The Mindboggle project: feature-based brain labeling

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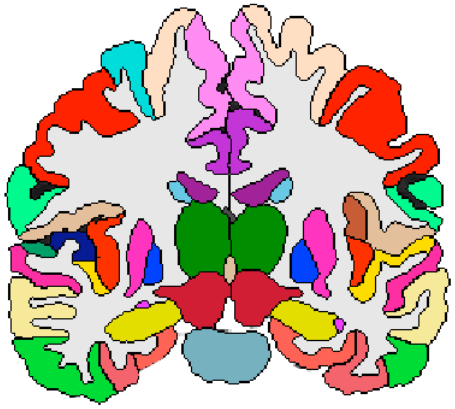
asst. professor of clinical neurobiology
columbia university

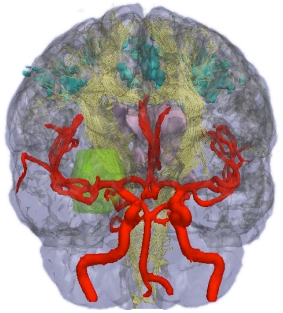


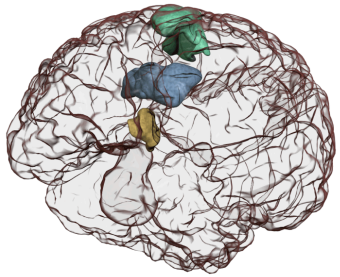
April 21, 2011
Cognitive Neuroscience Seminar

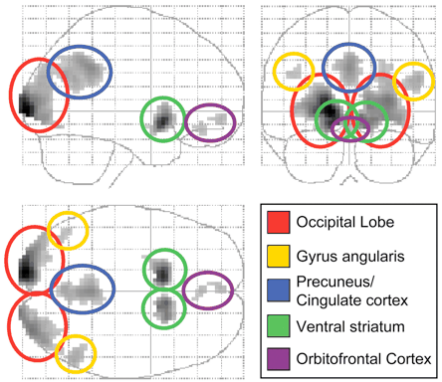
Why label brains?

Labels visually augment anatomy

- teach brain anatomy
- guide neurosurgery







http://www.cbd.ucla.edu/bios/iacoboni.html, http://brainvisa.info/, http://dx.doi.org/10.1126/science.1145876
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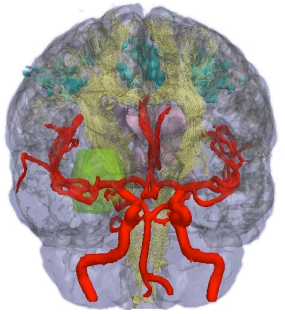
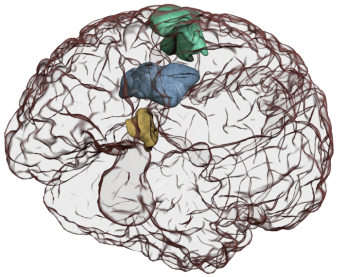
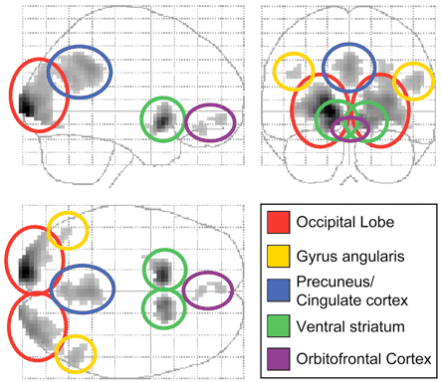


Labels compartmentalize image data

- assign results to brain regions
- quantify data by brain region





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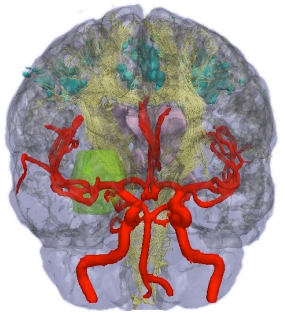

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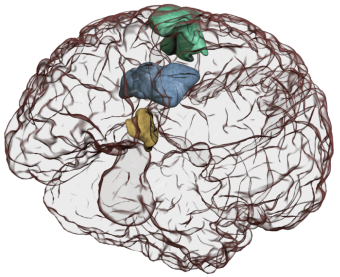
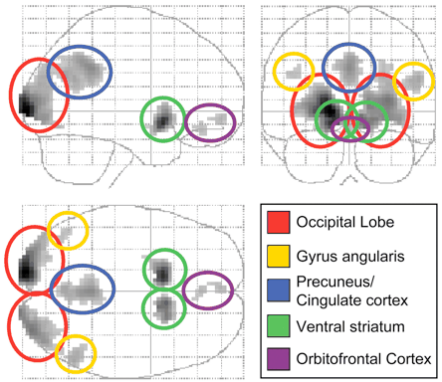


Labels provide a common nomenclature

- compare individuals within and across studies
- communicate results with a common language



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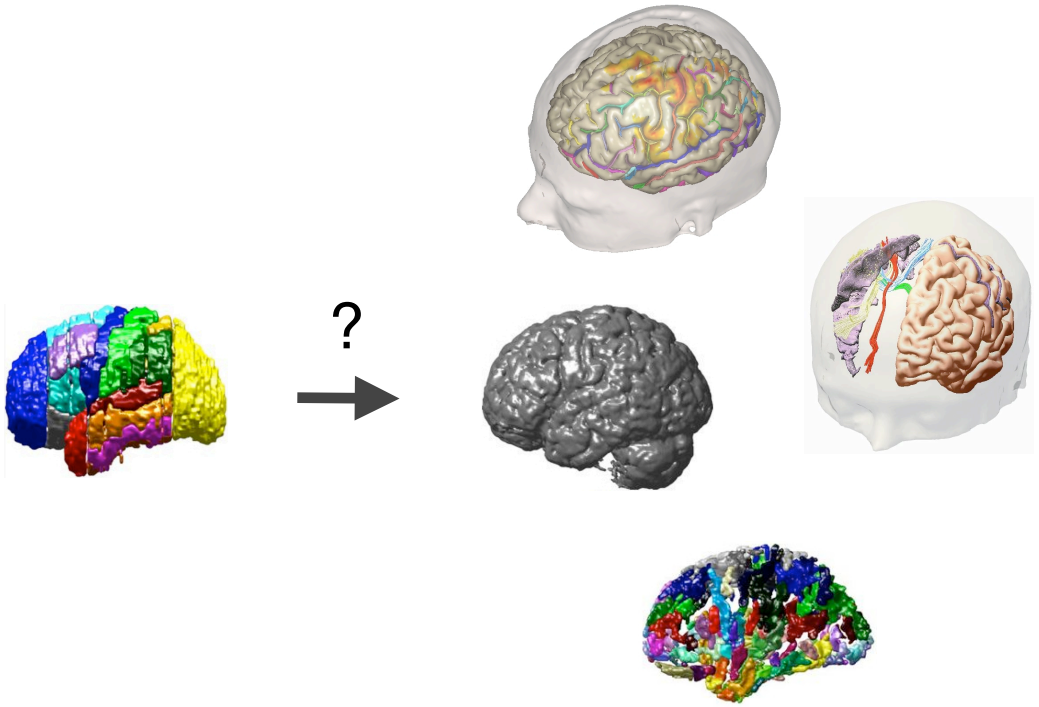
How should we label brains?



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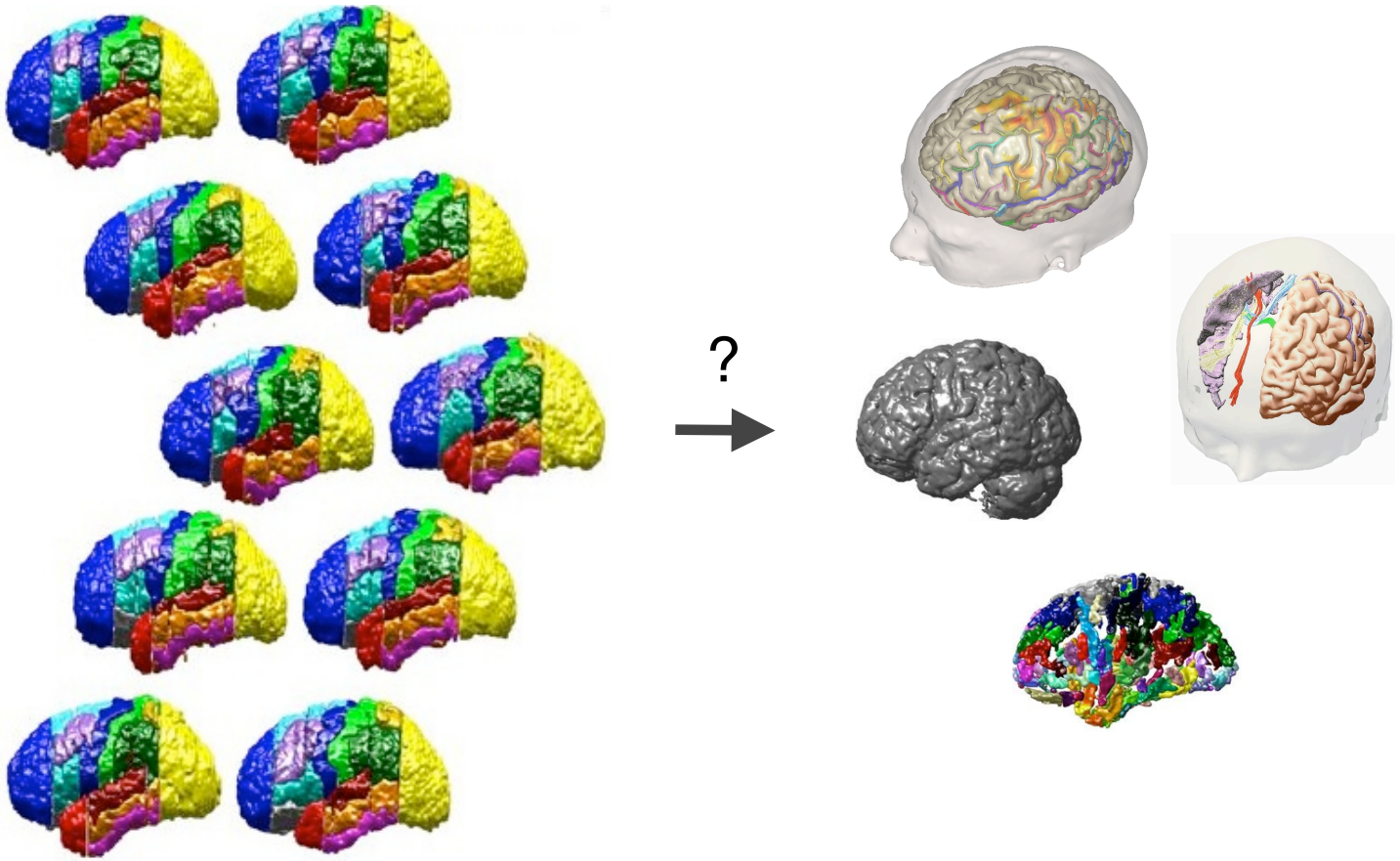

How should we label brains?

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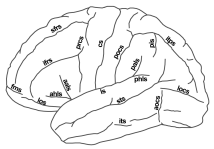
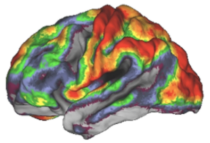
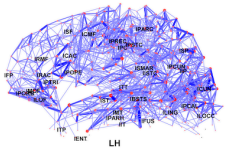


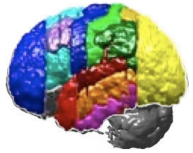
2. Functional mapping



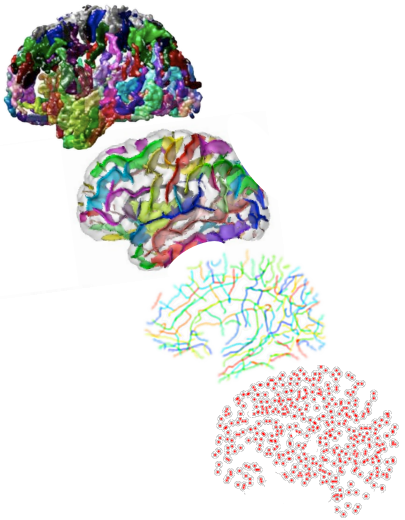
3. Tractography-based segmentation



4. Registration-based labeling



5. Feature matching



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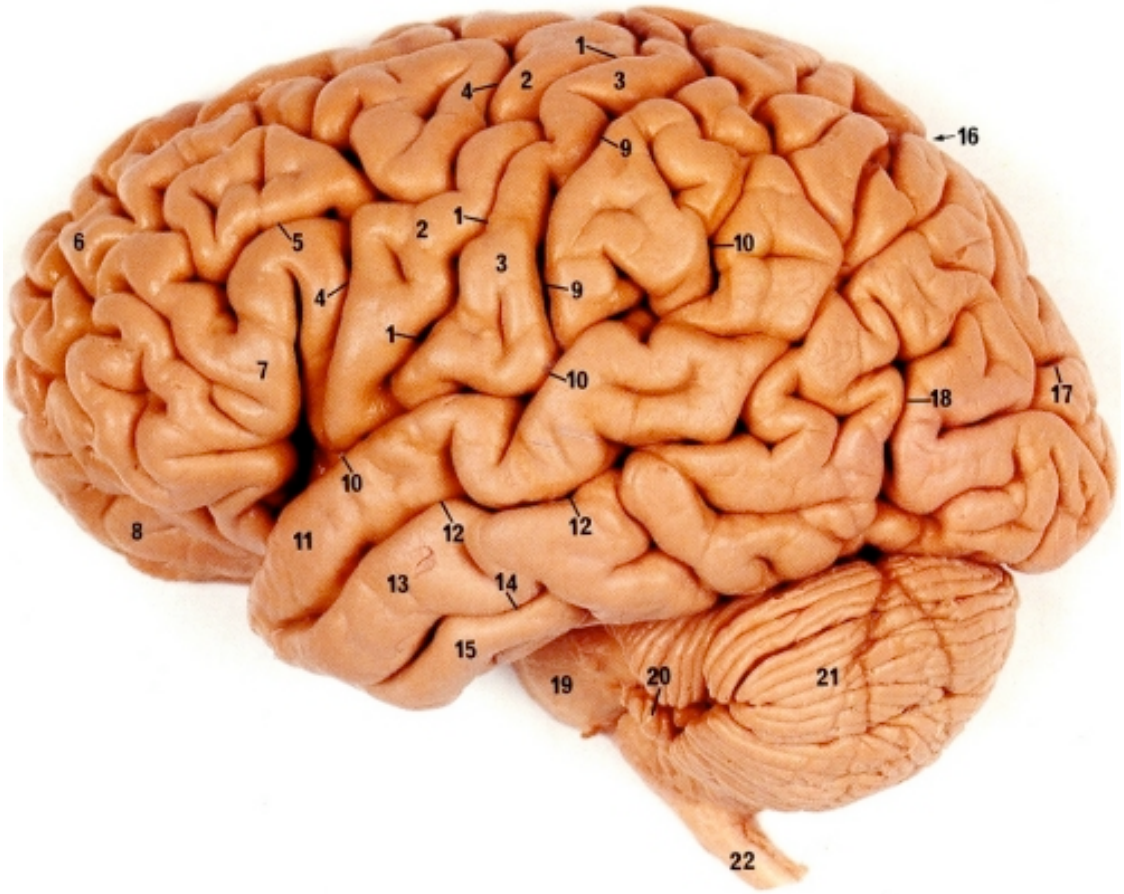
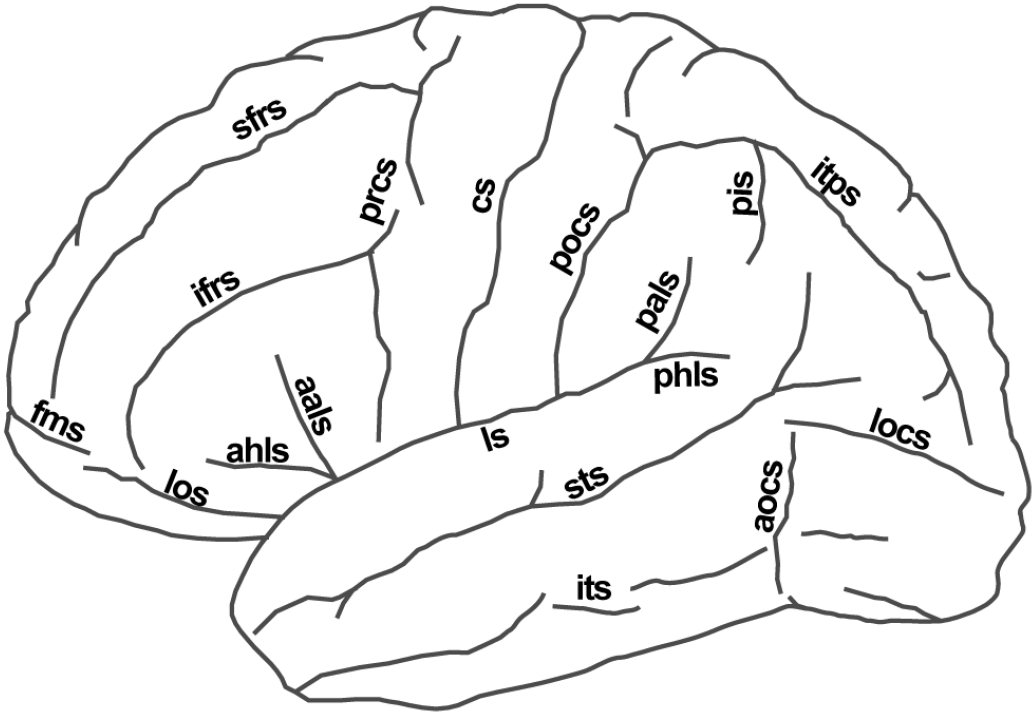
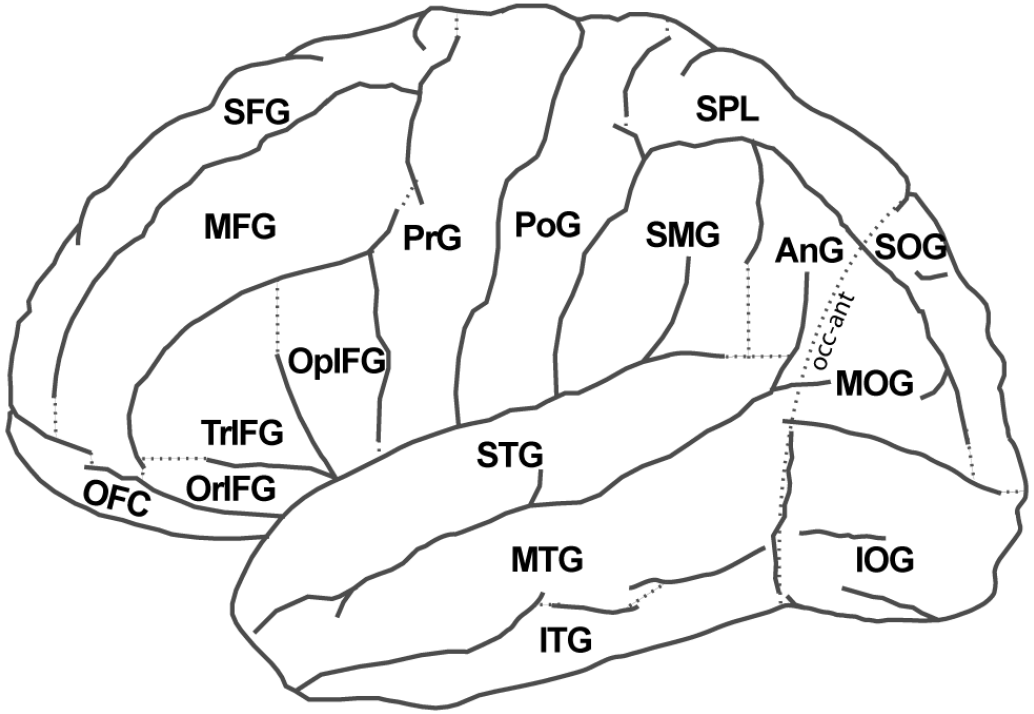
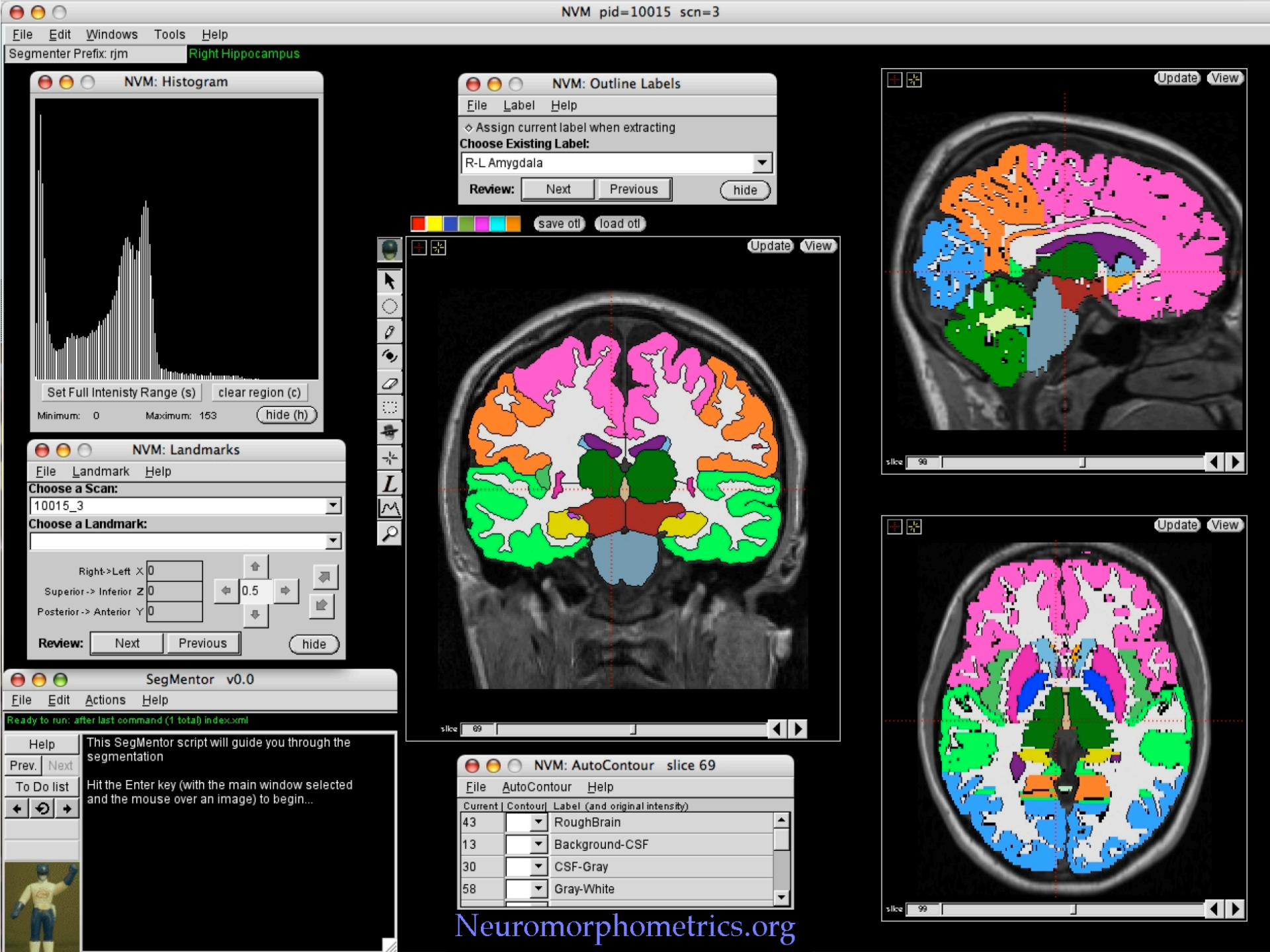


Sulcus definitions



Gyrus definitions

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NVM: Outline Labels
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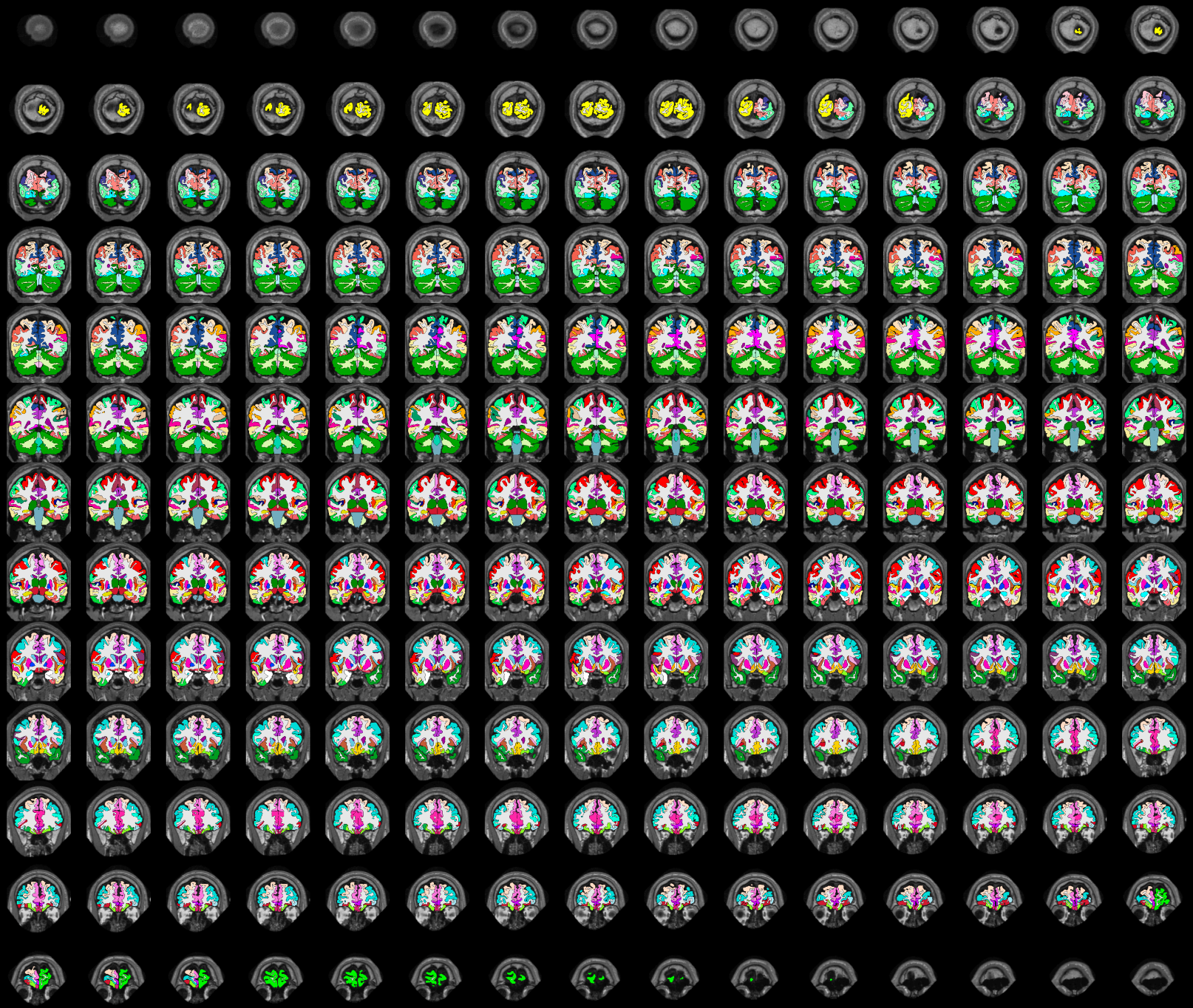
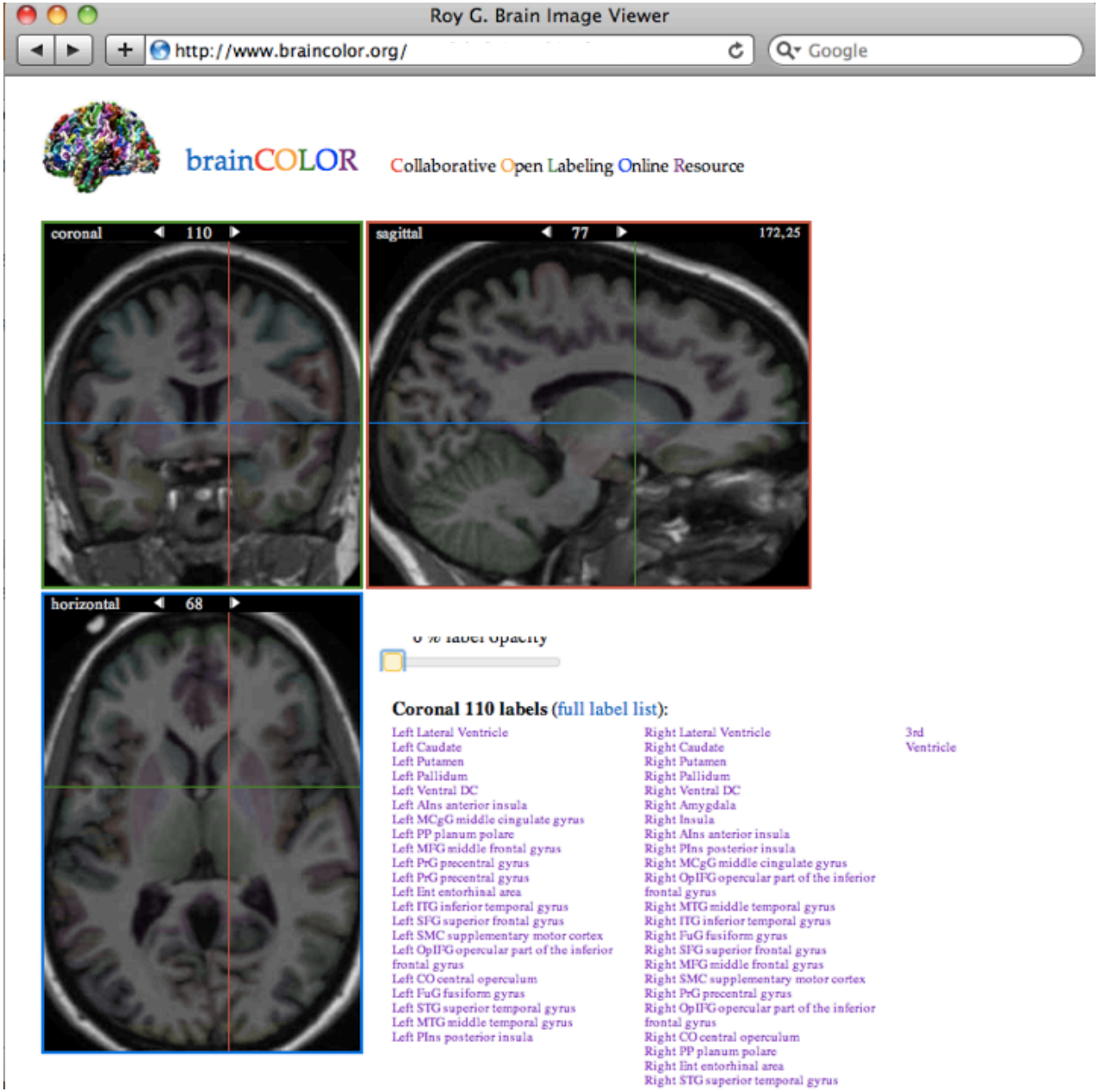
43 RoughBrain
13 Background-CSF
30 CSF-Gray
58 Gray-White
Neuromorphometrics.org




Roy G. Brain Image Viewer
http://www.braincolor.org/
Google
brainCOLOR
Collaborative Open Labeling Online Resource
coronal 110
sagittal 77 172,25
horizontal 68
Coronal 110 labels (full label list):
Left Lateral Ventricle
Left Caudate
Left Putamen
Left Pallidum
Left Ventral DC
Left AIns anterior insula
Left MCgG middle cingulate gyrus
Left PP planum polare
Left MFG middle frontal gyrus
Left PrG precentral gyrus
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Left ITG inferior temporal gyrus
Left SFG superior frontal gyrus
Left SMC supplementary motor cortex
Left OpIFG opercular part of the inferior frontal gyrus
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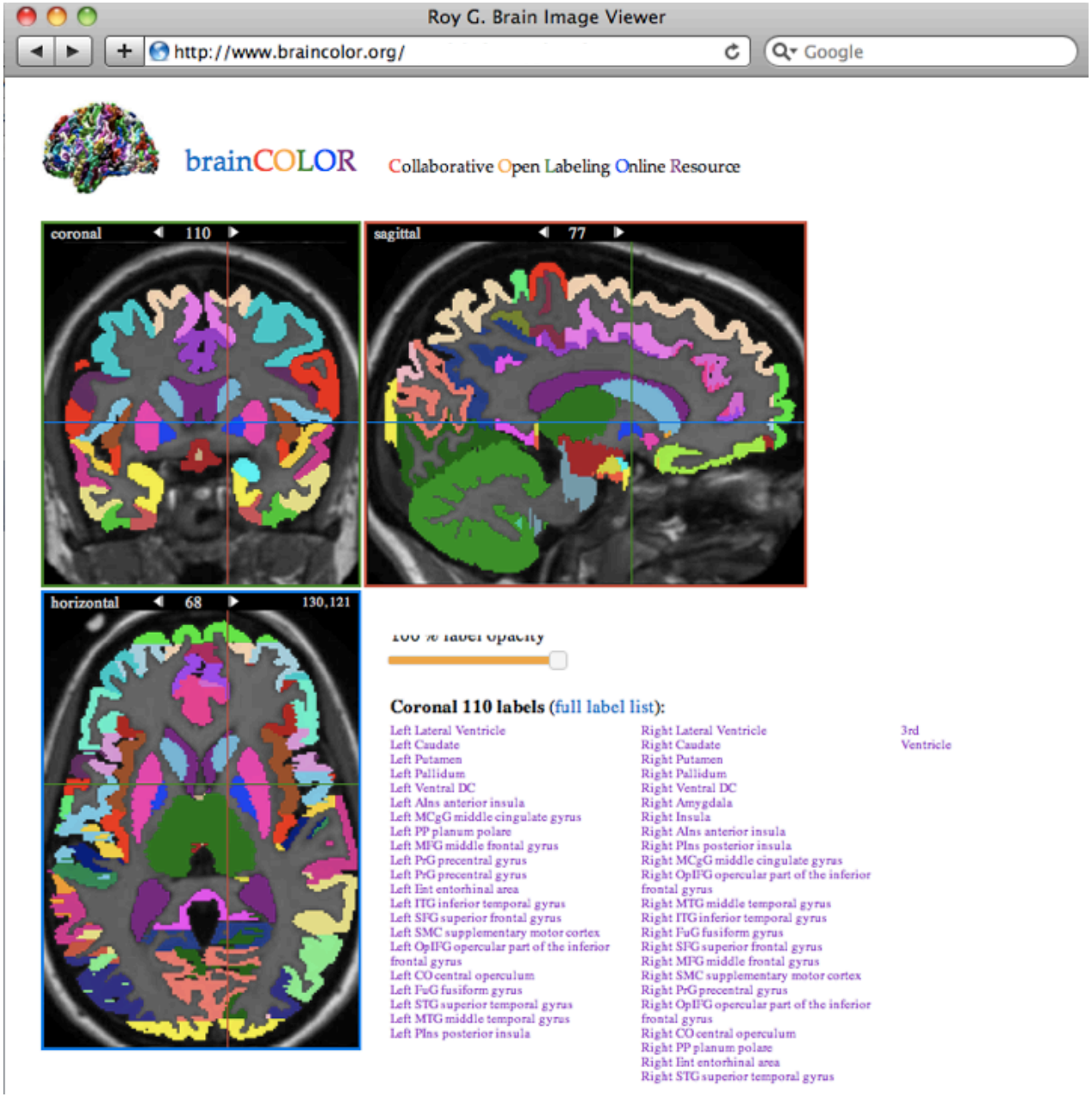
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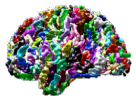


An interactive tool for constructing optimal brain colormaps

Arno Klein — NY State Psych. Inst. Columbia University, NY
Andrew Worth — Neuromorphometrics, Inc., MA
Jason Tourville — Cognitive & Neural Systems Boston University, MA
Bennett Landman — Vanderbilt University Nashville, TN
Tito Dal Canton — NY State Psych. Inst. Columbia University, NY
Satrajit S. Ghosh — Research Laboratory of Electronics, MIT, MA
David Shattuck — Laboratory of NeuroImaging UCLA, CA

Goal

Create a software tool to aid in the construction of optimal colormaps for viewing and labeling brain anatomical images.

Background

The application of color is an indispensible means of visually distinguishing anatomical regions of the brain [1,2]. The need to facilitate visualization of brain images has become particularly urgent with the inception of large-scale anatomical labeling projects, such as the BrainCOLOR project, in which hundreds of MR images of the human brain are being manually labeled (www.braincolor.org/protocols) as well as viewed online (www.braincolor.org/roygbiv).

Choosing a color space

Our colormap must consist of colors that are perceptually distinct, so it is reasonable to choose a color space that is perceptually uniform, where a separation between two colors in the color space is as discriminable as the same separation between two other colors in the color space.
The International Commission on Illumination (CIE) devised a color space in 1931 that facilitates color description (Fig.1). Subsequent improvements led to the CIELAB and CIELUV color spaces, as well as a cylindrical variant, CIELch, all of which attempt to be perceptually uniform.

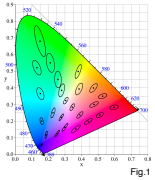


Fig.1

Constructing a colormap

We uniformly sampled hues from the CIELch cylinder (Fig.2) at different distances from the center (70-100% chrominance) and at different lightness values. The resulting colormap (Fig.3) has the same number of colors as regions we wish to color (49 cortical regions in the BrainCOLOR protocol). We intend to expand the number of colors to include subcortical and other regions.

Fig.2

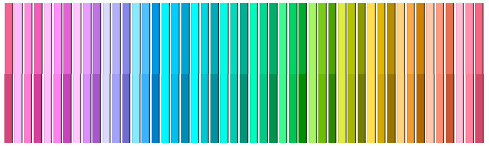


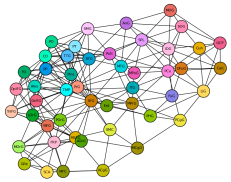
Fig.3

1. Schott GD (2010) Colored illustrations of the brain: some conceptual and contextual issues. Neuroscientist. 16(5):508-18.
2. Schoonover, C (2010) Portraits of the Mind: Visualizing the Brain from Antiquity to the 21st Century. Abrams (ISBN-13: 978-0810990334)

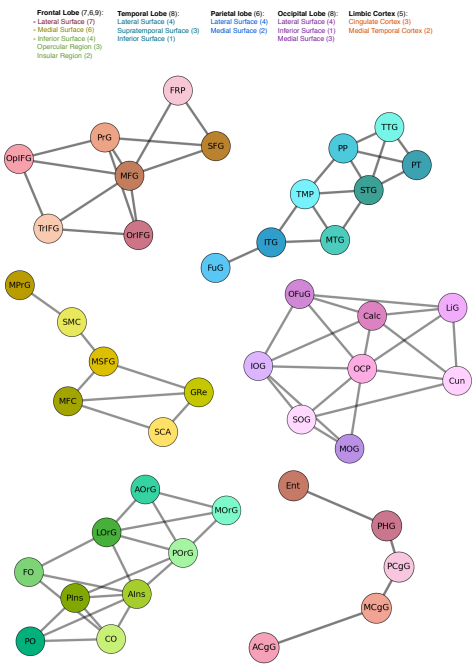
CIE1931 figure: http://en.wikipedia.org/wiki/File:CIExy1931_MacAdam.png
CIELch figure: http://www.colorbasics.com/ColorSpace/

Maximizing discriminability of adjacent regions

To easily distinguish brain regions from each other, we wish to maximize the color difference between adjacent regions. We do this by constructing a graph that represents connections (edges) between regions (nodes).

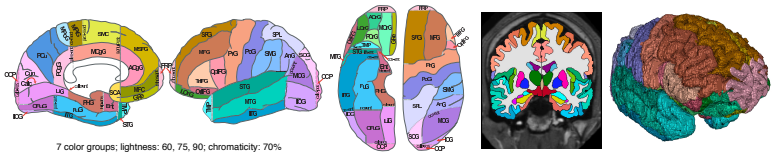


We define an *optimal mapping* of colors as the combination of colors assigned to nodes with the maximum sum of color differences between connected nodes, defined by the CIE2000 Delta E measure (http://en.wikipedia.org/wiki/Color_difference).
However, we cannot compute 8.8 x 10^{18} permutations of the 49 colors in the colormap, so we break up the brain into sublobes and compute the permutations of portions of the colormap at a time:

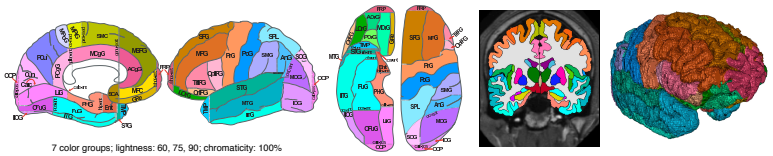


Grouping regions by using similar colors

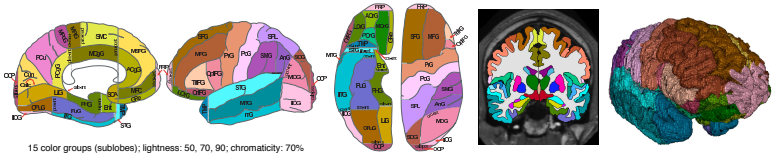
For labeling a brain image, maximum discriminability is paramount. For viewing a brain image, however, it is useful to visually group regions by assigning similar colors to the regions within a group. To create this visual grouping, we colored each subgraph with a neighborhood of colors (sampled within a wedge of the CIELch cylinder).



7 color groups; lightness: 60, 75, 90; chromaticity: 70%



7 color groups; lightness: 60, 75, 90; chromaticity: 100%



15 color groups (sublobes); lightness: 50, 70, 90; chromaticity: 70%

Conclusion and Future Work

We have created Python software for creating and applying colormaps to brain images.
Download the software from: http://binarybottle.github.com/brainCOLORmap
The software calls the Python libraries: *NumPy, NetworkX, Python-Colormath, Matplotlib, and xlrd*, to:

1. convert a table of adjacent regions (an adjacency matrix) to a weighted graph of colored nodes
2. compute permutations of colors for each subgraph to optimally distinguish colors of adjacent regions
3. apply similar colors to predefined groups of regions

There are many improvements we could pursue. We have targeted the following for future work:

- Develop an optimization algorithm for whole graphs or larger subgraphs.
- Restrict the color space to colors that can be displayed; currently, the CIELch colors that should appear different from one another may appear similar after conversion to SRGB colors.
- Seed color values to better control the range of colors for each group of regions.
- Accommodate visual concerns such as color blindness by adapting the colormap accordingly.

This project is funded as part of NIMH R01 MH084029-02 and NIMH R43 MH084358.

How should we label brains?

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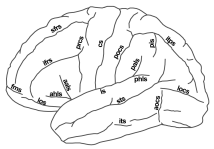

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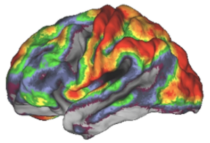

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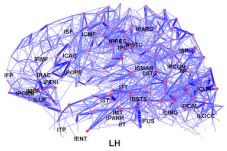
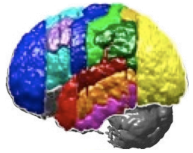


4. Registration-based labeling



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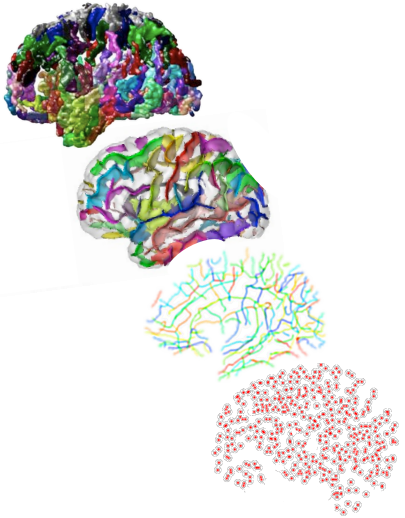
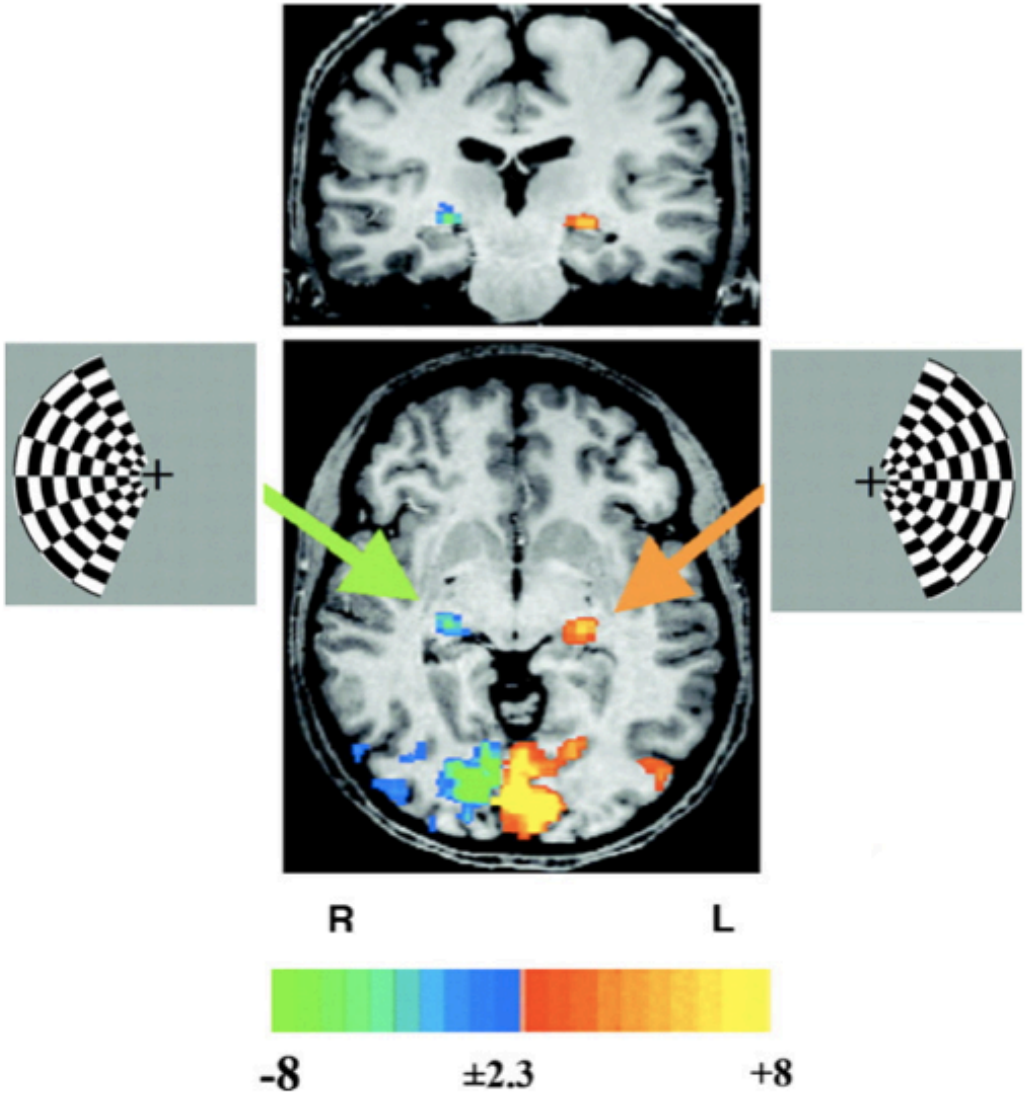
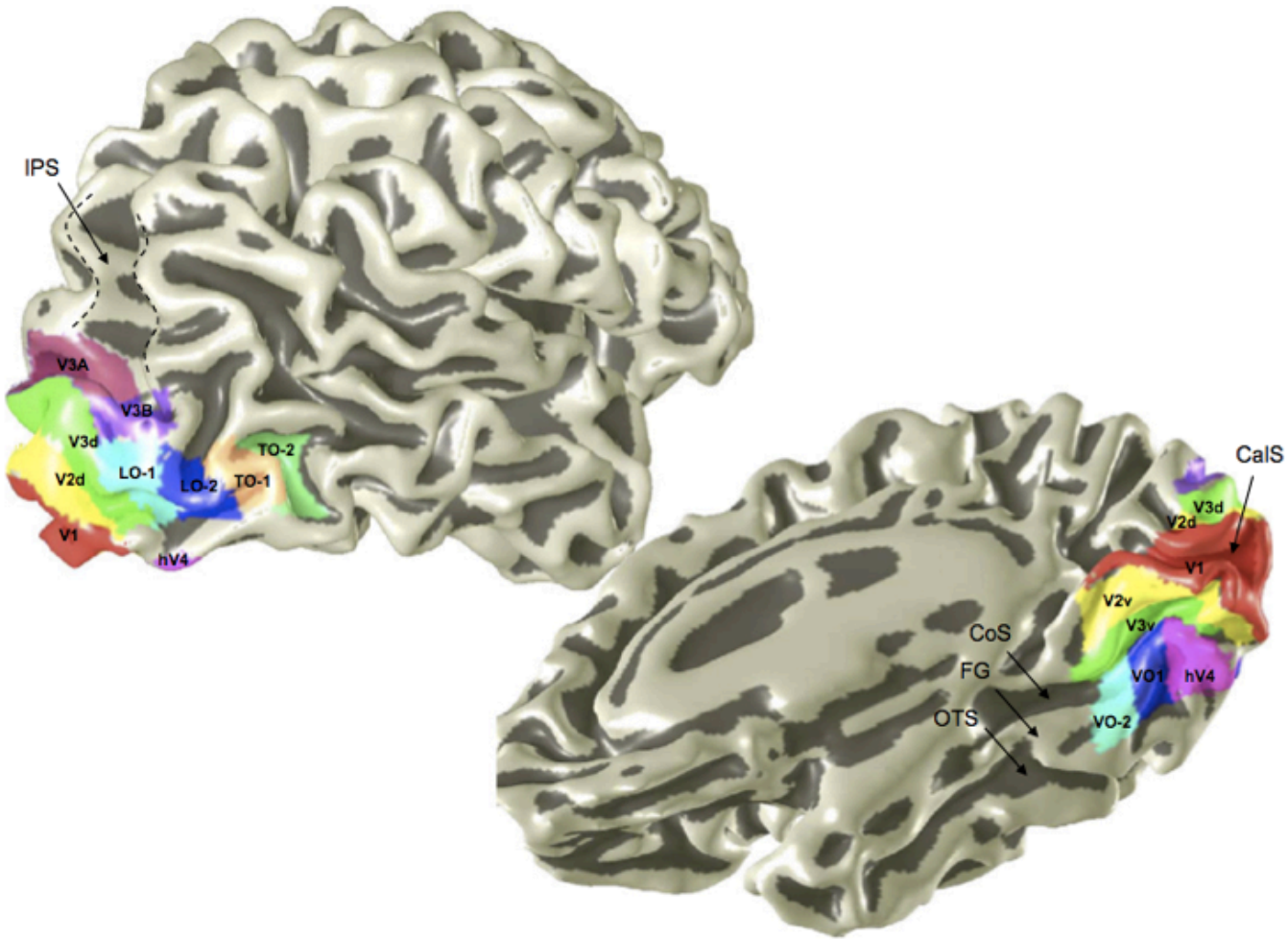


2. Functional mapping



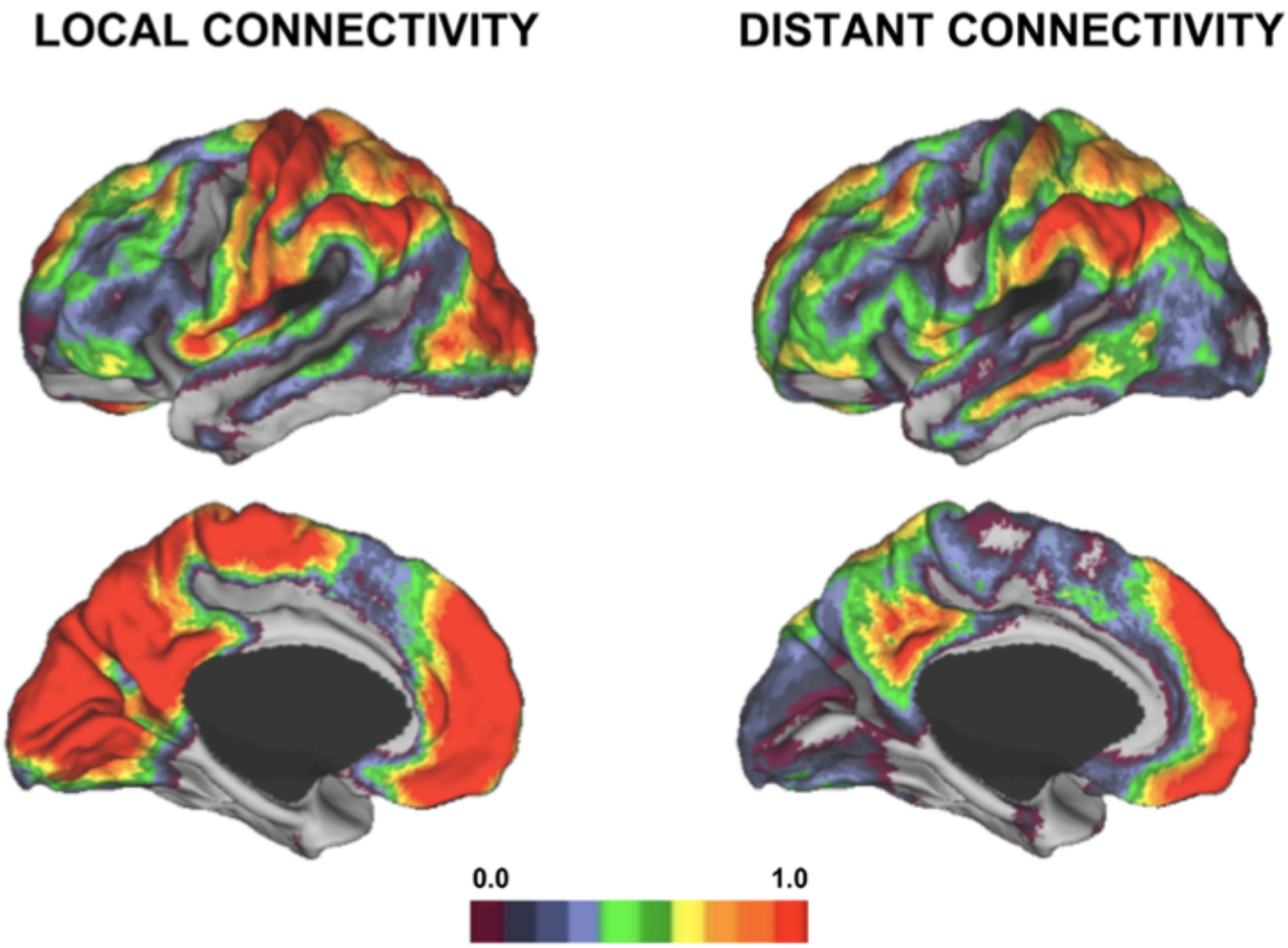
Kastner, et al., 2004

Visuotopic mapping



Wandell and Winawer, 2011

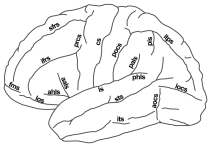
Functional “connectivity”



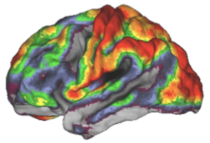
Sepulcre, et al., 2010

How should we label brains?

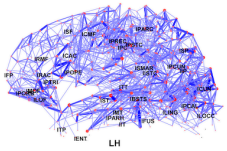
1. Manual labeling



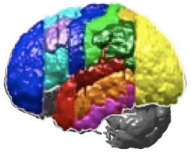
2. Functional mapping



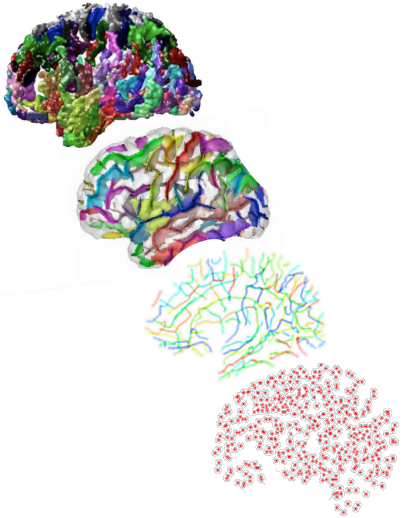
3. Tractography-based segmentation



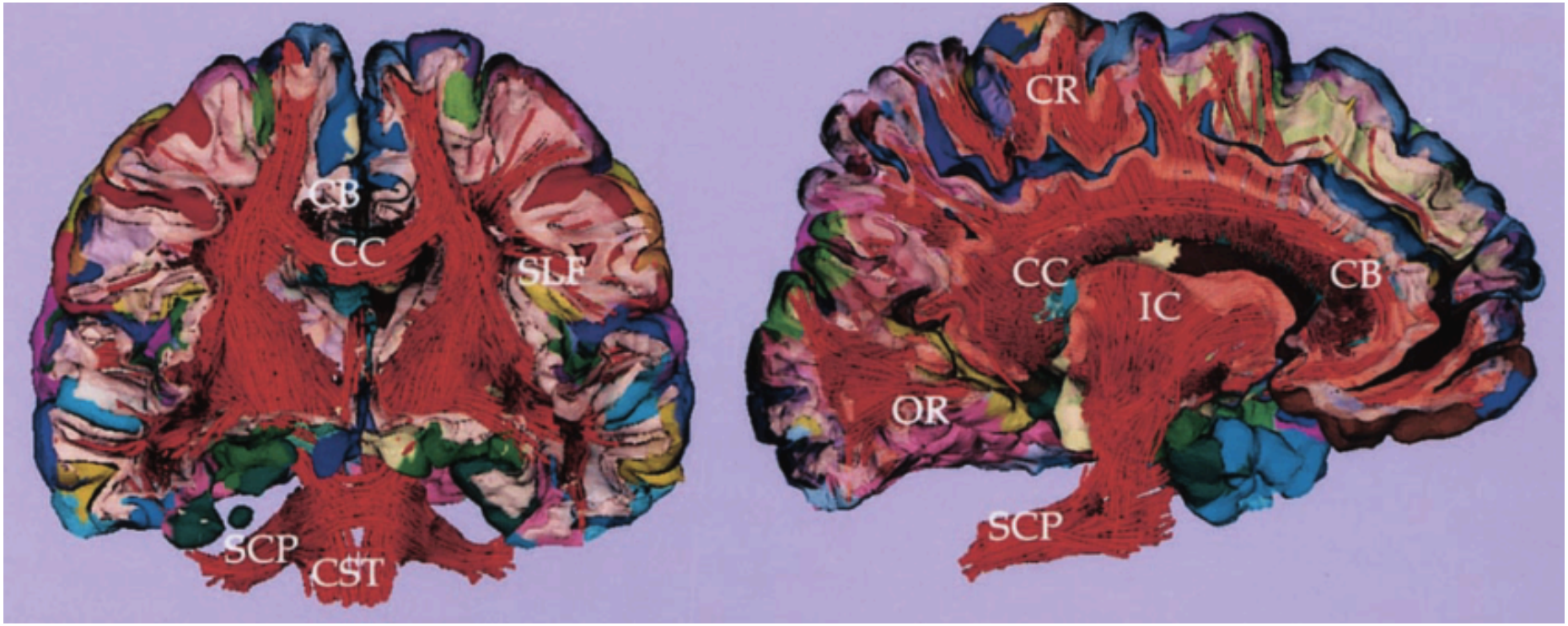
4. Registration-based labeling



5. Feature matching



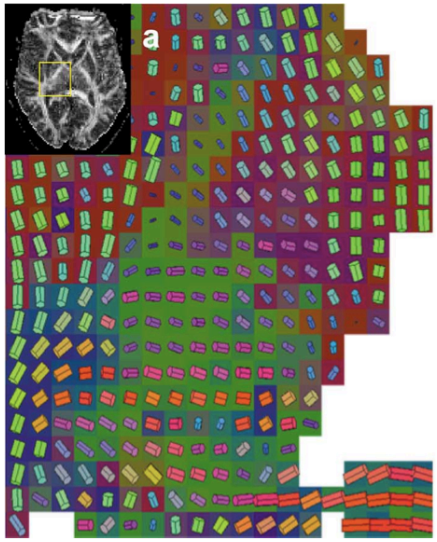
3. Tractography-based segmentation

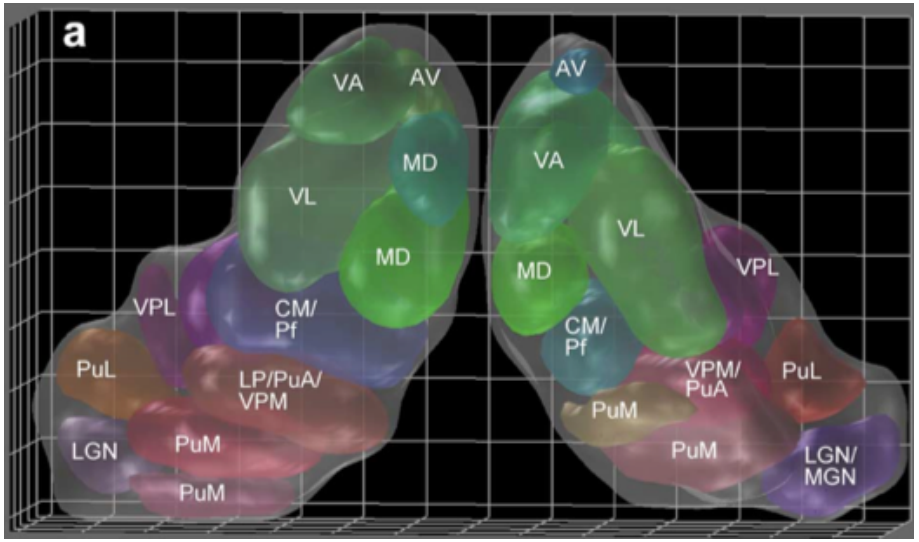


visualization of atlas-based labels + tractography

Park, et al., 2004

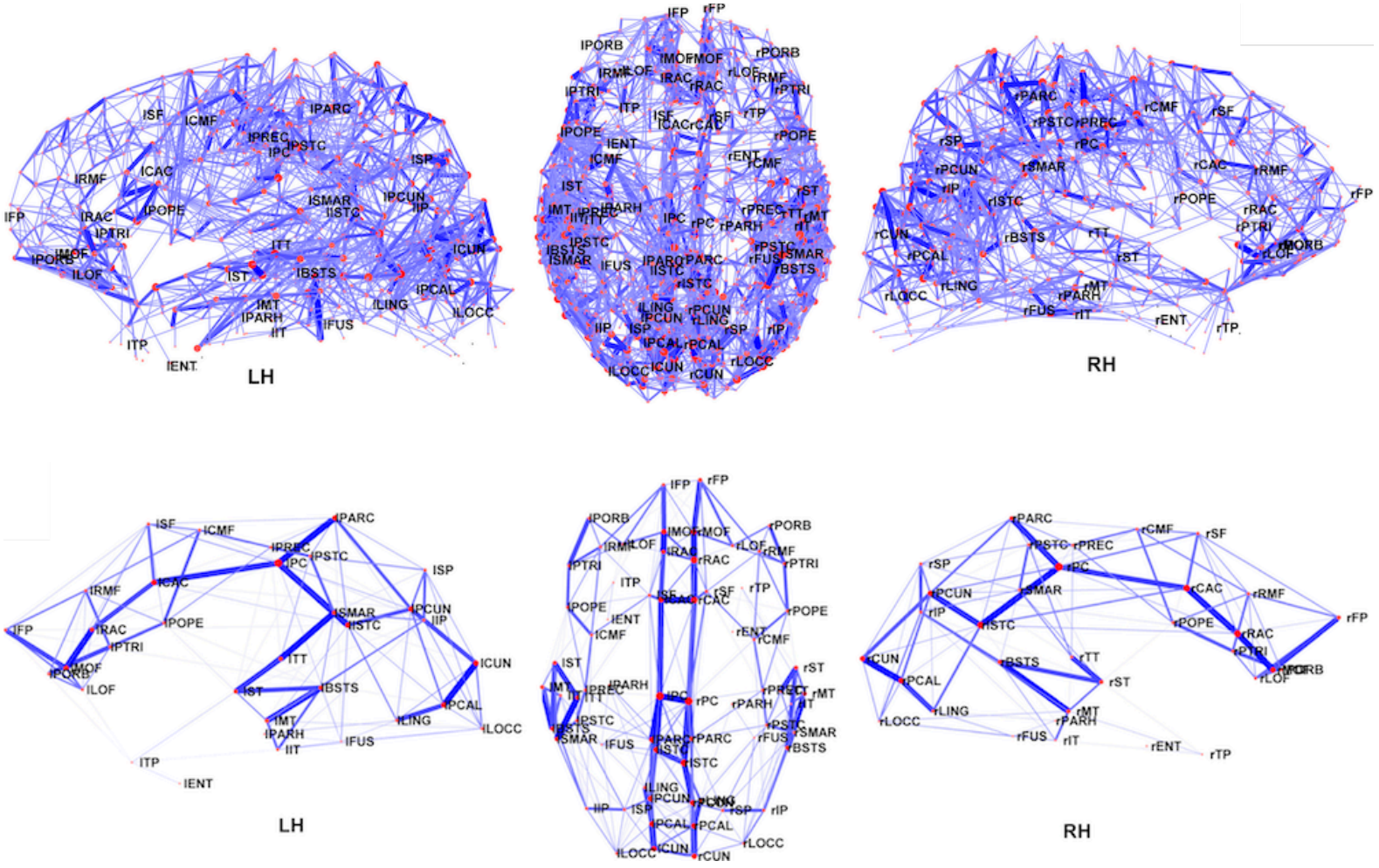
Tractography + atlas-based labeling





Wiegall et al., 2003; Cachia et al., 2008

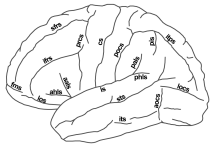
Labeled tractography-based networks



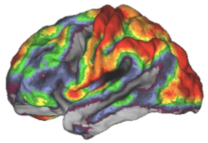
Hagmann, et al., 2008

How should we label brains?

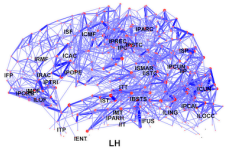
1. Manual labeling



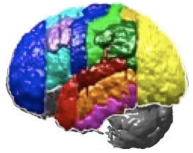
2. Functional mapping



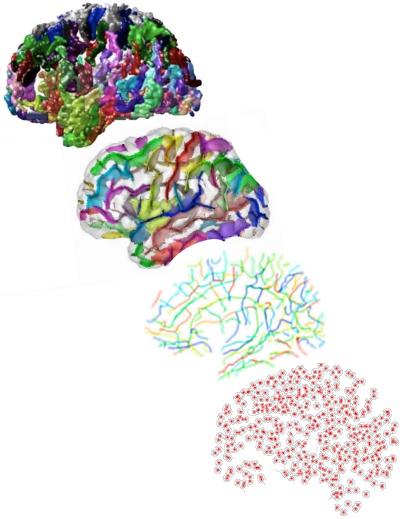
3. Tractography-based segmentation



4. Registration-based labeling

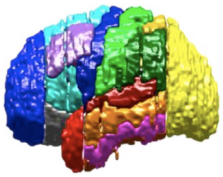


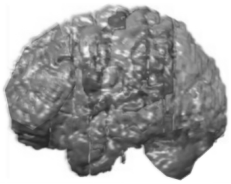
5. Feature matching



4. Registration-based labeling

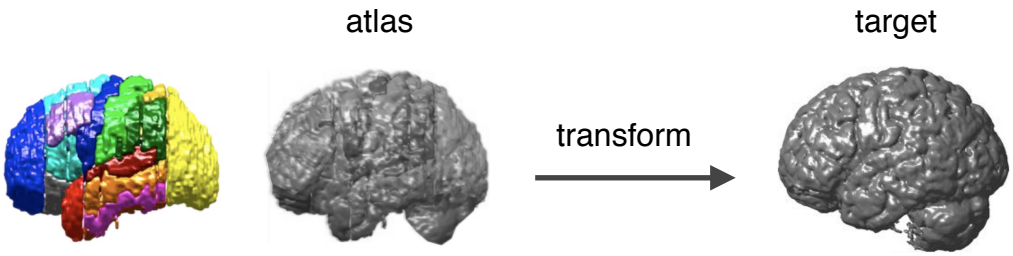
atlas



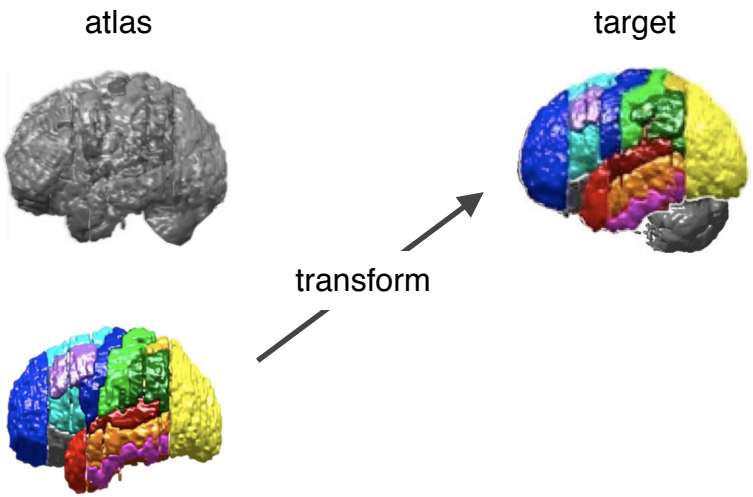


target

Step 1: compute the registration transform from the atlas to the target

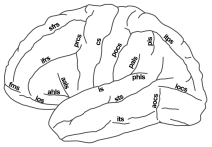


Step 2: apply the transform to the atlas labels

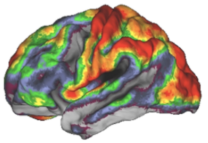


How should we label brains?

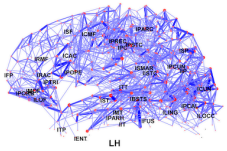
1. Manual labeling



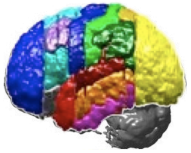
2. Functional mapping



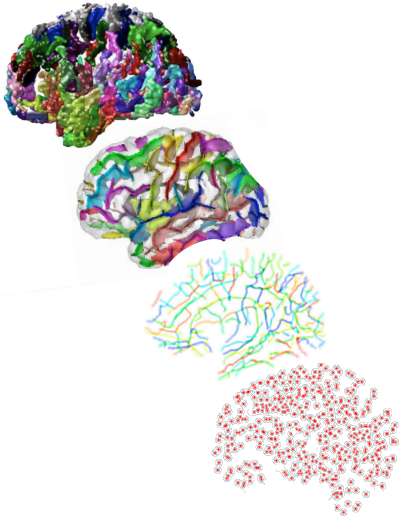
3. Tractography-based segmentation



4. Registration-based labeling



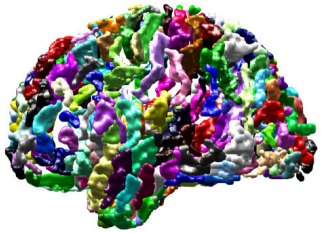
► 5. Feature matching

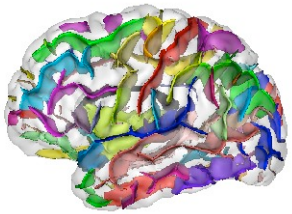


5. Feature matching

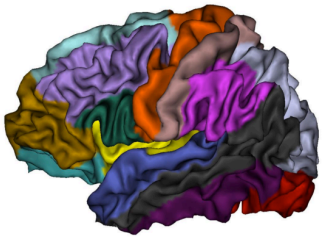
Sulcus structures

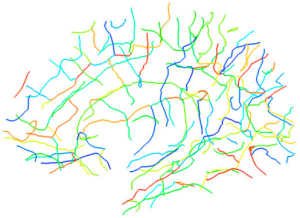
3-D: basins
skeletons



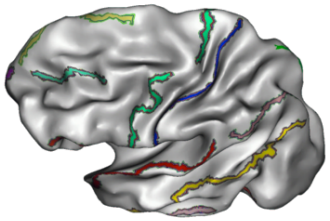


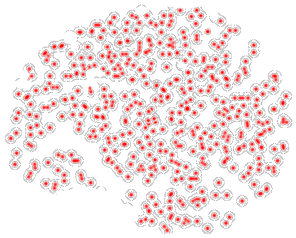
2-D: ribbons
surfaces



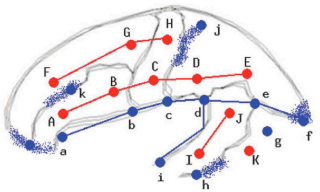


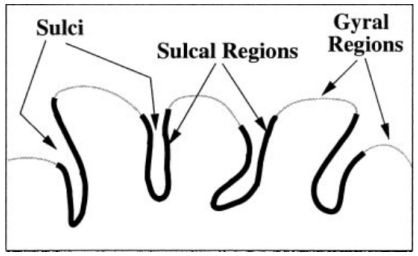
1-D: curves

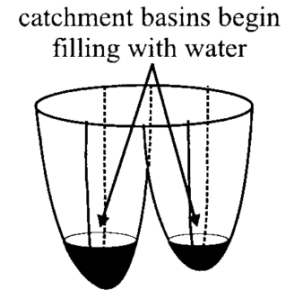


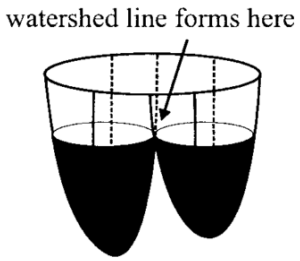


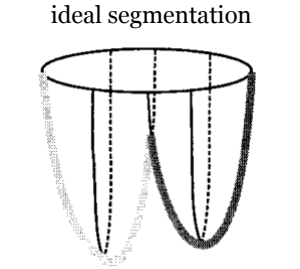
0-D: points
pits



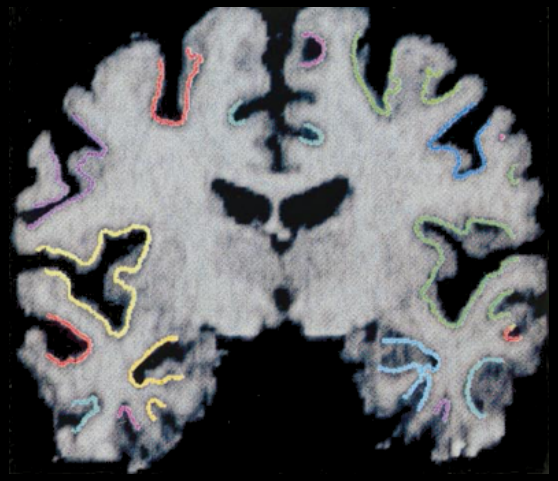


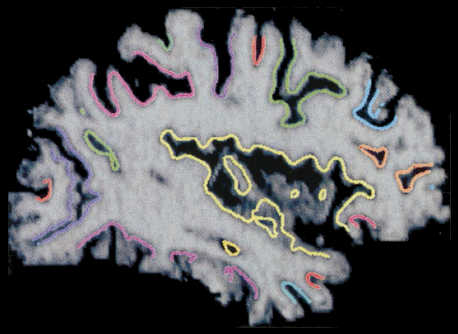




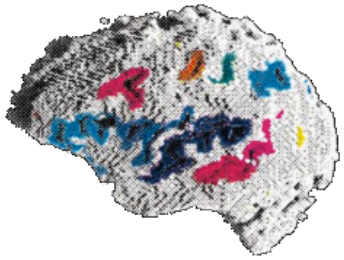


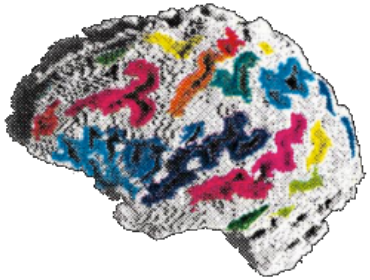
sulcus **basins**

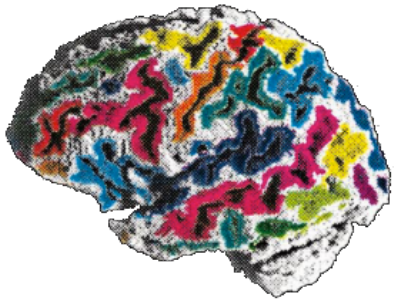


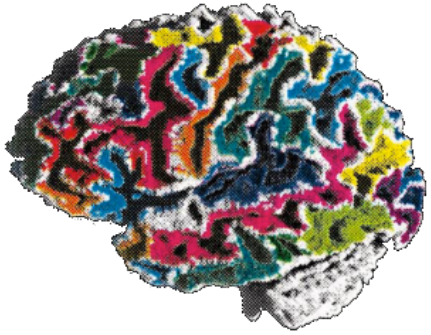


Rettman et al. 2002, Lohmann et al., 2000

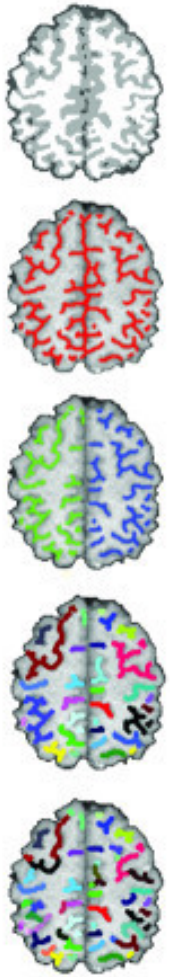


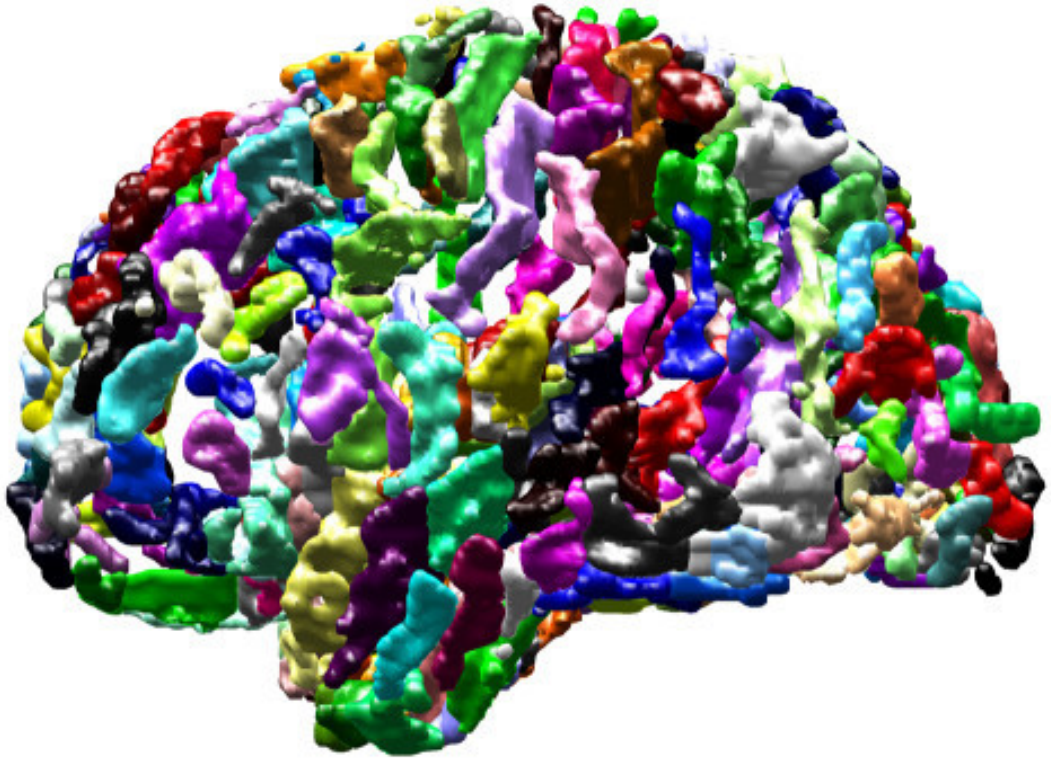




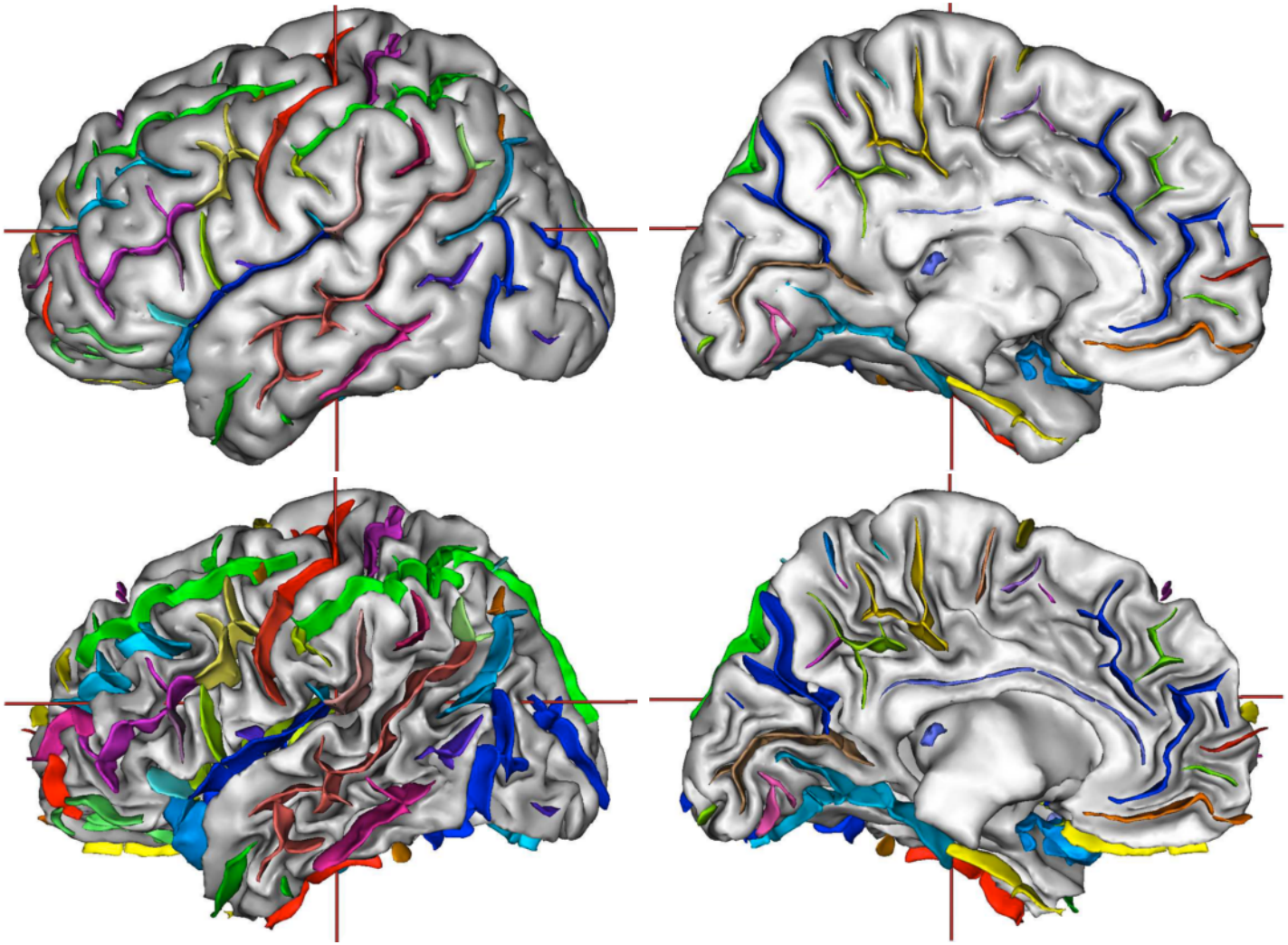


sulcus **skeletons**



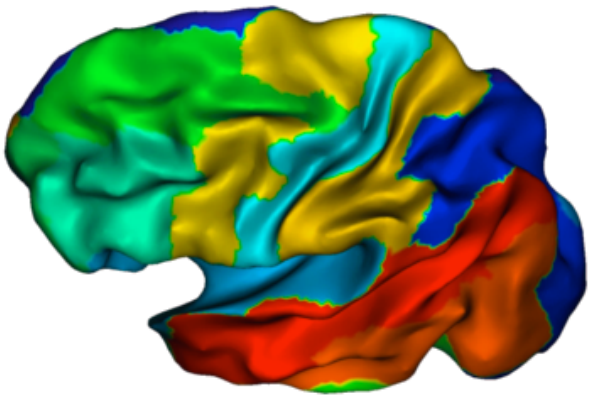


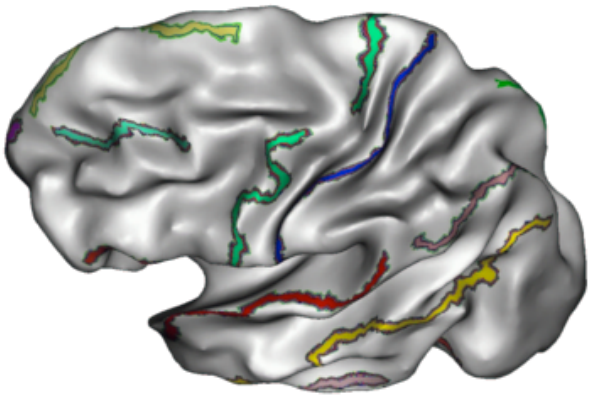
sulcus **ribbons**

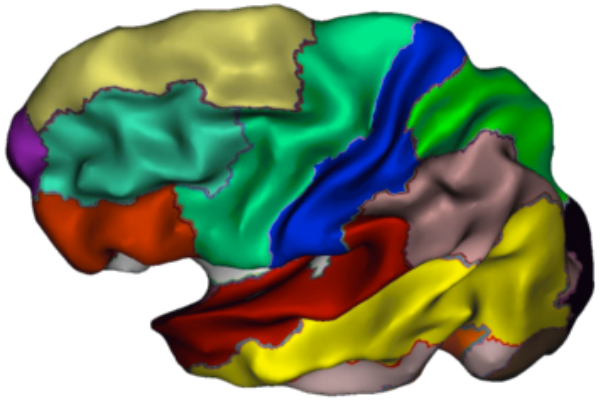


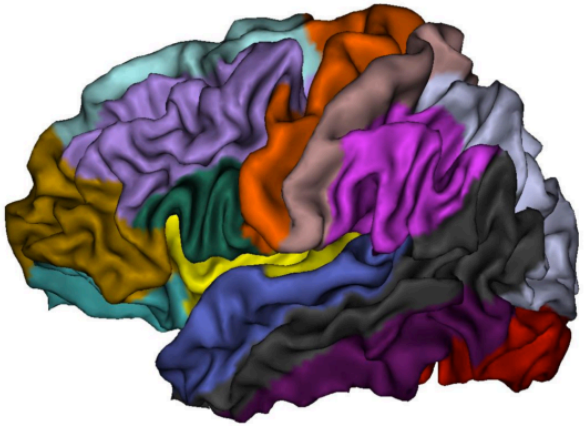
Clouchoux, 2008

sulcus & gyrus **surfaces**



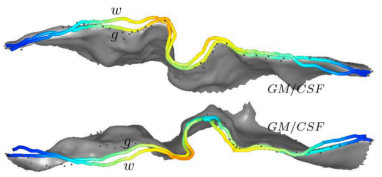


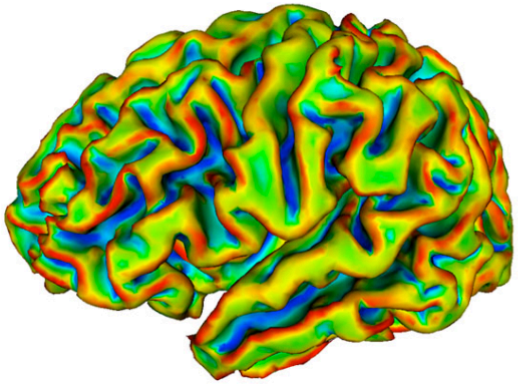


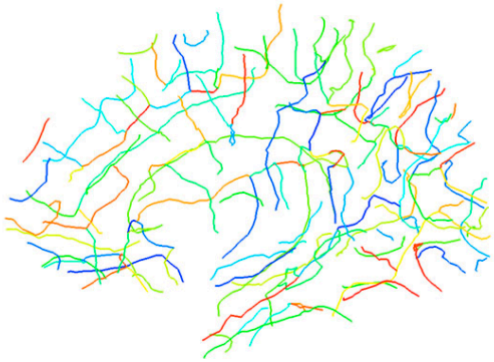


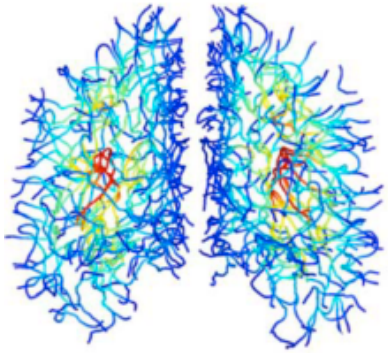
Cachia et al., 2003, Clouchoux et al., 2006

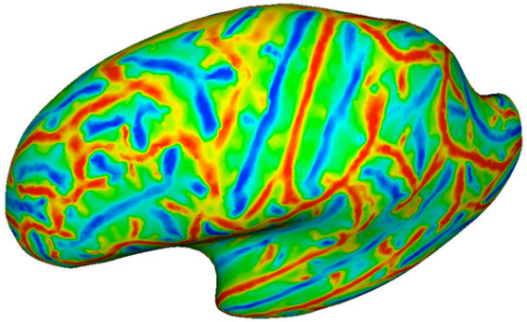
sulcus **curves**

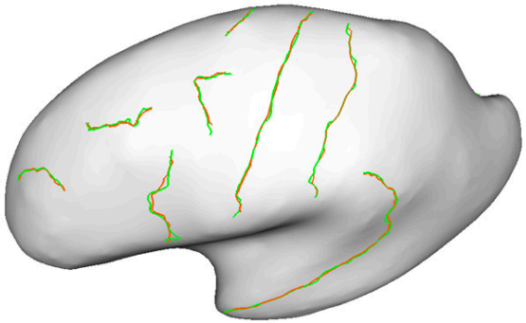


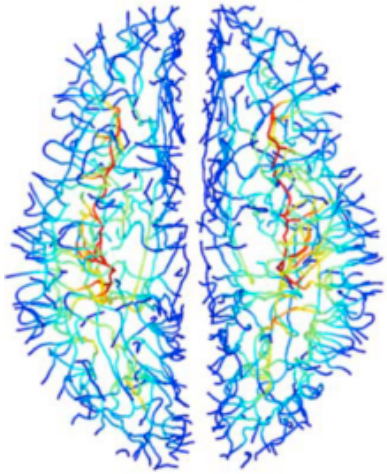






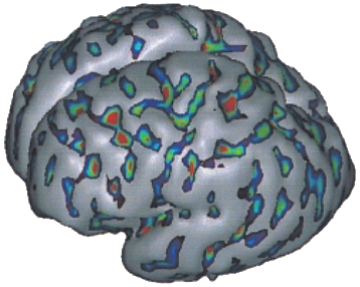


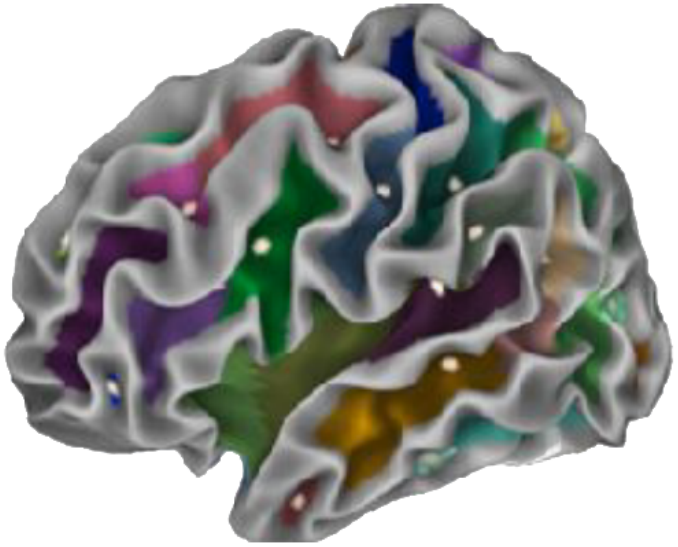


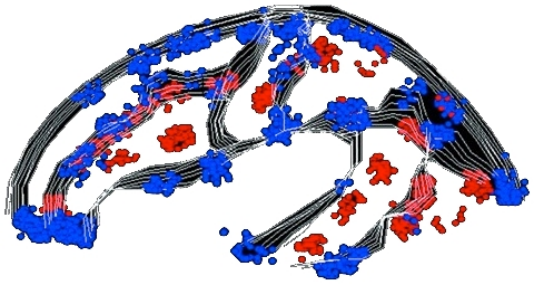


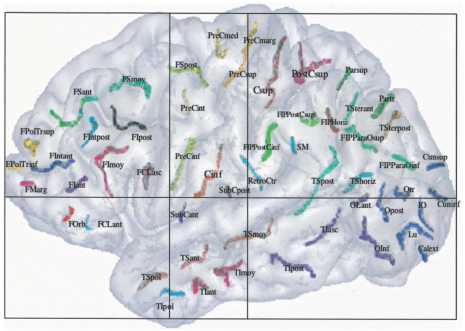
Li et al., 2008, Kao et al., 2007

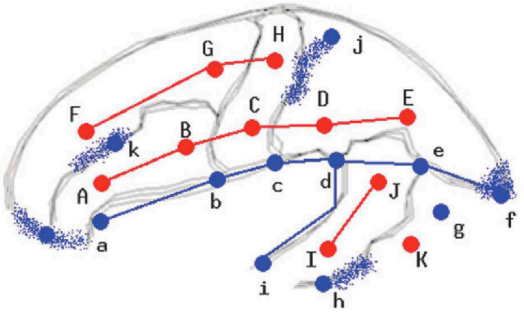
sulcus **pits**







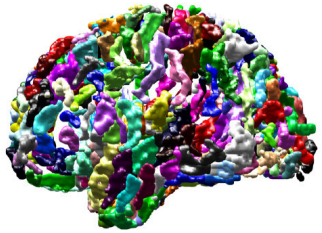


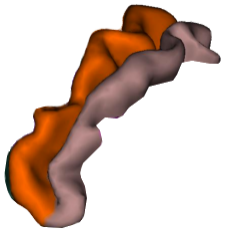


Regis et al., 2005, Im et al., 2010, Lohmann et al., 2007

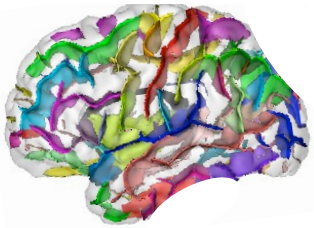
Combine stuctures in a nested hierarchy

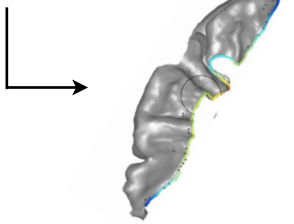
3-D



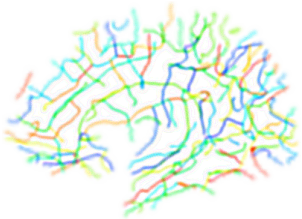


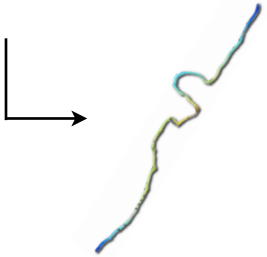
2-D



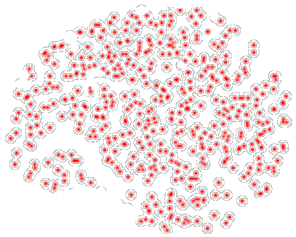


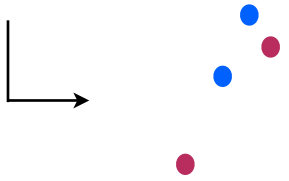
1-D





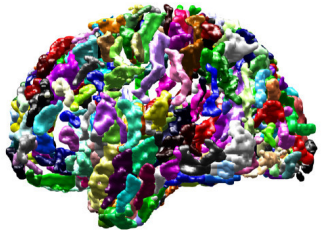
0-D

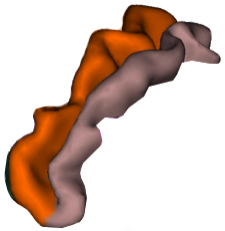




Characterize their shapes: **features**

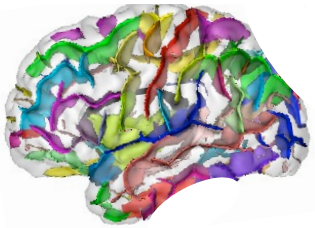
3-D





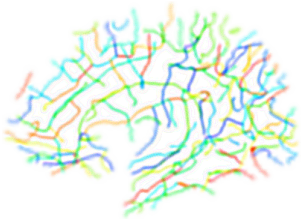
volume
surface area
lengths (thickness)
...

2-D



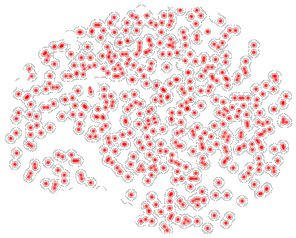
area
curvature
convexity
spectral components
...

1-D



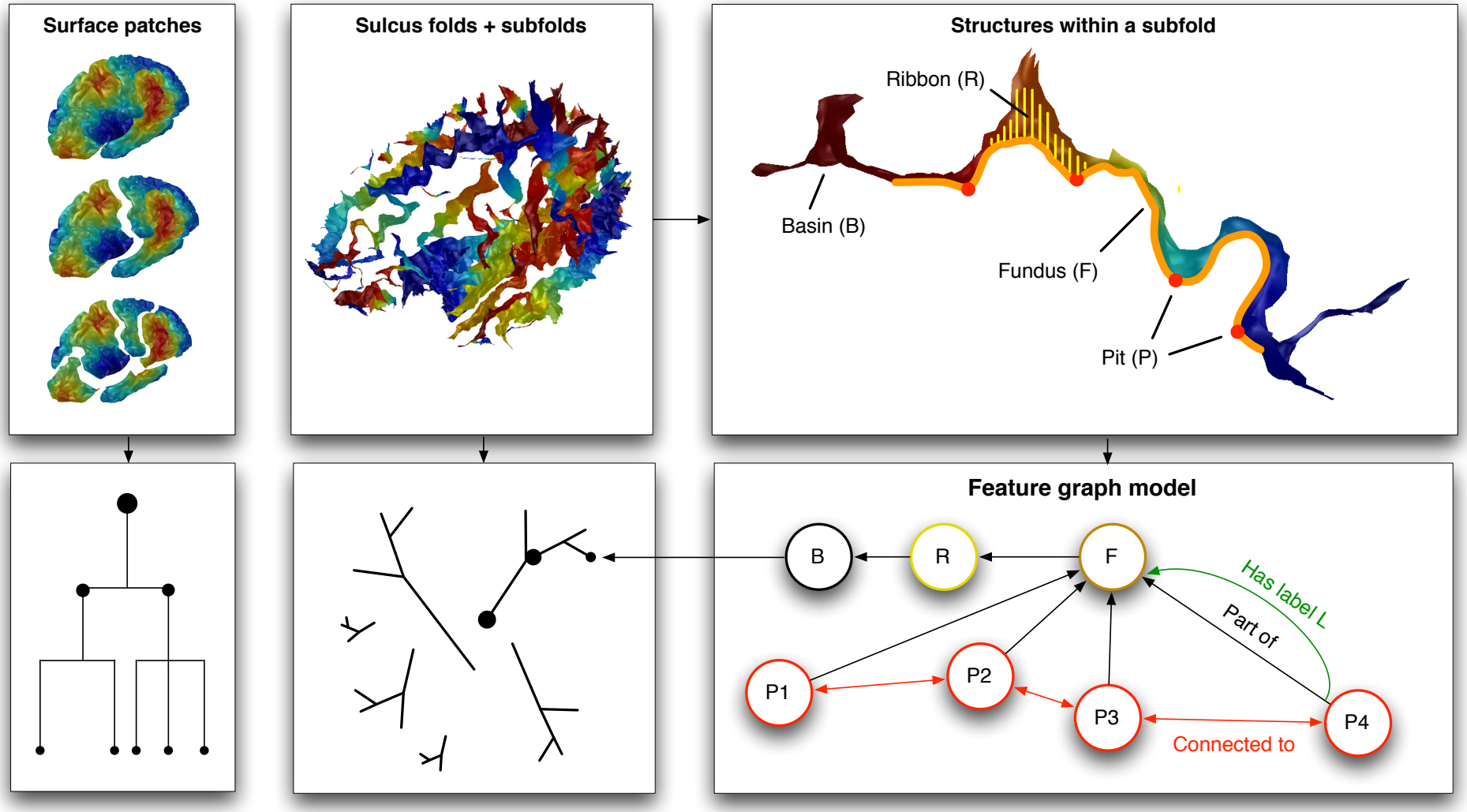
length
curvature
convexity
...

0-D



3-D convex hull volume
1-D sequence along a curve
...

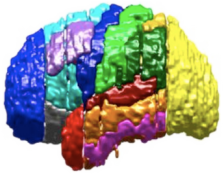
Represent nested features within a graph-based data model

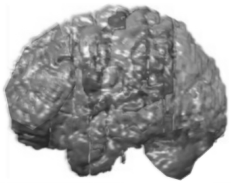


Top: structures: surface patches fragmented by application of the Laplace-Beltrami operator, sulcus folds and subfolds, and structures within a subfold.
Bottom: schematic diagrams representing the hierarchical relationships among nested structures.
Bottom right: features as properties of edges (relationships: Part of, Connected to, Has label) and nodes (geometric, shape, spectral, and connectivity measures).

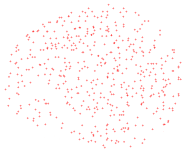
Mindboggle 2: feature-based labeling

atlas



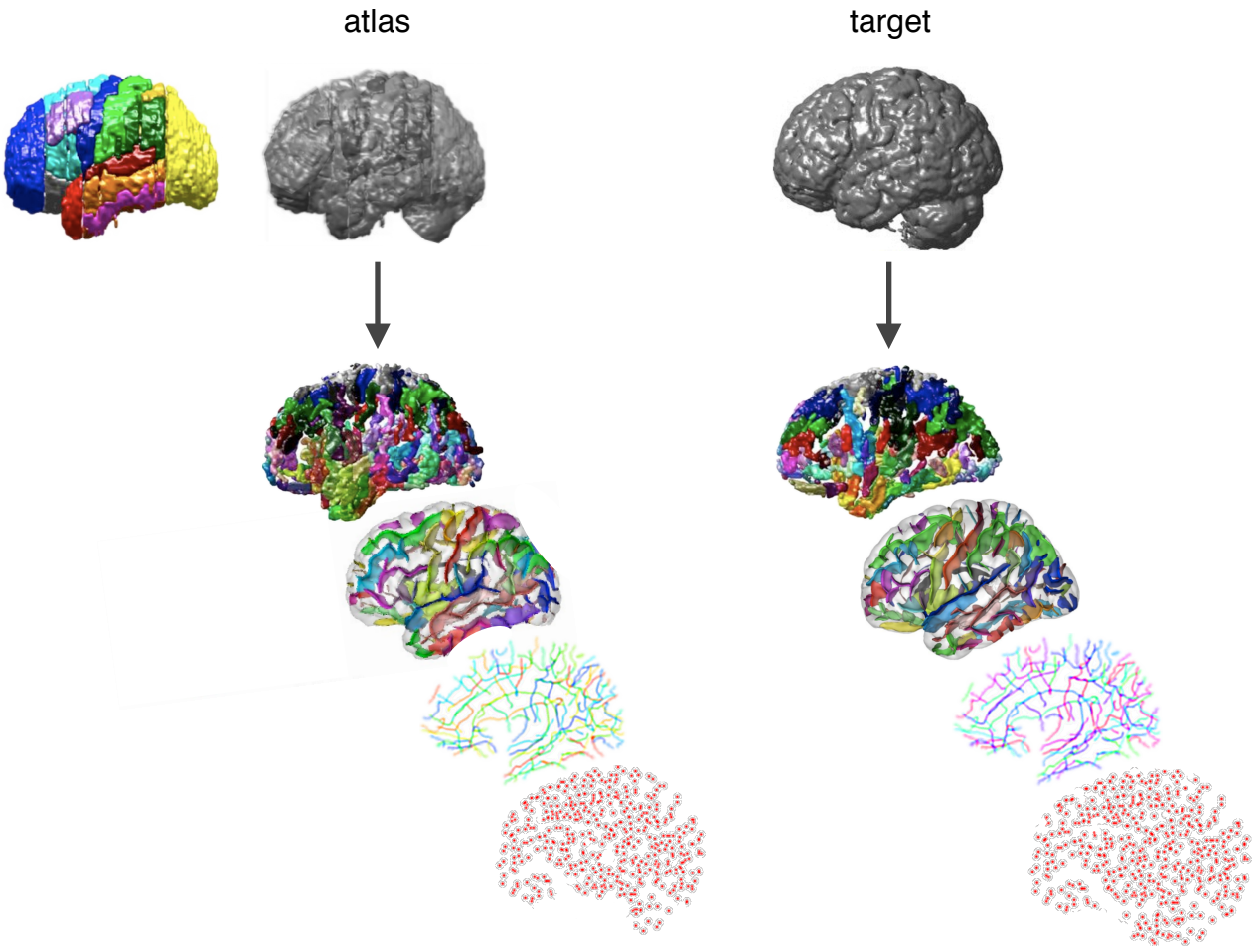


target



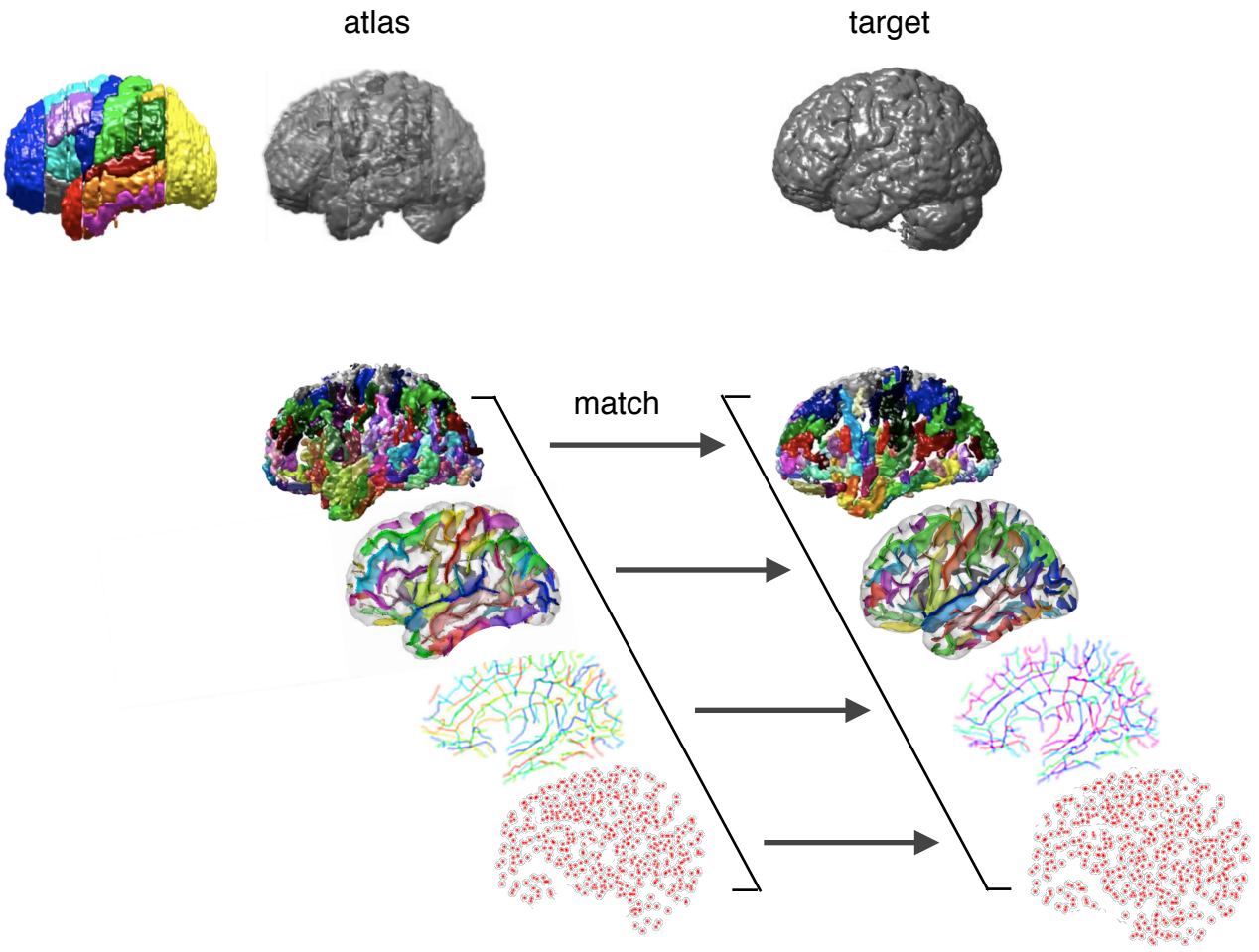
Mindboggle 2: feature-based labeling

Step 1: extract structures, compute their features



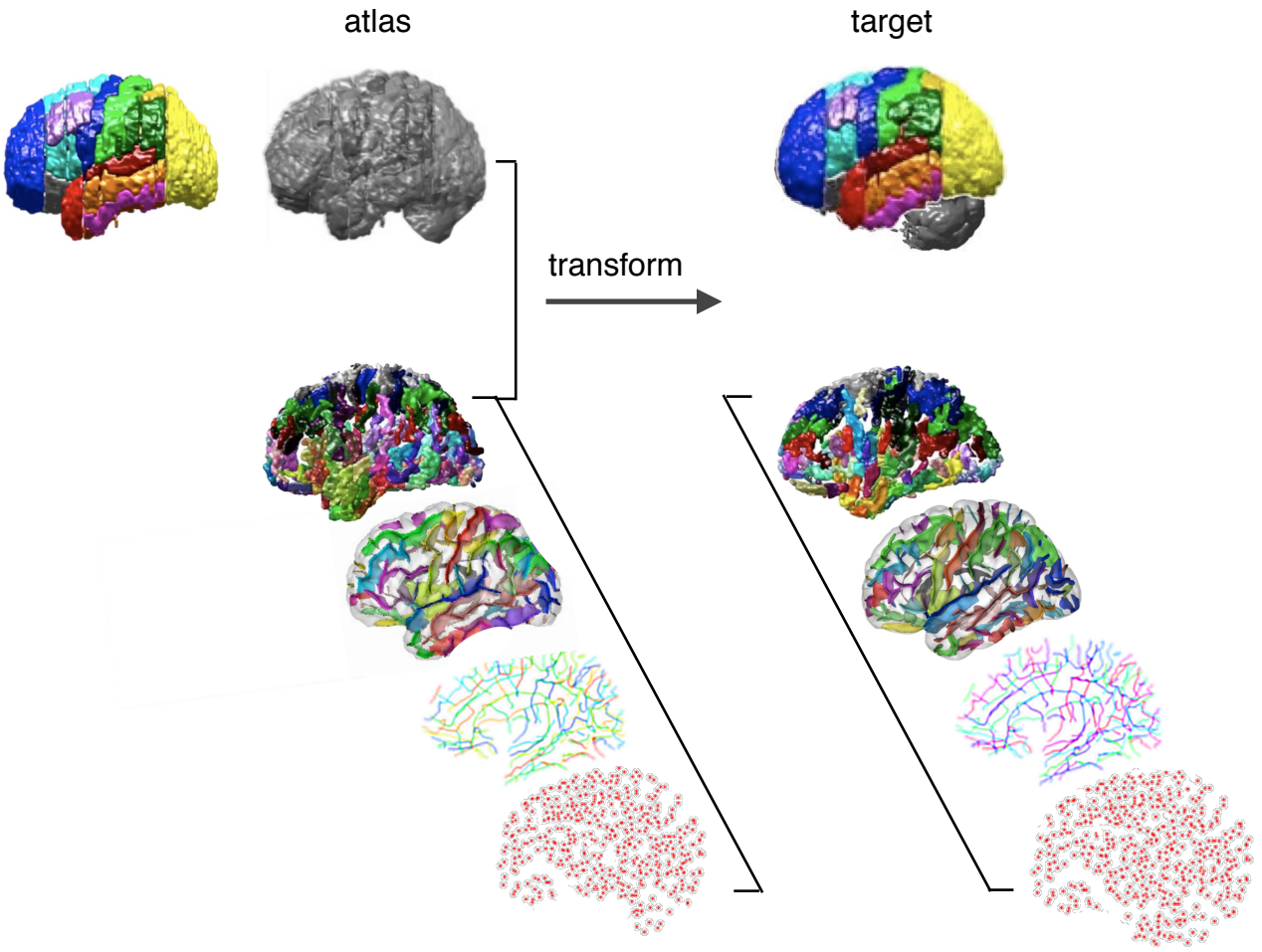
Mindboggle 2: feature-based labeling

Step 2: match atlas and target features



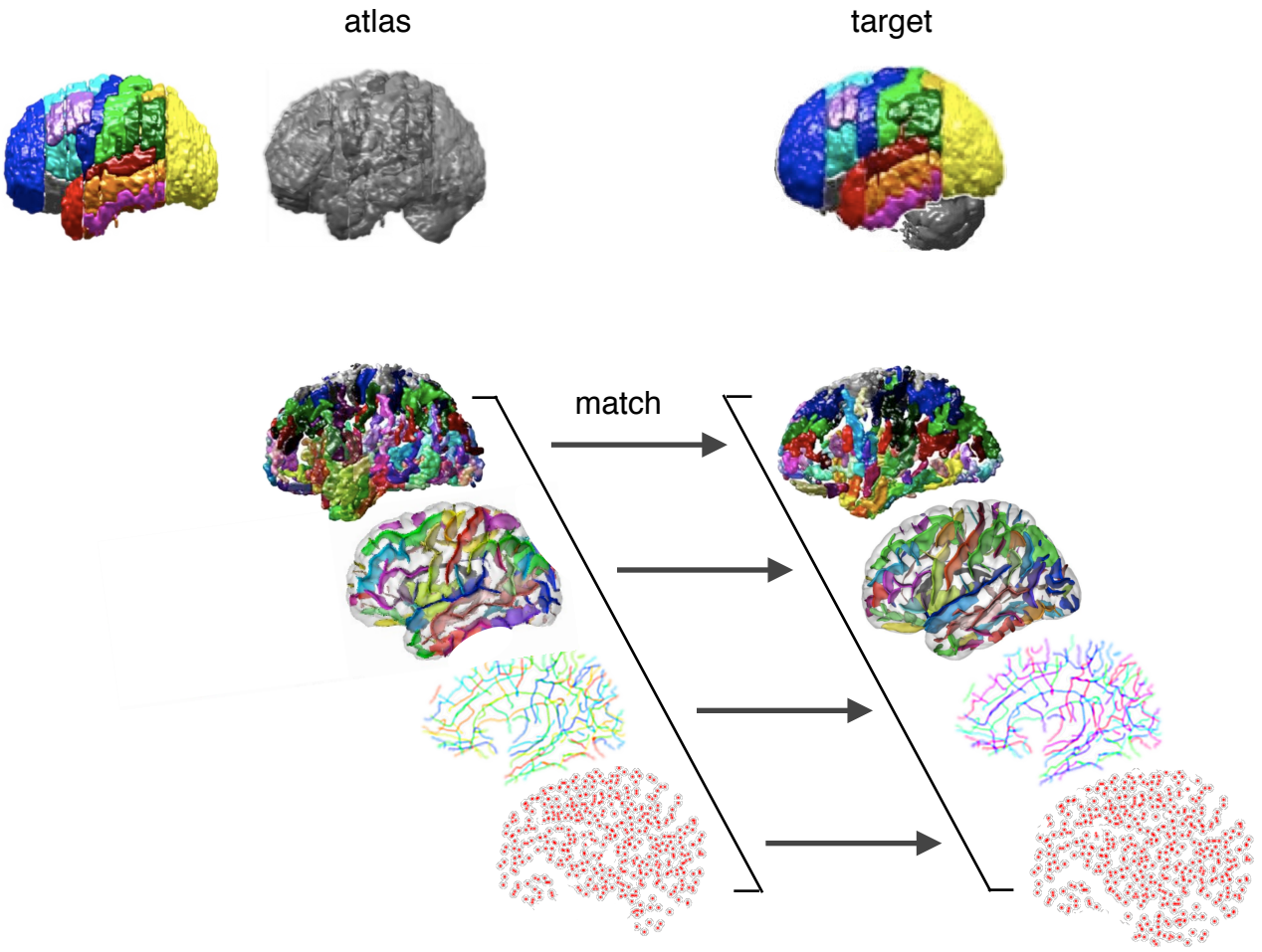
Mindboggle 2: feature-based labeling

Step 3: register atlas and target structures



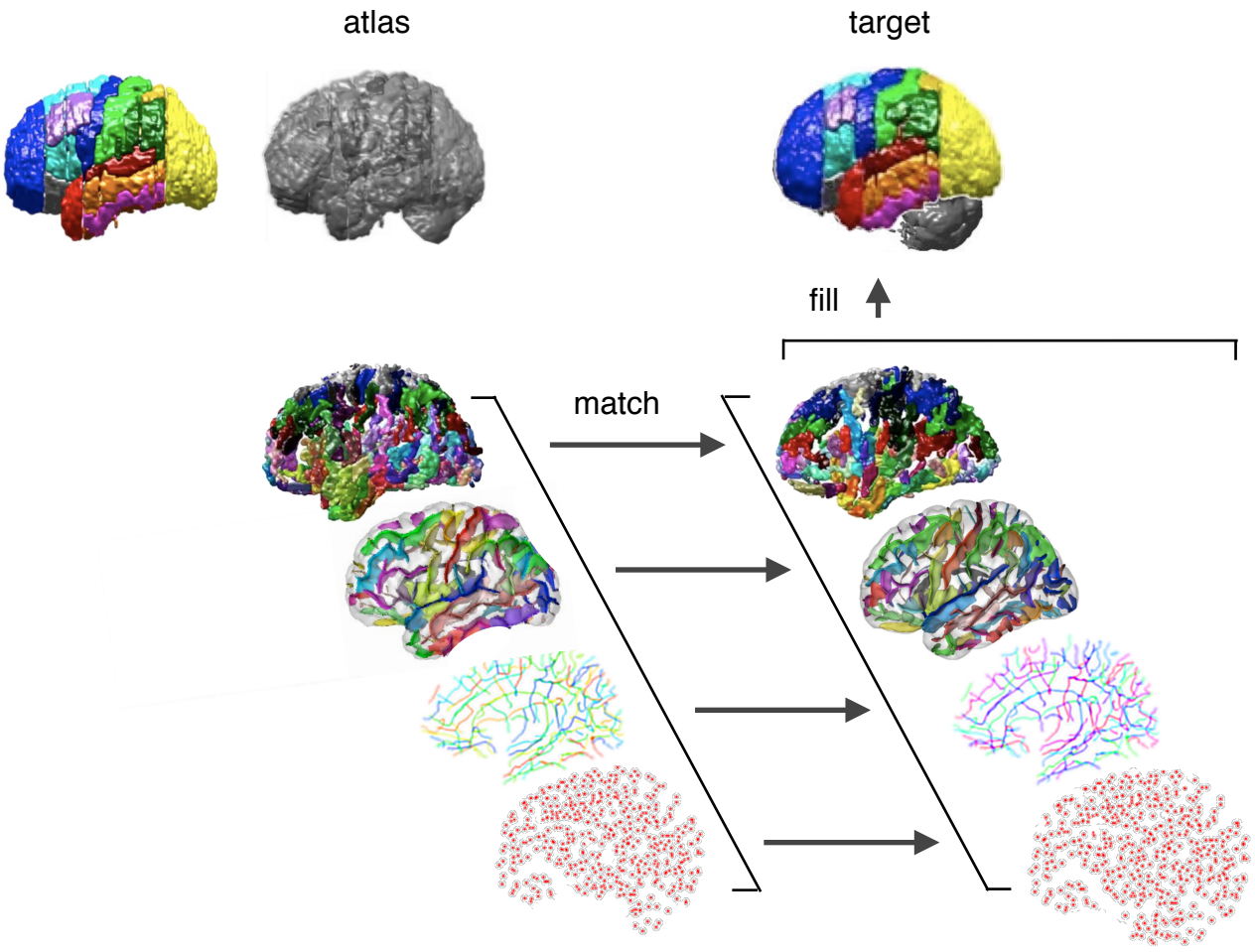
Mindboggle 2: feature-based labeling

Step 2: or match features...

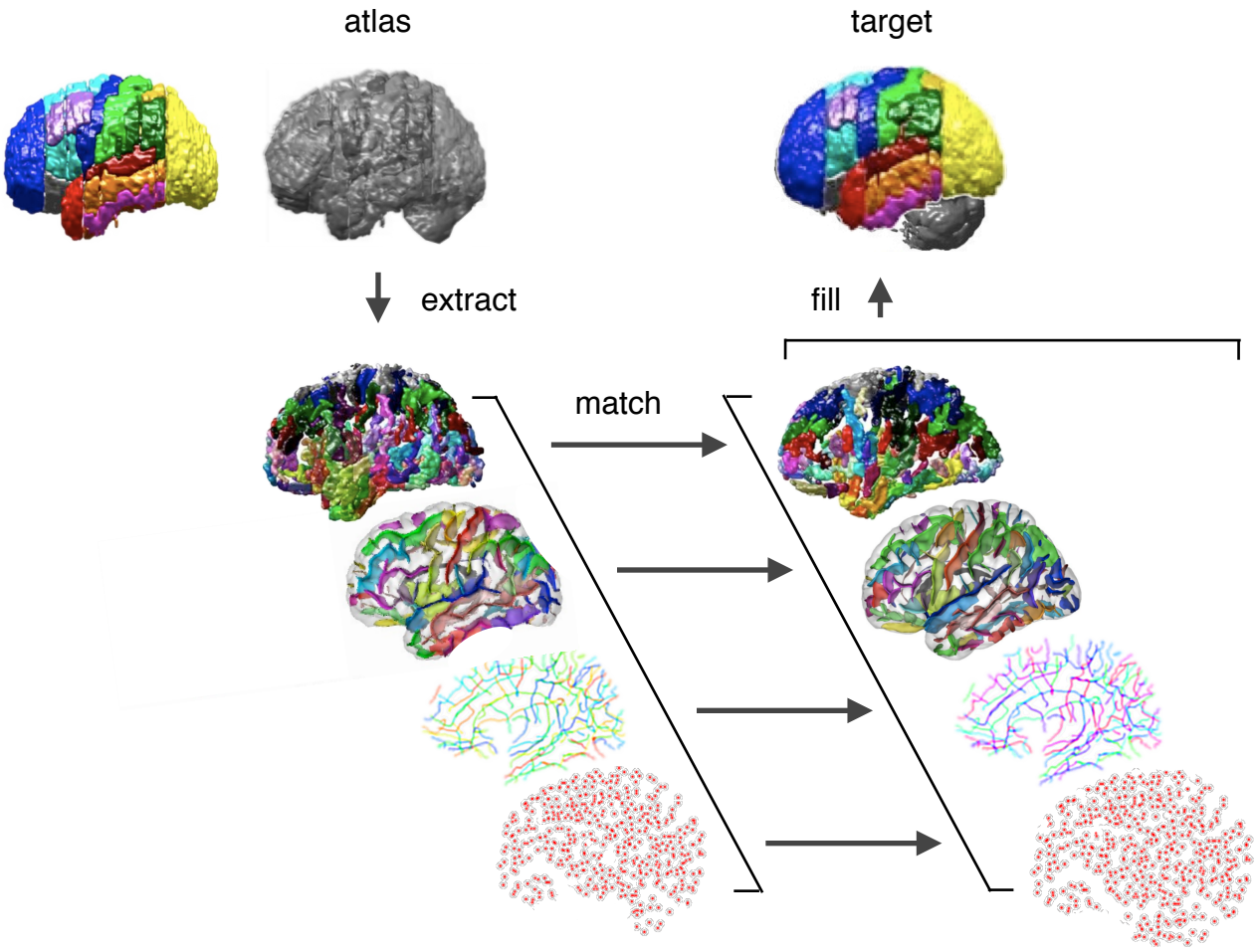


Mindboggle 2: feature-based labeling

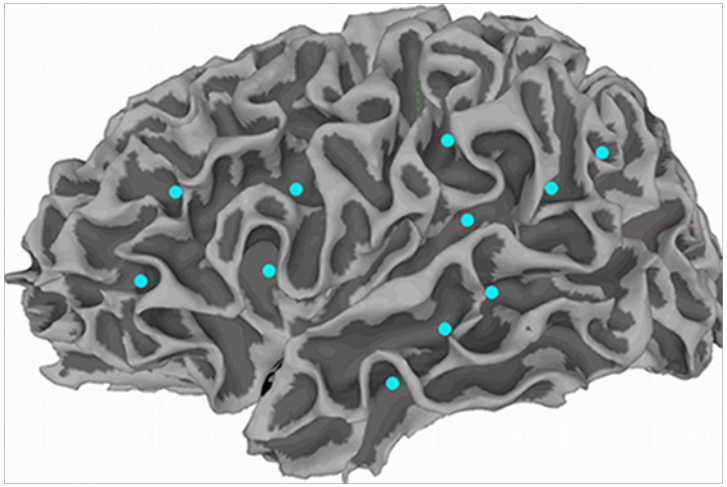
Step 3: then propagate labels within inferred label boundaries



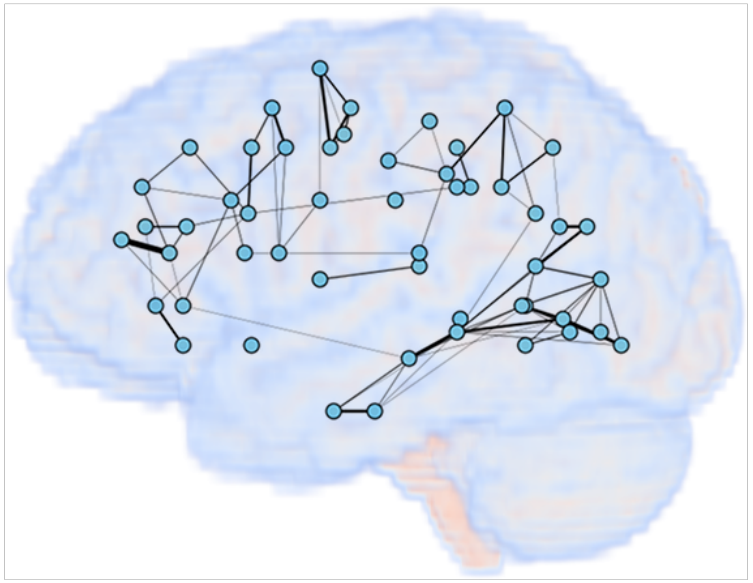
Mindboggle 2: feature extraction
feature matching
feature-based labeling



Combine structures across modalities

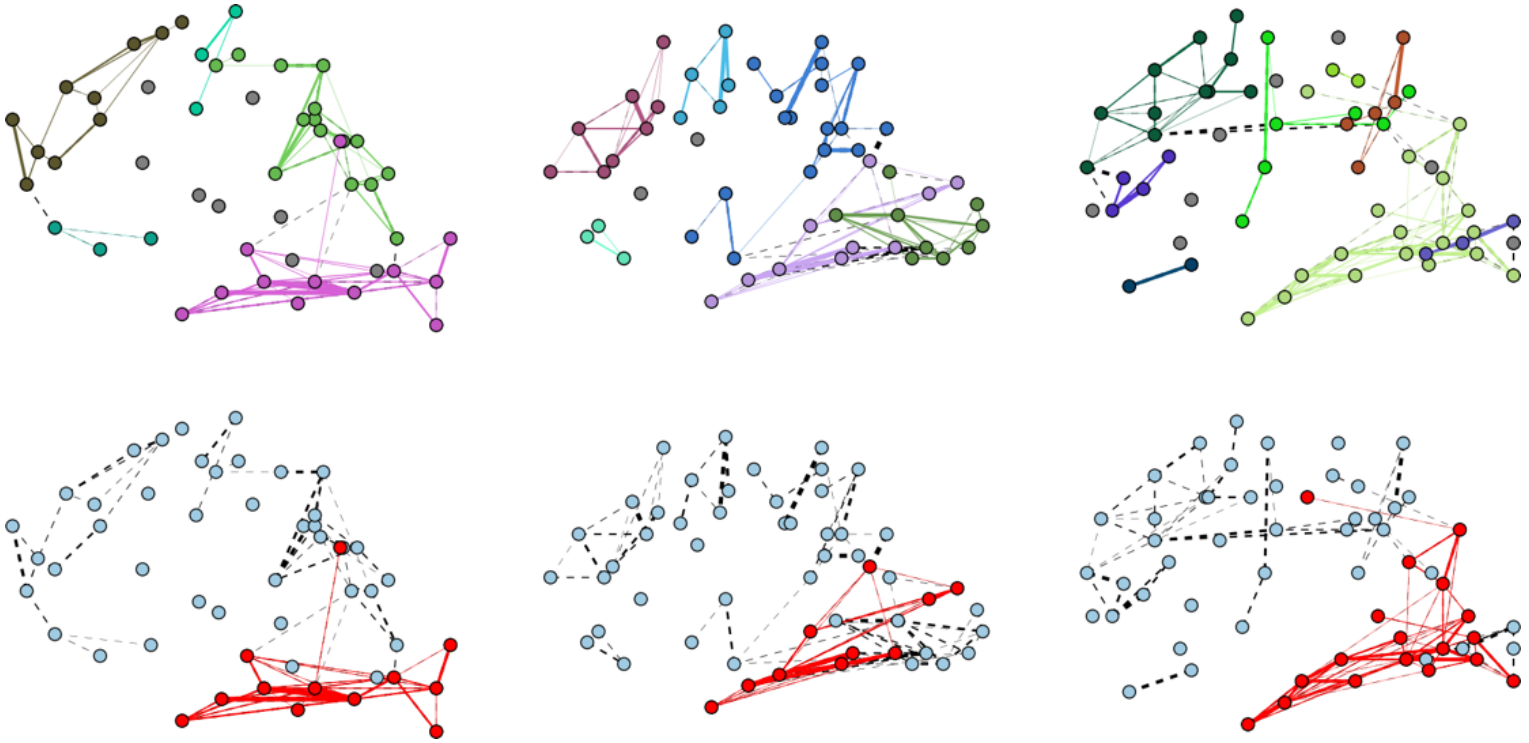


A gray/white matter surface (left lateral view) with visible sulcal pits highlighted (cyan circles). These features go by different names (sulcal roots, buried or annectant gyrii, plis de passage) and may be well conserved structures formed early in development.



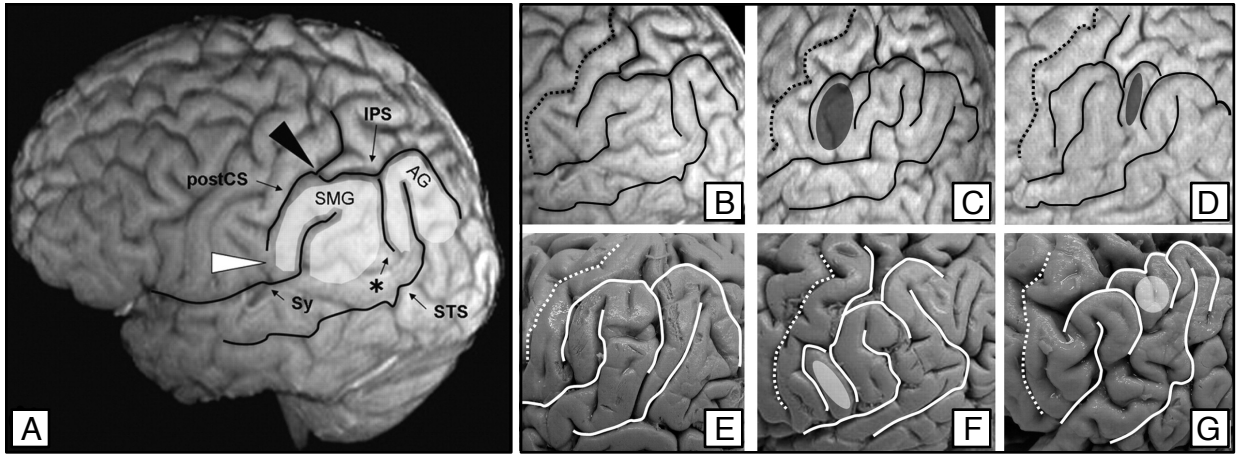
DTI connectivity graph (same subject). Vertices represent all extracted sulcal pits and each edge width indicates a connection probability greater than 0.01 between two vertices (and does not follow a tractography path).

Match “brain graphs”



Early attempt at subgraph extraction (upper row) and matching (lower row).
These graphs were constructed from (left to right) a remitter, non-remitter, and control subject.
The subgraphs in red in the lower row have the highest small-worldness ratio.

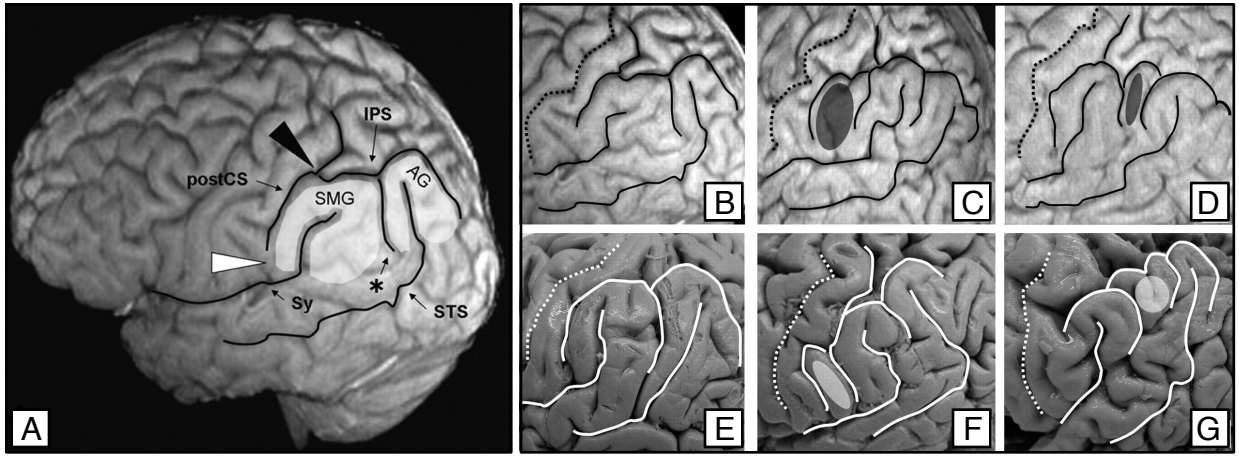
Characterize anatomical variability

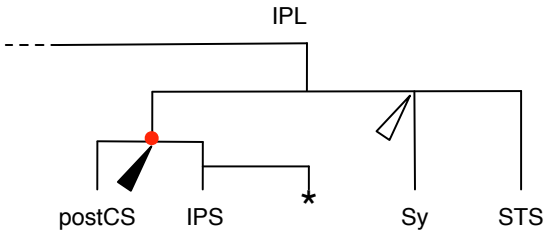


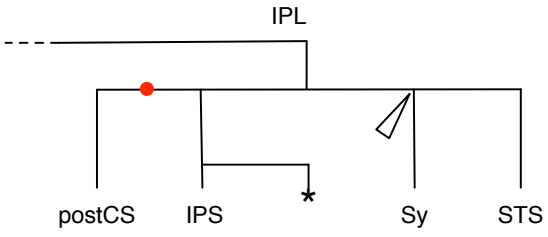
Example of natural morphological variability: left inferior parietal lobule (IPL; Kiriyama et al. 2009).
(A-D) are MRI data and (E-G) are post-mortem specimens.
(A) IPL is highlighted and folds are outlined.
(B,E) Typical folding pattern.
(C,F) PreSMG pattern: an additional gyrus (ellipse) lies between postCS and SMG.
(D,G) PreAG pattern: an additional gyrus (ellipse) lies between SMG and AG.

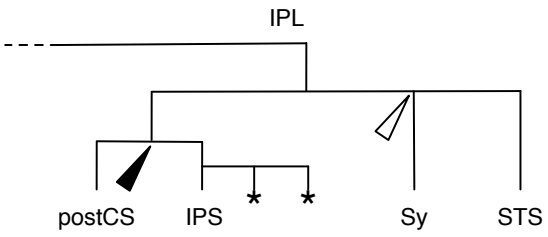
[SMG: supramarginal gyrus; AG: angular gyrus; postCS: postcentral sulcus; IPS: intraparietal sulcus;
Sy: Sylvian fissure, STS: superior temporal sulcus; *sulcus intermedius primus]

Convert one brain graph into another!









Noah Lee
Graph-based database architecture
Machine learning-based features

Forrest Bao
(Texas Tech)
Nested feature extraction

Denis Peruzzo
Graph matching
DTI tractography

Ray Razlighi
SIFT algorithm evaluation

Satrajit Ghosh (MIT)
Machine learning,
NiPype software pipeline

Brian Avants (UPenn)
Diffeomorphic registration