

Freesurfer and alternative solutions

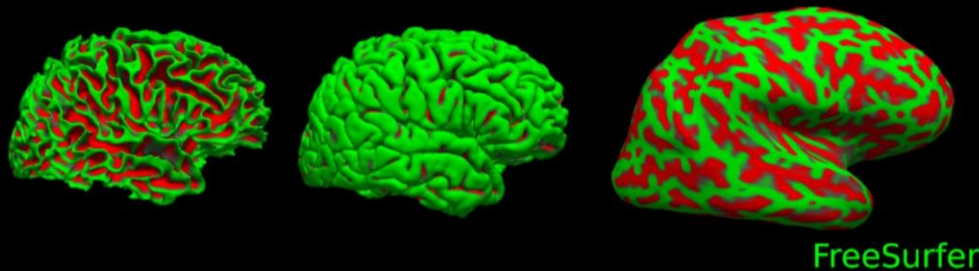
Guillaume Auzias

2022-11

Brainhack Marseille

Online videos, tutorials and courses

- <https://surfer.nmr.mgh.harvard.edu>
- <https://www.youtube.com/channel/UCruQerP8aa-gYttXkAcyveA>



FreeSurfer Wiki



FreeSurfer

@freesurfer7634
2,88 k abonnés

S'abonner

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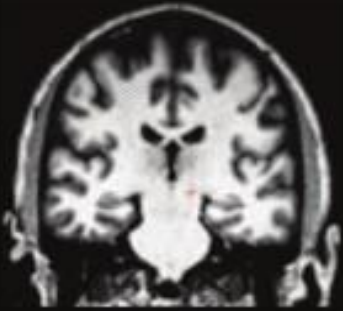


FreeSurfer Essentials ▶ Tout lire

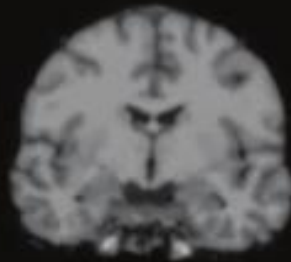


- <https://andysbrainbook.readthedocs.io/en/latest/index.html>

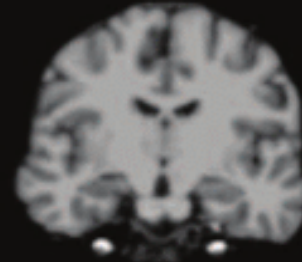
Recon-all pipeline for processing anatomical data



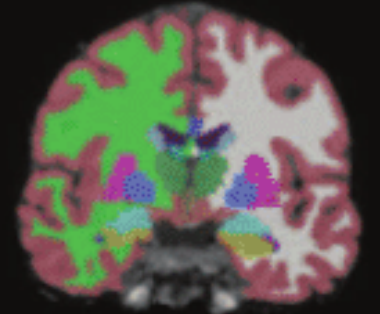
1. T1 Weighted
Input



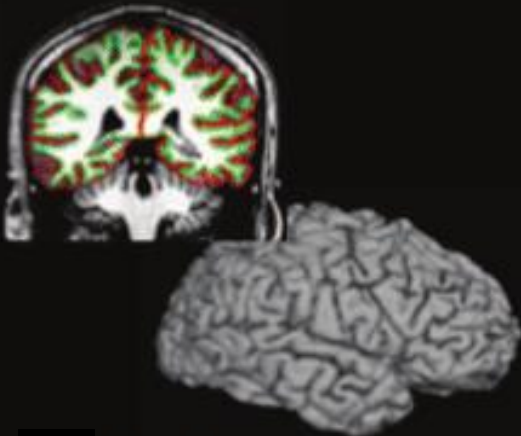
2. Skull Stripping



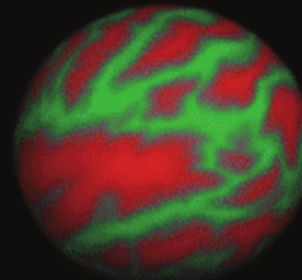
3. Intensity
Normalization



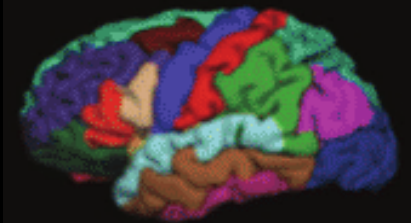
4. Segmentation



5. Surface Extraction

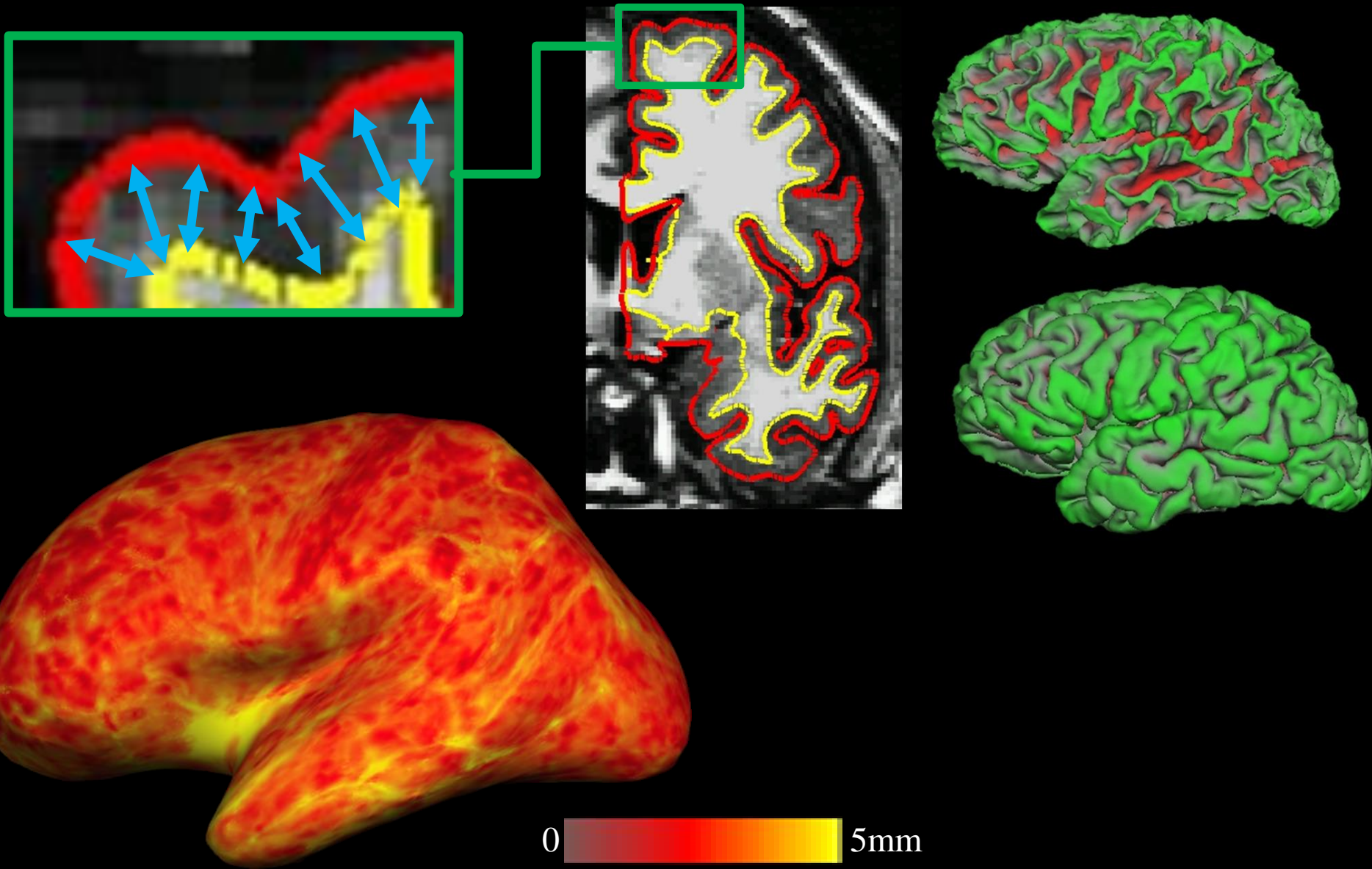


6. Surface Atlas
Registration

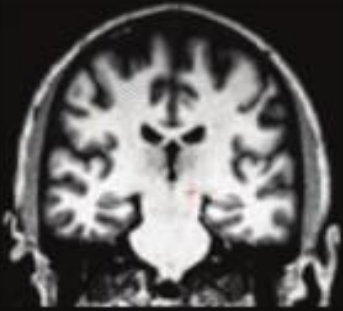


7. Gyrus Labeling

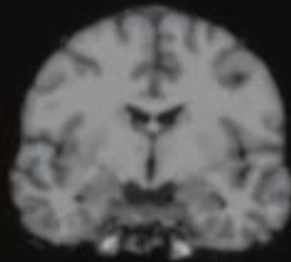
Surface extraction → cortical thickness



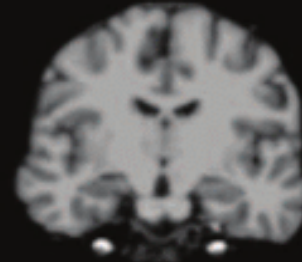
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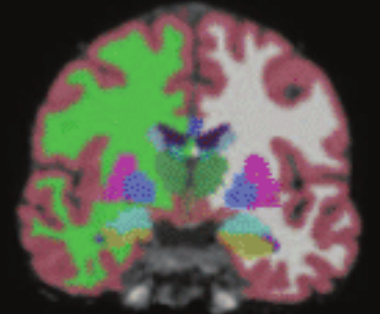
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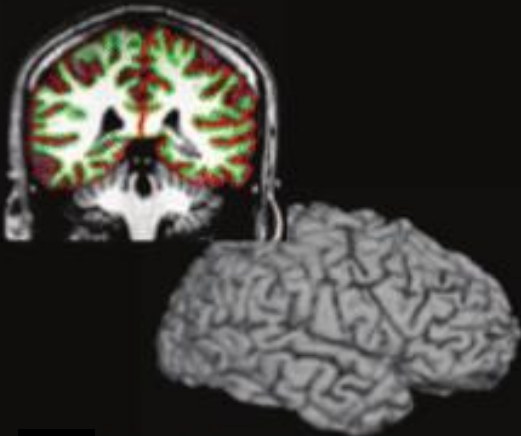
2. Skull Stripping



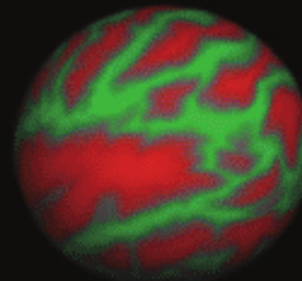
3. Intensity
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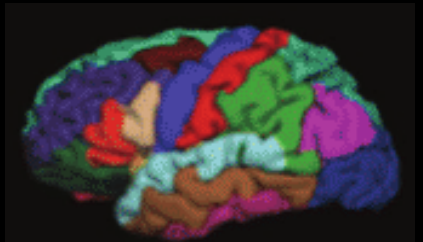
4. Segmentation



5. Surface Extraction

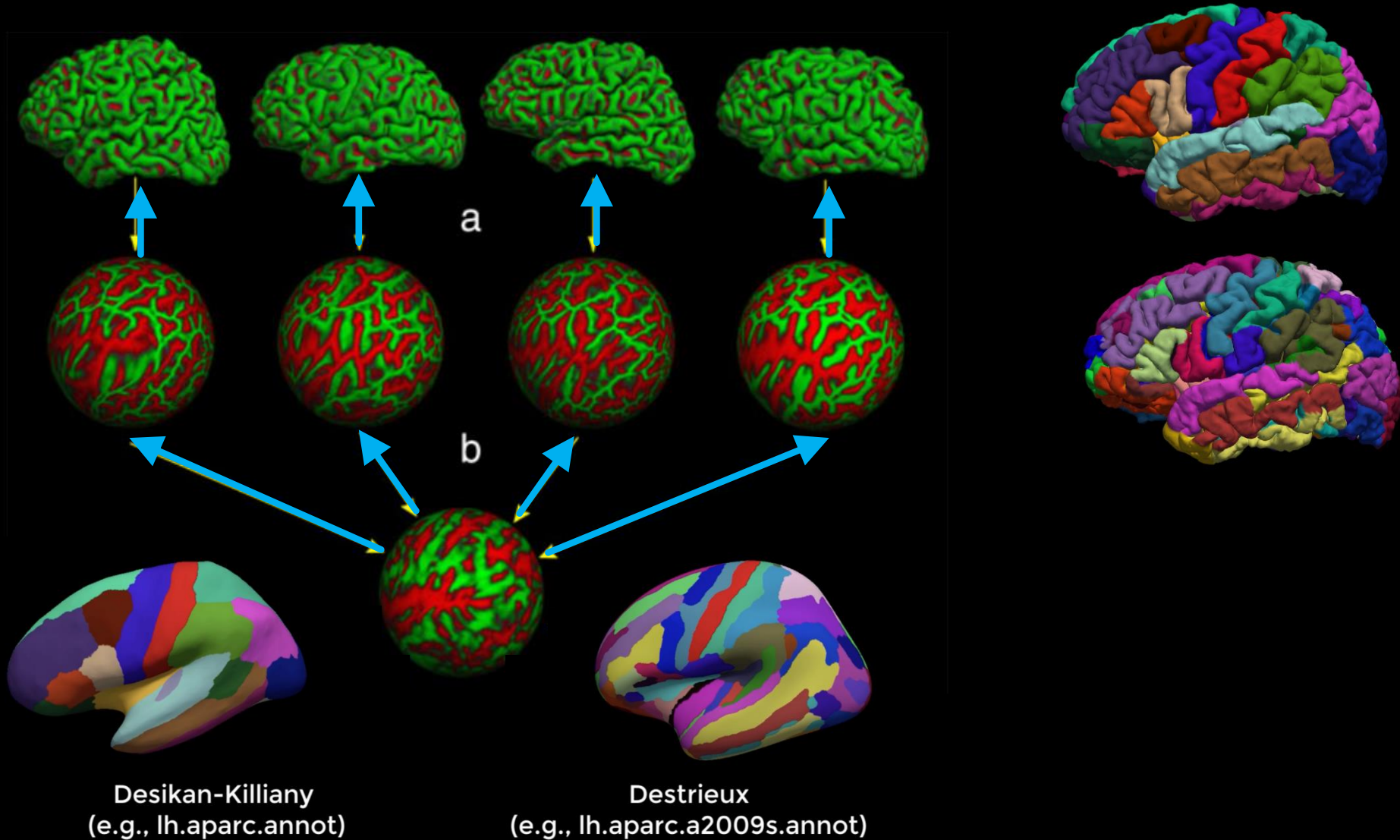


6. Surface Atlas
Registration

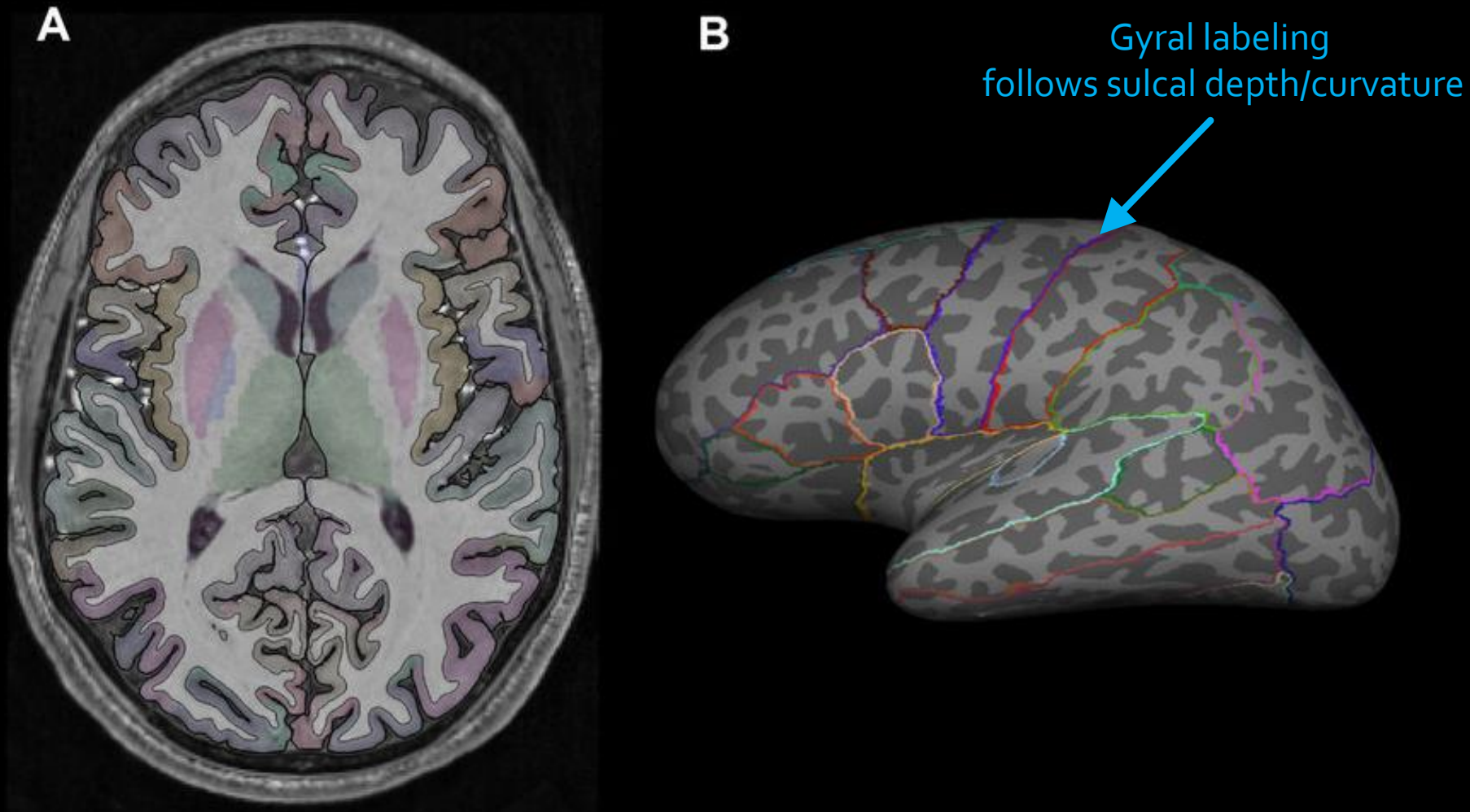


7. Gyrus Labeling

Gyral labeling via surface registration



High accuracy for high quality input MRI



Zaretskaya, N. et al. (2017). Advantages of cortical surface reconstruction using [submillimeter 7T MEMPRAGE](https://doi.org/10.1016/j.neuroimage.2017.09.060). NeuroImage. 165. 10.1016/j.neuroimage.2017.09.060.

Freeview

The Freeview software interface displays a 3D brain model with segmented regions. The left panel contains controls for file management, rendering, and segmentation. The main window shows a 3D view of the brain with segmented regions. The bottom panel displays coordinate information for the cursor and mouse.

Control Panel (Left):

- Volumes:** ☒ aseg, ☒ orig
- Surfaces:** ☒ lh.pial
- File name:** rfer/subjects/bert/surf/lh.pial
- Opacity:** 1.00
- Color:** Solid Color
- Render:** Surface
- ☐ Show vertices
- Curvature:** Threshold
- Mid point:** 0
- Slope:** 10
- Overlay:** Off
- Annotation:** Off
- Label:** Load, Delete
- Edge color:** (highlighted in red)
- Edge thickness:** 2
- Vector display:** Off

3D View (Main Window):

The 3D view shows a brain model with segmented regions. The regions are color-coded: red for the left hemisphere, yellow for the right hemisphere, and green for the brain surface. The background is black. The view is centered on the brain, with a red box highlighting the brain surface.

Coordinate Information (Bottom Panel):

Cursor	Mouse
RAS	RAS
TkReg...aseg	TkReg...aseg
Talair...(aseg)	Talair...(aseg)
aseg	aseg
orig	orig
lh.pial	lh.pial
Vertex	Vertex

Alternative solutions

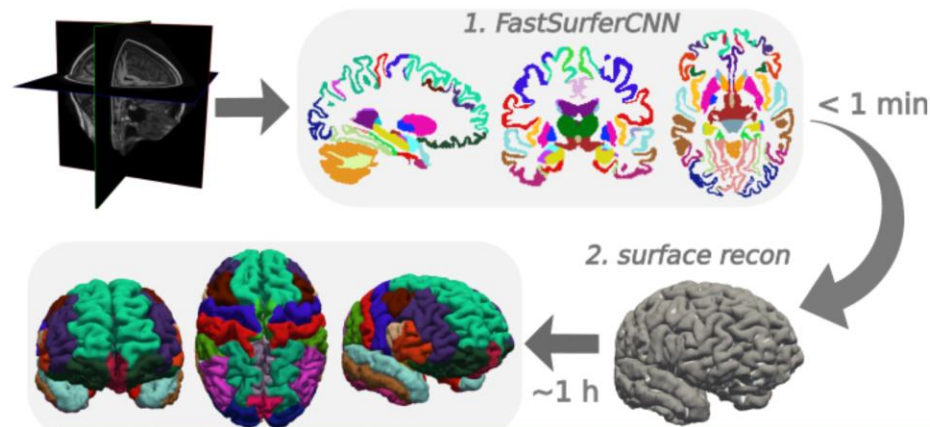
- <https://deep-mi.org/research/fastsurfer/>

FastSurfer - a fast and accurate deep-learning based neuroimaging pipeline

FastSurfer is a fast and [extensively validated](#) deep-learning pipeline for the fully automated processing of structural human brain MRIs. As such, it provides FreeSurfer conform outputs, enables scalable big-data analysis and time-critical clinical applications such as structure localization during image acquisition or extraction of quantitative measures.

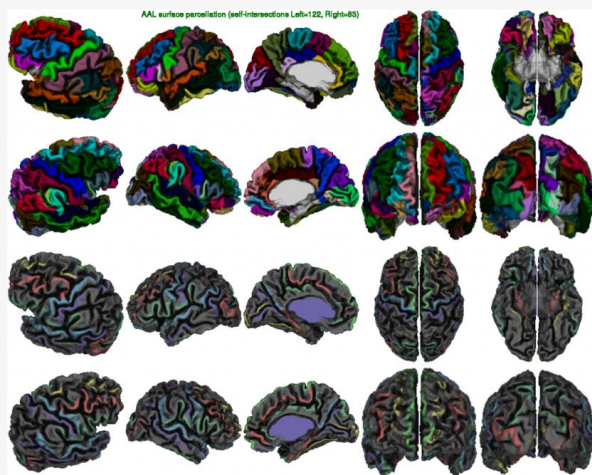
FastSurfer consists of two main parts building upon each other:

1. [FastSurferCNN](#) - an advanced deep learning architecture capable of whole brain segmentation into 95 classes in under 1 minute, mimicking FreeSurfer's anatomical segmentation and cortical parcellation (DKTatlas)
2. [recon-surf](#) - full FreeSurfer alternative for cortical surface reconstruction, mapping of cortical labels and traditional point-wise and ROI thickness analysis in approximately 60 minutes (+ optionally 30 min for group registration).



Alternative solutions

- <https://mcin.ca/technology/civet/>



AAL Surface Paracellation

Technical Features of CIVET


CIVET is implemented with high-level scripts, primarily using the common scripting language Perl, that runs computationally efficient image processing tools mainly implemented in C/C++. CIVET extends the previous in-house pipelines by the addition of corticometry analysis tools.

CIVET analysis includes our in-house morphometric analysis tools for:

- Linear and nonlinear brain registration
- Classification
- Partial volume correction
- NonUniformity correction (N3)
- Brain surface extraction (CLASP)
- Surface registration
- Cortical folding

Alternative solutions

- <http://brainsuite.org/>

 BrainSuite

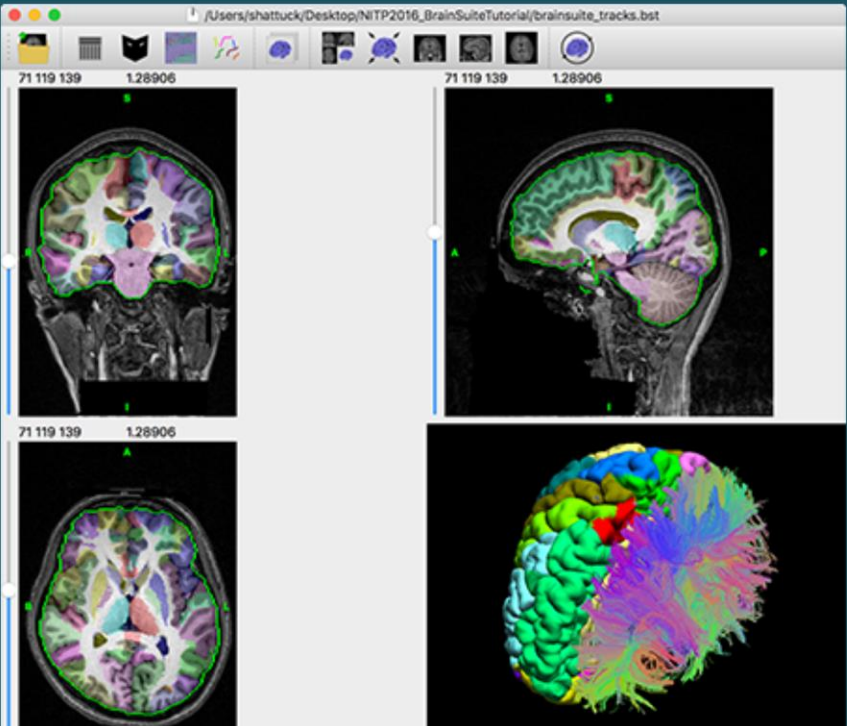
BrainSuite Homepage Download Forums Support

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BrainSuite21a now available


The latest version of BrainSuite (v.21a) is available for download.
This release features:

- GUI for Windows, Mac OSX, and Linux platforms
- **USCBrain Atlas** — A Hybrid High-Resolution Anatomical MRI Atlas with Subparcellation of Cortical Gyri using Resting fMRI — now included in the distribution
- New rewind feature for each stage of the BrainSuite anatomical (T1-weighted) pipeline
- Automated skull-stripping parameter tuning
- Command line tools for performing cortical surface extraction, surface/volume registration, and processing of diffusion weighted images

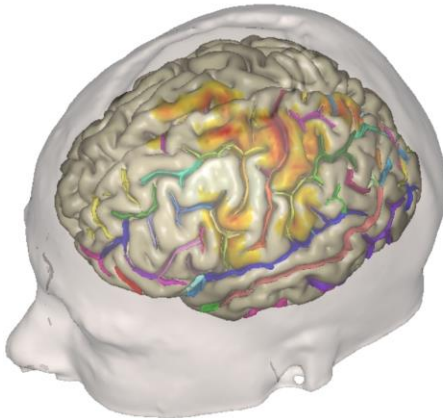


Alternative solutions

- <https://brainvisa.info/web/>
Emphasis on **sulcal anatomy**





Home Neuroimaging tools **Download** News Documentation ▾ Publications Support



BrainVISA
Anatomist
Neuroimaging software platform for mass data analysis

How to use

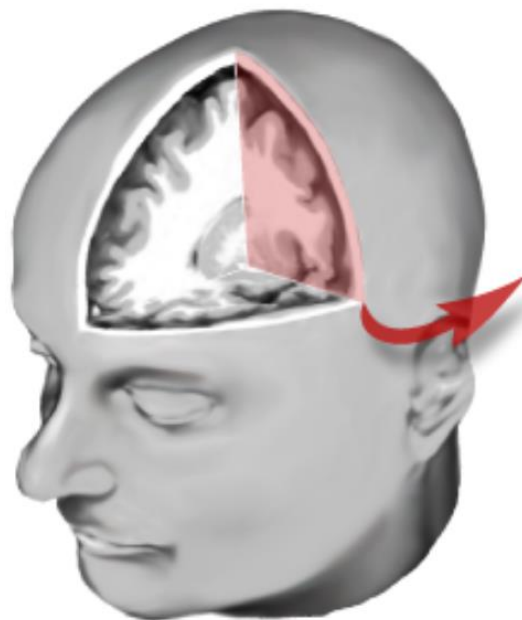
 Download

 Support

- Morphologist: brain segmentation and sulcal morphometry
- Processing tools and toolboxes
- Interactive 3D neuroimaging data visualization
- Software and data organization

BrainVISA 5.0.4 is available

- <https://neuro-jena.github.io/cat12-help/>
- https://andysbrainbook.readthedocs.io/en/latest/CAT12/CAT12_Overview.html#what-is-voxel-based-morphometry



coronal slice of the left hemisphere

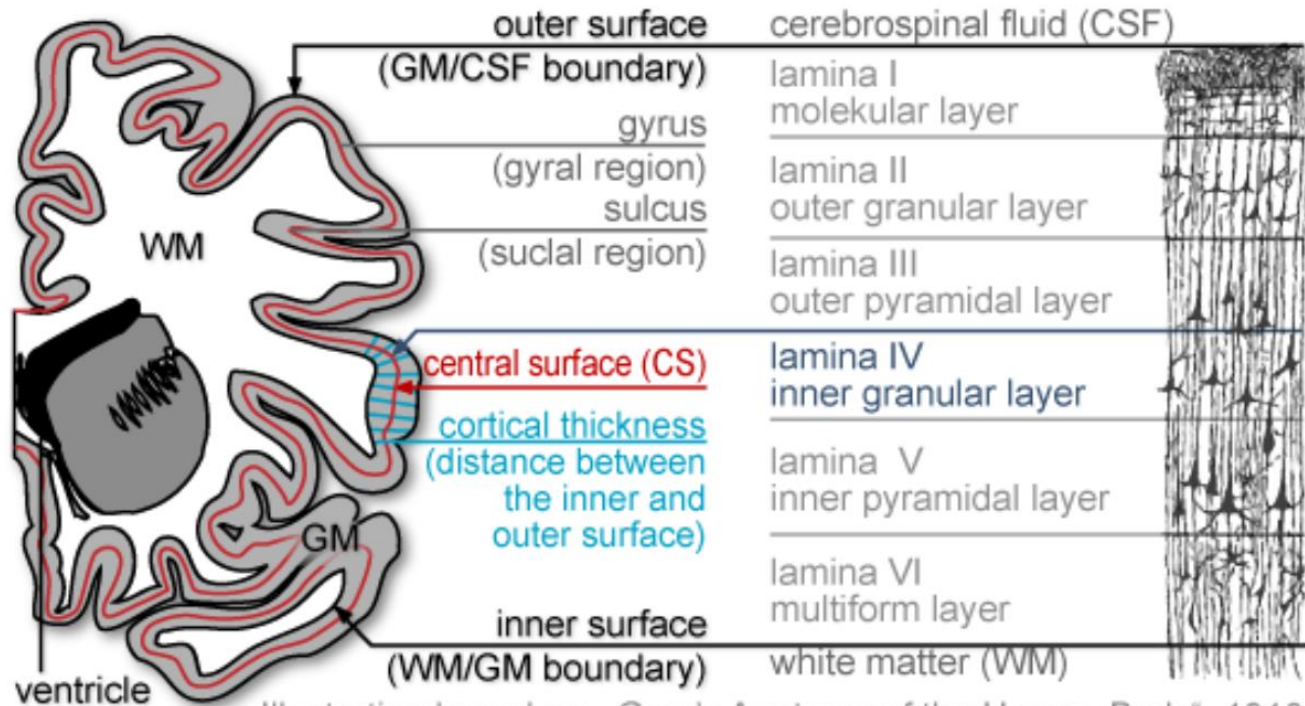


Illustration based on „Gray's Anatomy of the Human Body“, 1918

HCP workbench

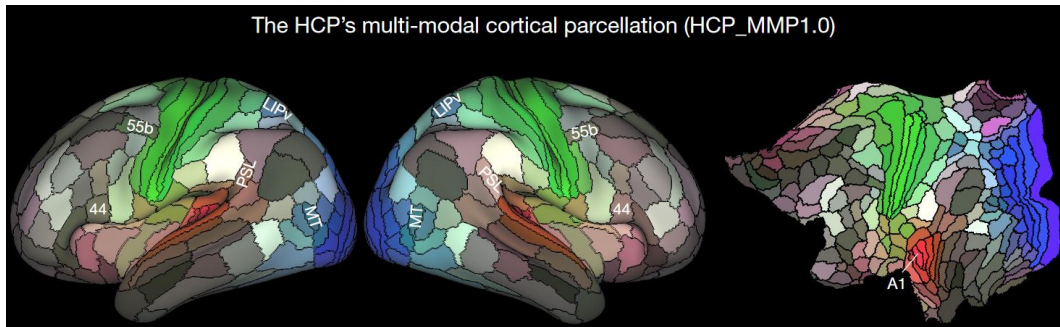
- <https://humanconnectome.org/software/connectome-workbench>

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Using Connectome Workbench

Connectome Workbench is an open source, freely available visualization and discovery tool used to map neuroimaging data, especially data generated by the Human Connectome Project. The distribution includes `wb_view`, a GUI-based visualization platform, and `wb_command`, a command-line program for performing a variety of algorithmic tasks using volume, surface, and grayordinate data. `wb_command` is necessary for running HCP data processing pipelines.

The HCP's multi-modal cortical parcellation (HCP_MMP1.0)



Glasser et al., Nature, 2016

Connectome Tools

- [ConnectomeDB](#)
- [Connectome Workbench](#)
- [Workbench Command](#)
- [HCP MR Pipelines Reference](#)
- [HCP MEG Pipelines Reference](#)
- [FSL](#)
- [FreeSurfer](#)
- [Brain Connectivity Toolbox](#)
- [Fieldtrip](#)