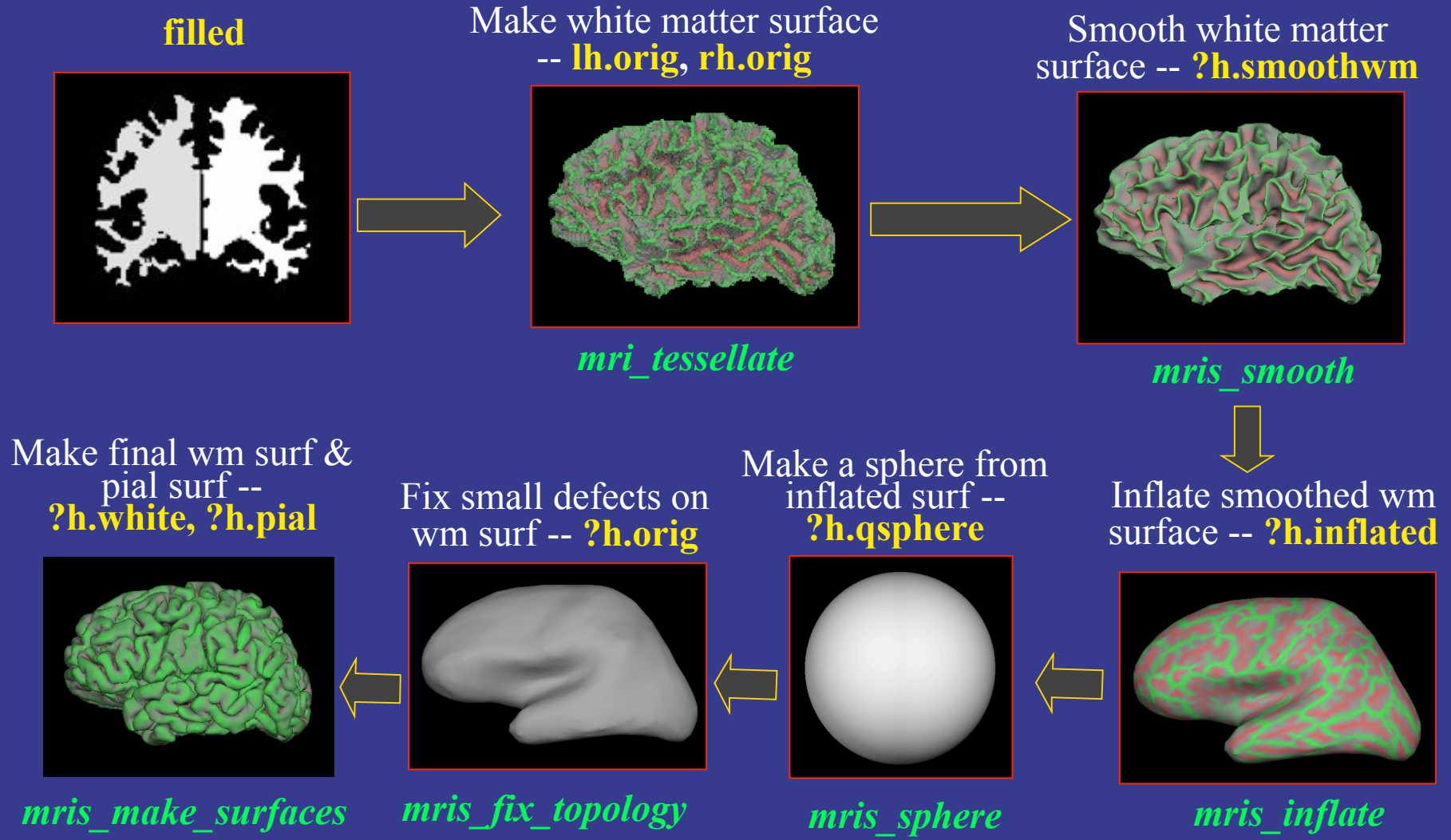
# Processing Steps for recon-all -autorecon1



# Processing Steps for recon-all -autorecon2

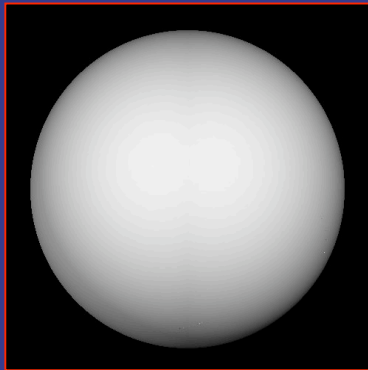


# Processing Steps for recon-all -autorecon2 (continued...)

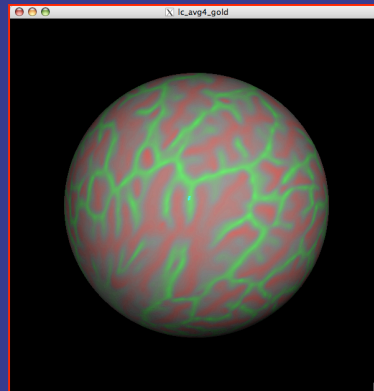


# Processing Steps for recon-all -autorecon3

**qsphere**

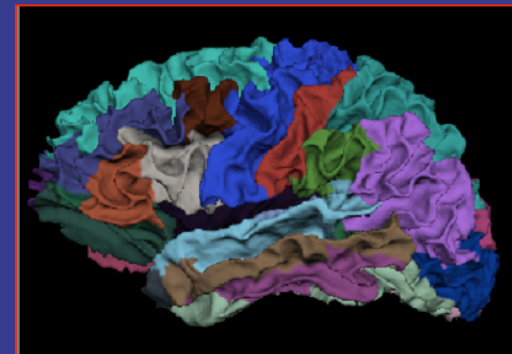


register individual sphere  
with sphere template --  
**?h.sphere.reg**



**mrisc\_register**

Cortical parcellation --  
**?h.aparc.annot**



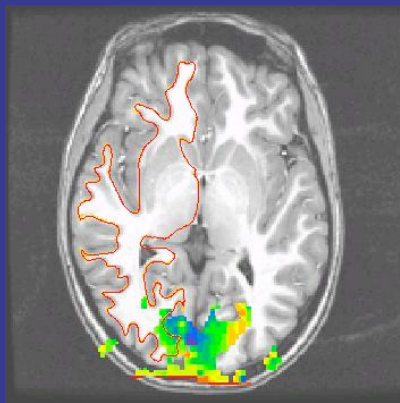
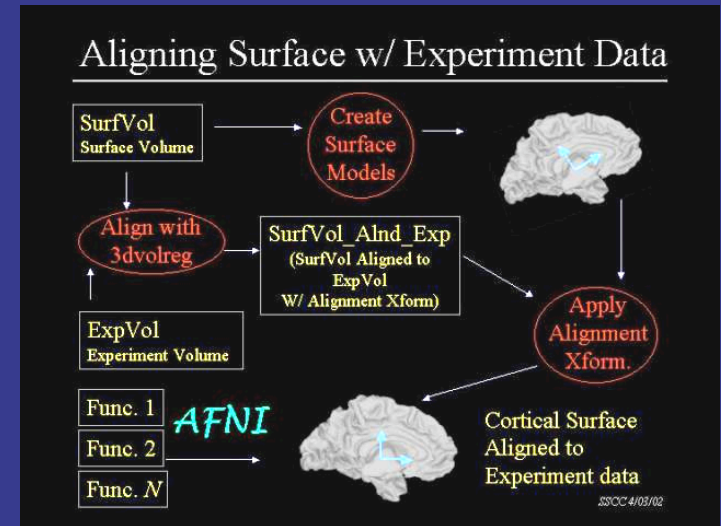
**mrisc\_ca\_label**



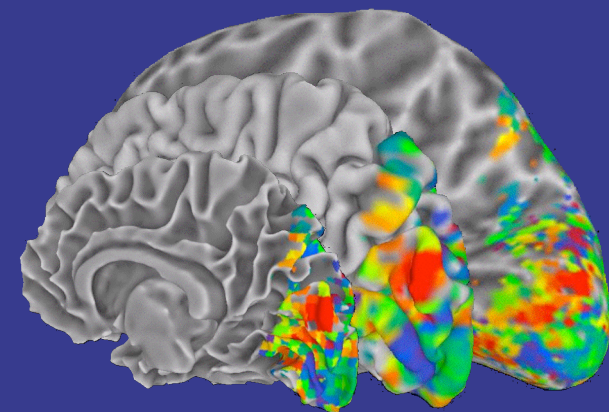
## 9. SUMA (Hands-On class 11-9-05)

- Convert surfaces to ASCII format
- Align surface volume to experiment volume
- Overlay functional data onto surface
- Create link between AFNI and SUMA
- View function on volume and surface simultaneously
- Visit SUMA website for details:

- <http://afni.nimh.nih.gov/ssc/ziad/SUMA/>



AFNI



SUMA

## FreeSurfer Links

FreeSurfer Website (articles, download, docs, FAQ):

<http://surfer.nmr.mgh.harvard.edu>

Mail Archives:

[www.mail-archive.com/freesurfer@mail.nmr.mgh.harvard.edu](http://www.mail-archive.com/freesurfer@mail.nmr.mgh.harvard.edu)