Surface-Based Brain Imaging Analysis and DPABISurf

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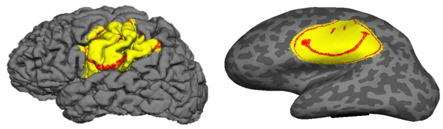
Why Surface-based Analysis

- Function has surface-based organization
- Inter-subject registration: anatomy, not intensity
- Smoothing
- Clustering
- 2D ReHo other than 3D ReHo



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Exploratory Spatial Analysis

- Generally requires spatial smoothing of data to increase SNR
- For group analysis, requires that subjects' brains be aligned to each other on a voxelwise basis.
- Neither needed for an ROI analysis
- Smoothing and inter-subject registration can be performed in the volume or surface.

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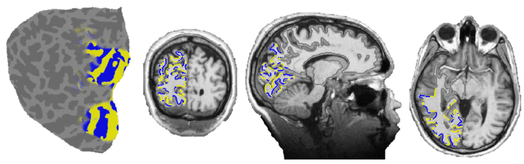
Why is a Model of the Cortical Surface Useful?

- Local functional organization of cortex is largely 2-dimensional! Eg, functional mapping of primary visual areas:



From (Sereno et al, 1995, Science).

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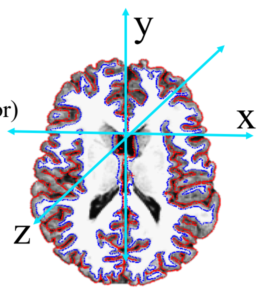
Coordinate Systems: 3D (Volumetric)

- 3D Coordinate System
  - XYZ
  - RAS (Right-Anterior-Superior)
  - CRS (Column-Row-Slice)
  - Origin (XYZ=0, eg, AC)
  - MR Intensity at each XYZ



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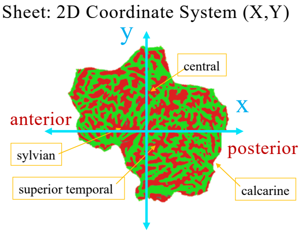
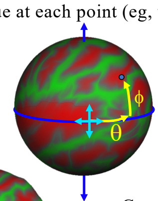
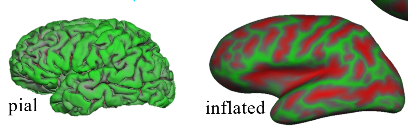
Coordinate Systems: 2D (Surface)

Sheet: 2D Coordinate System (X,Y)



Sphere: 2D Coordinate System
- Latitude and Longitude (θ, ϕ)
- Continuous, no cuts
- Value at each point (eg, thickness)





Curvature
- SULCUS (+)
- GYRUS (-)

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Inter-subject Registration

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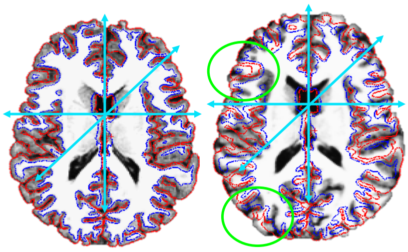
Volumetric Inter-subject Registration

- Affine/Linear
  - Translate
  - Rotate
  - Stretch
  - Shear
  - (12 DOF)



- Match Intensity, Voxel-by-Voxel
- Problems
- Can use nonlinear volumetric

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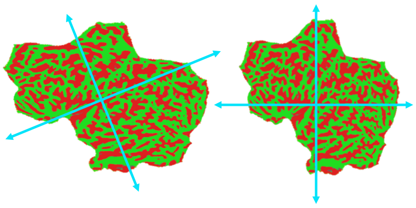
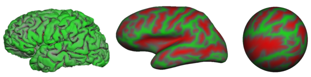
Surface-based Inter-subject Registration



- Translate, Rotate, Stretch, Shear (12 DOF)
- Match Curvature, Vertex-by-Vertex
- Nonlinear Stretching ("Morphing") allowed (area regularization)
- Actually done on sphere
- "Spherical Morph"



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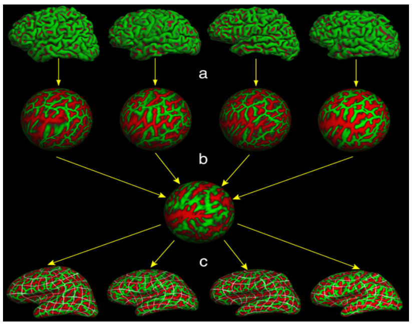
A Surface-Based Coordinate System



Common space for group analysis (like Talairach) 10

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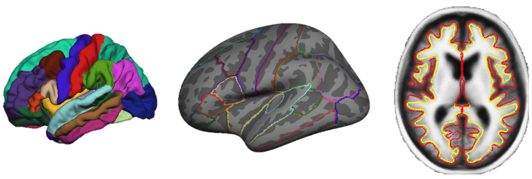
fsaverage



- Has "subject" folder like individual FS subjects
- "Buckner 40" subjects
- Default registration space
- MNI305 coordinates

?h.average.curvature.filled.buckner40.tif 11

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Surface-based Inter-subject Registration

- Gray Matter-to-Gray Matter (it's all gray matter!)
- Gyrus-to-Gyrus and Sulcus-to-Sulcus
- Some minor folding patterns won't line up
- Fully automated, no landmarking needed
- Atlas registration is probabilistic, most variable regions get less weight.
- Done automatically in recon-all
- fsaverage

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Spatial Smoothing

Why should you smooth?
- Might Improve CNR/SNR
- Improve intersubject registration

How much smoothing?
- Blob-size
- Typically 5-20 mm FWHM
- Surface smoothing more forgiving than volume-based

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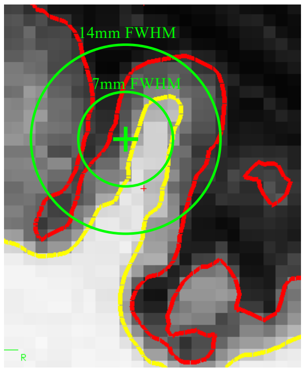
Volume-based Smoothing



- Smoothing is averaging of “nearby” voxels

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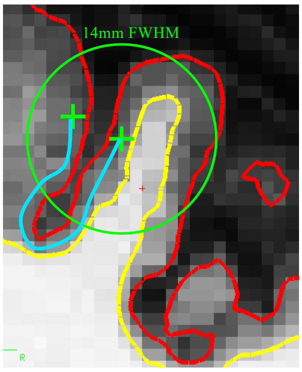
Volume-based Smoothing



- 5 mm apart in 3D
- 25 mm apart on surface!
- Kernel much larger
- Averaging with other tissue types (WM, CSF)
- Averaging with other functional areas

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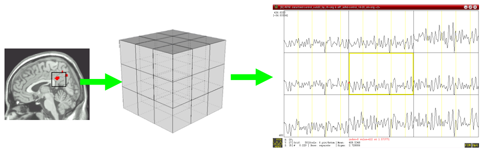
3D ReHo

Regional Homogeneity (ReHo)

Similarity or coherence of the time courses within a functional cluster



$$W = \frac{\Sigma(R_i)^2 - n(\bar{R})^2}{\frac{1}{12}K^2(n^3 - n)}$$

Zang et al., 2004. Neuroimage

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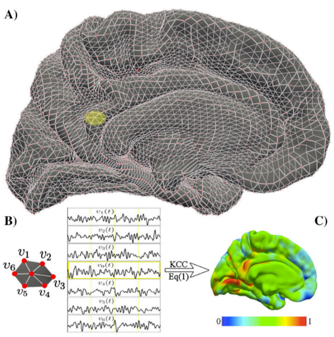
2D ReHo



Zuo et al., 2013. Neuroimage

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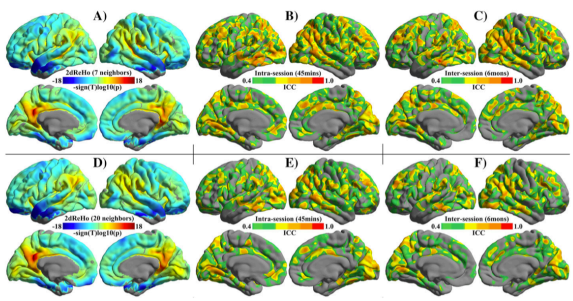
2D ReHo



Zuo et al., 2013. Neuroimage

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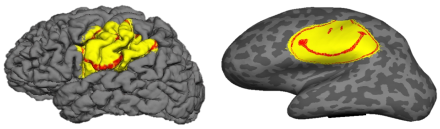

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Why Surface-based Analysis

PNAS PNAS PNAS PNAS

The impact of traditional neuroimaging methods on the spatial localization of cortical areas

Timothy S. Coalson[a], David C. Van Essen[a,1], and Matthew F. Glasser[a,b,1]

[a]Department of Neuroscience, Washington University School of Medicine, St. Louis, MO 63110; and [b]St. Luke's Hospital, St. Louis, MO 63017

Contributed by David C. Van Essen, May 17, 2018 (sent for review January 29, 2018; reviewed by Alexander L. Cohen, James V. Haxby, and Martin I. Sereno)

Localizing human brain functions is a long-standing goal in systems neuroscience. Toward this goal, neuroimaging studies have traditionally used volume-based smoothing, registered data to volume-based standard spaces, and reported results relative to volume-based parcellations. A novel 360-area surface-based cortical parcellation was recently generated using multimodal data from the Human Connectome Project, and a volume-based version of this parcellation has frequently been requested for use with traditional volume-based analyses. However, given the major methodological differences between traditional volumetric and Human Connectome Project-style processing, the utility and interpretability of such an altered parcellation must first be established. By starting from automatically generated individual-subject parcellations and processing them with different methodological approaches, we show that traditional processing steps, especially volume-based smoothing and registration, substantially degrade cortical area localization compared with surface-based approaches. We also show that surface-based registration using features closely tied to cortical areas, rather than to folding patterns alone, improves the alignment of areas, and that the benefits of high-resolution acquisitions are largely unexploited by traditional volume-based methods. Quantitatively, we show that the most common version of the traditional approach has spatial localization that is only 35% as good as the best surface-based method as assessed using two objective measures (peak areal probabilities and "captured area fraction" for maximum probability maps). Finally, we demonstrate that substantial challenges exist when attempting to accurately represent volume-based group analysis results on the surface, which has important implications for the interpretability of studies, both past and future, that use these volume-based methods.

mapping using Gaussian random-field theory requires volumetric smoothing to satisfy its underlying assumptions (e.g., ref. 8), resulting in the widespread adoption of smoothing in brain-imaging studies. Spatial smoothing has the seductive side effect of increasing the statistical significance of weak effects in small sample sizes, but at the expense of spatial localization precision (9, 10). Traditionally, smoothed group functional activations are then statistically thresholded and summarized by single 3D coordinates that may be assigned Brodmann's areas or gyral and sulcal designations. Unfortunately, these standard coordinates are imprecisely related to the underlying functional neuroanatomy—the cortical areas—whose neuronal populations generate the functional activations under study (9, 10).

Besides the reductions in precision from spatial smoothing and representing brain functional neuroanatomy with single 3D coordinates, another key issue is the approach used for cross-subject alignment. Because of the high degree of individual variability in cortical folding patterns, and in the location of many areal boundaries relative to folds (11, 12), traditional volume-based methods for aligning cortical areas are imprecise across much of the cerebral cortex (9). Progress in characterizing the functions of brain areas has been impeded by these factors, along with the distributed nature of many brain functions and the lack of an accurate map of human cortical areas.

Significance

Most human brain-imaging studies have traditionally used low-resolution images, inaccurate methods of cross-subject

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Why Surface-based Analysis

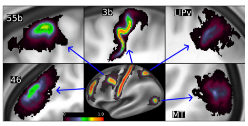
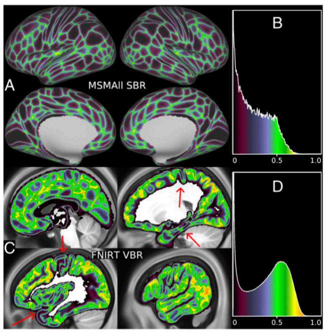


Fig. 1. Probabilistic maps for five areas using both MSMAll areal-feature-based surface registration and FNIRT volume alignment. The volume-basec peak probabilities are all lower than the surface-based probabilities fo these example areas. Each volume-based area is shown on a parasagittal slic through the peak volumetric probability. See *SI Appendix, Supplementa Methods M2 and M3*. Data are available at https://balsa.wustl.edu/xK0Z.



Coalson et al., 2018. PNAS

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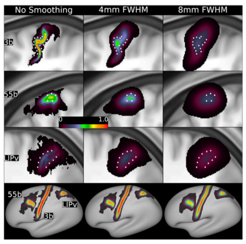

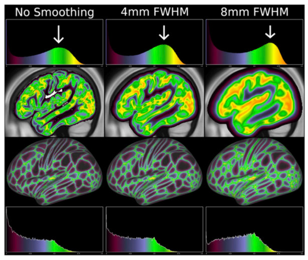

Coalson et al., 2018. PNAS

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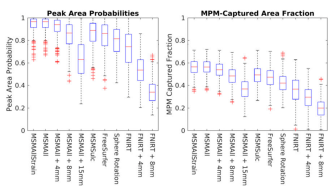
Why Surface-based Analysis



Widespread adoption of surface-based approaches has been slow: the desire to replicate or compare with existing studies that used the traditional volume-based approach; the relative lack of "turn-key" tools for running a surface-based analysis; the learning curve for adopting surface-based analysis methods; unawareness of the problems with traditional volume-based analysis; and uncertainty or even skepticism as to how much of a difference these methodological choices make.

Coalson et al., 2018. PNAS

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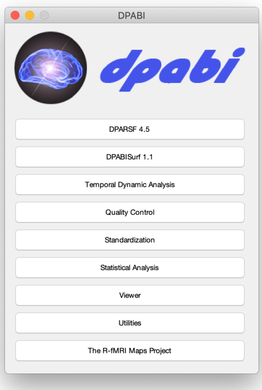

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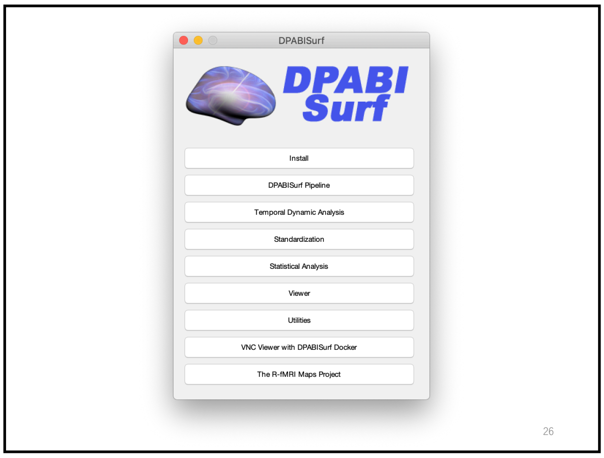

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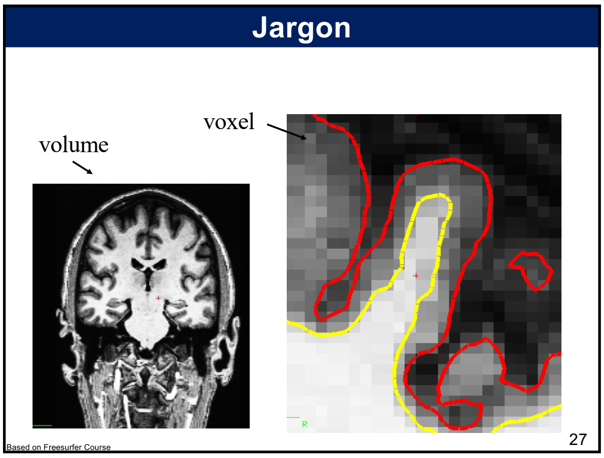

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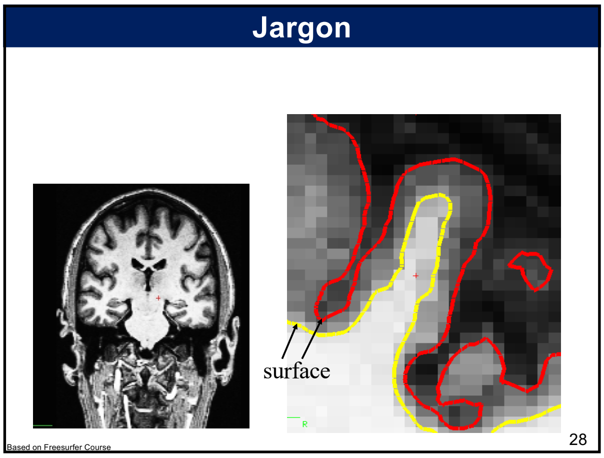

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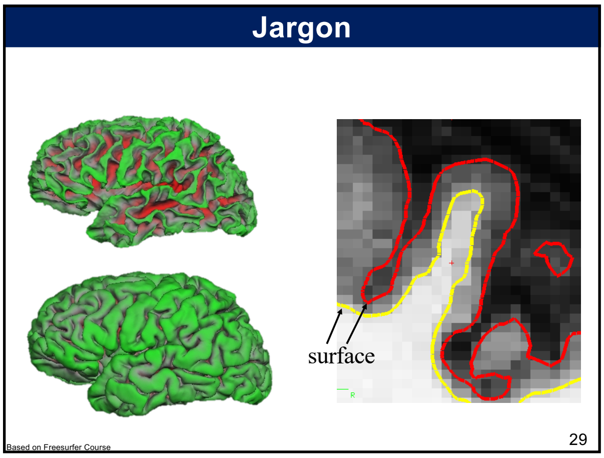

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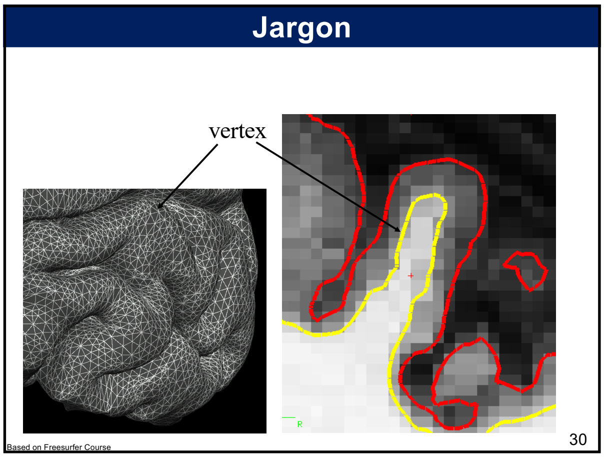

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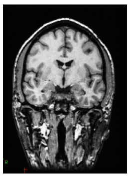
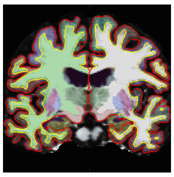
Call FreeSurfer…

FreeSurfer creates computerized models of the brain from MRI data.



Input:
T1-weighted (MPRAGE)
1mm³ resolution
(.dcm)



Output:
Segmented & parcellated conformed volume
(.mgz)

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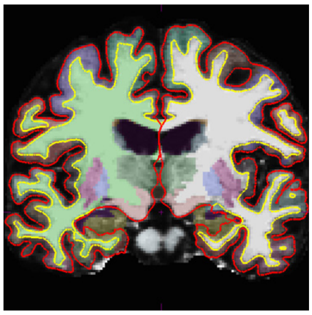
Recon



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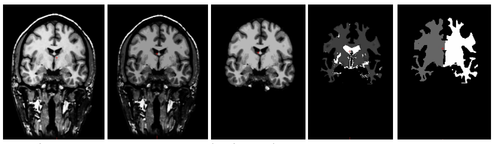
Volumes



orig.mgz T1.mgz brainmask.mgz wm.mgz filled.mgz (Subcortical Mass)

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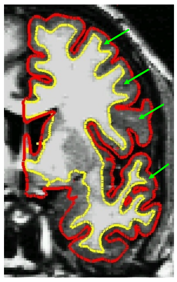
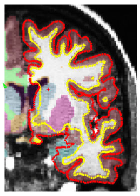
Cortical vs. Subcortical GM

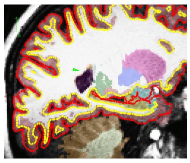
cortical gm



subcortical gm



coronal



sagittal

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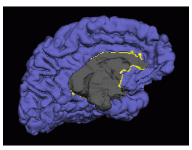
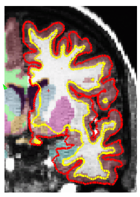
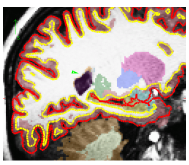
Cortical vs. Subcortical GM



subcortical gm



coronal



sagittal

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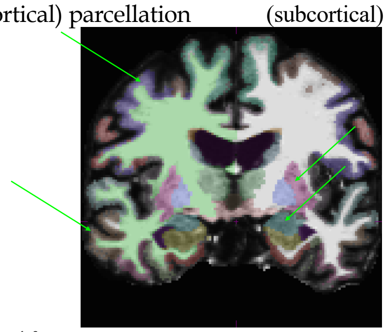
Parcellation vs. Segmentation

(cortical) parcellation (subcortical) segmentation



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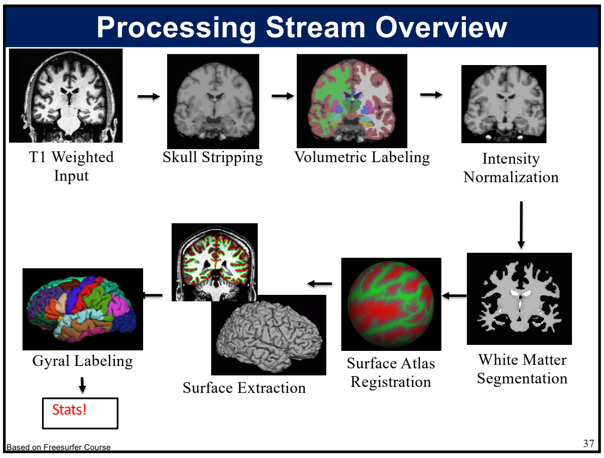

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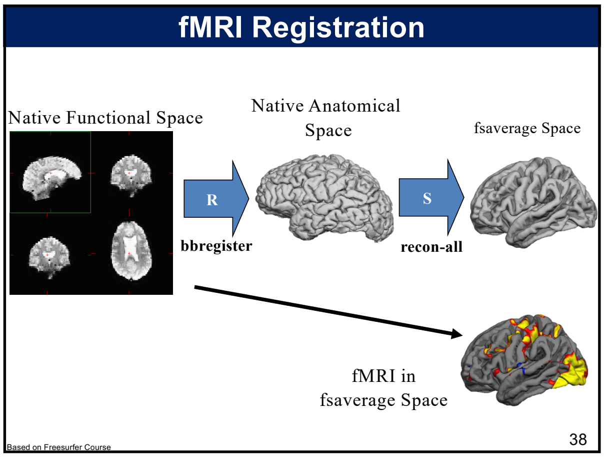

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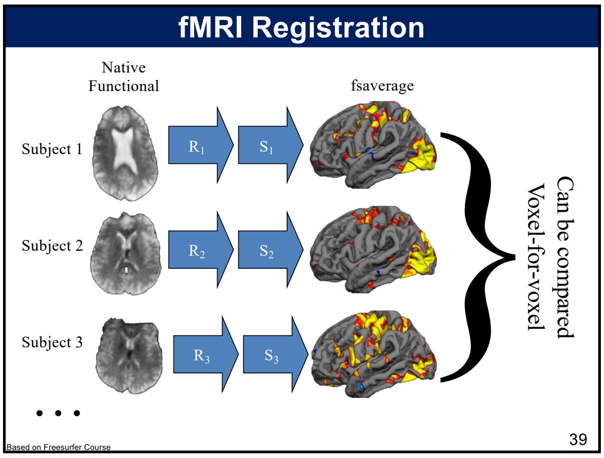

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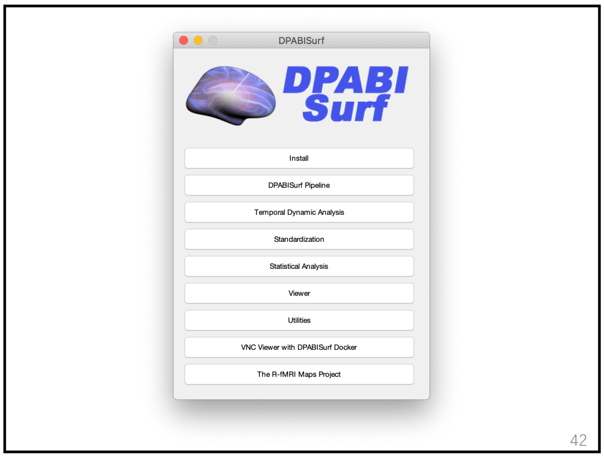

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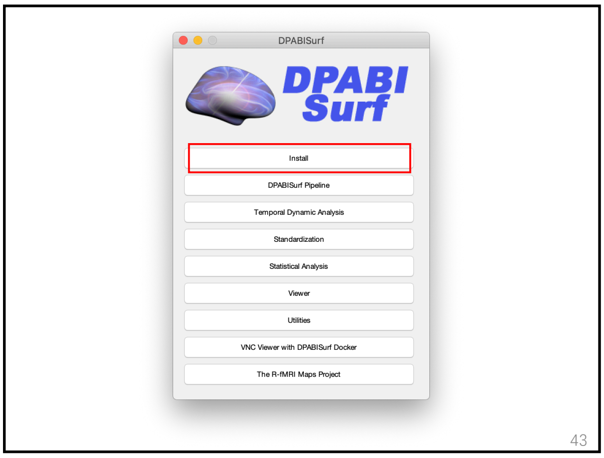

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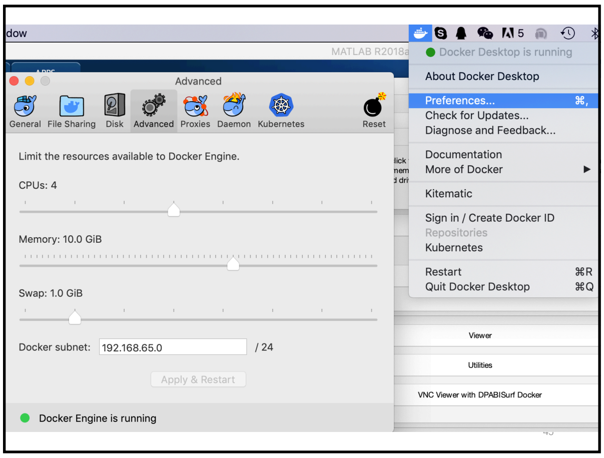

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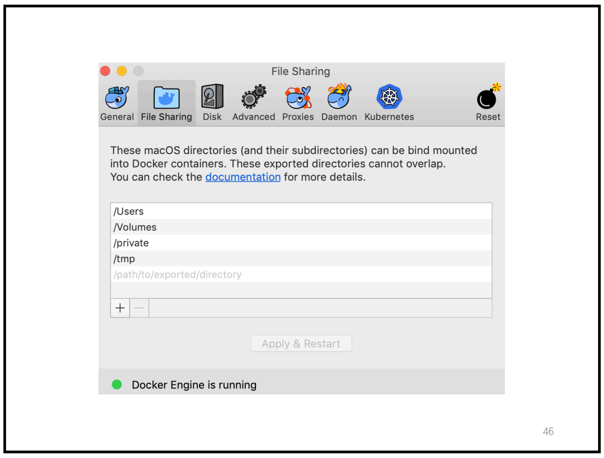

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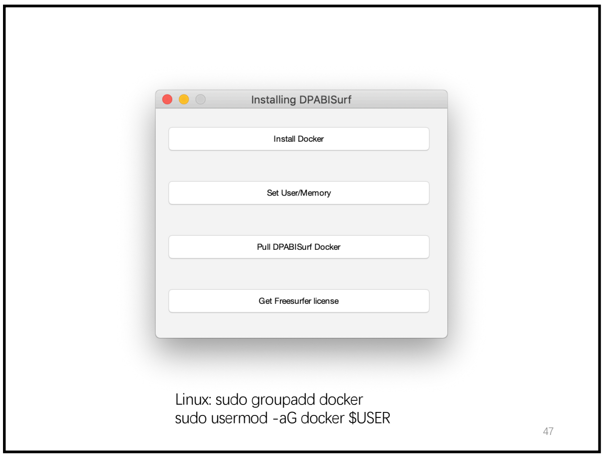

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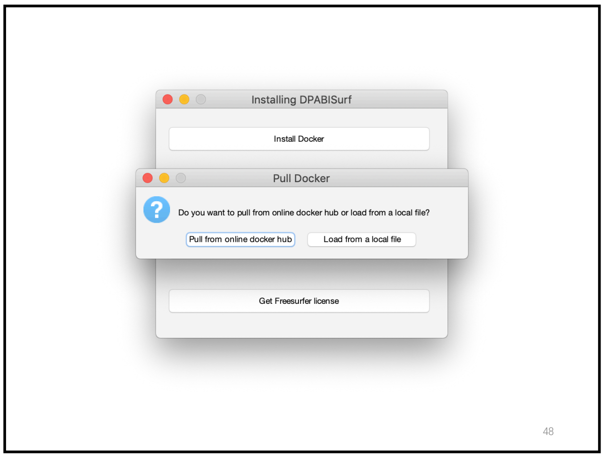

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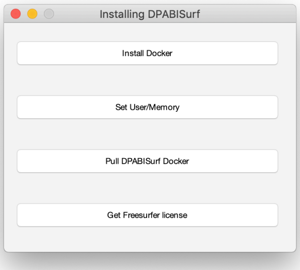

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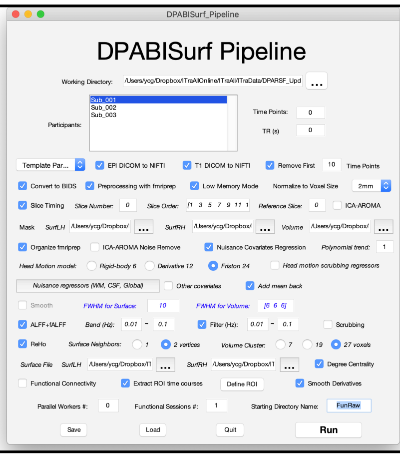

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Thanks for your attention!

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