

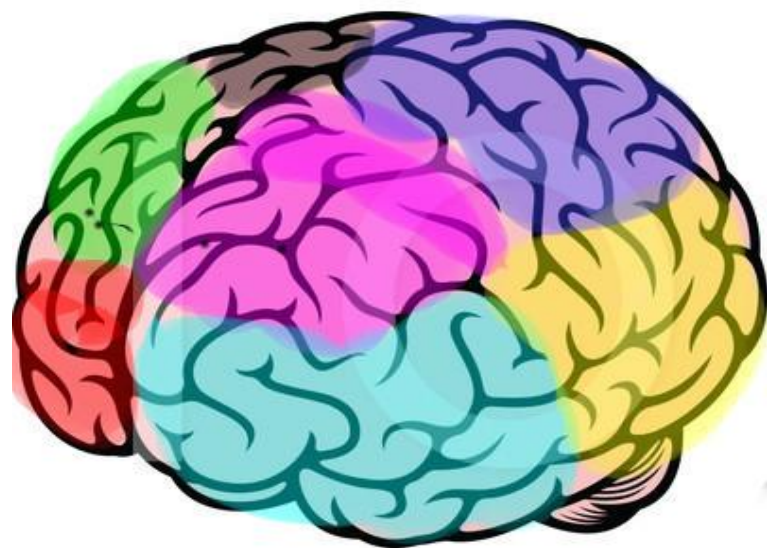
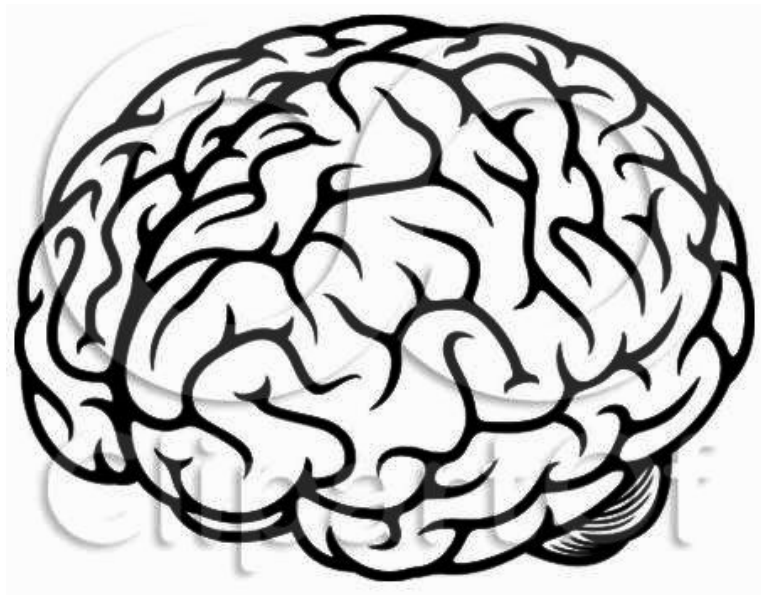
# MRI based brain parcellation

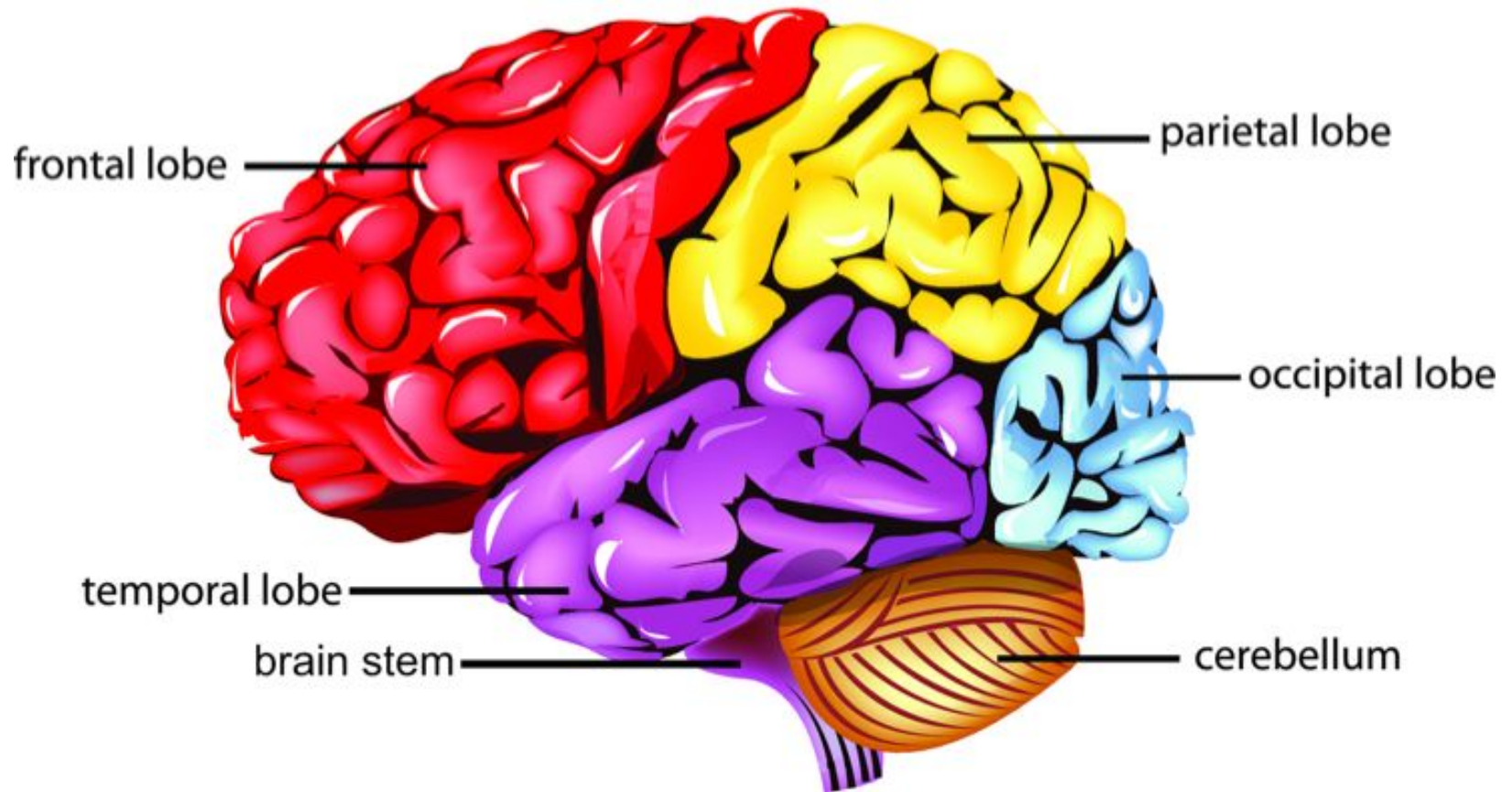
Kurmukov Anvar, 2020

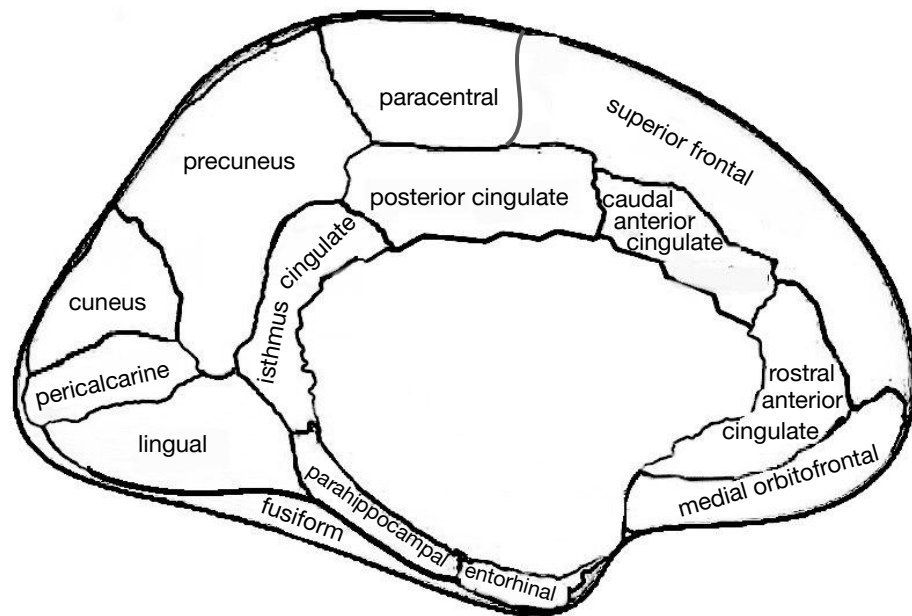
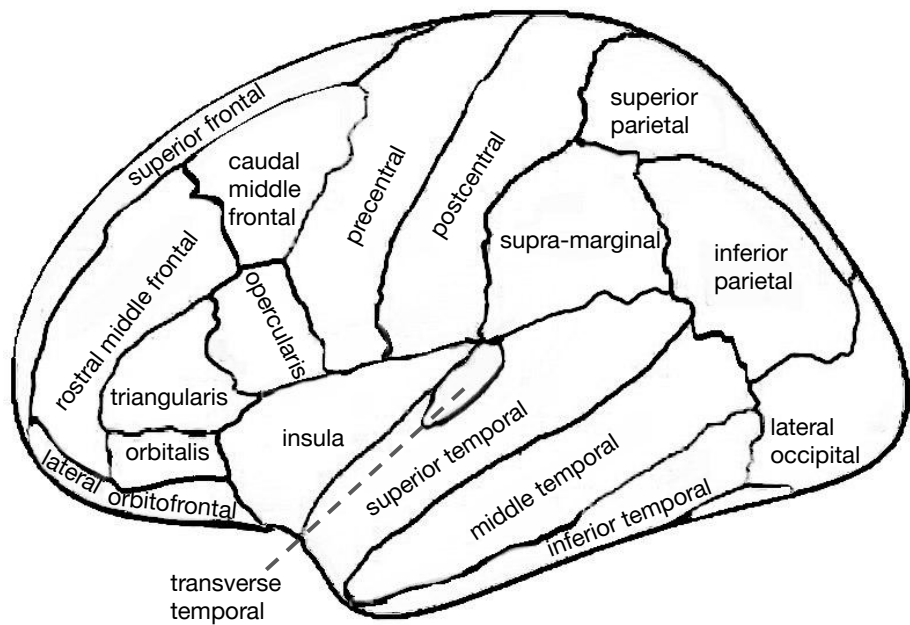
1. What is brain  
parcellation?

In computational neuroimaging, brain parcellation methods subdivide the brain into individual regions <...> to study its **structure and function.**

[Brain parcellation based on information theory](#)



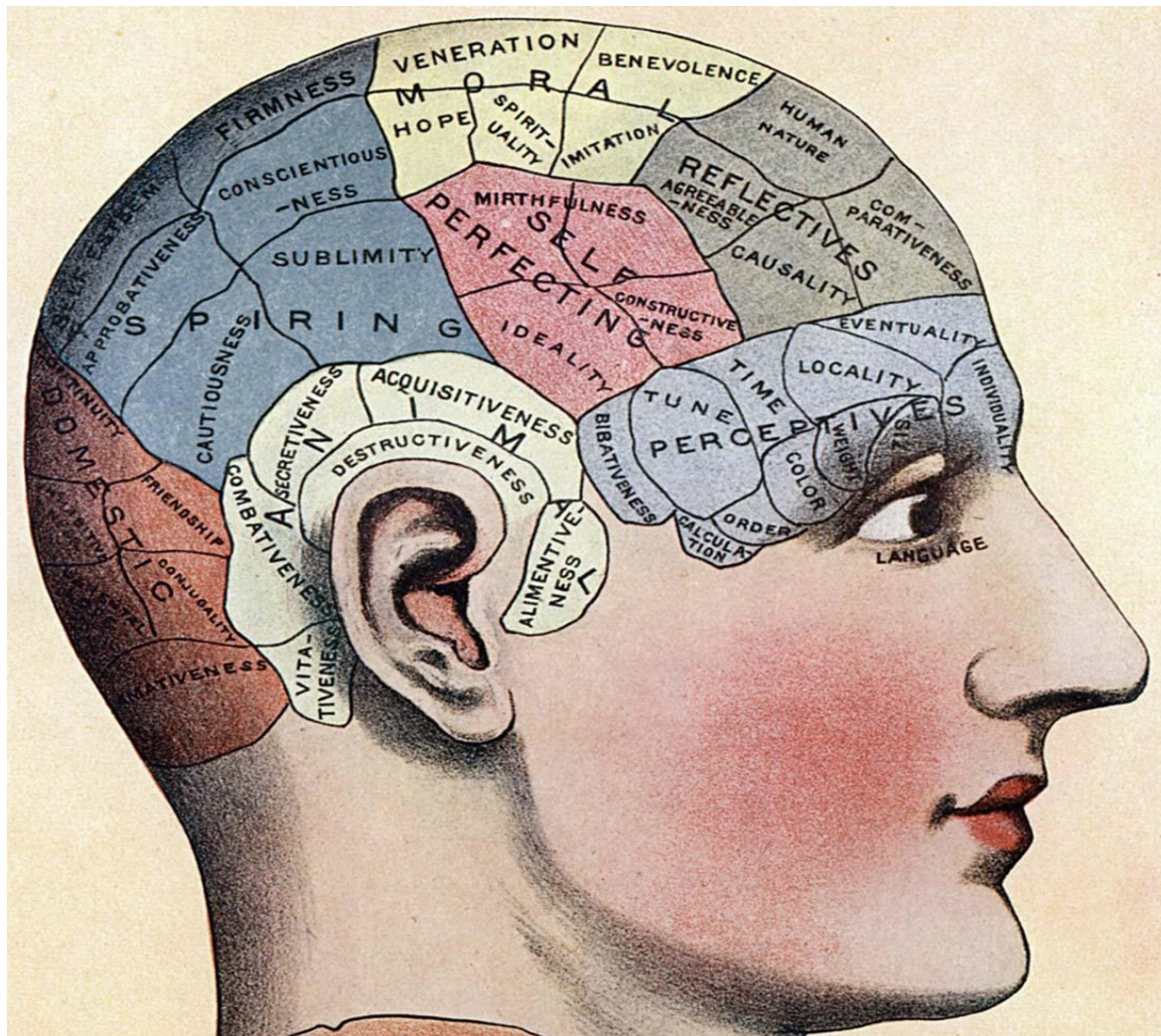




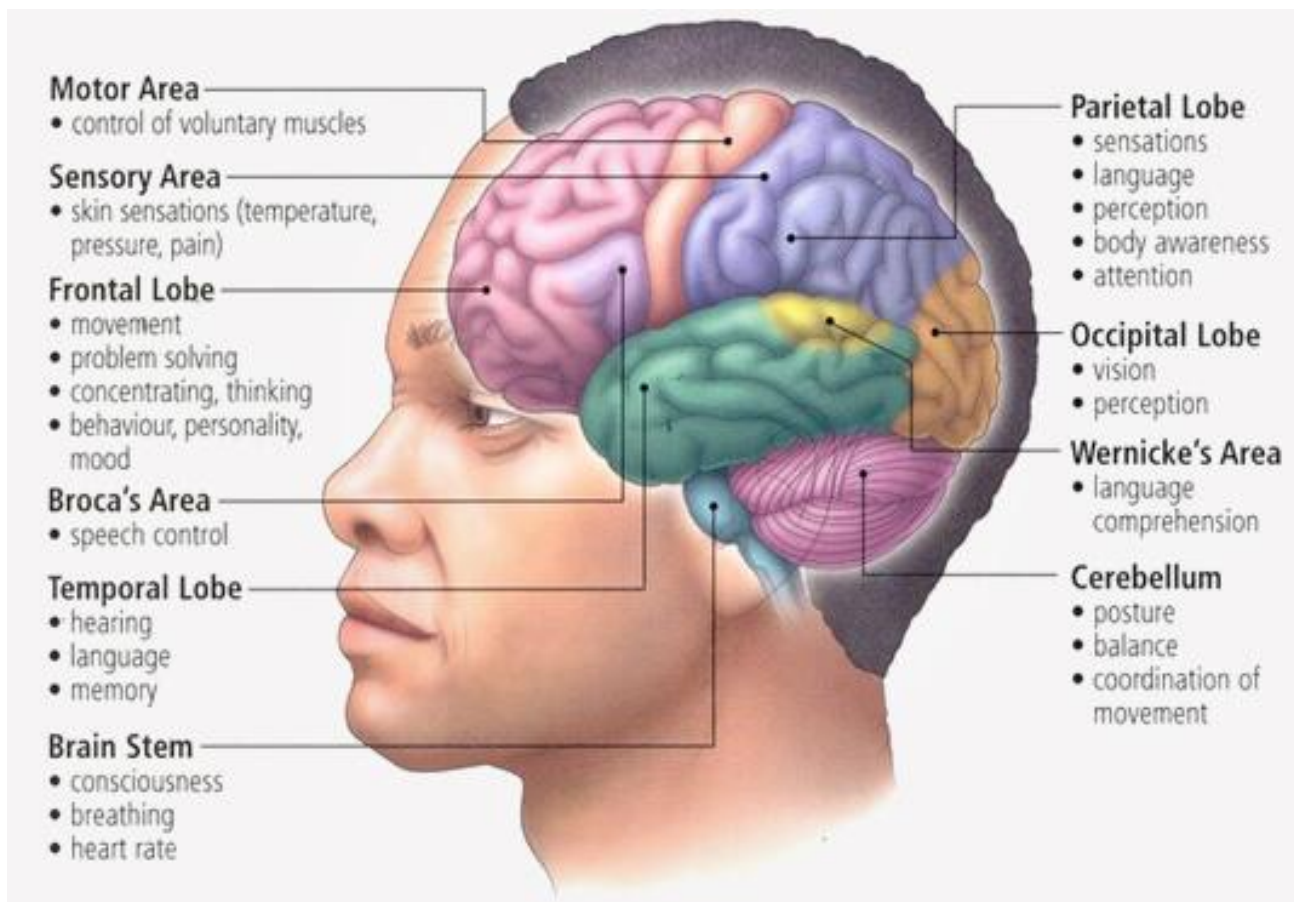
2. Why do we need  
parcellations?

1. Because brain structure is somehow related to its function.
2. Because typical MRI consists of  $\sim 10^5$  up to  $\sim 10^7$  voxels and typical study has  $\sim 10^1$  up to  $\sim 10^3$  observations (dimensionality reduction).
3. Because in multimodal studies we need to have 1 to 1 correspondence between different modalities.
4. Because in population studies we need to have 1 to 1 correspondence between subjects.
5. To build connectomes;)

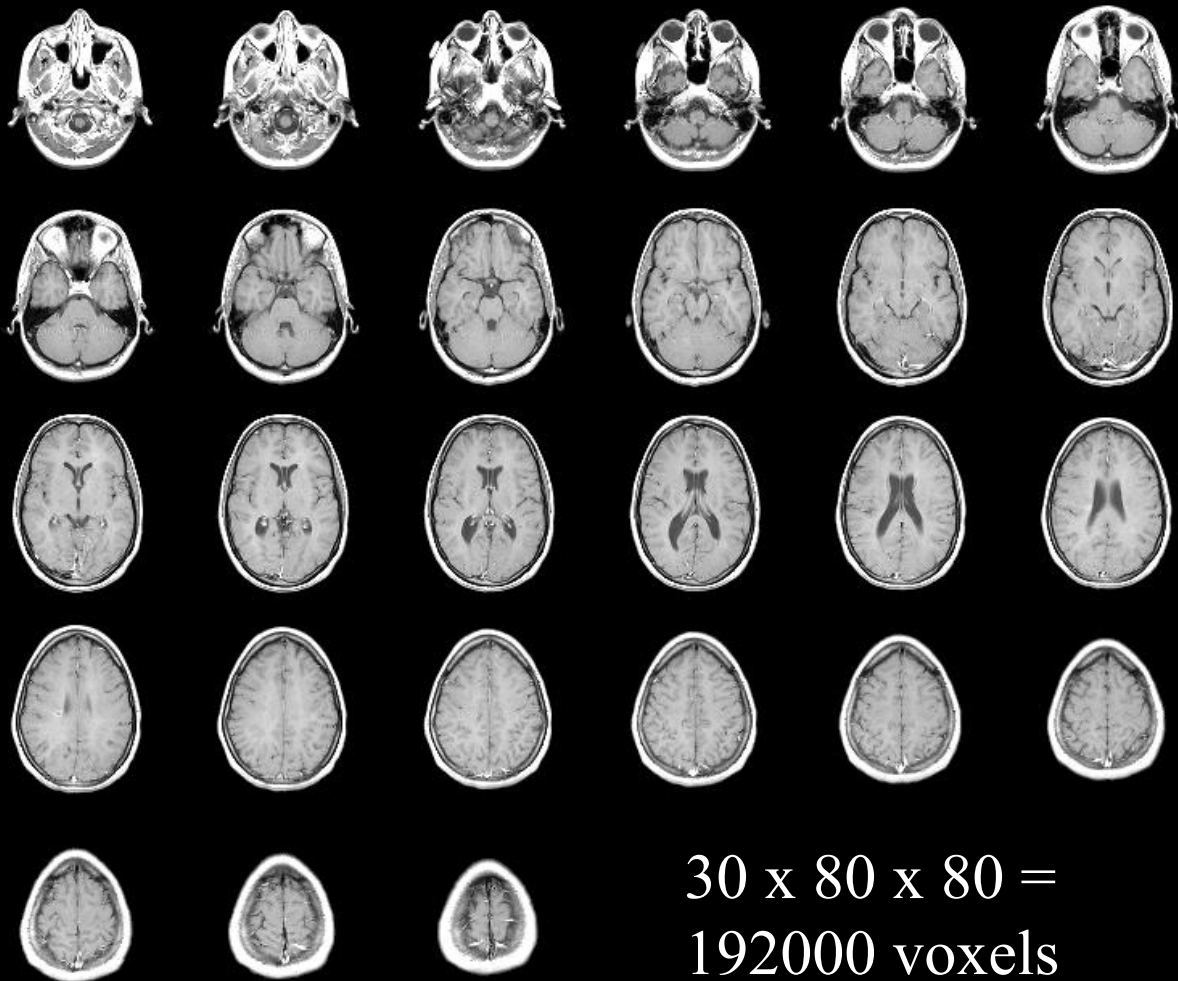




Phrenology  
(pseudoscience)

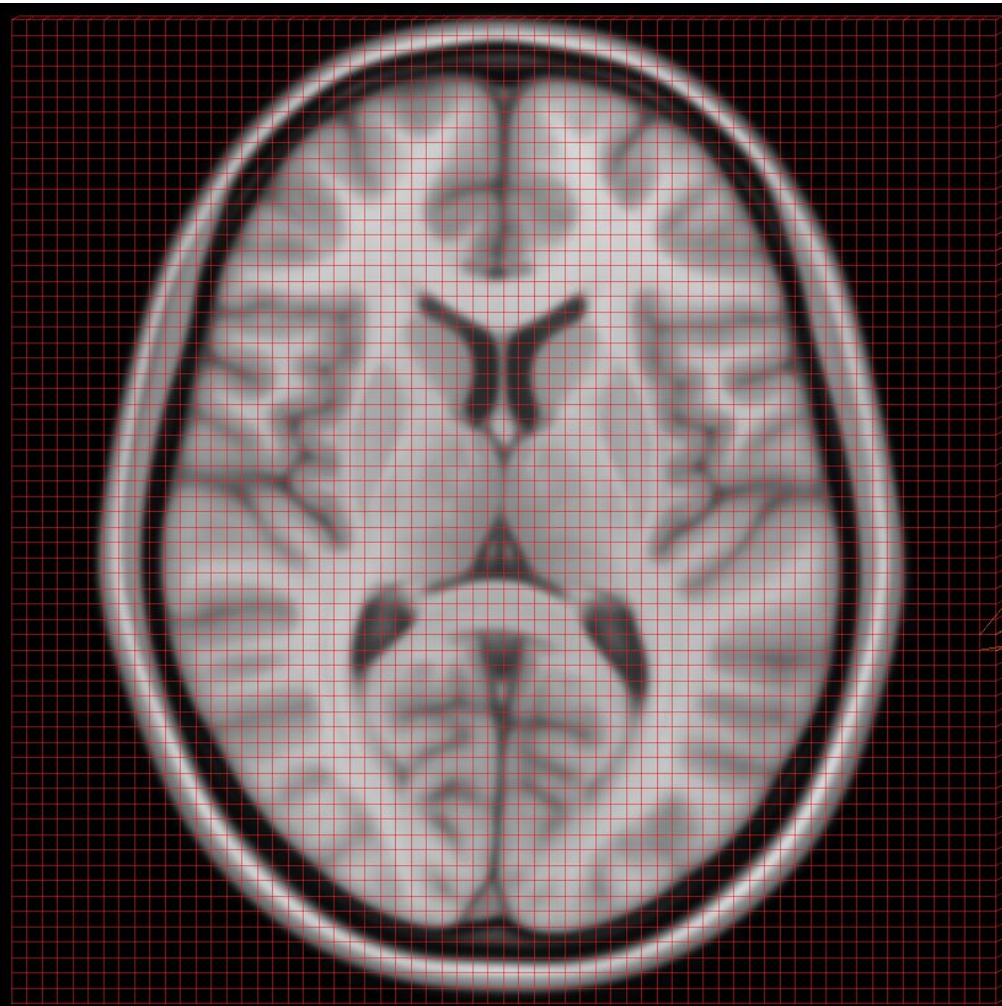


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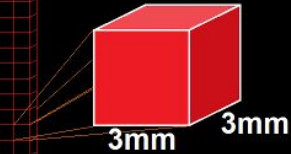
$30 \times 80 \times 80 =$   
192000 voxels





**Matrix size of slice:**  
64 x 64

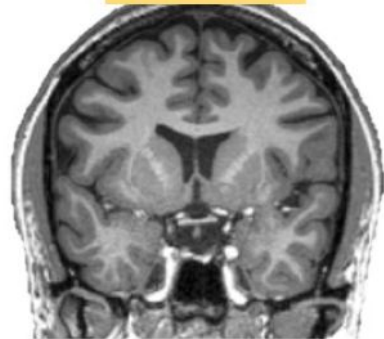
**Voxel size:**  
3mm x 3mm x 3mm



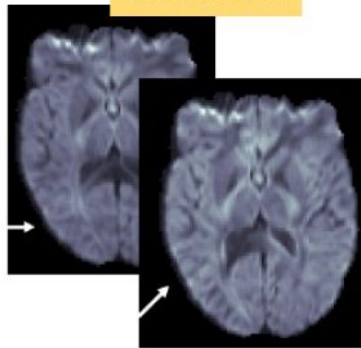
voxels are not  
necessarily squared

1. Because brain structure is somehow related to its function.
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3. **Because in multimodal studies we need to have 1 to 1 correspondence between different modalities.**
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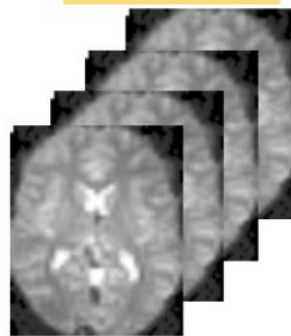
structure



diffusion



functional



FLAIR

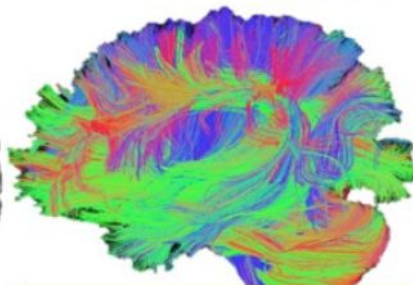


Fully automated processing pipelines  
on HPC clusters

unit: subject



volumes & surface



structural connectivity



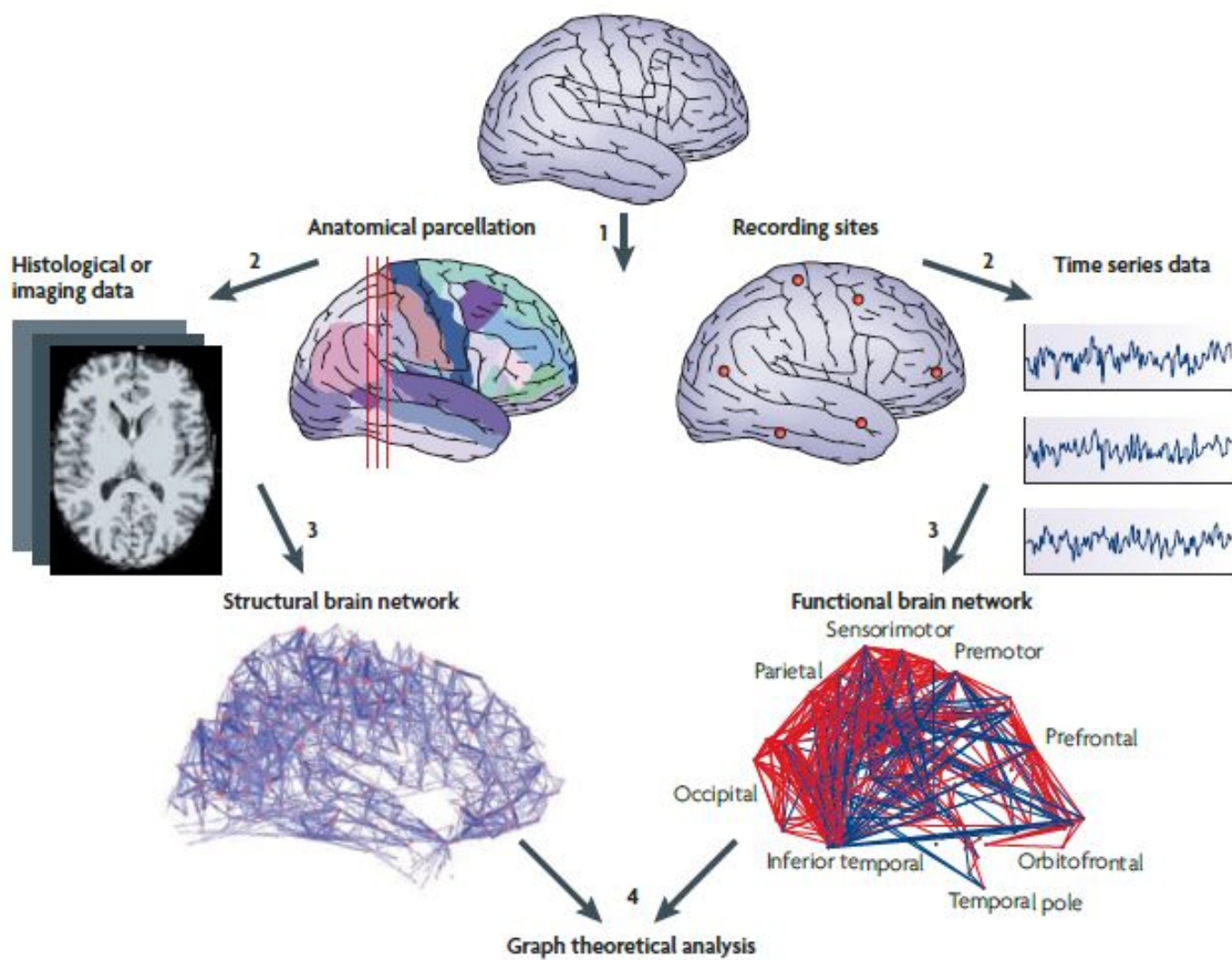
functional connectivity



brain lesions

ANALYSES

unit: features



Source is lost ;(



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Narrow-sense heritability:  $\Omega = 2 \cdot \Phi \cdot \sigma_g^2 + I \cdot \sigma_e^2$

$\text{Var}(y)\sigma_p^2 = \Omega$  – pedigree covariance,  $\Phi$  – kinship matrix  
 $\sigma_g^2$  – genetic variance,  $\sigma_e^2$  – environmental variance

\*Typically, done in family/twin studies

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$$h^2 = \sigma_g^2 / \sigma_p^2$$



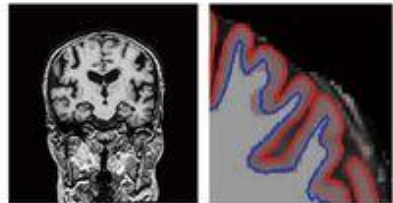
Interpretation:

Relative importance of **genetics vs. environment** for a given trait

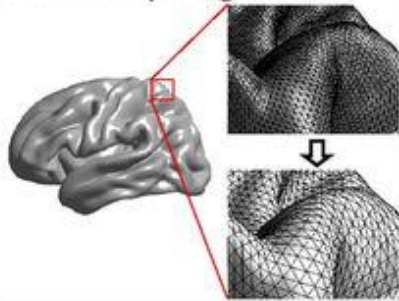
[Heritability of the shape of subcortical brain structures in the general population](#)

## Image preprocessing

Freesurfer

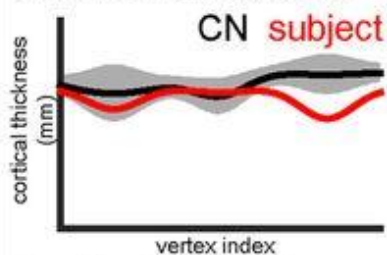


Resampling

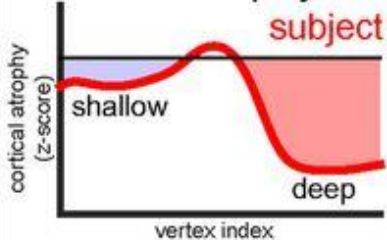


## Computing cortical atrophy map

Cortical thickness

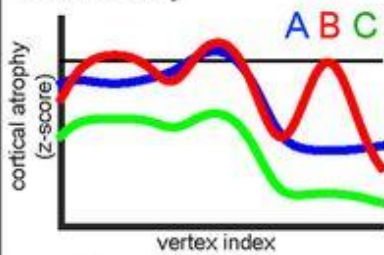


Cortical Atrophy



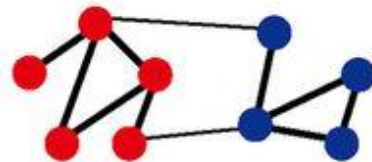
## Subtyping based on similarity

Similarity



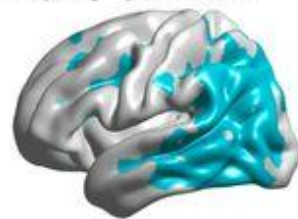
$$Corr_{AB} < Corr_{AC}$$

Modularity

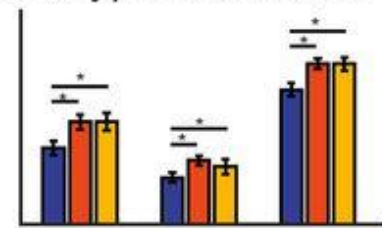


## Statistical analysis

Atrophy pattern



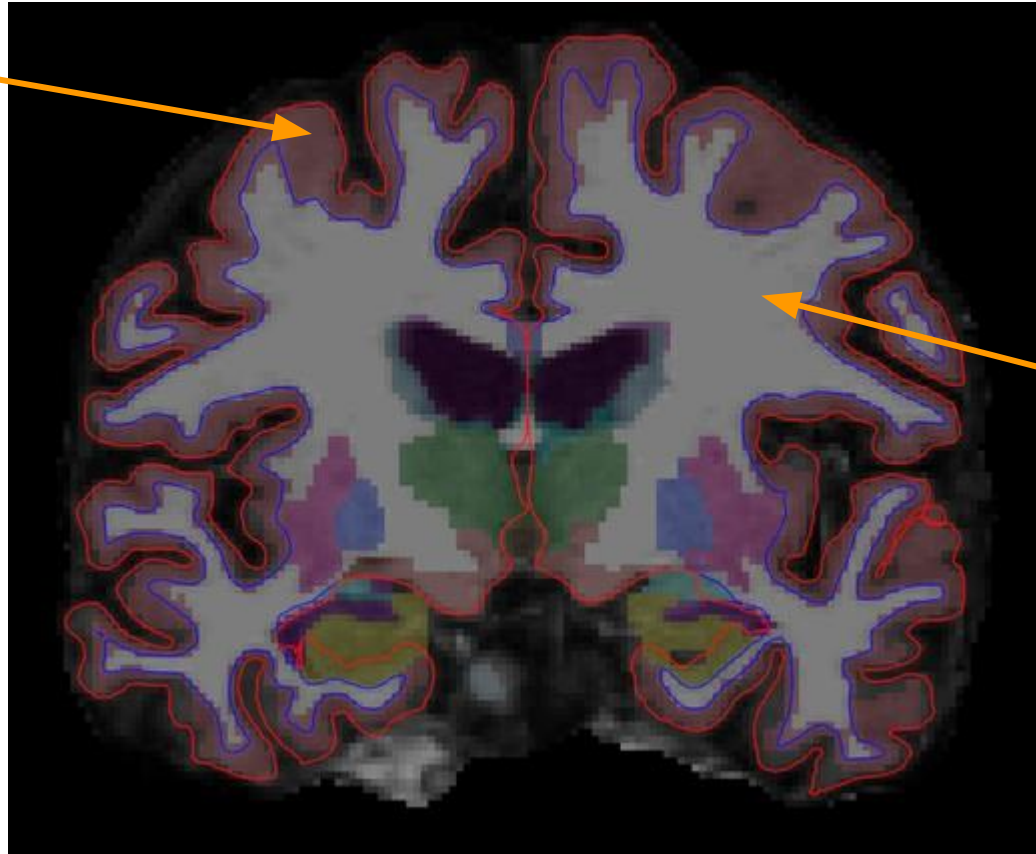
Subtype Hallmarks



[Robust Identification of Alzheimer's Disease subtypes based on cortical atrophy patterns](#)

Gray  
matter

Freesurfer  
segmentation

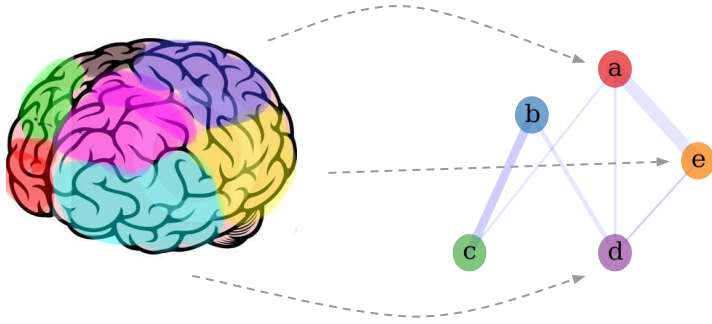


White  
matter

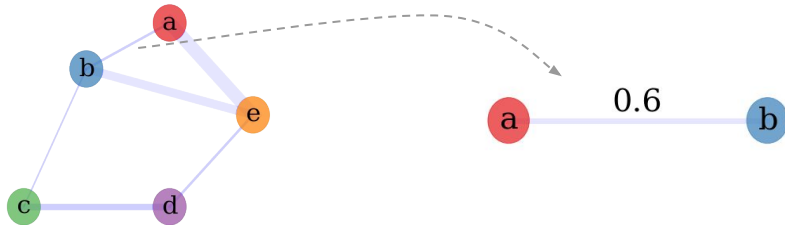
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# Brain network = Connectome

Brain regions become nodes



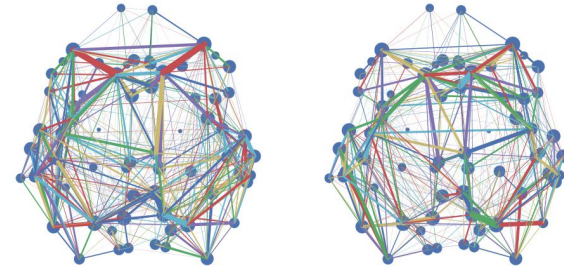
Neural connections between regions become edges



Graph  $G = (V, E, l, w)$ , where

- $V$  is the set of nodes
- $E$  is the set of edges
- $l$  is node's labeling mapping
- $w$  is edge's weighting mapping

is called a brain network or a **connectome**



[Classification of Normal and Pathological Brain Networks Based on Similarity in Graph Partitions](#)

# 3. Anatomical parcellations

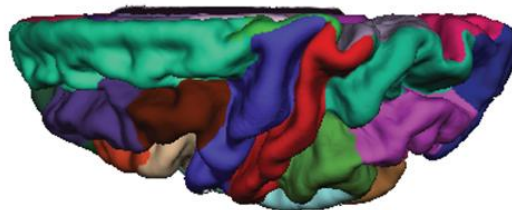
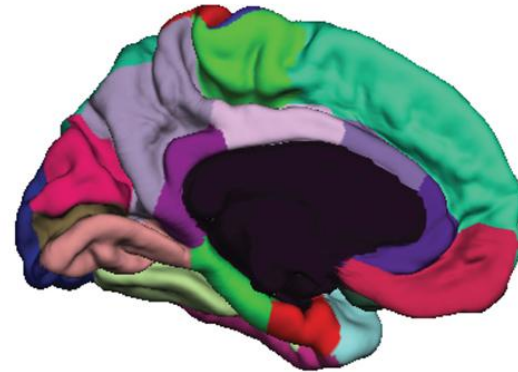
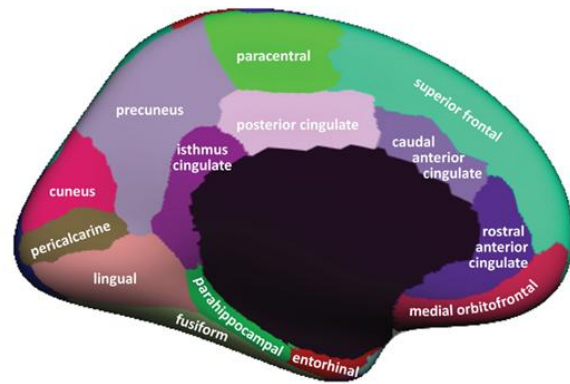
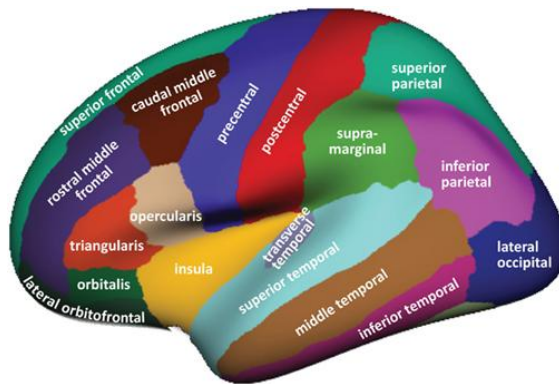
Cortical parcellations = parcellation of the brain surface, popular examples are:

1. [Destrieux Atlas](#)
2. [Desikan-Killiany Atlas](#)
3. [DKT Atlas](#)
4. [Lausanne atlas](#)
5. [Harvard-Oxford atlas](#)
6. [Automated Anatomical Labeling](#)
7. [more](#)



101 labeled brain images  
and a consistent human  
cortical labeling protocol

They used DKT protocol.  
Manual segmentation of  
anatomical areas



# Lausanne atlas



83 ROI



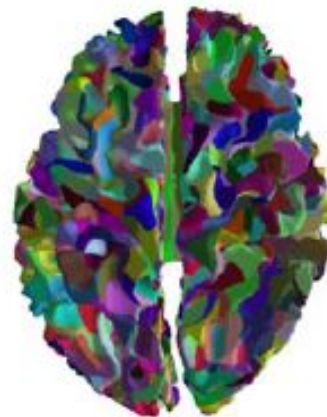
129 ROI



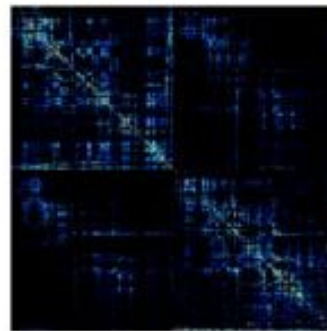
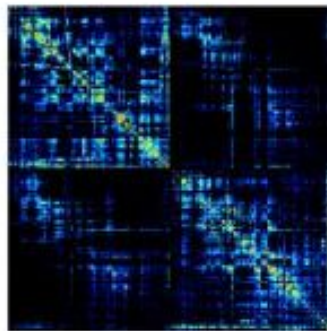
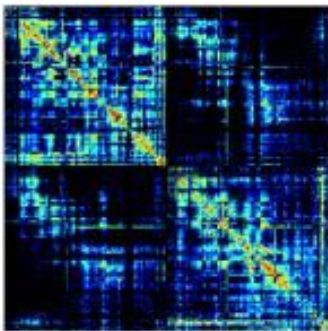
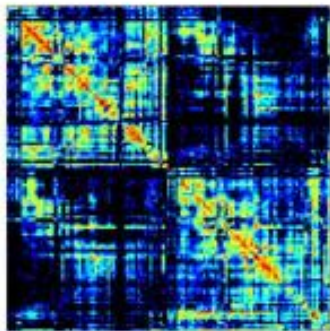
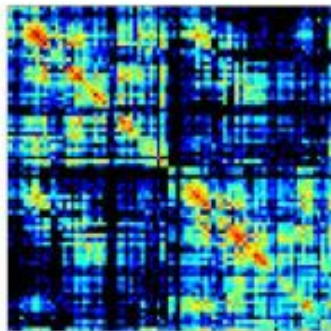
234 ROI



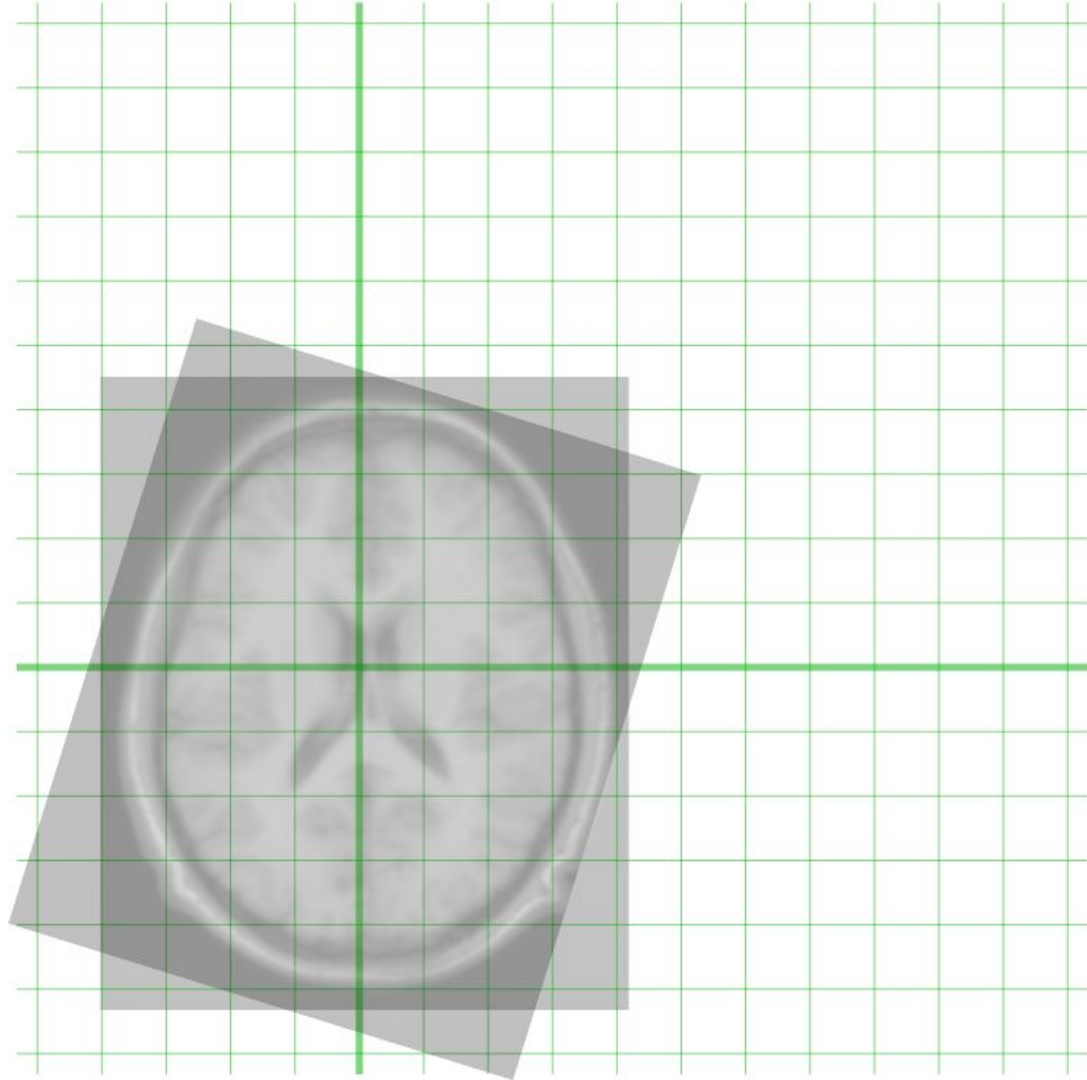
463 ROI



1015 ROI

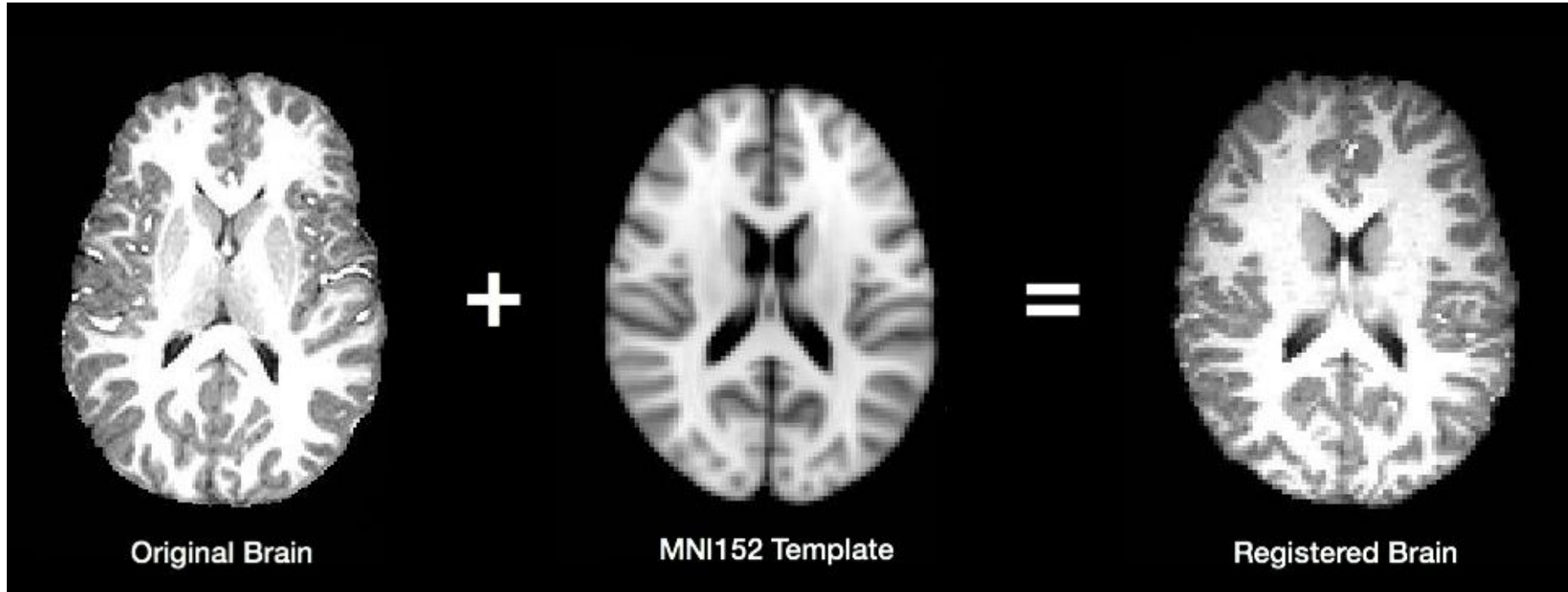


# 4. Couple of words on Image Registration



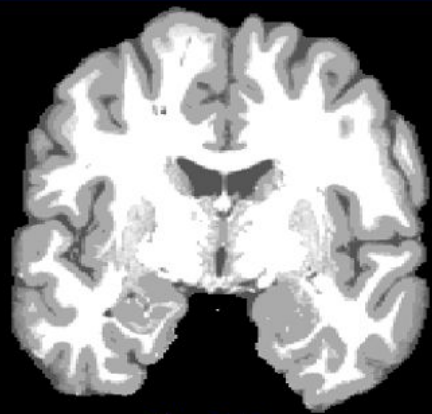
# Voxel-wise registration

# Register on template



[About MNI space](#)





Atlas Brain



Subject Brain

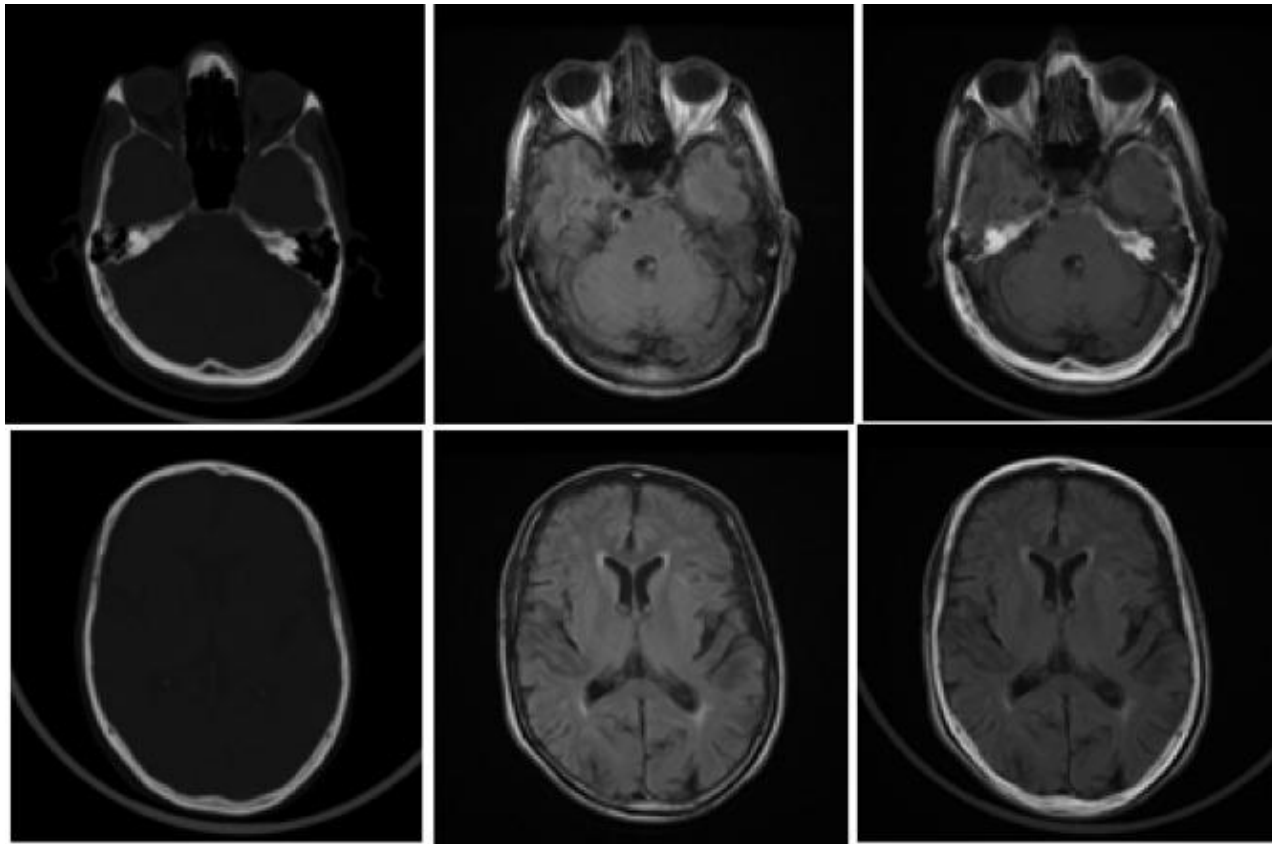


Warped atlas by surface-  
constrained mapping



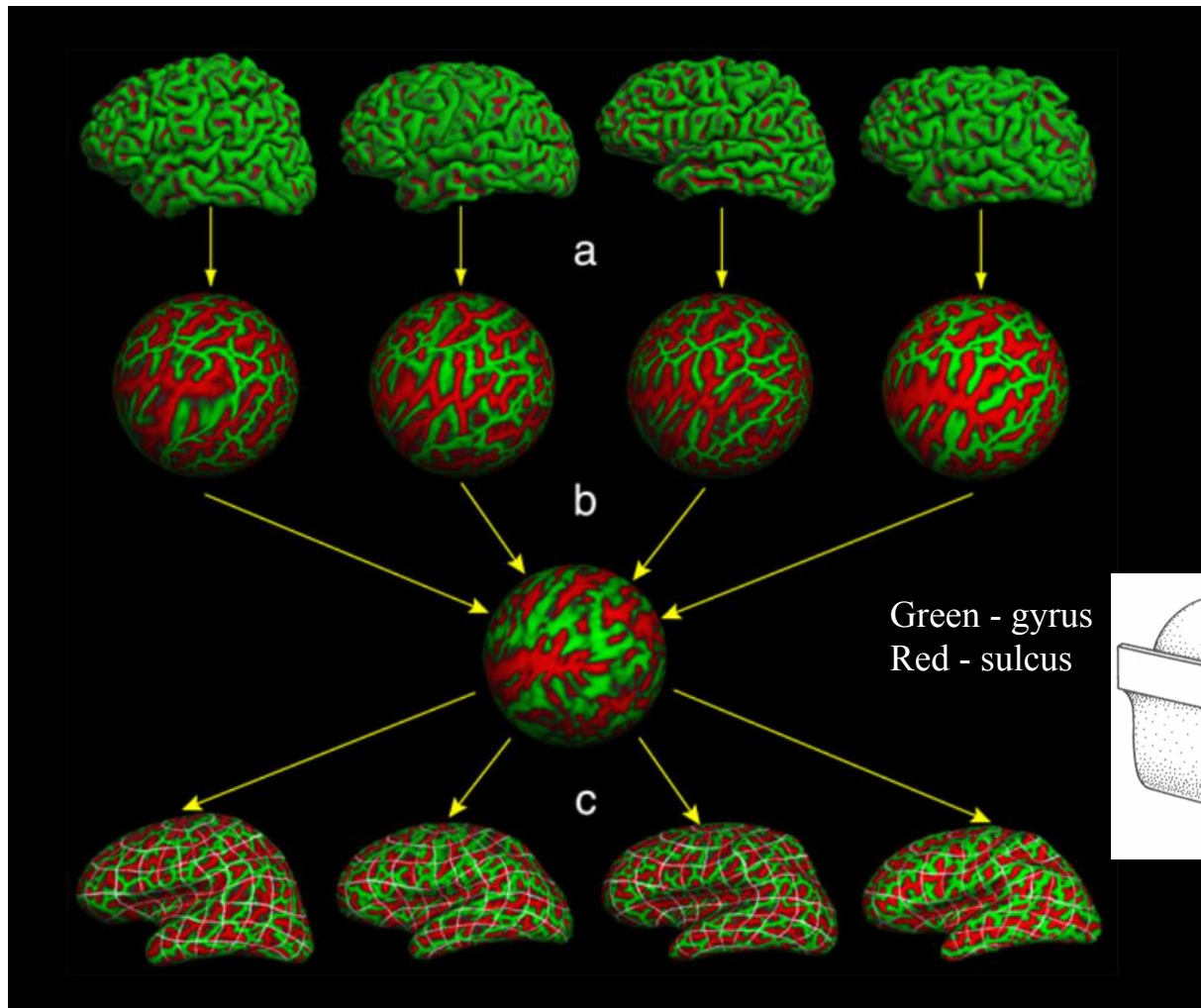
Warped atlas after  
intensity registration

# Register on modality





# Surface-based registration



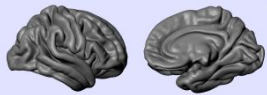
**n=7**

V = 163842  
E = 491520  
F = 327680



**n=6**

V = 40962  
E = 122880  
F = 81920



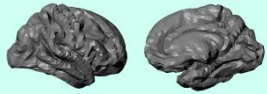
**n=5**

V = 10242  
E = 30720  
F = 20480



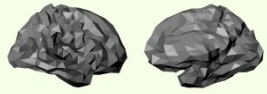
**n=4**

V = 2562  
E = 7680  
F = 5120



**n=3**

V = 642  
E = 1920  
F = 1280



**n=2**

V = 162  
E = 480  
F = 320



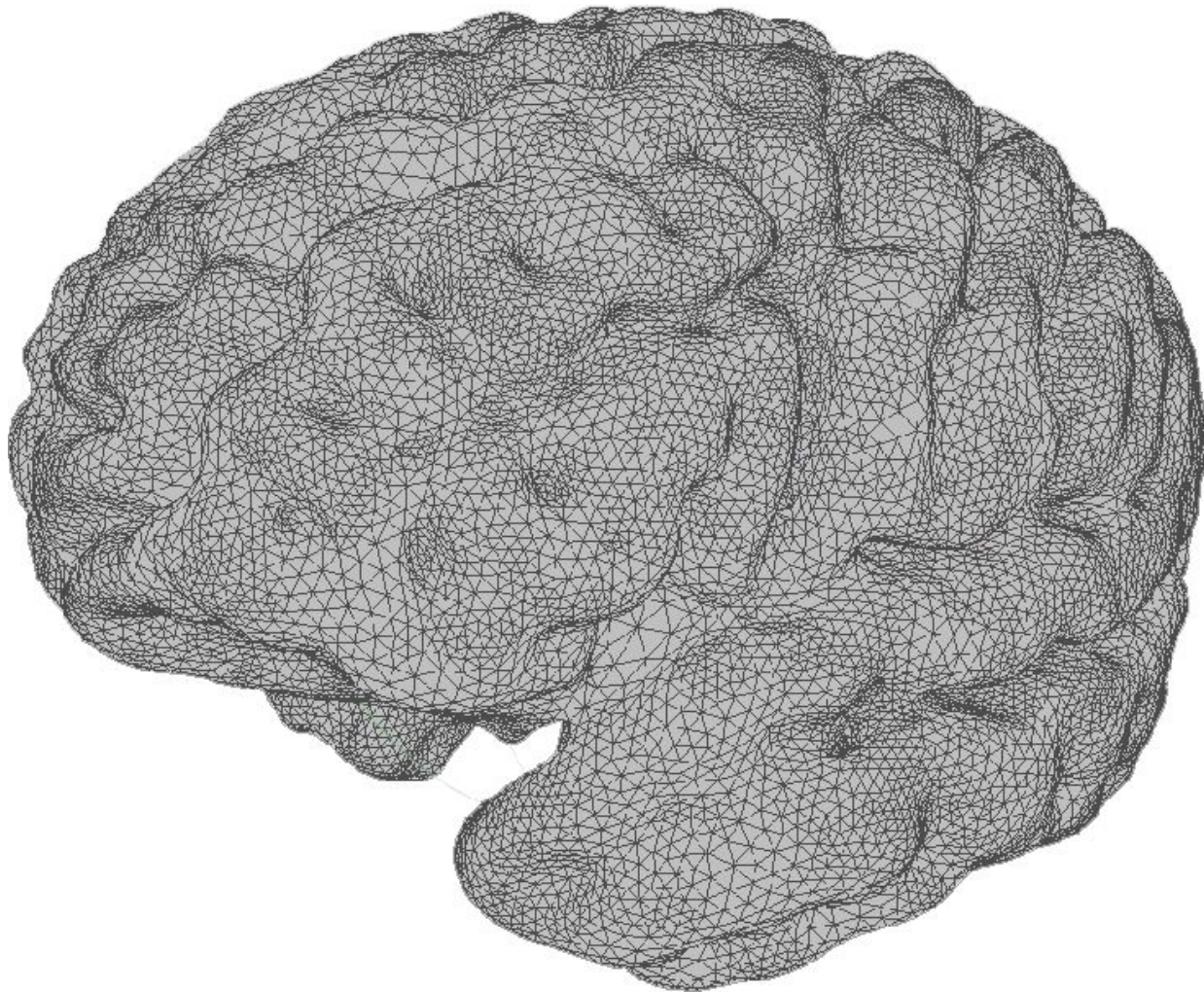
**n=1**

V = 42  
E = 120  
F = 80



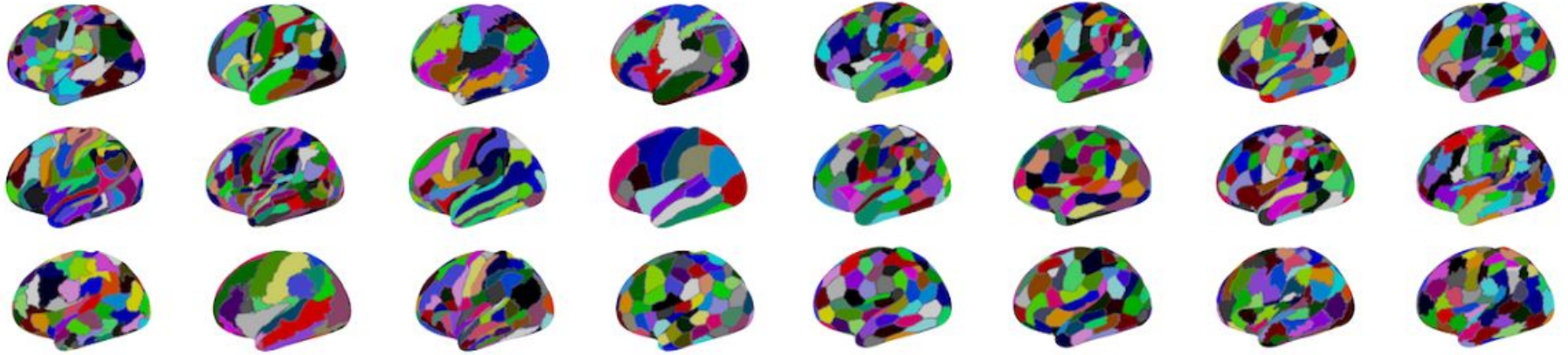
**n=0**

V = 12  
E = 30  
F = 20



# 4. Data driven brain parcellations

Dozens (or even hundreds) of them

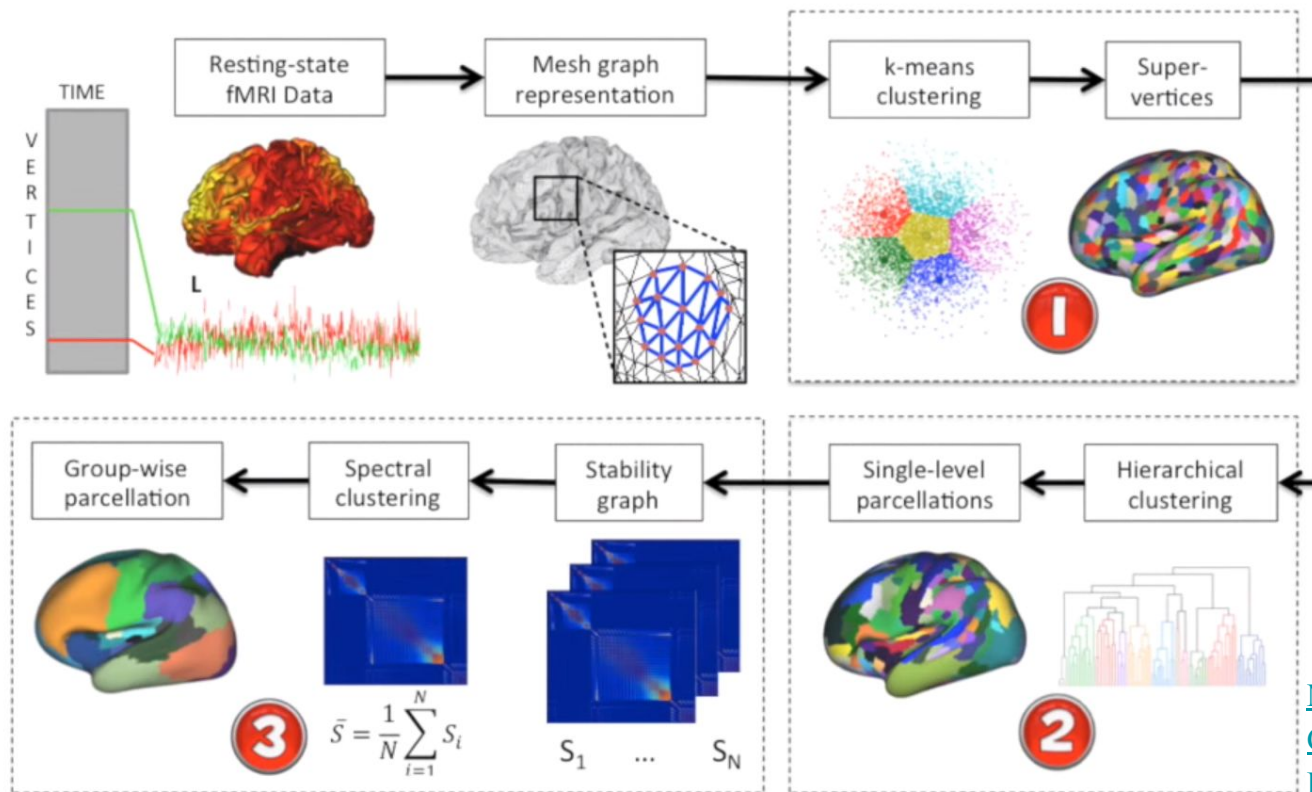


[Human Brain Mapping: A Systematic Comparison of Parcellation Methods for the Human Cerebral Cortex](#)



1. **2015** Multi-Level Parcellation of the Cerebral Cortex Using Resting-State fMRI, Salim Arslan, Daniel Rueckert  
[https://www.doc.ic.ac.uk/~sa1013/pub/2015\\_S\\_Arslan\\_MICCAI.pdf](https://www.doc.ic.ac.uk/~sa1013/pub/2015_S_Arslan_MICCAI.pdf)
  - a. 100 HCP subjects. Initial parcellation using k-means, distance is a combination of geodesic distance and time series correlation (from **fMRI**) -> hierarchical (agglomerative) clustering of these supervertices into larger ones -> Construct meta-graph edges - #times vertices co-occur in the same community -> Cluster this graph using n-cut
2. **2015** A Continuous Flow-Maximisation Approach to Connectivity-driven Cortical Parcellation, Sarah Parisot, Martin Rajchl, Jonathan Passerat-Palmbach, Daniel Rueckert, 2015
  - a. Start with random parcellation (spatially constrained) -> Update parcel centers seeking for a point with maximum correlation with all other nodes in a parcel (correlation from **fMRI**) -> Attach each node to a parcel with the highest correlation (s.t. Spatially smoothness constraints) -> Repeat until convergence.
  - b. 25 HCP Subjects
3. **2008** Normalized Cut Group Clustering of Resting-State fMRI Data, Martijn van den Heuvel, Rene Mandl, Hilleke Hulshoff Pol, 2008,  
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0002001#s2>
  - a. 2-level procedure. 1 construct subject level parcellation from **fMRI** (correlation, 0.4 cutoff) - 20 clusters (authors call them resting-state networks RSNs). Individual graph consist of 8500-9500 nodes. Use ncut clustering, no spatial constraints. Construct group graph edge +1 between 2 nodes if they were in the same cluster (for a subject). Finally group graph was clustered using ncut. 26 fMRI subjects.
4. **2012** A whole brain fMRI atlas generated via spatially constrained spectral clustering, R. Cameron Craddock, G. Andrew James, Paul E. Holtzheimer, Xiaoping P. Hu, and Helen S. Mayberg, 2012
  - a. Build a network from **fMRI**, such that every node is a voxel and an edge between two nodes exist only if they are in 3D neighborhood (for every voxel there are 26 neighborhood voxels), the weight on an edge is a correlation. Cluster it using ncut, group atlas generated either by averaging subject networks and cluster an averaged one, or by using the same technique as in [3] (Martijn van den Heuvel, 2008)
5. **2014** OPTIMIZING BRAIN CONNECTIVITY NETWORKS FOR DISEASE CLASSIFICATION USING EPIC Gautam Prasad, Shantanu H. Joshi, and Paul M. Thompson <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4232940/>
  - a. Start with Desikan atlas proposed algorithm combine separate regions into bigger ones, recompute connectivity matrix and run a classification algorithm on it (using PCA as prep step). In such a way authors find “optimal” in terms of classification (AD vs NC) brain parcellation. The search of best combination of regions is done in a probabilistic manner (simulated annealing/random search).

# Methodology

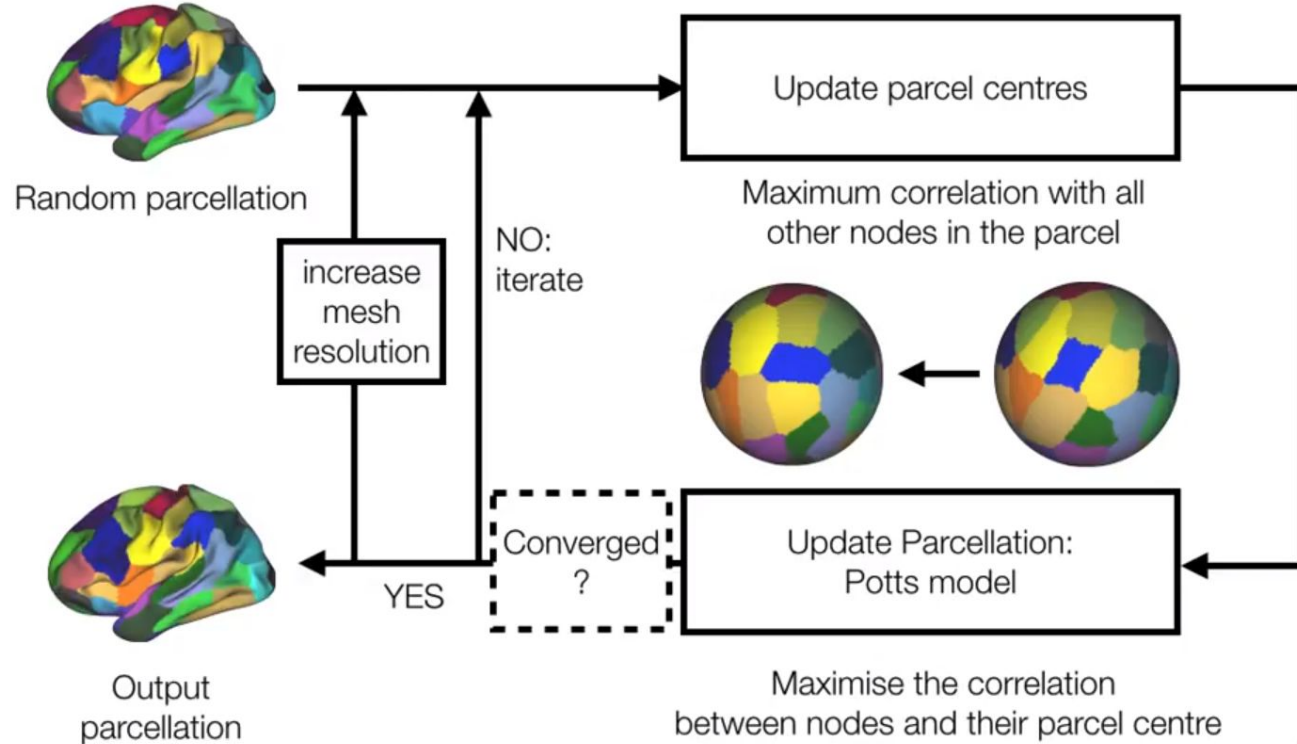


[Short presentation video](#)

[Multi-Level Parcellation of the Cerebral Cortex Using Resting-State fMRI](#)



# Method Overview

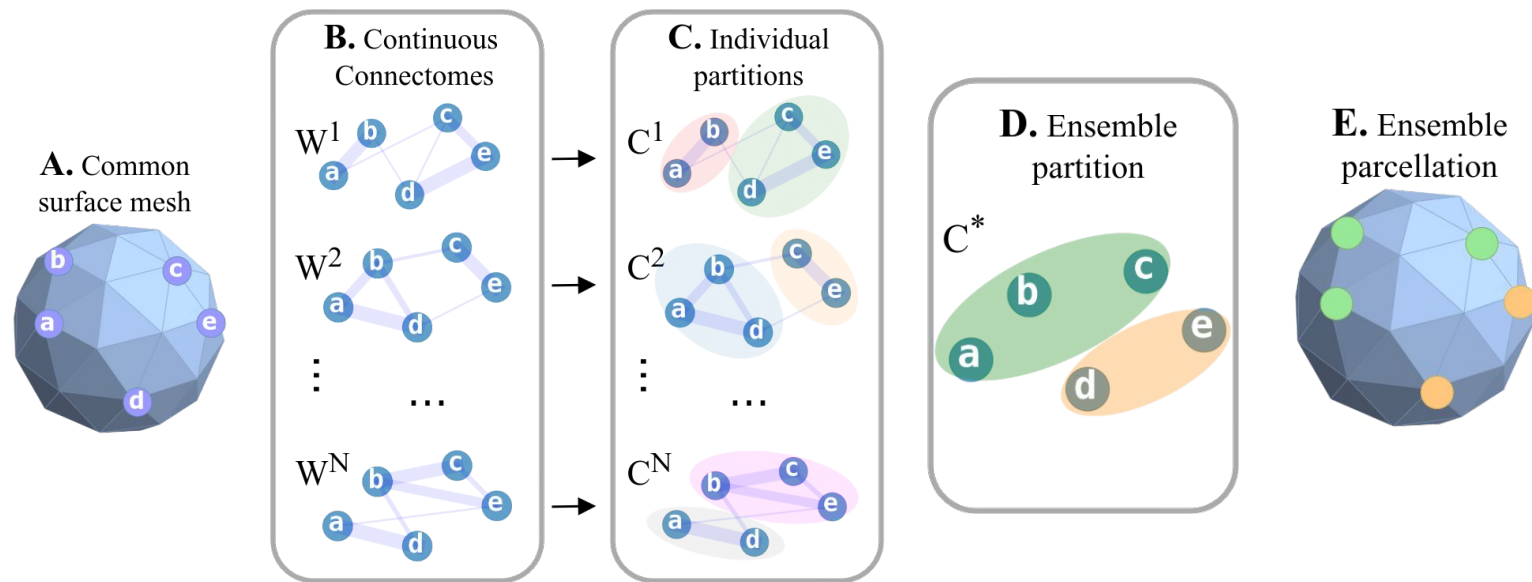


[Short presentation video](#)

[A Continuous Flow-Maximisation Approach to Connectivity-driven Cortical Parcellation](#)



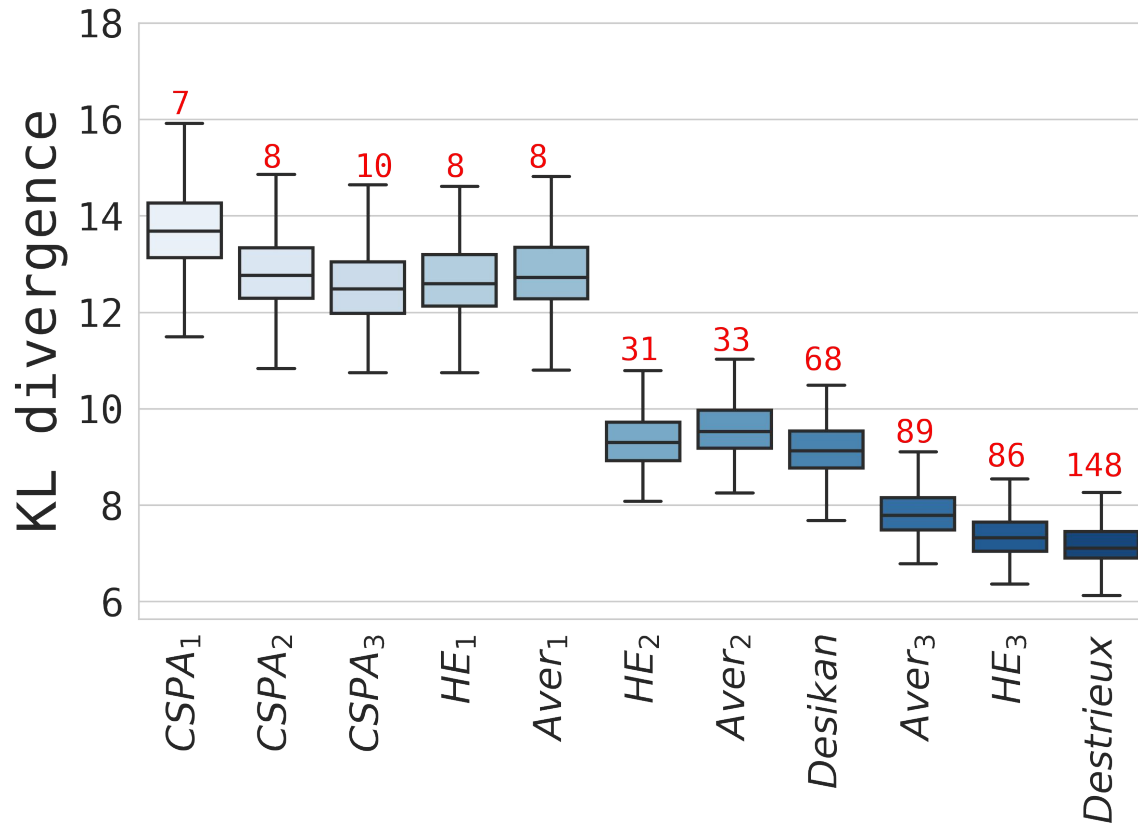
# Connectivity-Driven Brain Parcellation via Consensus Clustering



# Features

- Obtained parcellation is highly symmetrical (left vs right hemisphere)
- Has substantial intersection with classical gyral based parcellations
- Spatially continuous without specific spatial constraints
- Arbitrar subject to clustering approach and averaging approach
- Could be used for subject or group analysis

# Network connections preservation



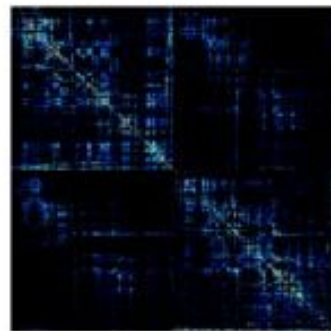
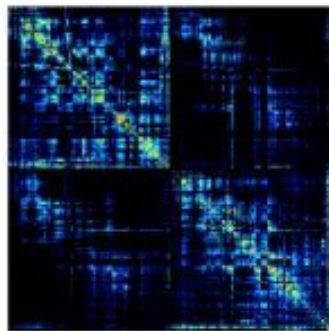
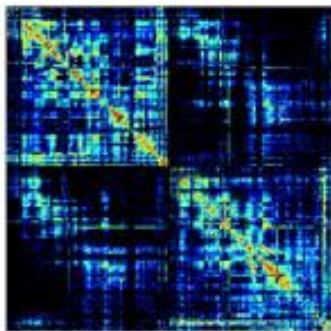
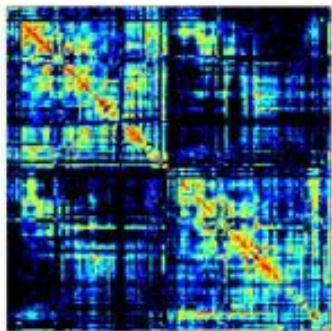
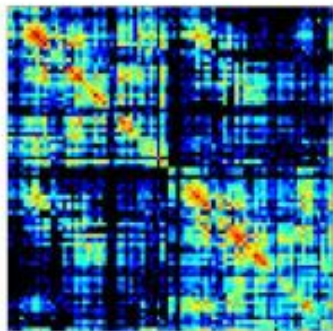
$$KL(\lambda, \gamma) = \int_{-\infty}^{+\infty} \lambda(u) \log \frac{\lambda(u)}{\gamma(u)} du$$

# Нестрогая интуиция почему это важно

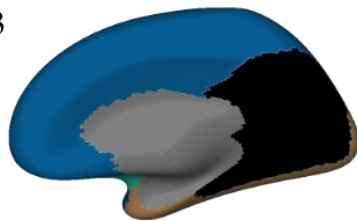
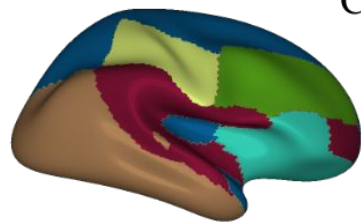
## Szemerédi regularity lemma

From Wikipedia, the free encyclopedia

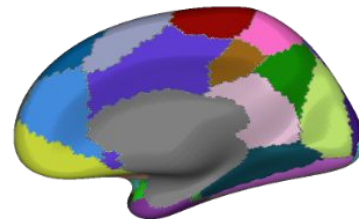
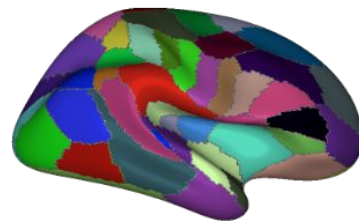
In [mathematics](#), the **Szemerédi regularity lemma** states that every large enough [graph](#) can be divided into subsets of about the same size so that the edges between different subsets behave almost randomly. [Szemerédi \(1975\)](#) introduced a weaker version of this lemma, restricted to bipartite graphs, in order to prove [Szemerédi's theorem](#),<sup>[1]</sup> and in ([Szemerédi 1978](#)) he proved the full lemma.<sup>[2]</sup> Extensions of the regularity method to [hypergraphs](#) were obtained by [Rödl](#) and his collaborators<sup>[3][4][5]</sup> and [Gowers](#).<sup>[6][7]</sup>



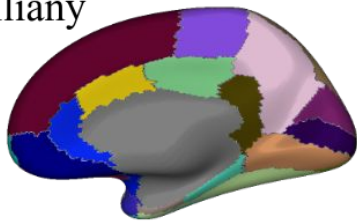
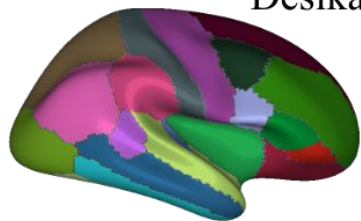
CSPA<sub>3</sub>



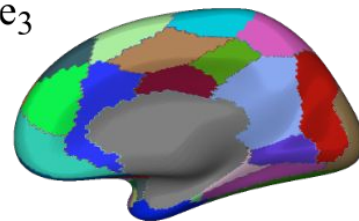
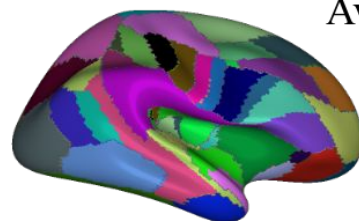
HE<sub>3</sub>



Desikan-Killiany



Average<sub>3</sub>



# Conclusion

- Problems:
  - Huge amount of different parcellation approaches
  - No obvious way to choose amongst them
- Solution:
  - Use common sense
  - Use anatomical parcellations, they are good enough in most cases.
  - Do not use parcellation at all (if possible).
  - In case of structural connectomes use Connectivity-driven parcellation!

# Picture sources

1. [http://www.clipartpanda.com/clipart\\_images/black-and-white-human-brain-3-29489506](http://www.clipartpanda.com/clipart_images/black-and-white-human-brain-3-29489506)
2. <https://braintumor.org/brain-tumor-information/signs-and-symptoms/brain-illustration/>
3. <https://www.britannica.com/topic/phrenology>
4. <https://www.humanbrainfacts.org/basic-structure-and-function-of-human-brain.php>
5. <http://cs.wellesley.edu/~cs112/courseMaterials/assignments/assign5/assign5.html>
6. <https://miykael.github.io/nipype-beginner-s-guide/neuroimaging.html>
7. [http://www.clinica.run/doc/Pipelines/T1\\_FreeSurfer/](http://www.clinica.run/doc/Pipelines/T1_FreeSurfer/)
8. <https://fcp-indi.github.io/docs/user/anat.html>
9. <http://brainsuite.org/processing/svreg/details/>
10. [https://en.wikipedia.org/wiki/Image\\_registration](https://en.wikipedia.org/wiki/Image_registration)
11. <https://www.spiedigitallibrary.org/conference-proceedings-of-spie/10133/1/Multi-atlas-based-CT-synthesis-from-conventional-MRI-with-patch/10.1117/12.2254571.short?SSO=1>
12. <https://www.sciencedirect.com/science/article/pii/S2319417017300653>
13. <https://www.semanticscholar.org/paper/Shape-analysis-of-the-human-brain.-Nitzken-Joseph/c47a238ce4a943a30da38f1047c01580a47fab7d/figure/63>
14. <https://www.semanticscholar.org/paper/Shape-analysis-of-the-human-brain.-Nitzken-Joseph/c47a238ce4a943a30da38f1047c01580a47fab7d>
15. <https://brainder.org/2016/05/31/downsampling-decimating-a-brain-surface/>