FreeSurfer
http://surfer.nmr.mgh.harvard.edu

freesurfer@nmr.mgh.harvard.edu
Cortical Surface Reconstruction

FreeSurfer creates computerized models of the brain from MRI data.

Input:
• T1-weighted (MPRAGE, SPGR)
• 1 mm$^3$ resolution
Cortical Surface Reconstruction

- Finds white/gray boundary – wm surface
- Finds pial/CSF boundary – pial surface
- To “Find” uses:
  - Intensity information, spatial location, geometric structure
  - Tessellation, neighboring voxels, talairach coordinates

- Subcortical Segmentation
Output of Cortical Surface Reconstruction
Cortical Reconstruction Goals

• Geometrically Accurate surfaces
  – Accurately follow the boundaries seen on the scan for each of your individual subjects

• Topologically Correct surfaces
  – Each surface is a 2-D continuous, non self-intersecting sheet and can be inflated into a perfect sphere

• Surfaces are only as good as your scan.
MR Anatomy Caveats

• Dependent on data quality
  – Contrast to noise
  – Signal to noise
  – Voxel resolution
• MR Artifacts
  – MR susceptibility
  – MR distortions
• Variations in MR tissue parameters across regions of the brain are altered in different populations
FreeSurfer Output

- Volumes
- Surfaces
- Surface Overlays
- ROI Summaries
Volumes

- orig.mgz
- T1.mgz
- brainmask.mgz
- wm.mgz
- filled.mgz
- aseg.mgz
- aparc+aseg.mgz

- $SUBJECTS_DIR/bert/mri
- All “Conformed” 256^3, 1mm

Volume Viewer: tkmedit
Surface Model

- Mesh ("Finite Element") – measurable size & unchanging with other steps in processing stream
- Allows us to measure Area, Distance, Curvature, Thickness
- Vertex = point of 6 triangles
- Triangles/Faces ~ 150,000
Surfaces

- orig
- white
- pial

- inflated
- sphere, sphere.reg
- flat

- $SUBJECTS_DIR/bert/surf
- Number/Identity of vertices stays the same (except flat)
- XYZ Location Changes
- Flattening not done as part of standard reconstruction

Surface Viewer: tksurfer
Surface Overlays

- Value for each vertex
- Color indicates value
- Color: gray, red/green, heat, color table
- Rendered on any surface
- fMRI/Stat Maps too

lh.sulc on inflated
lh.curv on inflated
lh.thickness on inflated
lh.sulc on pial
lh.curv on inflated
lh.aparc.annot on inflated
fMRI on flat
ROI Summaries

**aseg.stats**
- volumes of subcortical structures (mm$^3$)

**aparc.stats**
- thickness of cortical parcellation structures (mm)
- total white matter volume (mm$^3$)
- number of vertices in cortex
- surface area of cortex (mm$^2$)
### ROI Summaries:

```plaintext
$SUBJECTS_DIR/subjid/stats
  aseg.stats – volume summaries
  ?h.aparc.stats – desikan/killiany atlas summaries
  ?h.aparc.a2005s.stats – destrieux atlas summaries
```

<table>
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<th>SegId</th>
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</table>

Routines to generate spread sheets of group data
- asegstats2table --help
- aparcstats2table --help
Getting Stats into Table Format

`asegstats2table --subjects 001 002 003 004 005 006 007 --meas vol --t asegstats.txt`

`cd $SUBJECTS_DIR` to find `asegstats.txt`

From Excel, File > Open, search for `asegstats.txt` (make sure viewing all file types) > Choose Delimited, Space, and Finish
Getting Stats into Table Format

aparcstats2table --subjects 001 002 003 004 005 006 007 --h rh --meas volume --t aparc_rh_vol_stats.txt

aparcstats2table --subjects 001 002 003 004 005 006 007 --h rh --meas thickness --t aparc_rh_thick_stats.txt

aparcstats2table --subjects 001 002 003 004 005 006 007 --h rh --meas area --t aparc_rh_area_stats.txt

*Repeat above for lh; .txt files in SUBJECTS_DIR
ROI Summaries: Make Your Own

yourROI.label
- Draw your own surface label
- use "mris_anatomical_stats -l" to get data

mris_volume
- Total volume within a surface you specify

mris_wm_volume
- Total volume within white surface ignoring non-wm voxels in aseg.mgz
Before running FreeSurfer, **must** set $FREESURFER_HOME and $SUBJECTS_DIR
Each data set has its own unique SubjectId (eg, bert)
FreeSurfer Directory Tree

Directories used often are in green.

```
bert
  
  bem  stats  src  mri  scripts  surf  tmp  label  trash

  aseg.stats  lh.aparc.stats  rh.aparc.stats  wmparc.stats
```

Subject ID
MGZ File Format

- mgz = compressed MGH file
- Can store 4D (like NIFTI)
- cols, rows, slices, frames
- Generic: volumes and surfaces

- Eg, Typical Anatomical volume: 256 x 256 x 128 x 1

FreeSurfer can read/write:
  - NIFTI, Analyze, MINC
  - Careful with NIFTI! (32k limit)

FreeSurfer can read:
  - DICOM, Siemens
  - IMA, AFNI
Other FreeSurfer File Formats

Unique to FreeSurfer

• **Surface**: lh.white, lh.pial, lh.orig

• **Curv**: lh.curv, lh.sulc, lh.thickness

• **Annotation**: lh.aparc.annot

• **Label**: lh.pericalcarine.label
Starting the Reconstruction Process

Before running FreeSurfer, **must** set $FREESURFER_HOME and $SUBJECTS_DIR

**recon-all** -i /path/to/your/raw/data1 -i /path/to/your/raw/data2 -all -s subject_id

- This will create the subject directory ‘subject_id’ in your $SUBJECTS_DIR and convert your 2 raw acquisitions to mgz and use them as input for the ‘-all’ command.
Some other relevant commands

• `recon-all --make all --s <subjid>`
  – reruns stream from most outdated step

• `recon-all --all --clean --s <subjid>`
  – reruns subject without using existing edits

• `recon-all --all --legacy`
  – use on data processed w/ previous version of FS to keep prior edits

• `recon-all --arg` – `dontrun`
  – prints command to run without executing it

http://surfer.nmr.mgh.harvard.edu/fswiki/OtherUsefulFlags
Alternative: Add Your Data

- `cd $SUBJECTS_DIR`
- `mkdir -p bert/mri/orig`
- `mri_convert yourdicom.dcm bert/mri/orig/001.mgz`
- `mri_convert yourdicom.dcm bert/mri/orig/002.mgz`
- `recon-all --all --s bert`
Individual Steps

Volumetric Processing Stages (subjid/mri):
1. Motion Cor, Avg, Conform (orig.mgz)
2. Non-uniform inorm (nu.mgz)
3. Talairach transform computation (talairach/talairach.xfm)
4. Intensity Normalization 1 (T1.mgz)
5. Skull Strip (brainmask.mgz)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization (norm.mgz)
8. CA Non-linear Volumetric Registration
9. CA Label (Volumetric Labeling) (aseg.mgz)
10. Intensity Normalization 2 (T1.mgz)
11. White matter segmentation (wm.mgz)
12. Edit WM With ASeg
13. Fill and cut (filled.mgz)

Surface Processing Stages (subjid/surf):
14. Tessellate (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. QSphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
19. Final Surfs (?h.white ?h.pial ?.thickness)
20. Smooth2 (?h.smoothwm)
21. Inflate2 (?h.inflated)
22. Aseg Statistics (stats/aseg.stats)
23. Cortical Ribbon Mask (?h.ribbon.mgz)
24. Spherical Morph
25. Spherical Registration (?h.sphere.reg)
26. Map average curvature to subject
27. Cortical Parcellation (Labeling)
28. Cortical Parcellation Statistics
29. Cortical Parcellation mapped to Aseg
30. White Matter Parcellation (wmparc.mgz)

Note: ?h.orig means lh.orig or rh.orig

recon-all -help

Blue = Manual Intervention
Reconstruction Stages

recon-all is broken into three stages
– autorecon1
– autorecon2
– autorecon3
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Motion Correction and Averaging

Does not change native resolution.
Conform

Changes to $256^3$, $1\text{mm}^3$
All volumes will be conformed.

mri_convert -conform
Non-Uniform Intensity Correction

- Uses MNI tool
- Removes B1 bias field

nu Volume

mri_nu_correct.mni
Talairach Transform

- Computes 12 DOF transform matrix
- Does NOT resample
- MNI305 template
- Used to help find structures (eg, CC)
- Can also be used to localize functional activation
- mri/transforms/talairach.xfm
Intensive Normalization

- Presegmentation (T1.mgz)
  - All WM = 110 intensity
  - Pre- and Post-Skull Strip

mri_normalize
Skull Strip

- Removes all non-brain
  - Skull, Eyes, Neck, Dura
- brainmask.mgz

Orig Volume  Brainmask Volume
Each data set has its own unique SubjectId (eg, bert)
-autorecon2

Volumetric Processing Stages (subjid/mri):
1. Motion Cor, Avg, Conform (orig.mgz)
2. Non-uniform inorm (nu.mgz)
3. **Talairach transform computation** (talairach/talairach.xfm)
4. **Intensity Normalization 1** (T1.mgz)
5. **Skull Strip** (brainmask.mgz)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization (norm.mgz)
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9. CA Label (Volumetric Labeling) (aseg.mgz)
10. **Intensity Normalization 2** (T1.mgz)
11. **White matter segmentation** (wm.mgz)
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Surface Processing Stages (subjid/surf):
14. **Tessellate** (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. QSphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
19. Final Surfs (?h.white ?h.pial ?.thickness)
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**Note:** lh processed completely first, then rh.
Automatic Volume Labeling

- Label subcortical structures and wm/gm
- Determine volumes of subcortical structures
- Used to fill in subcortical structures for later steps

Atlas: RB_all_2007-08-08
Volume-based Labeling

Labeling is determined by location and intensity.
Validation of Volume Labeling *

Manual labeling done by Center for Morphometric Analysis (CMA)

*Thanks to Drs Larry Seidman and Jill Goldstein for providing this data.
White Matter Segmentation

- Separates white matter from everything else
- “Fills in” subcortical structures
- Cerebellum removed, brain stem still there
Fill and Cut (Subcortical Mass)

• Fills in any voids
• Removes any islands
• Removes brain stem
• Separates hemispheres (each hemi has different value)
• filled.mgz = “Subcortical Mass”
FreeSurfer Directory Tree

Each data set has its own unique SubjectId (eg, bert)
Tessellation

- Mosaic of triangles ("tessellation")
- Errors: Donut holes, handles
  - Subsequently fixed by the automatic topology fixer
Inflation: Visualization

Dale and Sereno, 1993; Dale et al., Dale et al., 1999; Fischl et al., 1999; Fischl et al., 2000; Fischl et al., 2001
Automatic Topology Fixer

- Holes
- Handles
- Automatically Fixed
White Matter Surface

- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex Identity stays constant
Pial Surface

- Nudge white surface
- Follow T1 intensity gradients
- Vertex Identity Stays
Optimal Surface Placement

Gray-White Boundary

Outer Cortical Surface
Cortical Thickness
Thickness Maps

- Red regions are thinner
- Yellow regions are thicker
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18. Automatic Topology Fixer (?h.orig)
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recon-all -help

Note: lh processed completely first, then rh.
Surface-Based Spherical Coord System
"Spherical" Registration

Inflated Surface (Sulcal Map) → Spherical Inflation → Atlas (Target)

High-Dimensional Registration to Spherical Template

Template: average.curvature.filled.buckner.40.tif
Spherical Inflation
Registration to Atlas

Individual Subject

Atlas (Target)
Cortical Parcellation

Spherical Template based on Manual Parcellation

Map to Individual Thru Spherical Reg

Fine-tune based on individual anatomy

Atlases: curvature.buckner40filled.desikan_killiany, atlas_2005_simple
Cortical Parcellation: 2

Atlases: curvature.buckner40filled.desikan_killiany, atlas_2005_simple

Thanks to Christophe Destrieux for this slide.
There is also aparc.a2005s+aseg.mgz for Destrieux atlas
FreeSurfer Directory Tree

Each data set has its own unique SubjectId (eg, bert)
FreeSurfer Directory Tree

Each data set has its own unique SubjectId (eg, bert)
Actual Workflow: version 1

recon-all –all (Stages 1-30) ~30 hours

Check talairach transform, skull strip, normalization
Check surfaces
  1. Add control points: recon-all –autorecon2-cp –autorecon3 (Stages 10-30)
  2. Edit wm.mgz: recon-all –autorecon2-wm –autorecon3 (Stages 13-30)
  3. Edit brainmask.mgz: recon-all –autorecon2-pial -autorecon3 (Stage 19-30)
Note: all stages can be run individually
Actual Workflow: version 2

1. recon-all –autorecon1 (Stages 1-5) ~45 min
   Check talairach transform, skull strip, normalization
2. recon-all –autorecon2 (Stages 6-23) ~20 hours
   Check surfaces
   1. Add control points: recon-all –autorecon2-cp (Stages 10-23)
   2. Edit wm.mgz: recon-all –autorecon2-wm (Stages 13-23)
   3. Edit brainmask.mgz: recon-all –autorecon2-pial (Stage 19-23)
3. recon-all –autorecon3 (Stages 24-30) ~6 hours

Note: all stages can be run individually
Troubleshooting

recon-all fails

- check recon-all.log
- try to rerun step that failed
- look at volume from last successful step
- examine data quality to see what might cause error
- if it fails again, attempt to run modified version of command if possible
- search FreeSurfer mailing list for other instances of this problem:
  http://www.mail-archive.com/freesurfer@nmr.mgh.harvard.edu/
- email the mailing list if still need help
FreeSurfer Directory Tree

Each data set has its own unique SubjectId (eg, bert)
Bug Reporting

- Report version currently using
  - see top of recon-all.log
  - more $FREESURFER_HOME/build-stamp.txt
- command line tried to run
- attach recon-all.log
- Output in terminal window if appropriate
- Operating System
Shortcuts

• Aliases

alias tkm tkmedit \!* brainmask.mgz rh.white -aux T1.mgz -aux-surface lh.white -segmentation aseg.mgz -segmentation-opacity 0.2 -tcl ~/analysis_scripts/allisons_surfaces.tcl

SetZoomLevel 2
RedrawScreen

SetSurfaceLineColor 0 0 0 1
SetSurfaceLineColor 1 0 0 1
SetSurfaceLineWidth 0 0 2
SetSurfaceLineWidth 0 2 2
SetSurfaceLineWidth 1 0 2
SetSurfaceLineWidth 1 2 2
SetDisplayFlag 5 0
SetCursorColor .5 0 .5
Aliases

alias subdir 'setenv SUBJECTS_DIR `pwd`'
alias sourcefs 'source /usr/freesurfer/location'
alias project 'cd /data/location; source /freesurfer/version; setenv SUBJECTS_DIR /data/location ; /bin/echo –en "\033]0; Project Title\007"'
Aliases

emacs ~/.alias
source ~/.alias (in csh)

Must stay at bottom of script

• alias subdir 'echo $SUBJECTS_DIR'
• alias fshome 'echo $FREESURFER_HOME'
• alias csubdir 'cd $SUBJECTS_DIR'
• alias cfshome 'cd $FREESURFER_HOME'