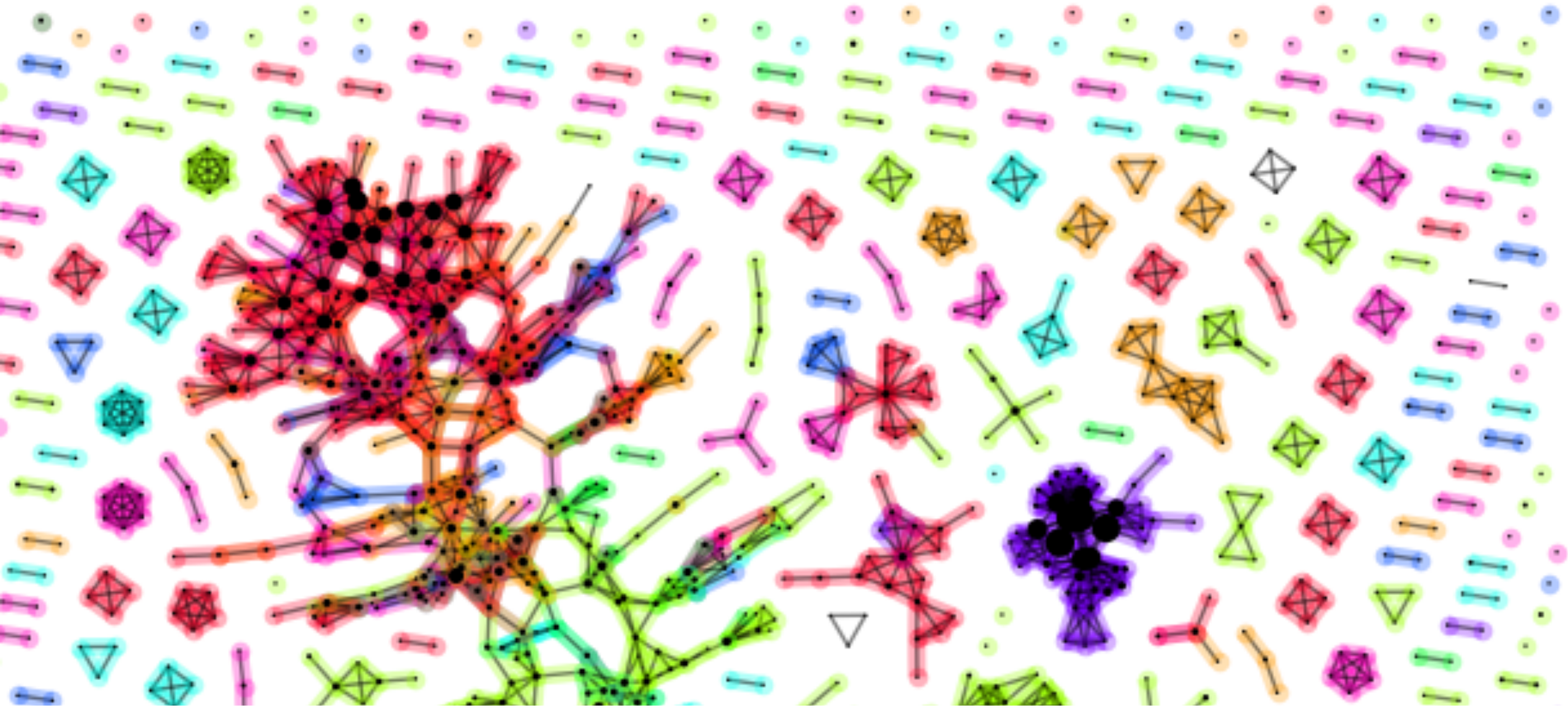


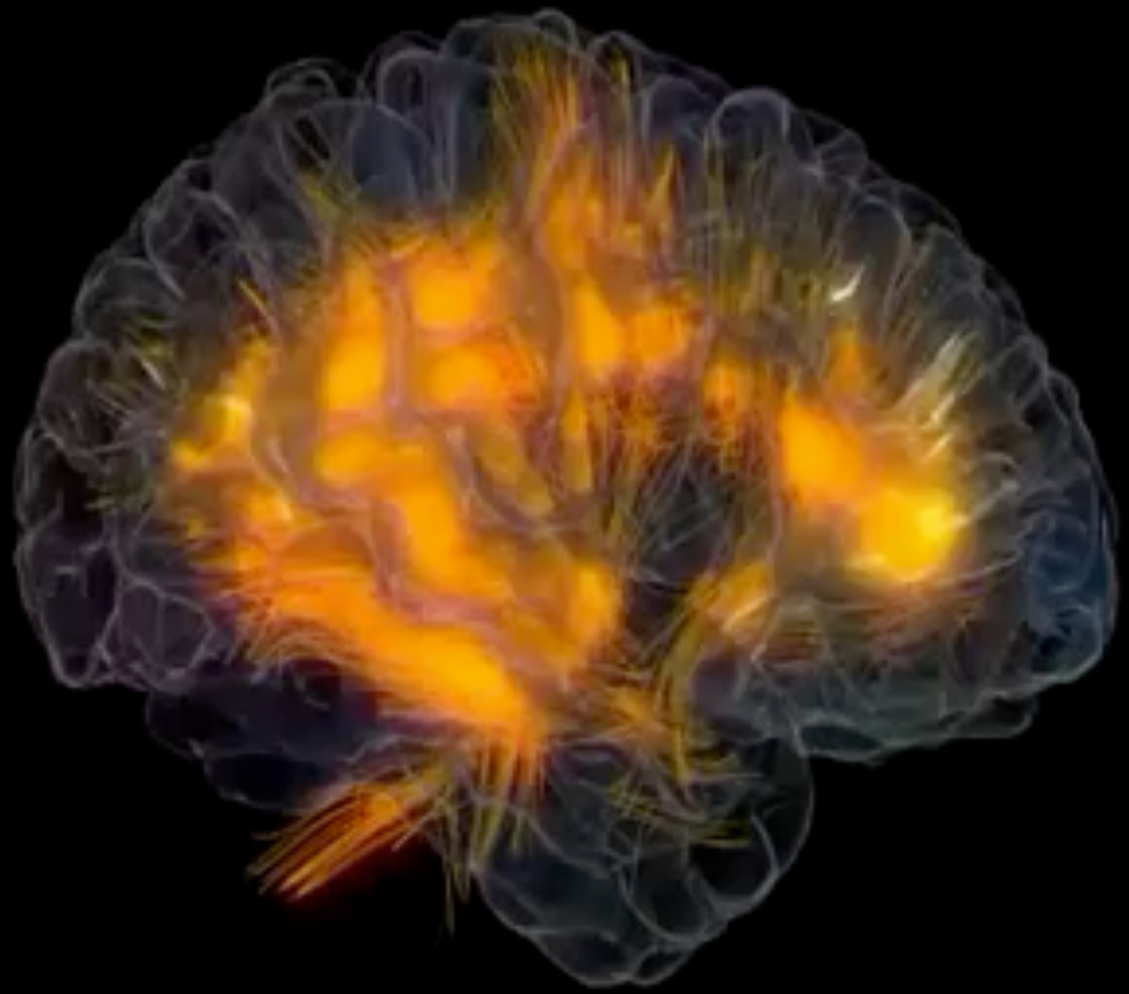
LA MENTE SI PARLA: LA COMPLESSITÀ DELLE CONNESSIONI CEREBRALI

Giovanni Petri, ISI Foundation

Brain Awareness Week, 12.03.2019

LA MENTE SI PARLA: LA **COMPLESSITÀ** DELLE CONNESSIONI CEREBRALI

LA MENTE SI PARLA: LA COMPLESSITÀ DELLE **CONNESSIONI CEREBRALI**



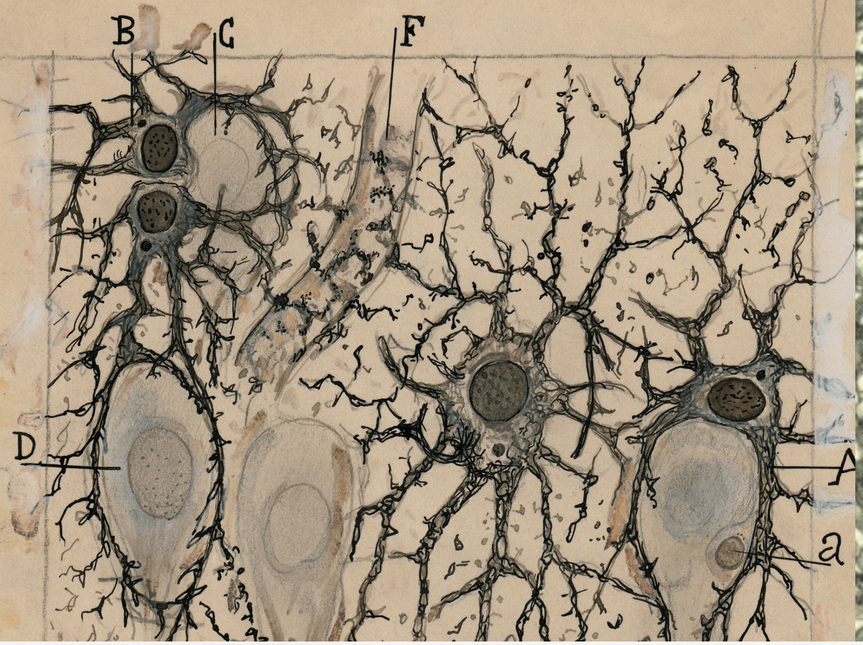
EEG powered by BCILAB | SIFT

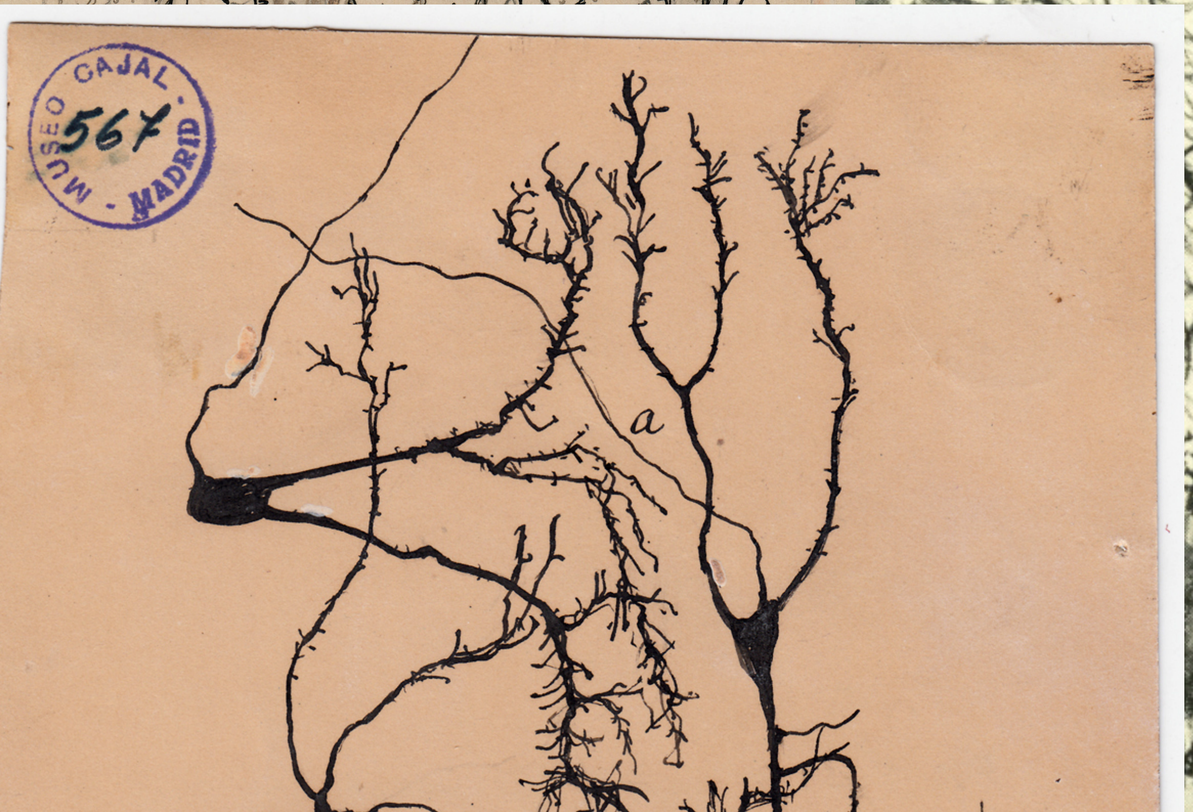
INTERPRETAZIONE

ANALISI

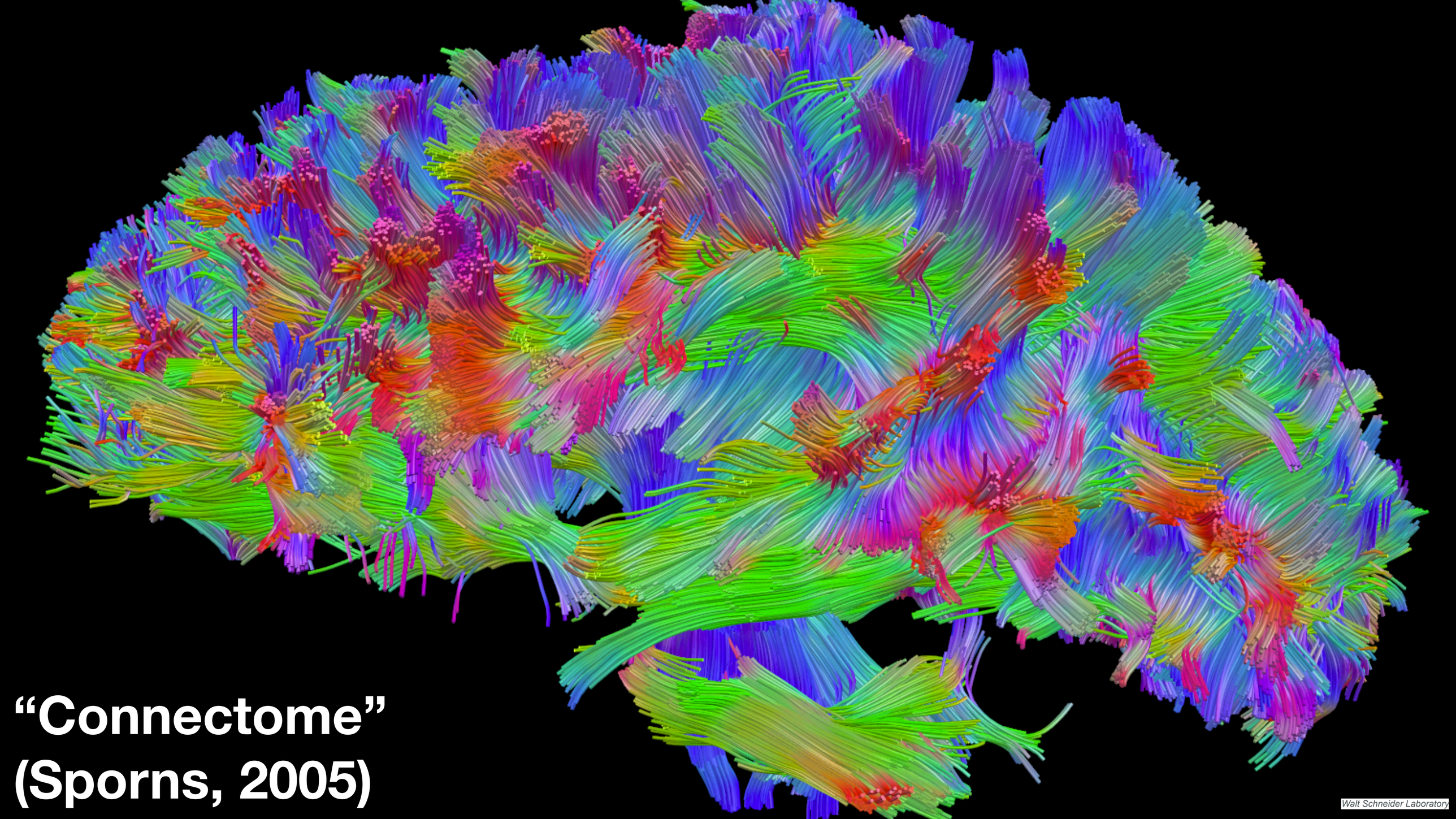
DATI

LA MENTE SI PARLA: LA **COMPLESSITÀ** DELLE CONNESSIONI CEREBRALI

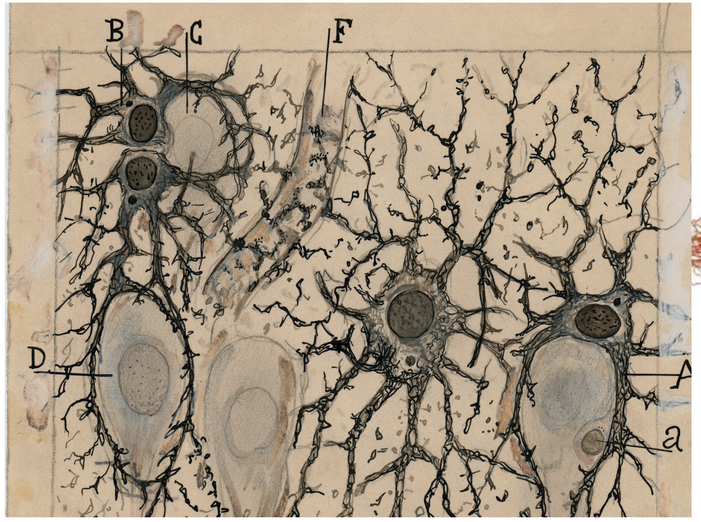




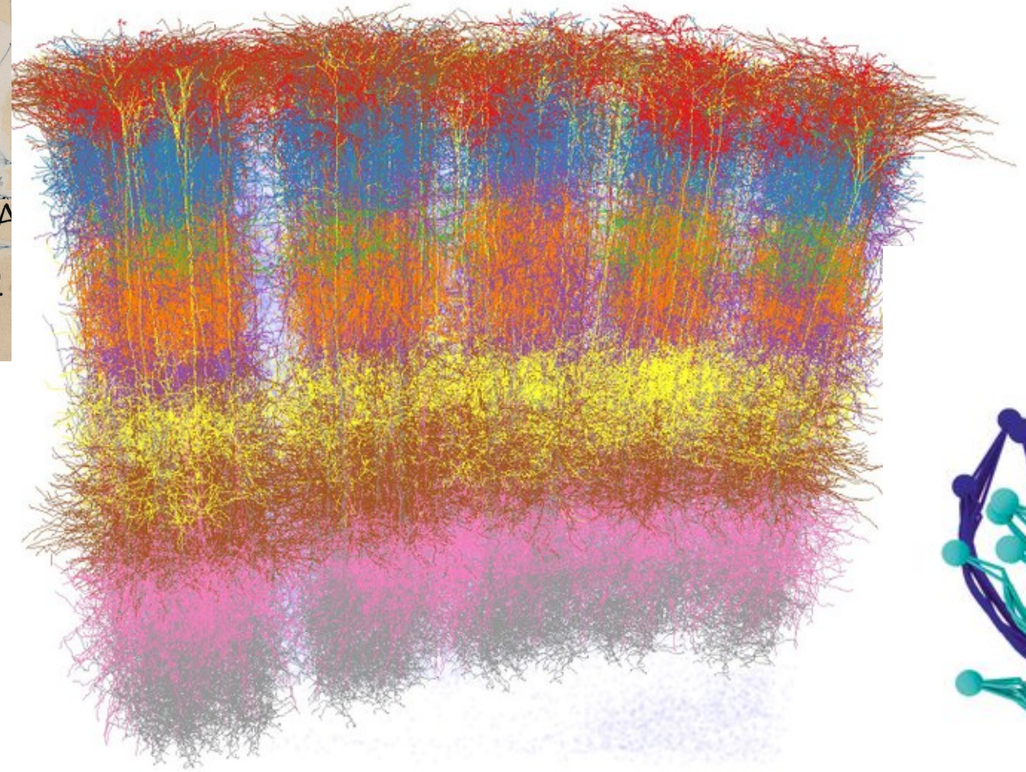
Ramon y Cajal 1906


“Connectome”
(Sporns, 2005)
Walt Schneider Laboratory

1 micrometer



100 micrometer

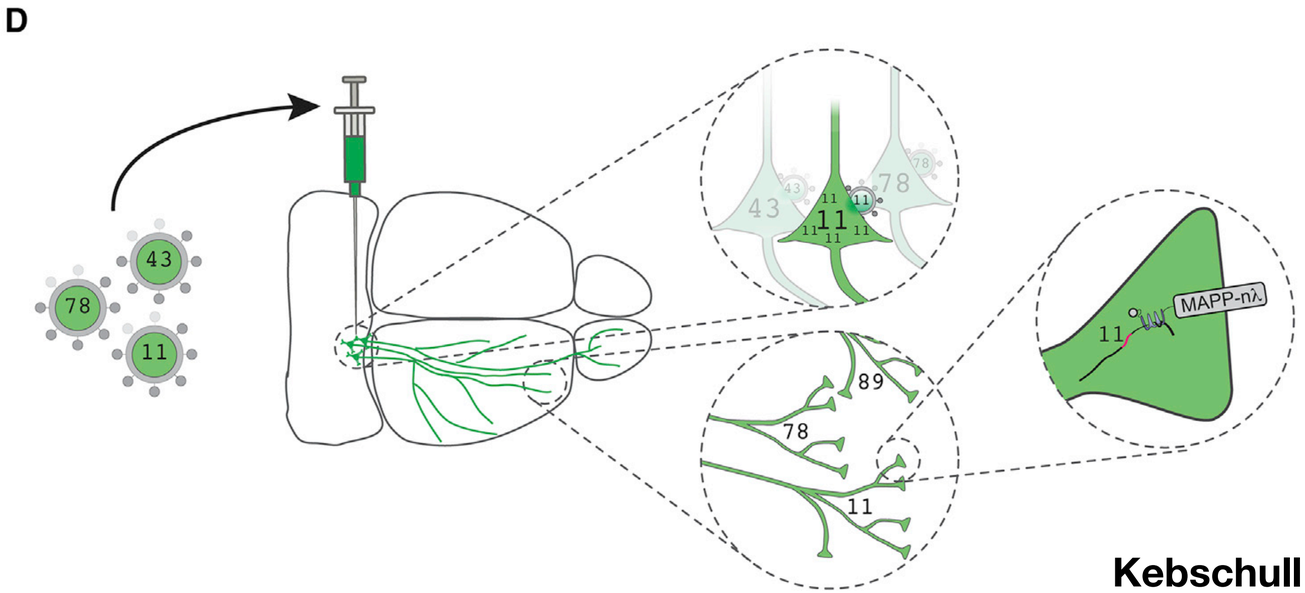


Meyer et al 2013

Millimeter

Dance, Nature 2015

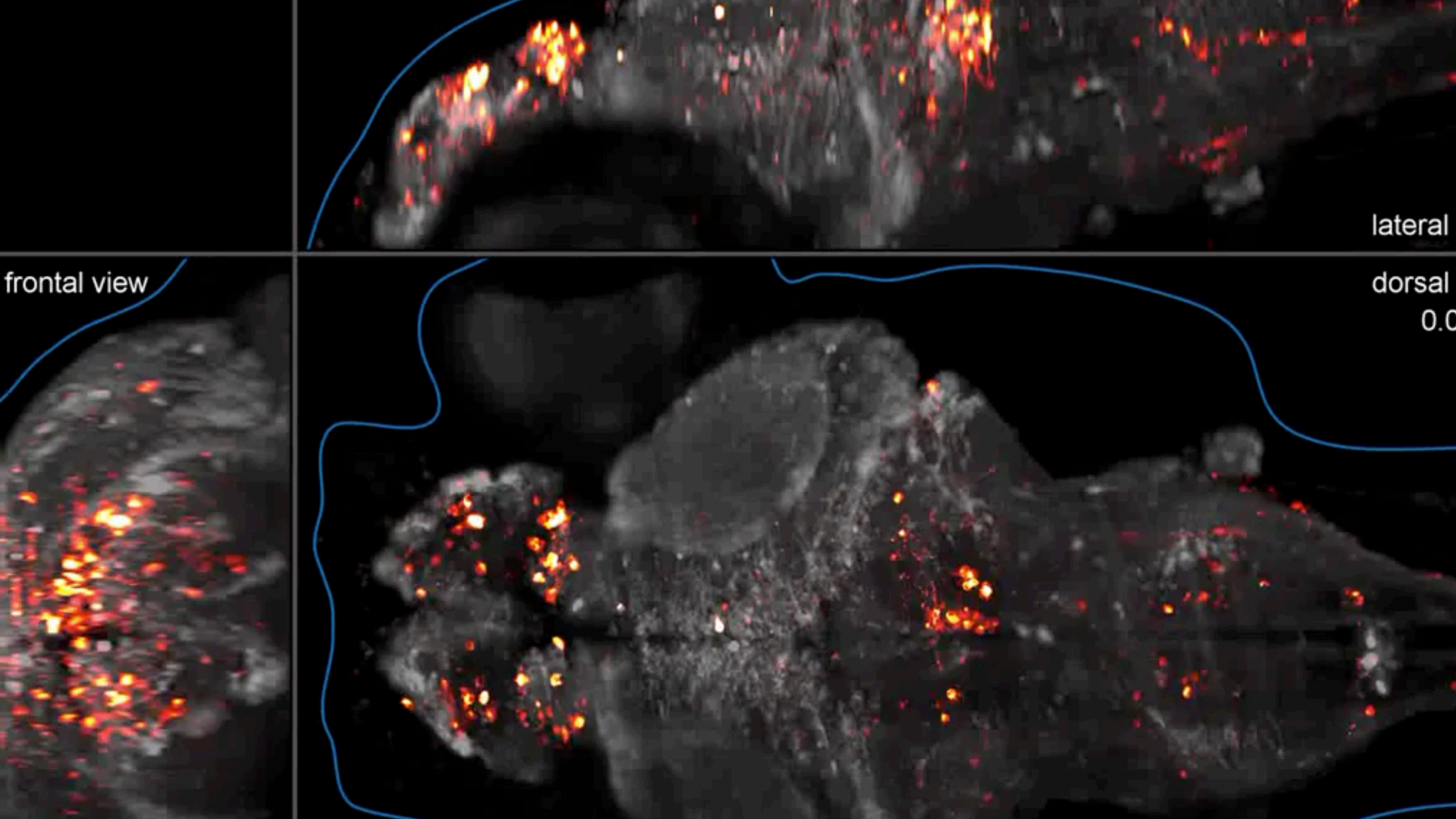
- **Microscales:**
  - **Electron microscopes**
  - **Cell staining**
  - **Viral neuronal tracing**
- **Mesoscales:**
  - **Tract-tracing**
  - **High-field MRI**
- **Macroscales:**
  - **Diffusion MRI**
  - **Diffusion tensor imaging**

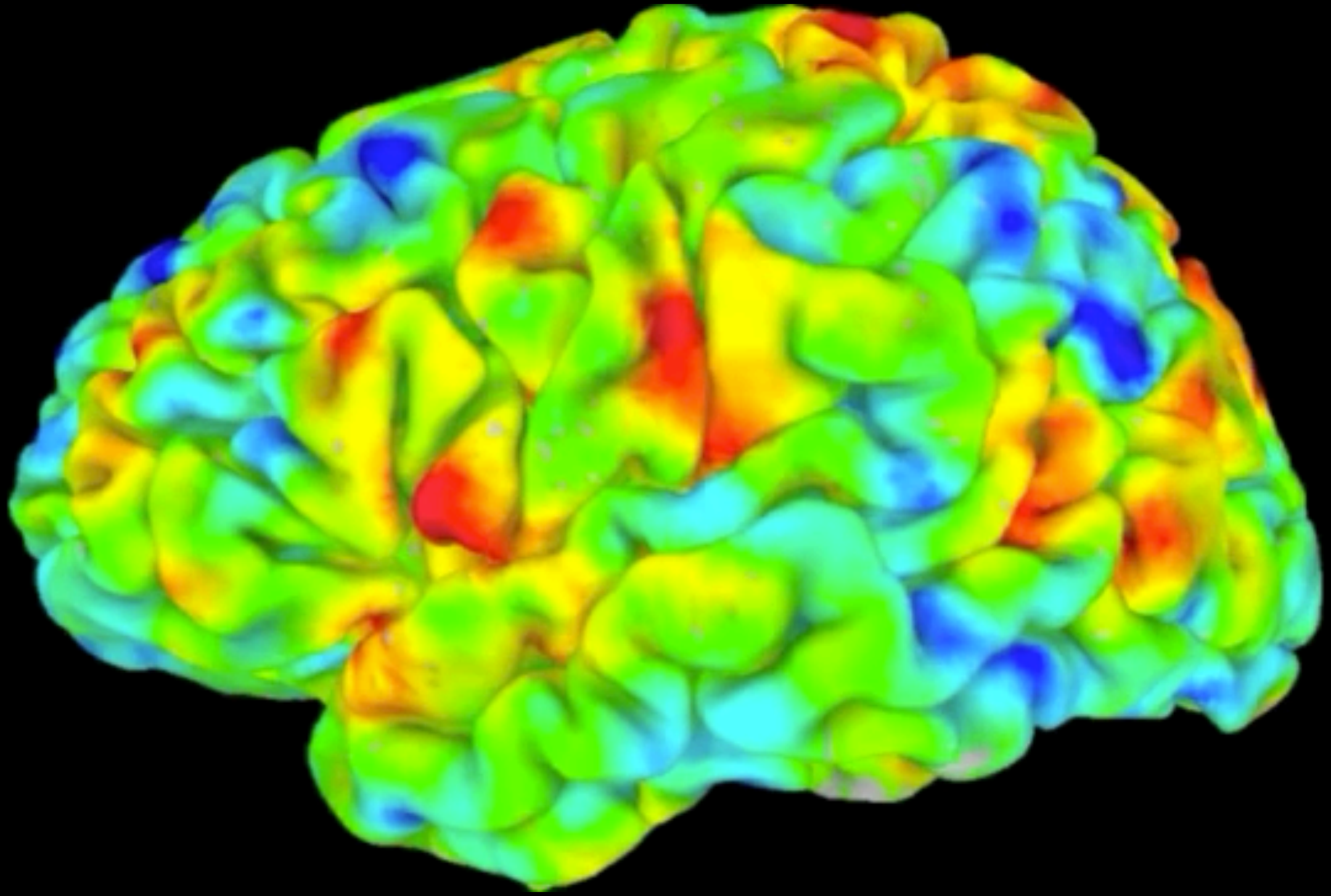


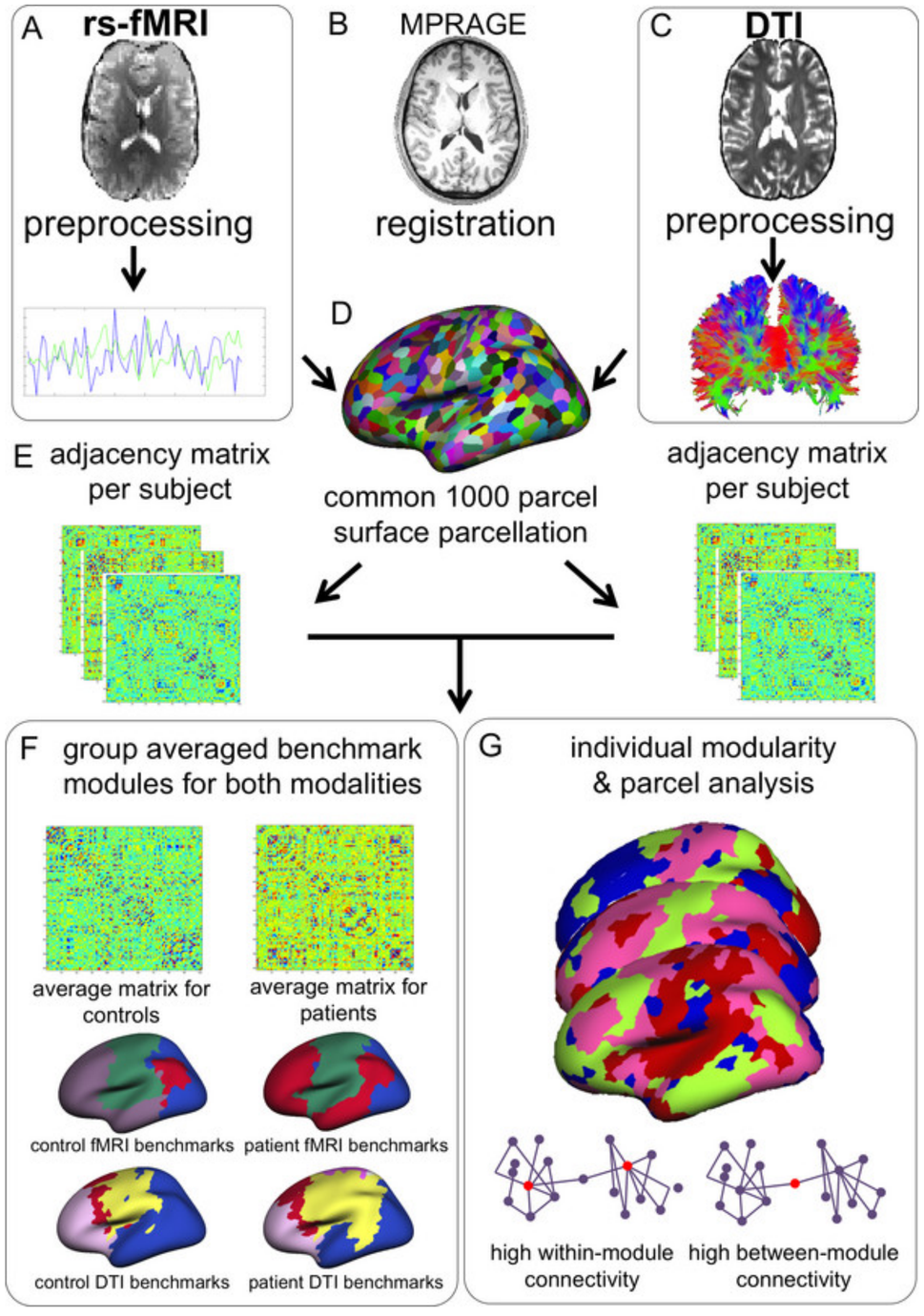
Kebschull et al, 2016

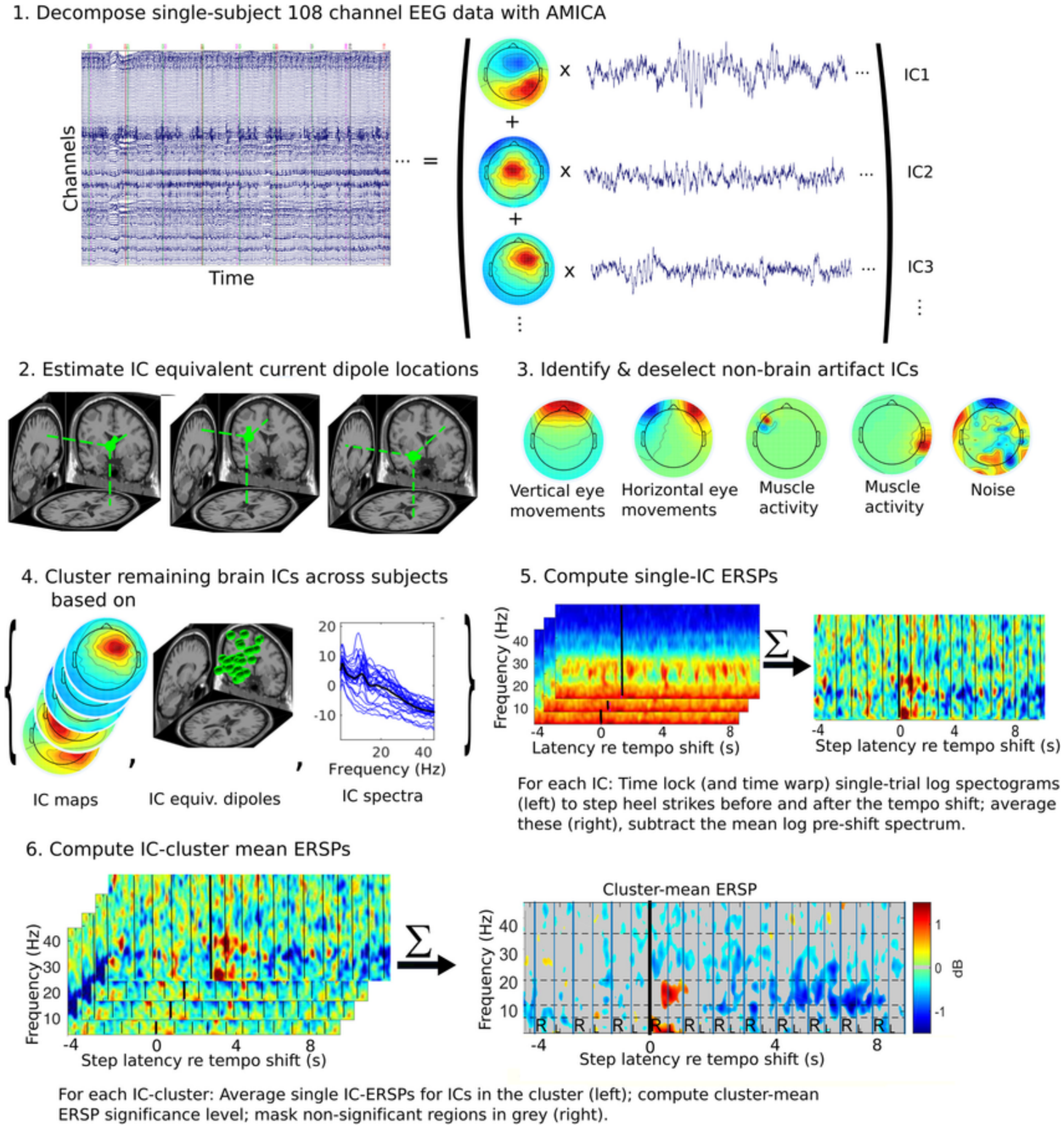
Research has **successfully constructed the full connectome of one animal:** the roundworm *Caenorhabditis elegans* (White *et al.*, 1986,[2] Varshney *et al.*, 2011[3]). **Partial connectomes** of a mouse retina[4] and mouse primary visual cortex[5] **have also been successfully constructed**. Other reconstructions, such as Bock *et al.*'s 2011 complete **12 terabyte dataset**, are publicly available through services such as *NeuroData*.[6]

"…to map the human cerebral cortex, HCP researchers analysed **6 terabytes of MRI data from 210 healthy young adults**, says Kamil Ugurbil, the HCP's co-principal investigator at the University of Minnesota in Minneapolis. Labs can download those data from the project's website or, for larger data sets, **order 8-terabyte hard drives for US$200 apiece**…"

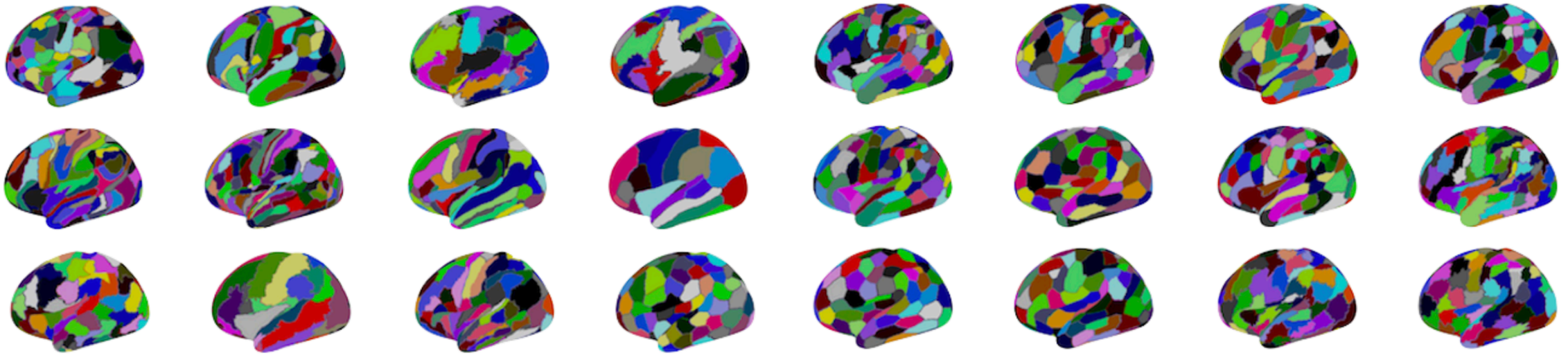

lateral
frontal view
dorsal
0.0




A rs-fMRI
preprocessing
B MPRAGE
registration
C DTI
preprocessing
D
common 1000 parcel surface parcellation
E adjacency matrix per subject
adjacency matrix per subject
F group averaged benchmark modules for both modalities
average matrix for controls
average matrix for patients
control fMRI benchmarks
patient fMRI benchmarks
control DTI benchmarks
patient DTI benchmarks
G individual modularity & parcel analysis
high within-module connectivity
high between-module connectivity


1. Decompose single-subject 108 channel EEG data with AMICA
Channels
Time
IC1
IC2
IC3
2. Estimate IC equivalent current dipole locations
3. Identify & deselect non-brain artifact ICs
Vertical eye movements
Horizontal eye movements
Muscle activity
Muscle activity
Noise
4. Cluster remaining brain ICs across subjects based on
IC maps
IC equiv. dipoles
IC spectra
Frequency (Hz)
5. Compute single-IC ERSPs
Latency re tempo shift (s)
Step latency re tempo shift (s)
For each IC: Time lock (and time warp) single-trial log spectograms (left) to step heel strikes before and after the tempo shift; average these (right), subtract the mean log pre-shift spectrum.
6. Compute IC-cluster mean ERSPs
Step latency re tempo shift (s)
Cluster-mean ERSP
dB
For each IC-cluster: Average single IC-ERSPs for ICs in the cluster (left); compute cluster-mean ERSP significance level; mask non-significant regions in grey (right).

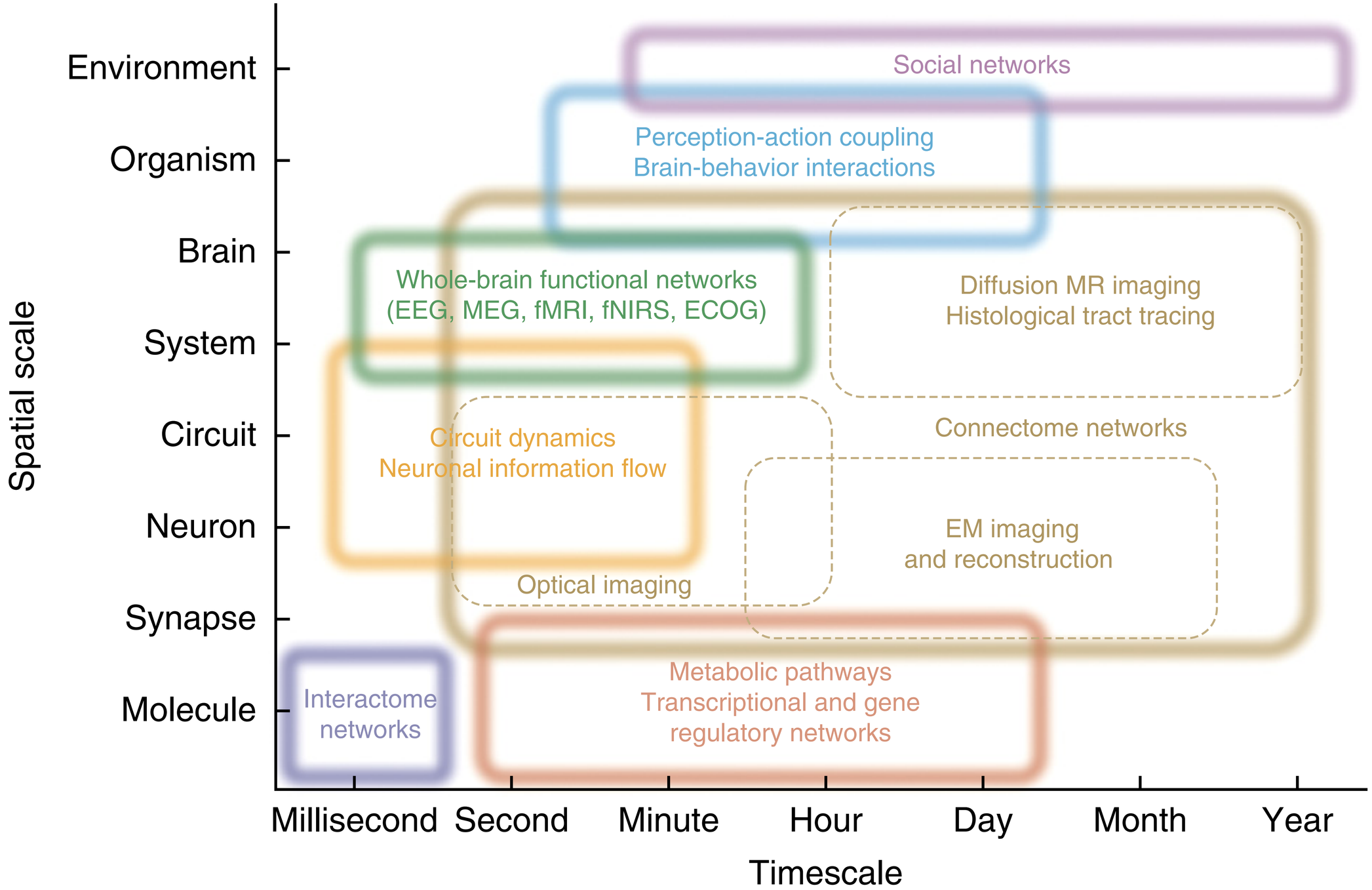
Brain Parcellation Survey

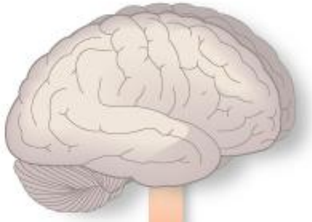


"Using resting-state functional MRI (rs-fMRI) data and several quantitative evaluation techniques, **10 subject-level** and **24 groupwise parcellation methods** are evaluated at different resolutions. The accuracy of parcellations is assessed from four different aspects: (1) reproducibility across different acquisitions and groups, (2) fidelity to the underlying connectivity data, (3) agreement with fMRI task activation, myelin maps, and cytoarchitectural areas, and (4) network analysis."

Parcellations are SMALL!

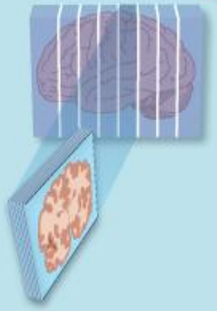
https://biomedia.doc.ic.ac.uk/brain-parcellation-survey/


Environment
Organism
Brain
System
Circuit
Neuron
Synapse
Molecule
Spatial scale
Social networks
Perception-action coupling
Brain-behavior interactions
Whole-brain functional networks
(EEG, MEG, fMRI, fNIRS, ECOG)
Diffusion MR imaging
Histological tract tracing
Circuit dynamics
Neuronal information flow
Connectome networks
EM imaging
and reconstruction
Optical imaging
Metabolic pathways
Transcriptional and gene
regulatory networks
Interactome
networks
Millisecond
Second
Minute
Hour
Day
Month
Year
Timescale



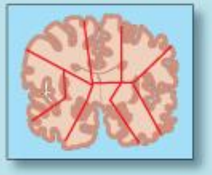
TISSUE PROCESSING

Cut into slabs



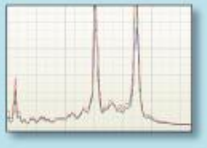
Section histology

Block into 2x3 and section



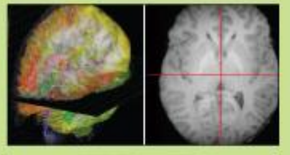
Anatomic sampling

RNA processing

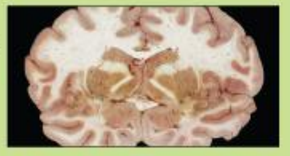


DATA COLLECTION

Scanning
DTI
MRI



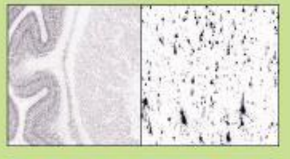
Block face images



Histology
Nissl
SMI-32

Annotation

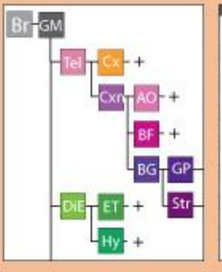
ISH



Microarray

DATA INTEGRATION, STORAGE AND RETRIEVAL

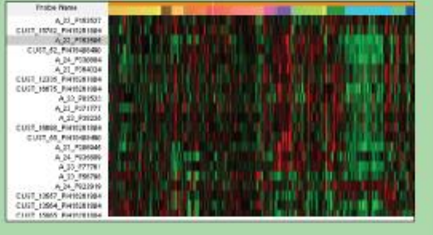
Ontology



LIMS

INFORMATICS AND DATA ANALYSIS

- Image preprocessing
- Microarray and ISH Data Processing
- Data normalization
- 3D Mapping and reconstruction

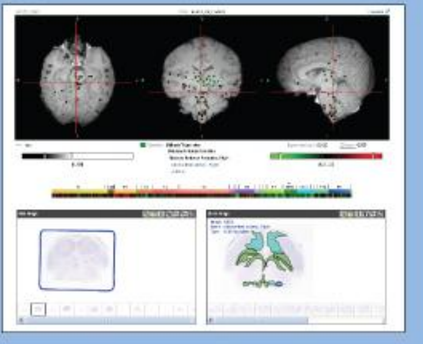


ALLEN HUMAN BRAIN ATLAS

Data Access • Visualization • Mining

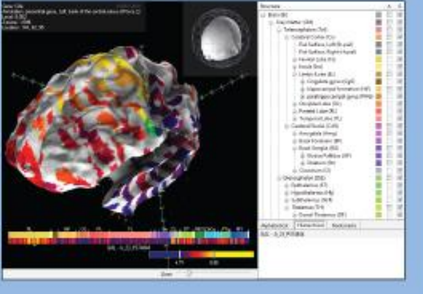
SEARCH FUNCTIONALITY

- Gene
- Structure
- Neuroblast- correlation search



- Histology - Nissl, SMI-32, ISH, LCM
- Heat Maps, MRI, DTI,
- Raw Data Download

3D Brain Explorer



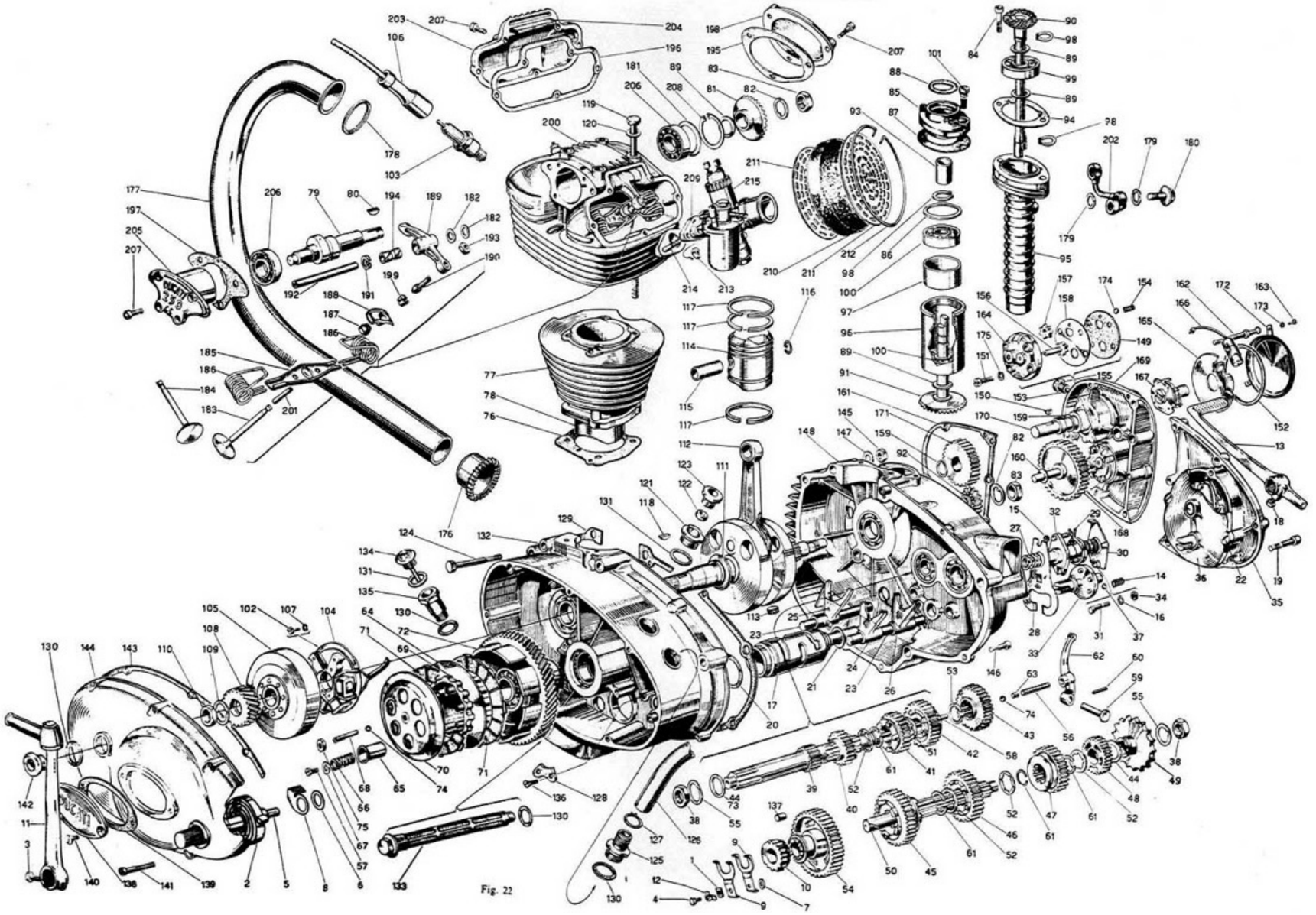
ANALISI/SISTEMA

DATI

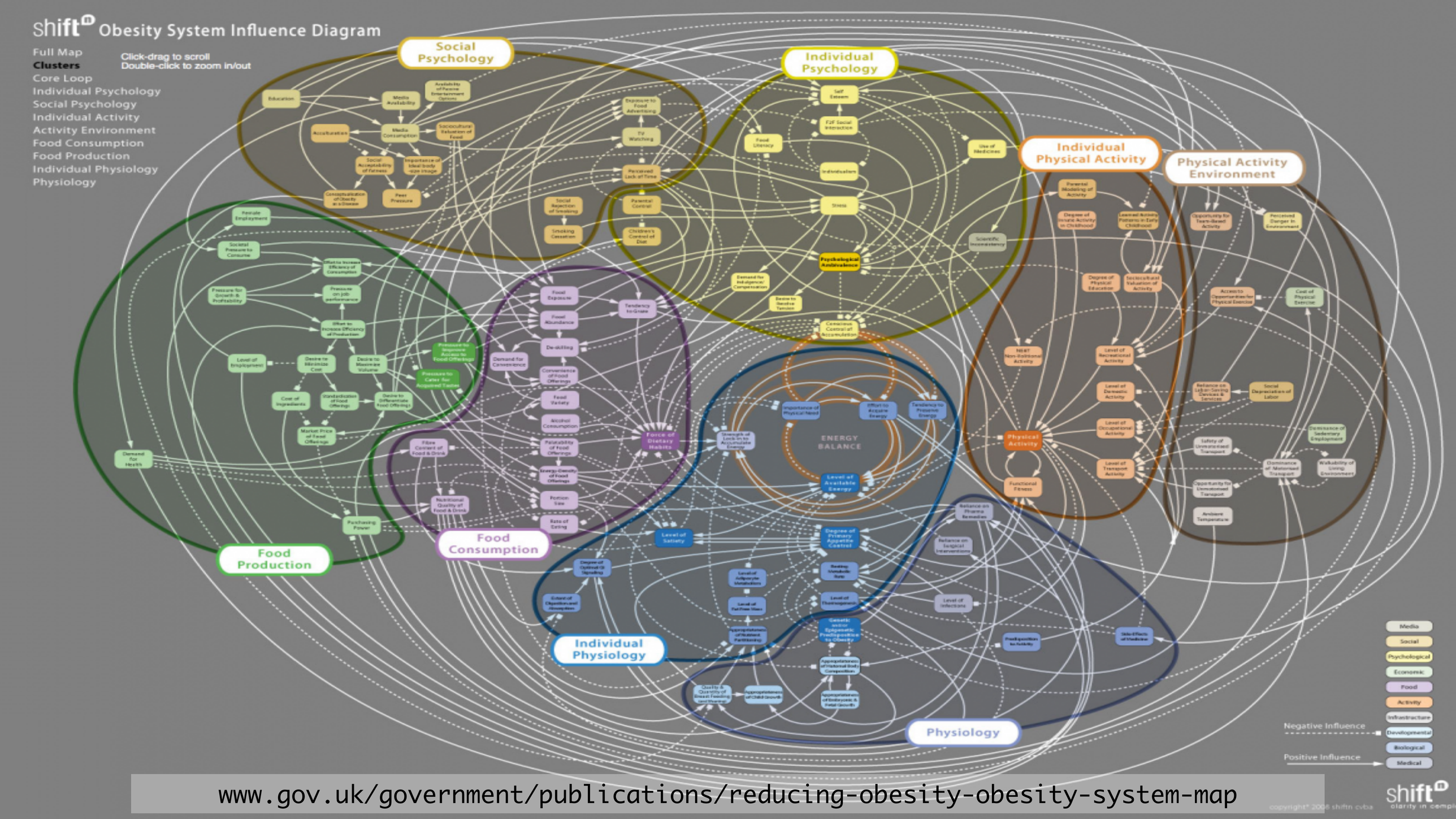
LA MENTE SI PARLA: LA **COMPLESSITÀ**

DELLE CONNESSIONI CEREBRALI

complexity: *not* like this



http://www.ducatimeccanica.com/single_engine.jpg


shift Obesity System Influence Diagram
Full Map
Clusters
Core Loop
Individual Psychology
Social Psychology
Individual Activity
Activity Environment
Food Consumption
Food Production
Individual Physiology
Physiology
Click-drag to scroll
Double-click to zoom in/out
Social Psychology
Individual Psychology
Individual Physical Activity
Physical Activity Environment
Food Production
Food Consumption
Individual Physiology
Physiology
ENERGY BALANCE
Negative Influence
Positive Influence
Media
Social
Psychological
Economic
Food
Activity
Infrastructure
Developmental
Biological
Medical
www.gov.uk/government/publications/reducing-obesity-obesity-system-map
copyright© 2008 shiftn cvba
shift
clarity in complexity

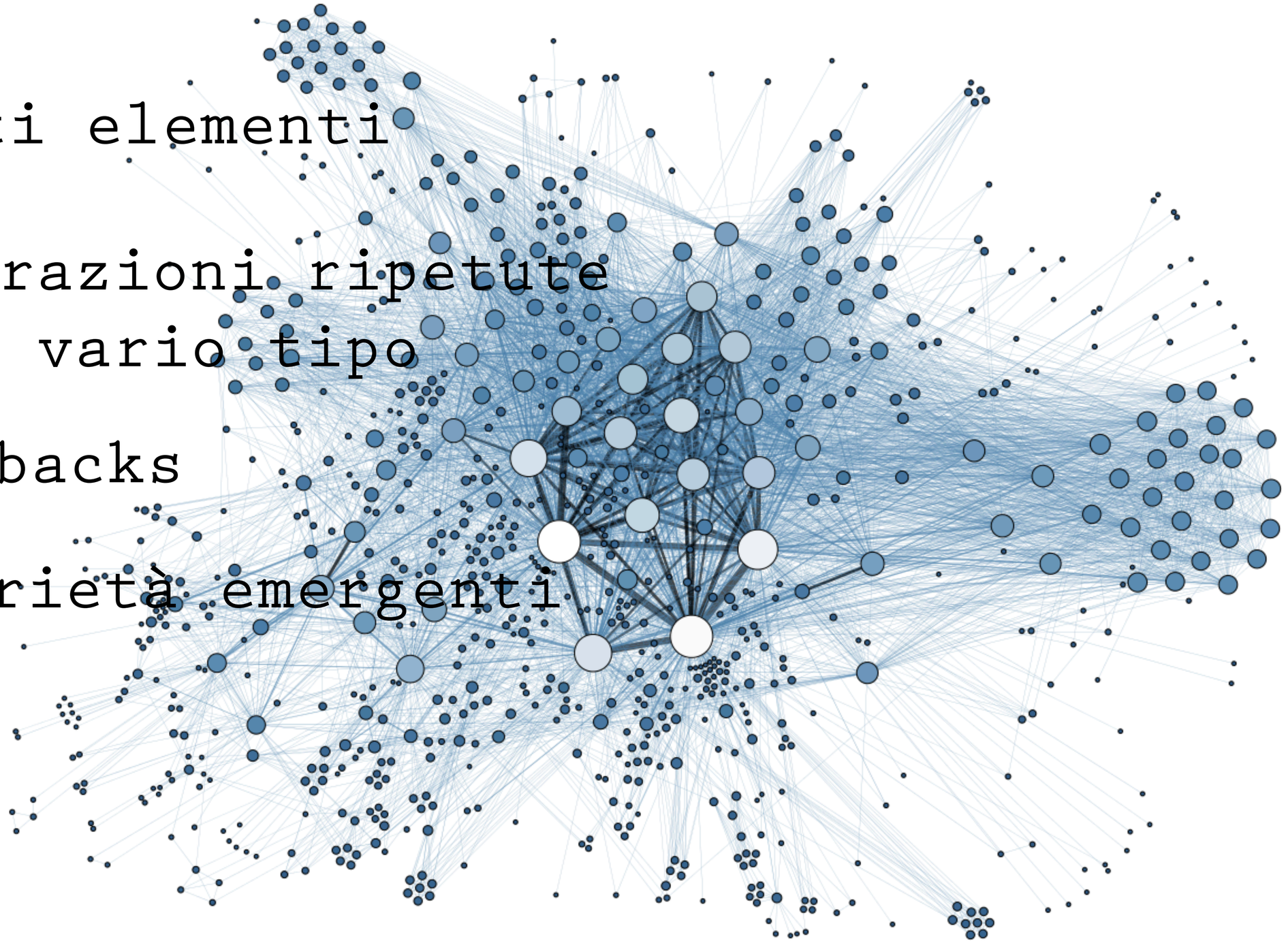
facebook
YouTube
Instagram
XING
facebook

Molti elementi

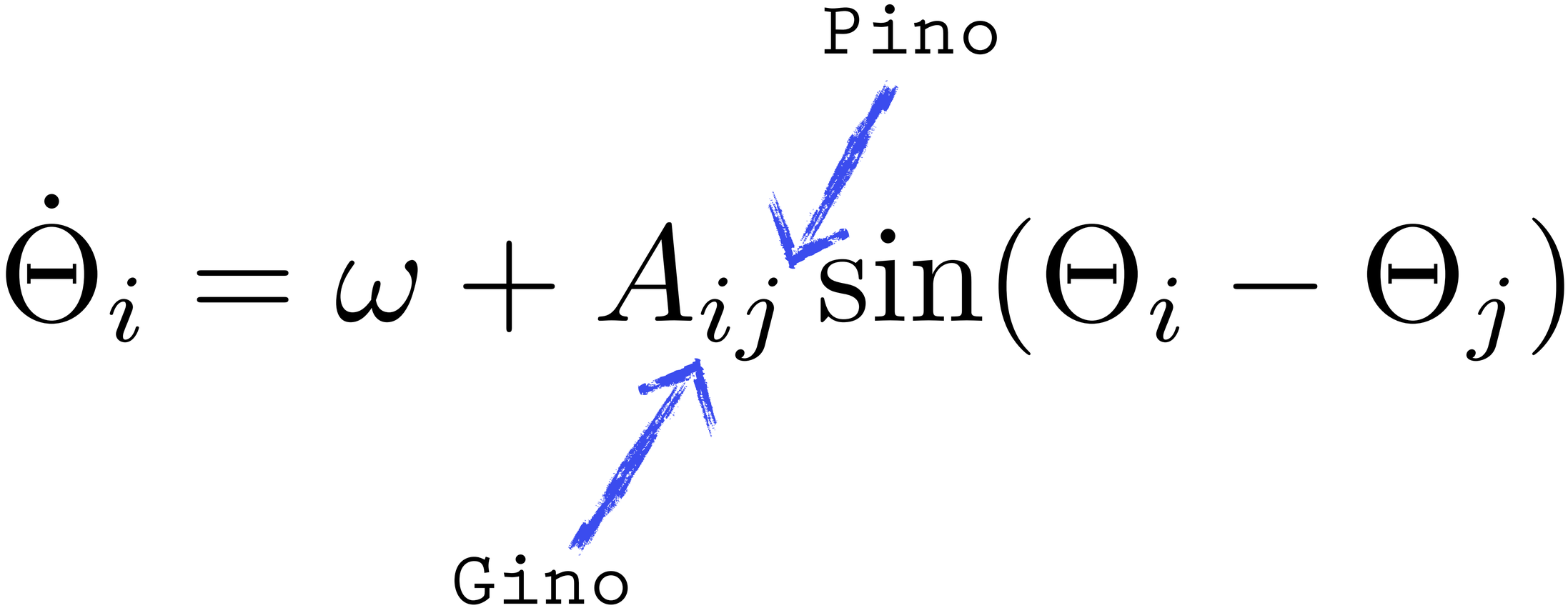
Interazioni ripetute
e di vario tipo

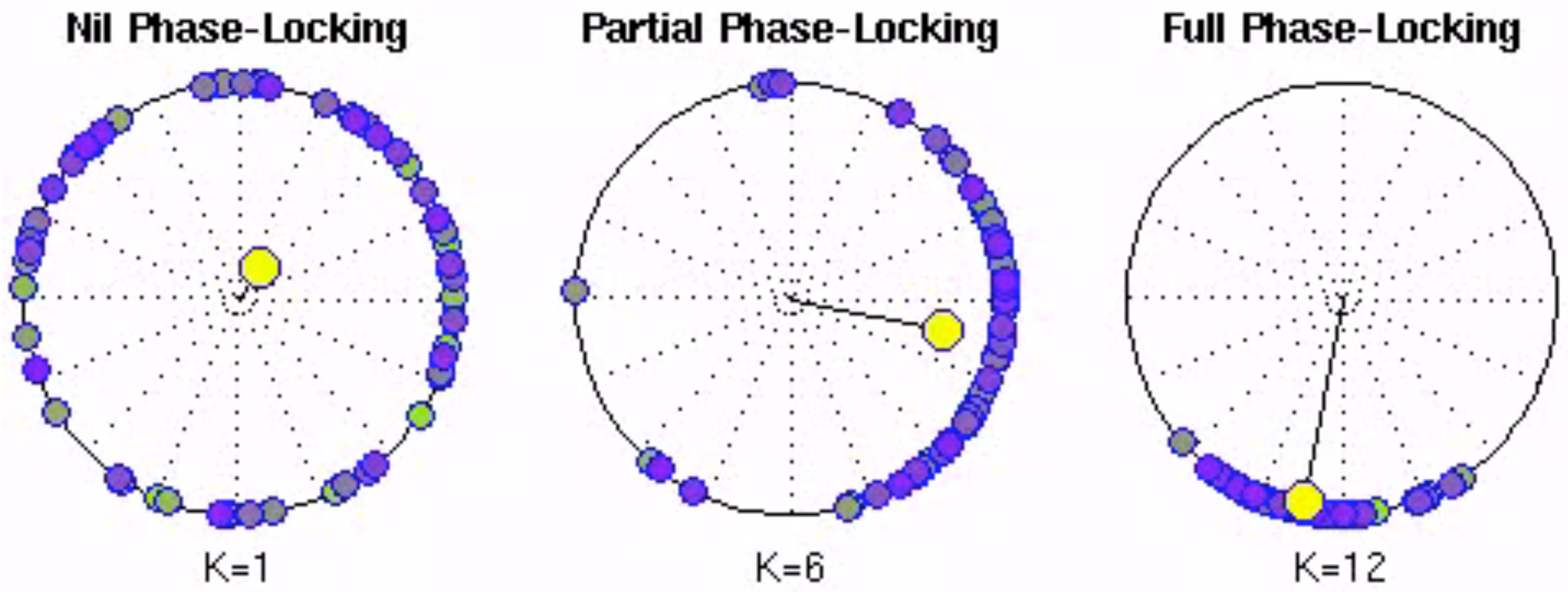
Feedbacks

Proprietà emergenti

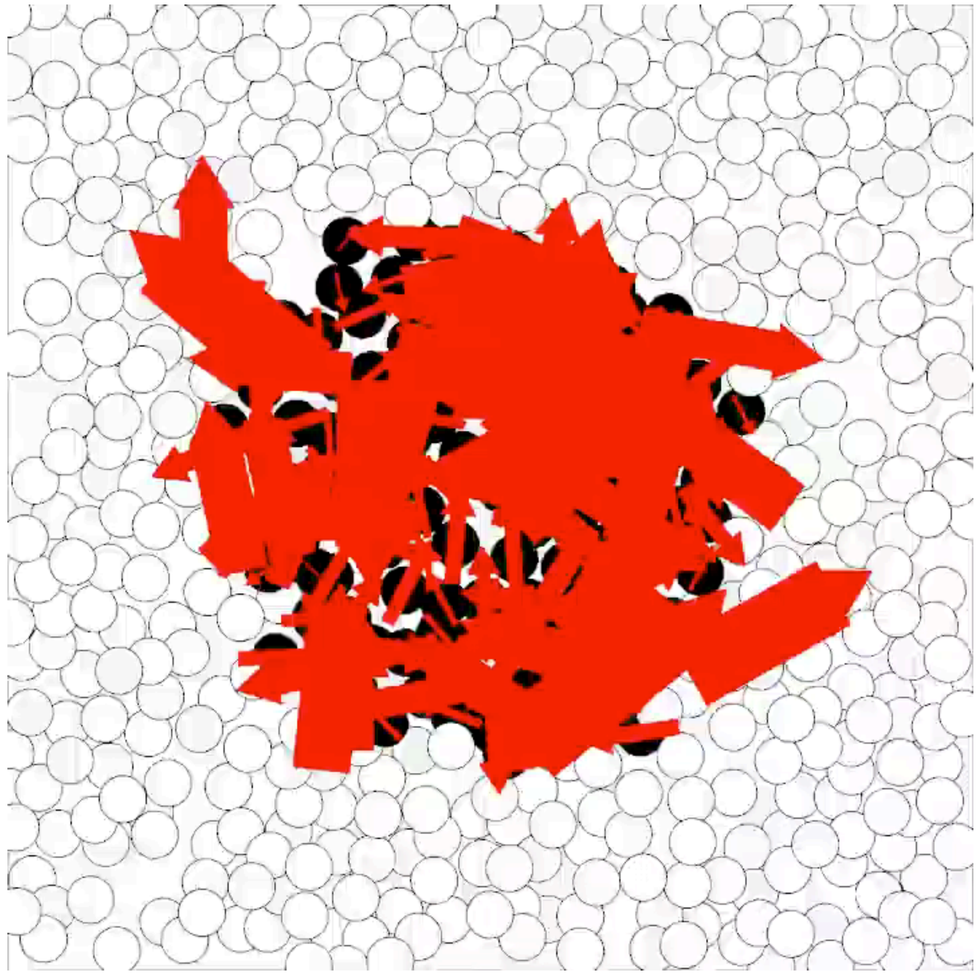


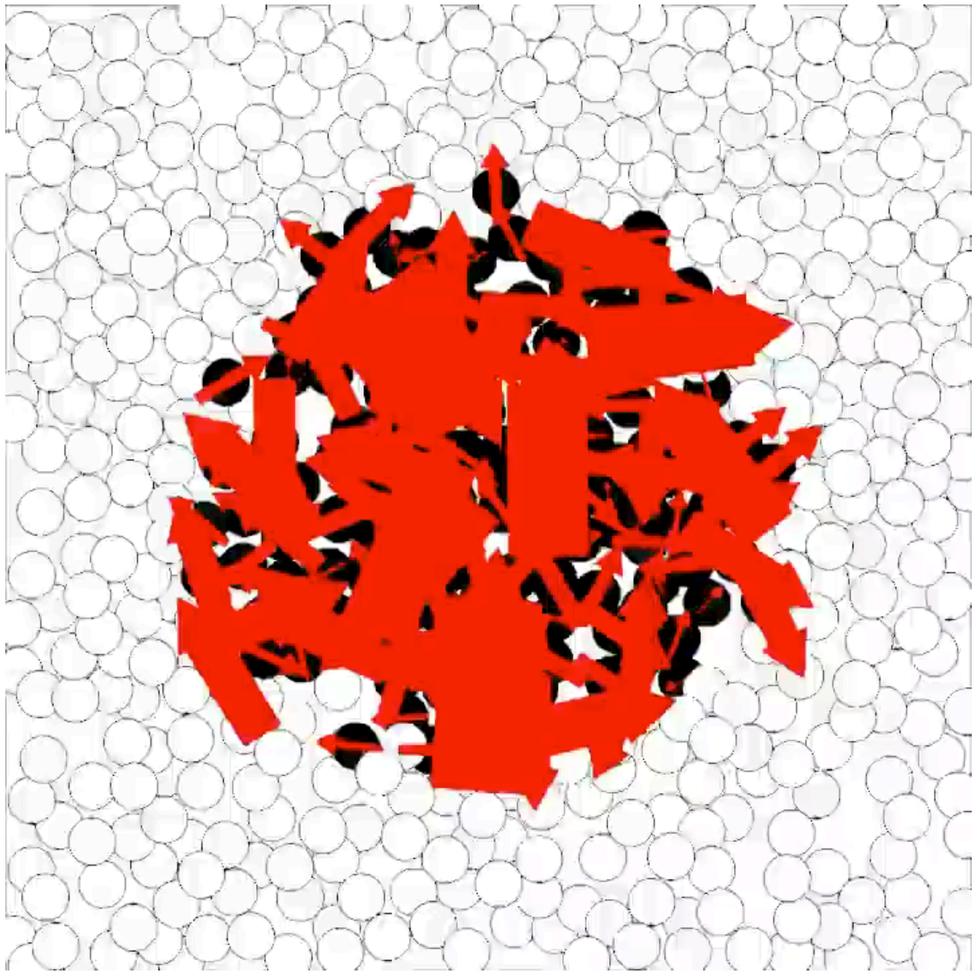
PATHÉ


Pino
$\dot{\Theta}_i = \omega + A_{ij} \sin(\Theta_i - \Theta_j)$
Gino



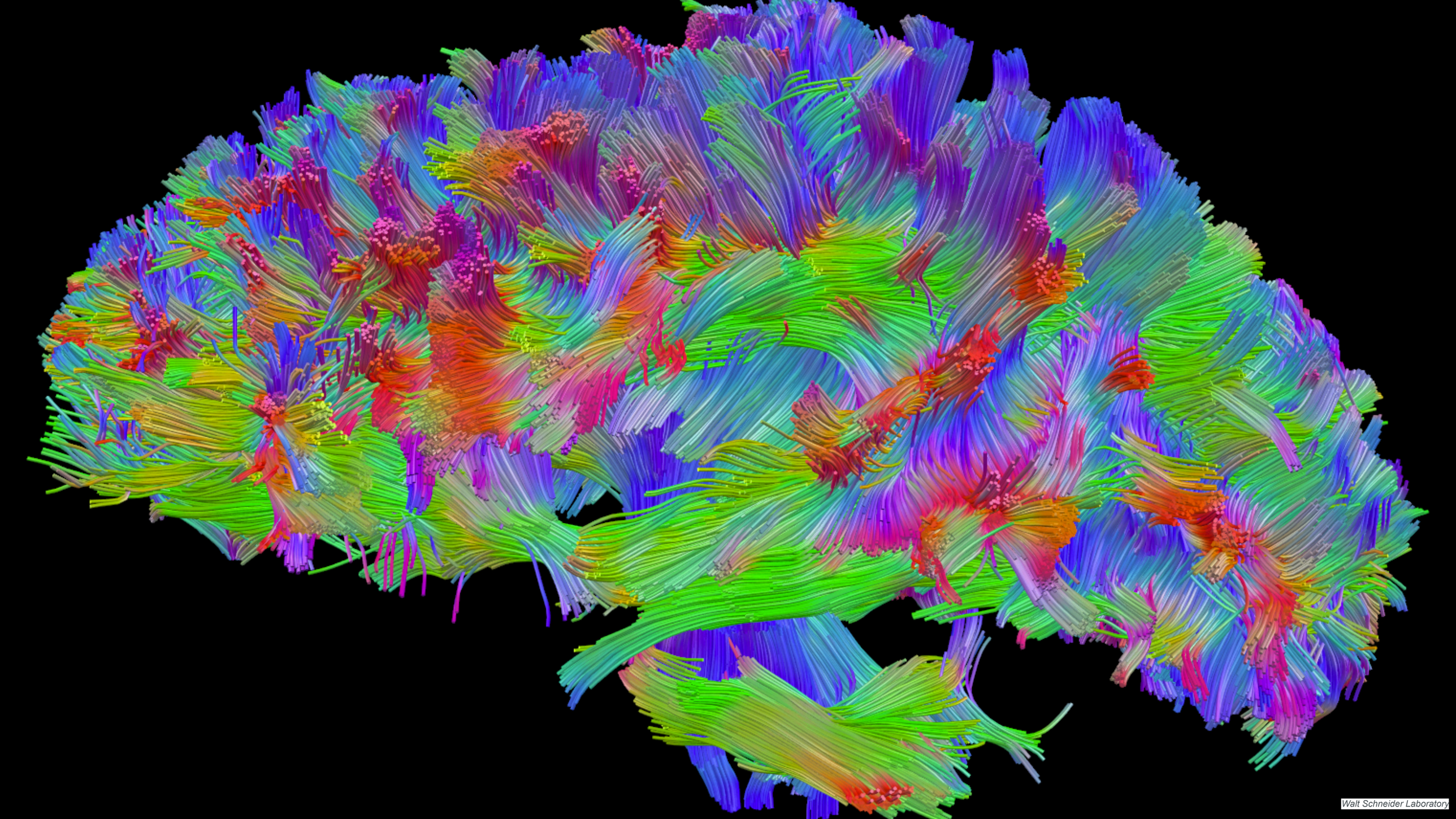
$$\dot{\Theta}_i = \omega + A_{ij} \sin(\Theta_i - \Theta_j)$$





Hallatschek and co-author Daniel Fisher of Stanford University

NASA


Walt Schneider Laboratory

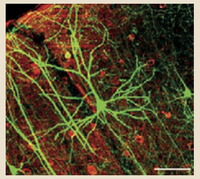
Network measurement

High-throughput molecular screening

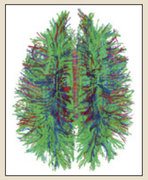
Statistical associations

Molecular binding

High-resolution anatomical mapping

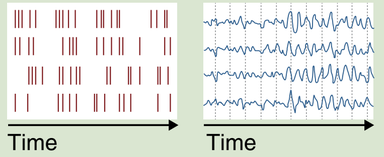


Synaptic connections



Projections

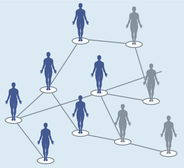
High-density functional recording



Statistical dependence
Causal efficacy
Information flow

High-volume behavioral tracking

Individual: sensorimotor coupling

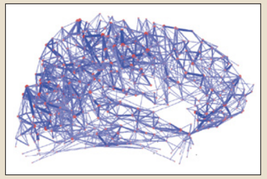


Collective: social interactions

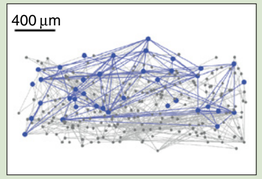
Network construction

Statistical inference, normalization, quality control, reduction of measurement bias and noise, artifact detection/elimination

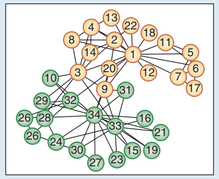
Transcriptome interactome



Connectome

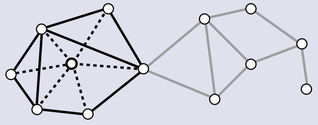


Functional/effective connectivity

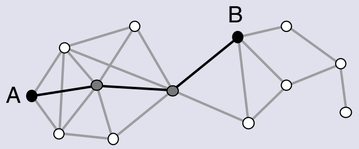


Social network

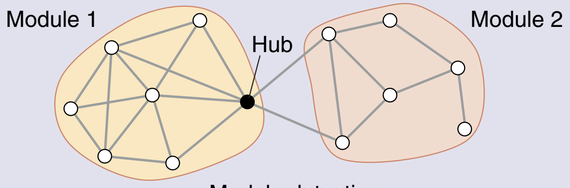
Network analysis



Local topology (degree, clustering)



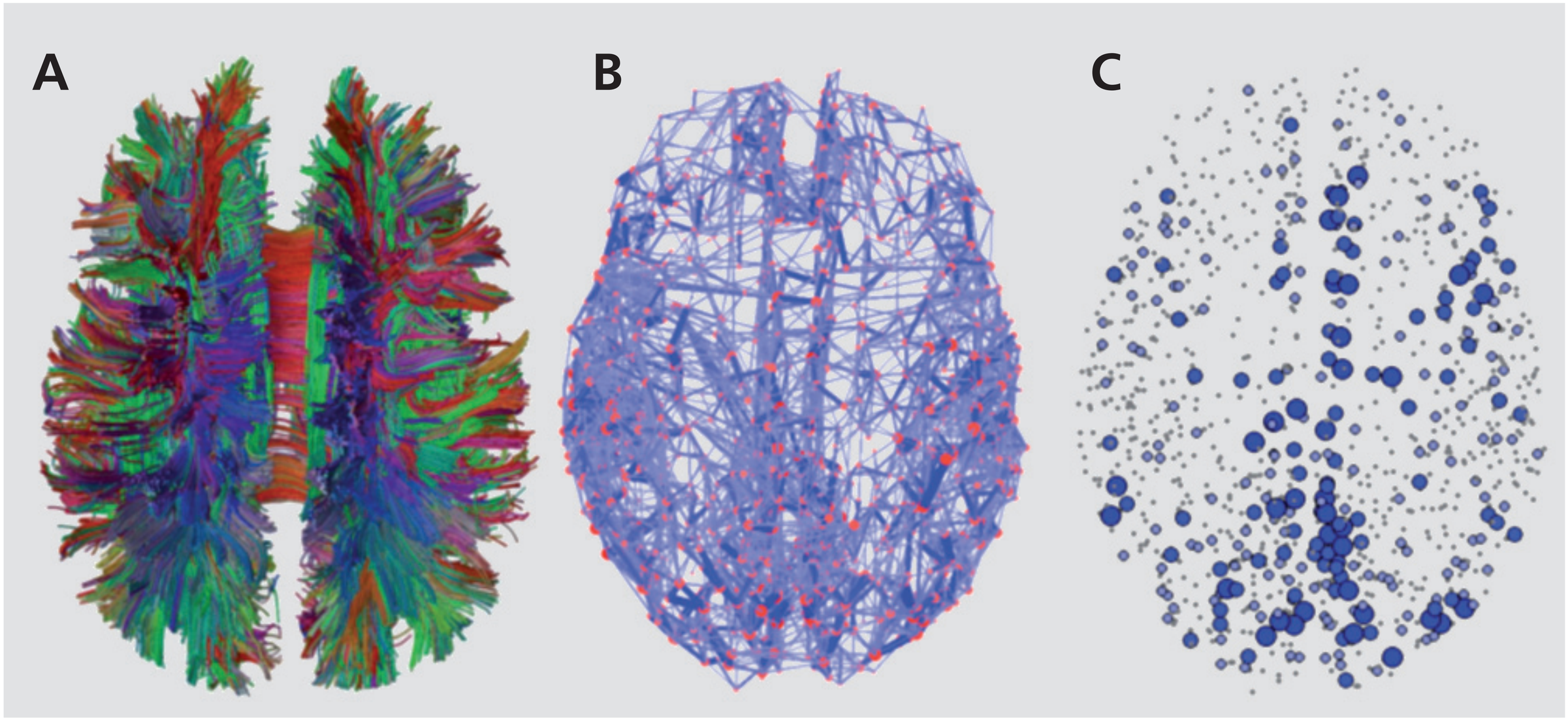
Paths, distances, communication

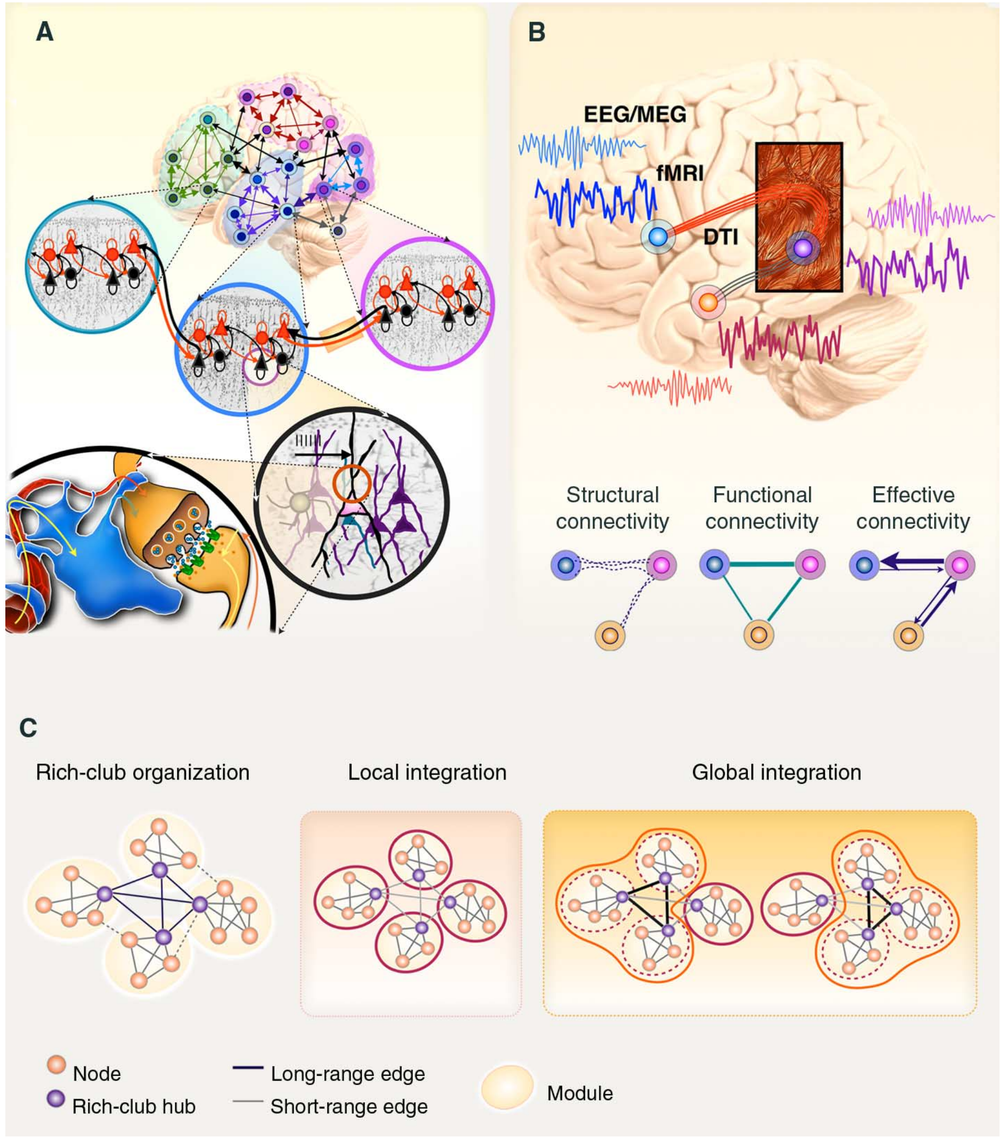


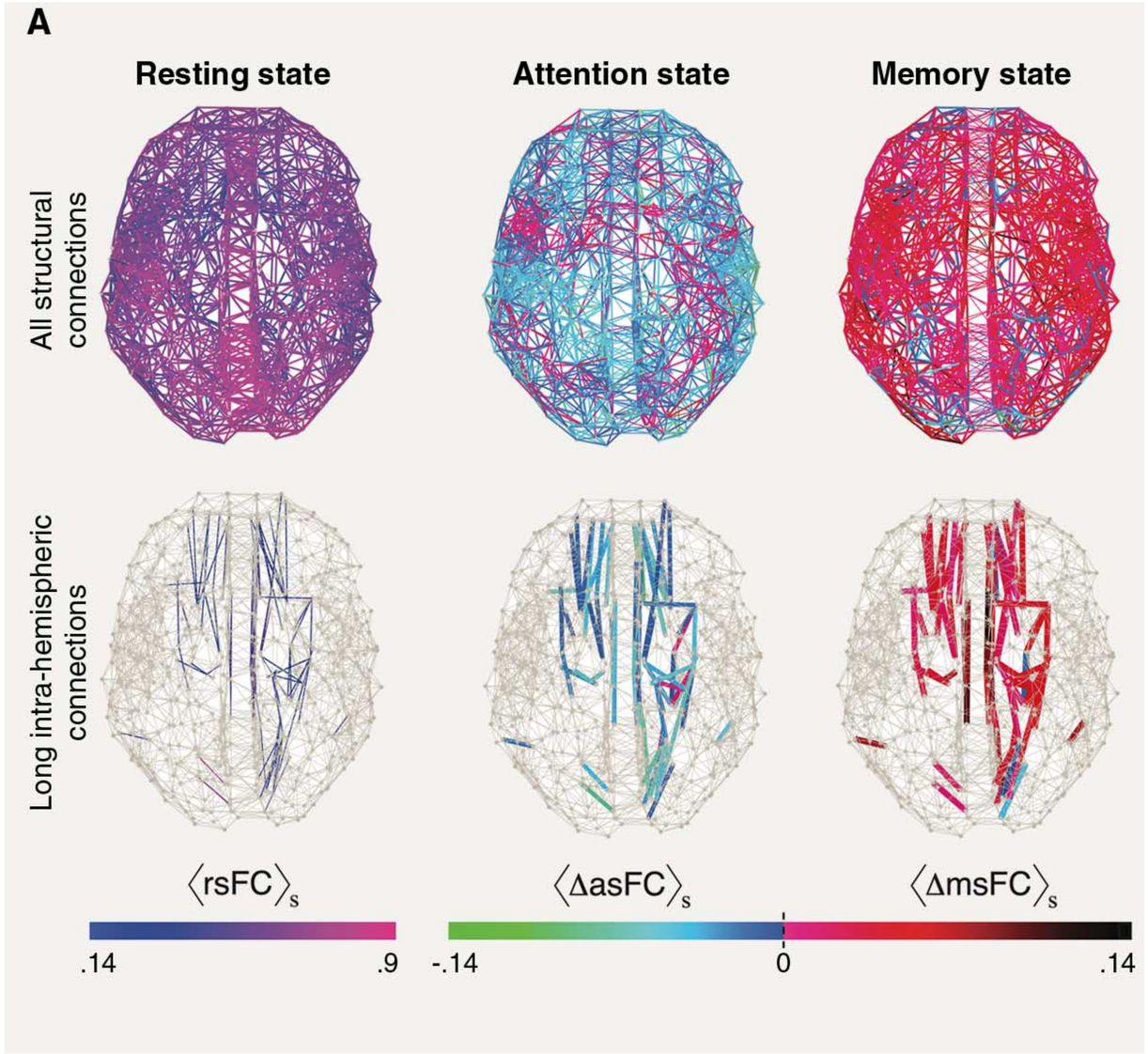
Module detection centrality

Data sharing and deposition in bio/neuroinformatics data banks, visualization, computer simulation and integrative modeling, experimental validation, refinement of measurement and analysis techniques

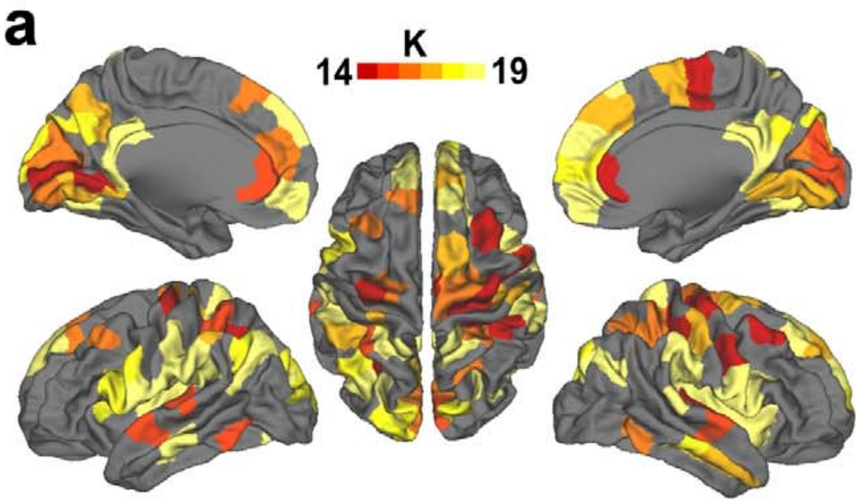
OK, so what?

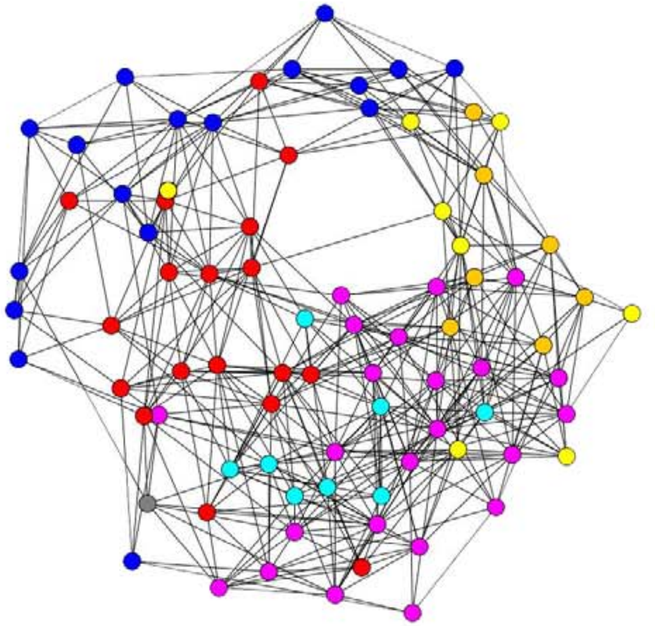

A
B
C

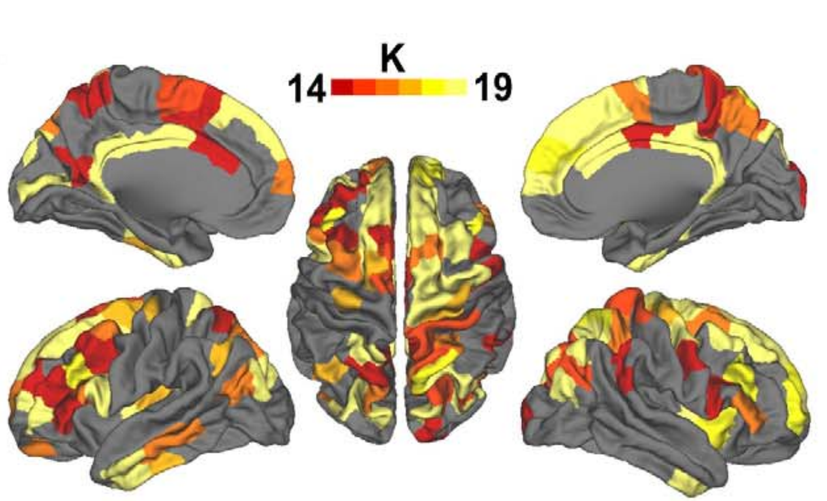


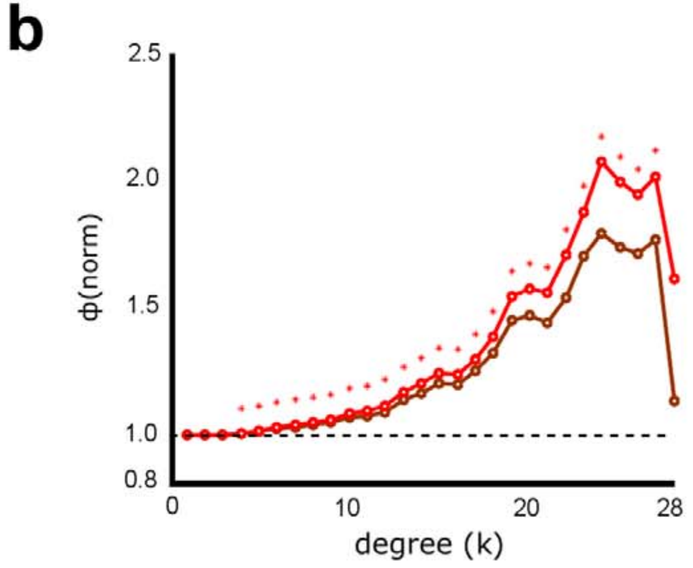


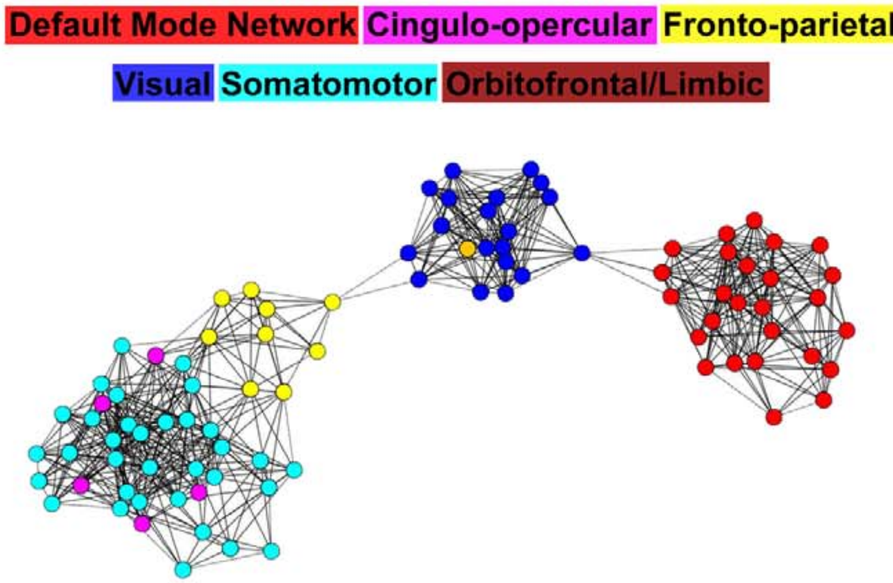
Park and Friston 2013

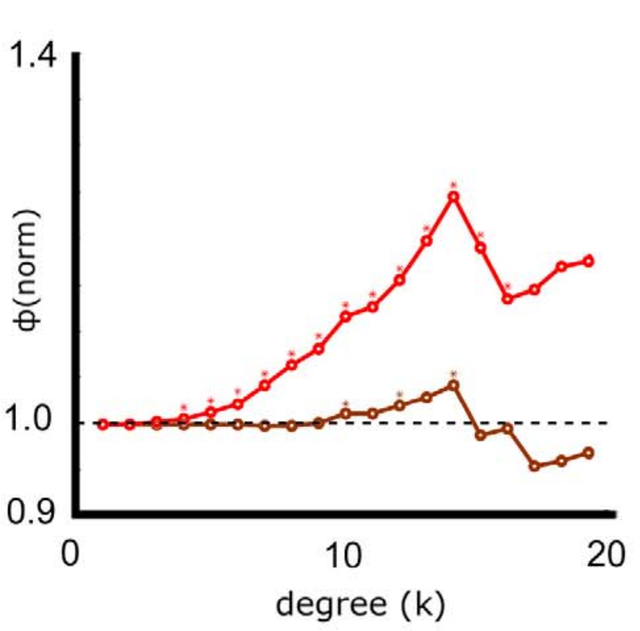












Grayson et al 2013

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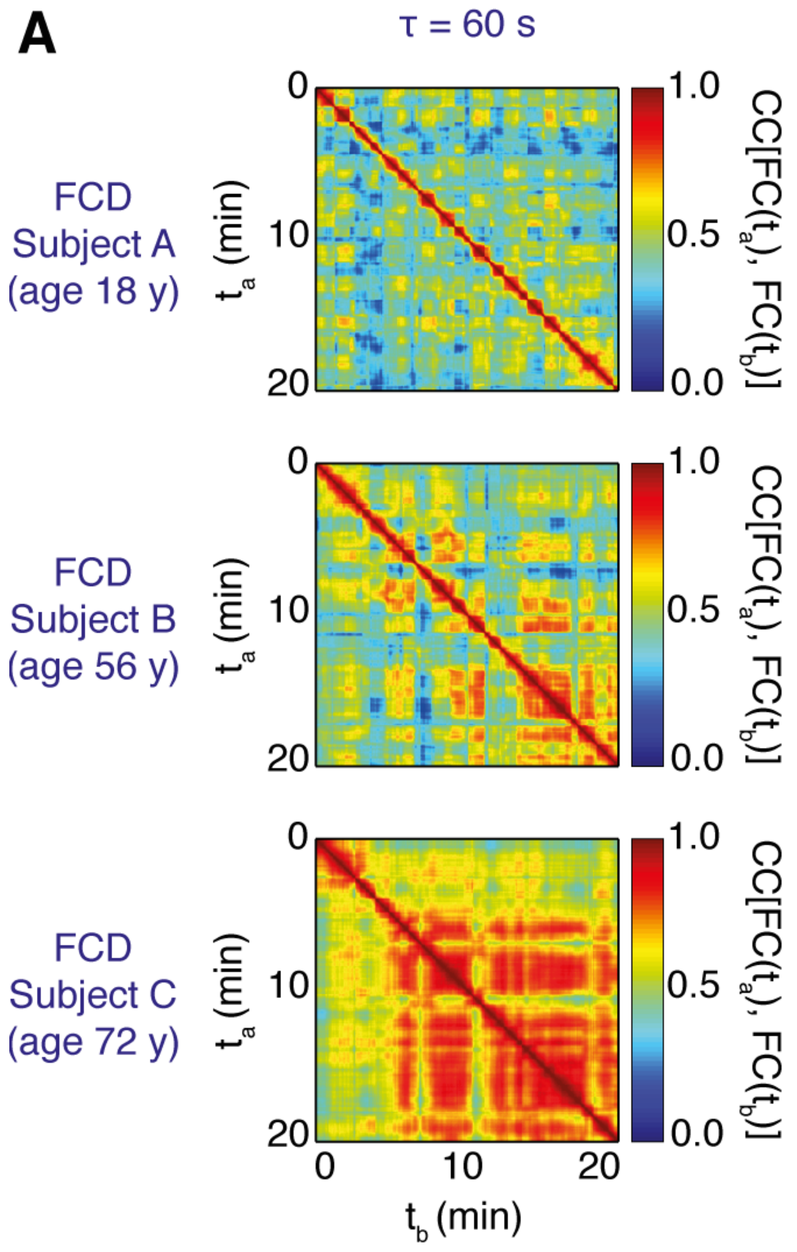
rsif.royalsocietypublishing.org

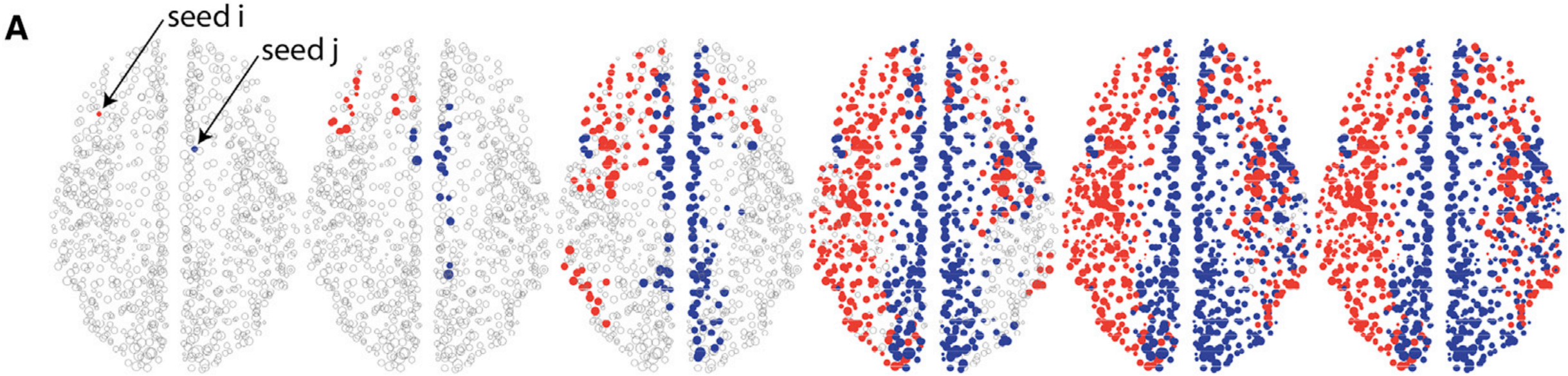
Homological scaffolds of brain functional networks

G. Petri[1], P. Expert[2], F. Turkheimer[2], R. Carhart-Harris[3], D. Nutt[3], P. J. Hellyer[4] and F. Vaccarino[1,5]



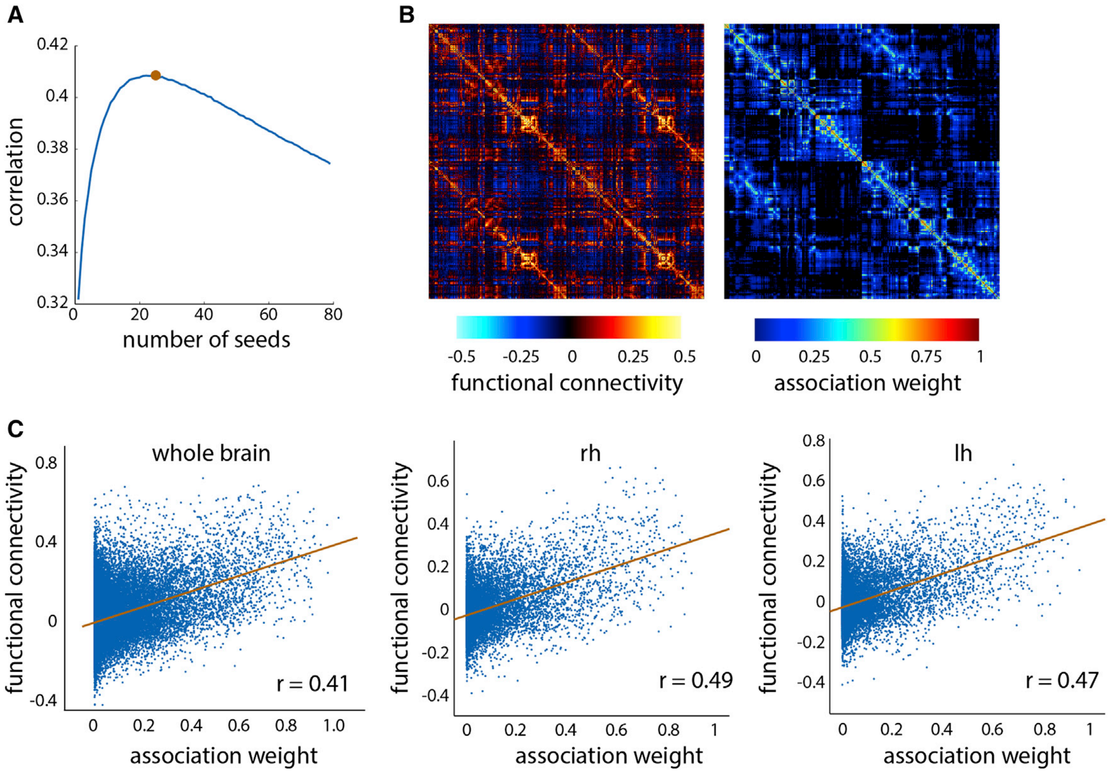
Battaglia et al. 2017

Simple models?



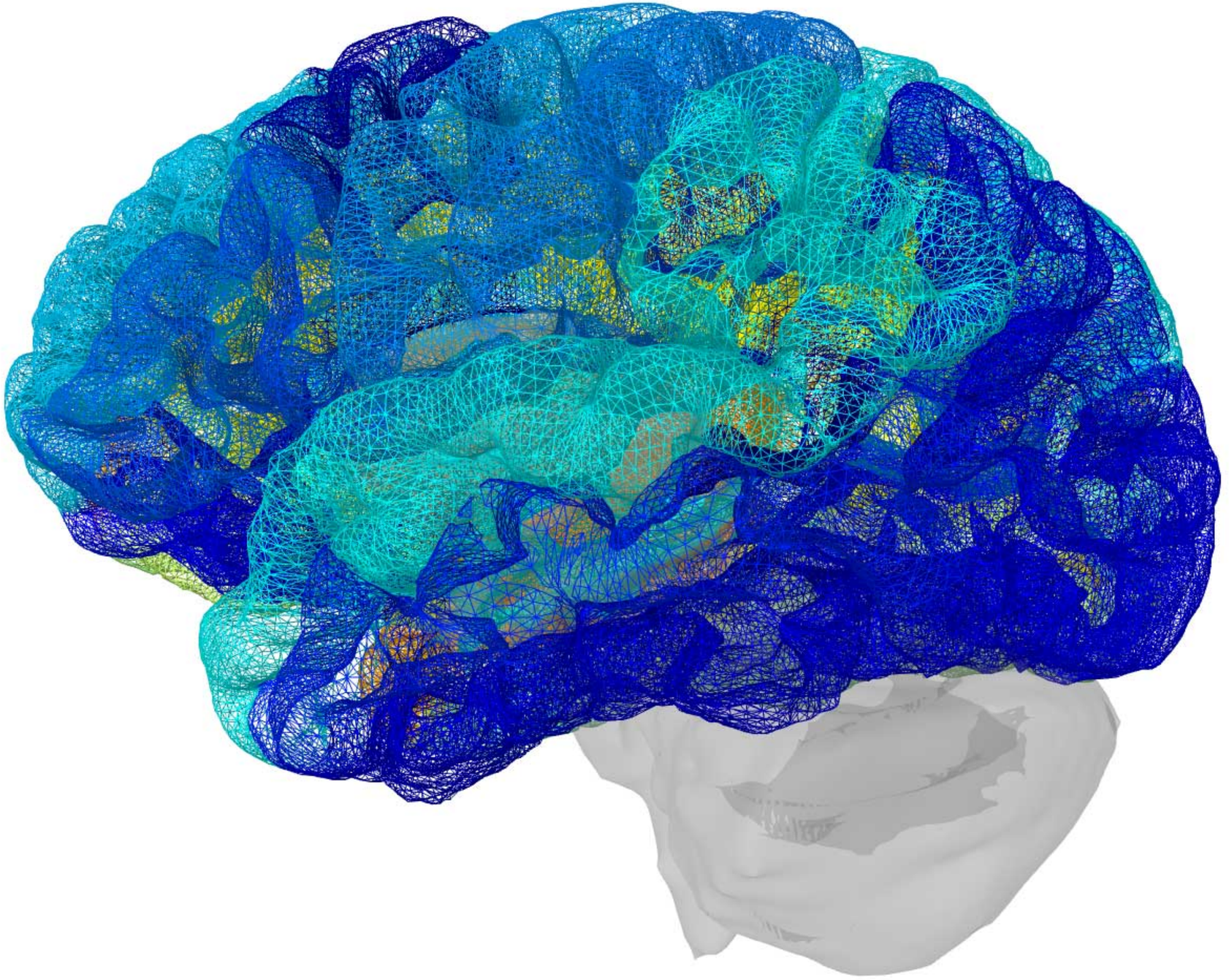
Highlights

- We use a simple model to study global spreading dynamics on human brain networks
- Hub regions and a backbone of core pathways facilitate early spreading of cascades
- Shortest path structure of brain networks accelerates spreading
- Cascades integrate by converging on polysensory associative areas

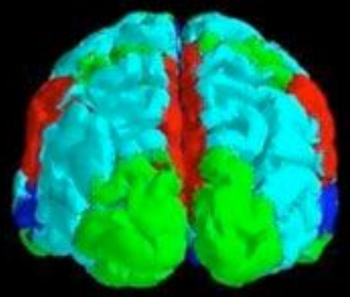


Misic et al. 2015

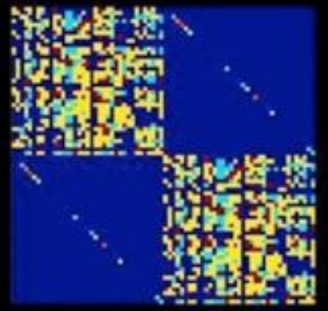
Mmmm can we simulate?



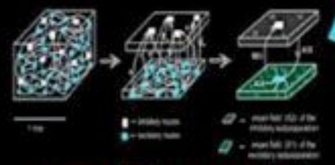
WWW.THEVIRTUALBRAIN.ORG



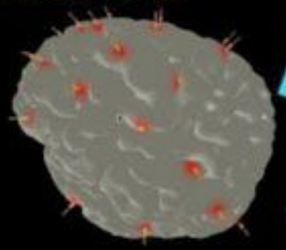
cortical surface



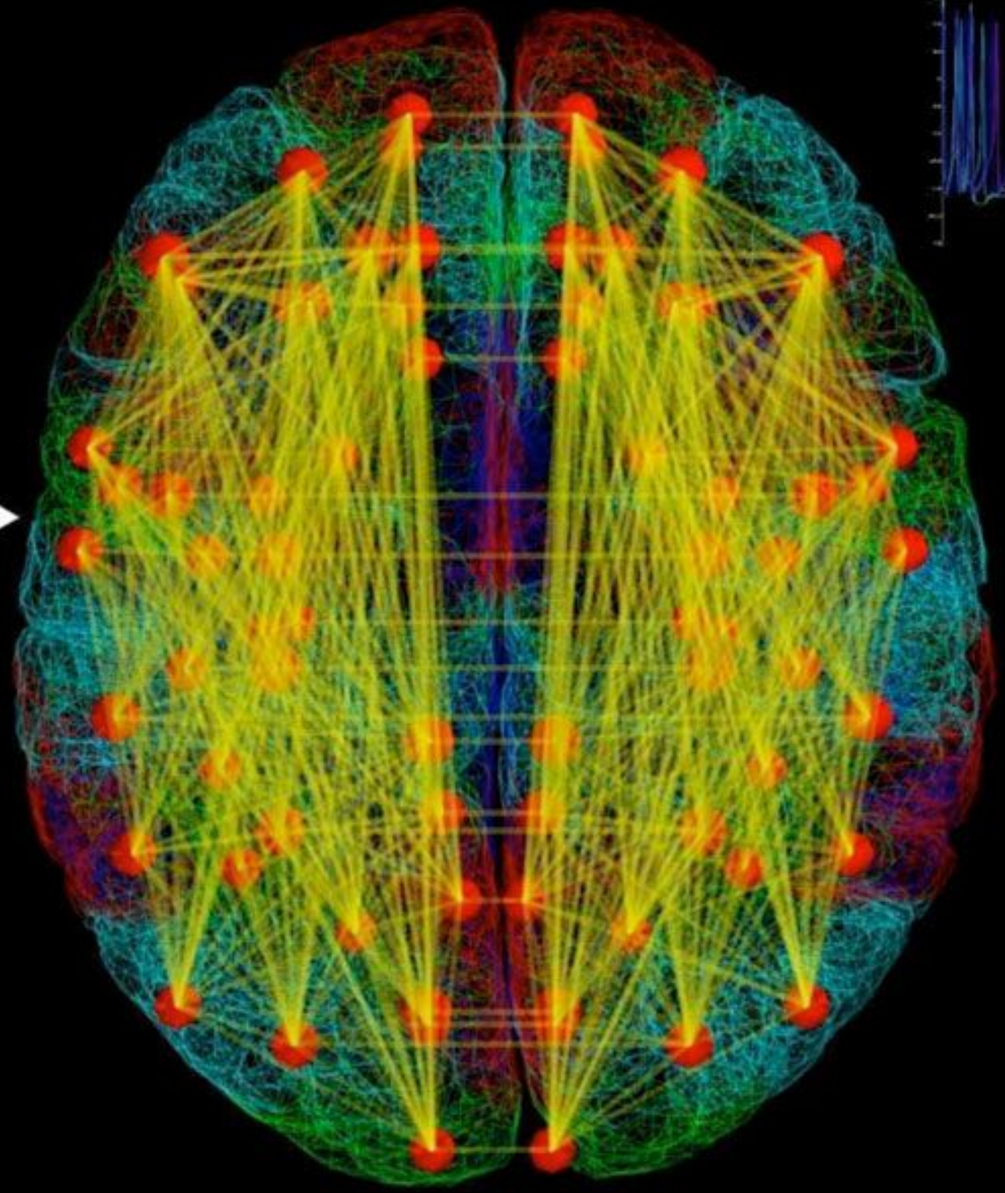
connectivity matrix

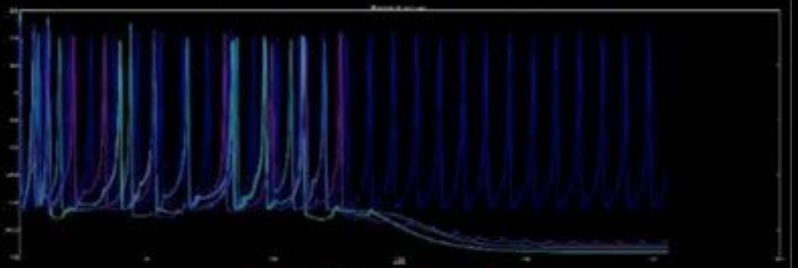


population model

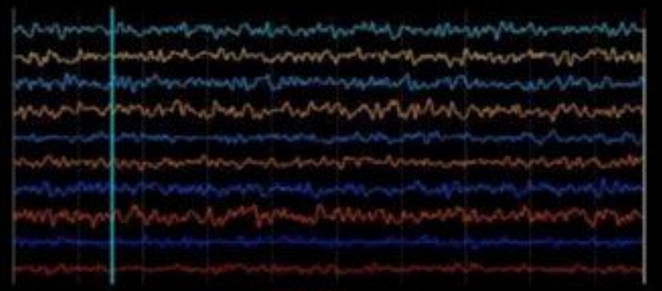


stimulation

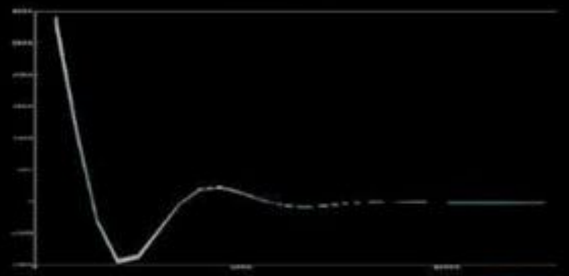




raw time series

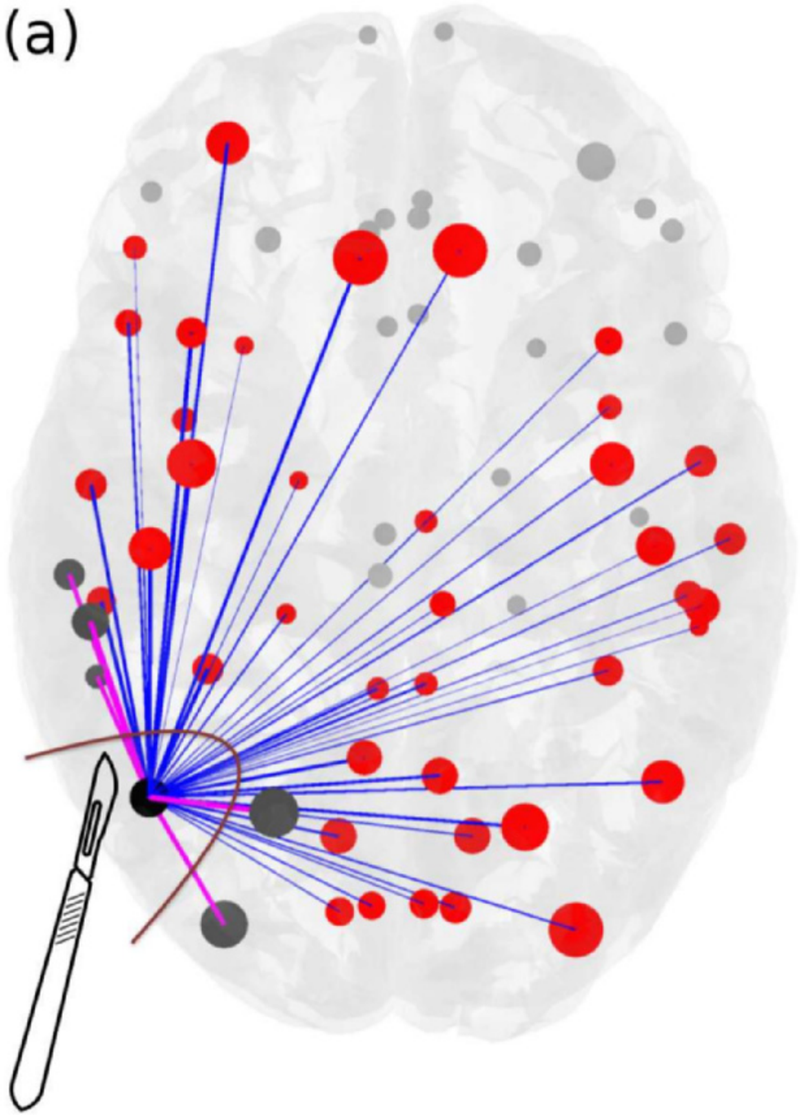


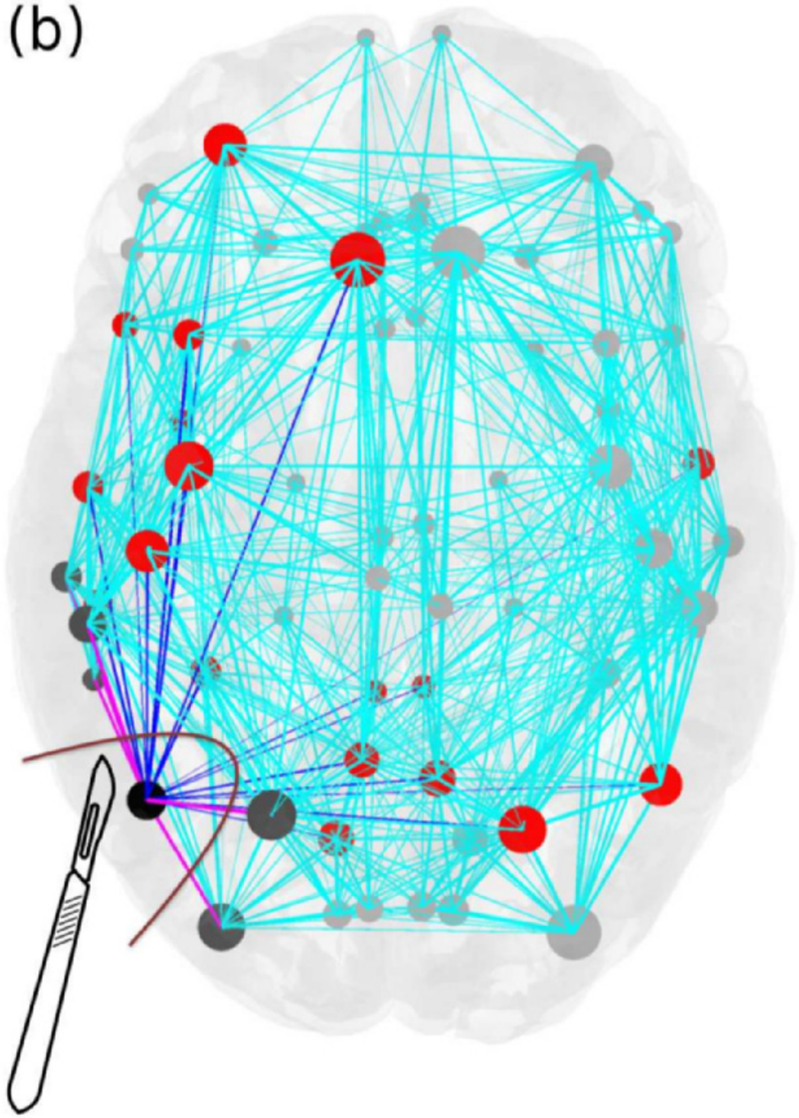
eeg

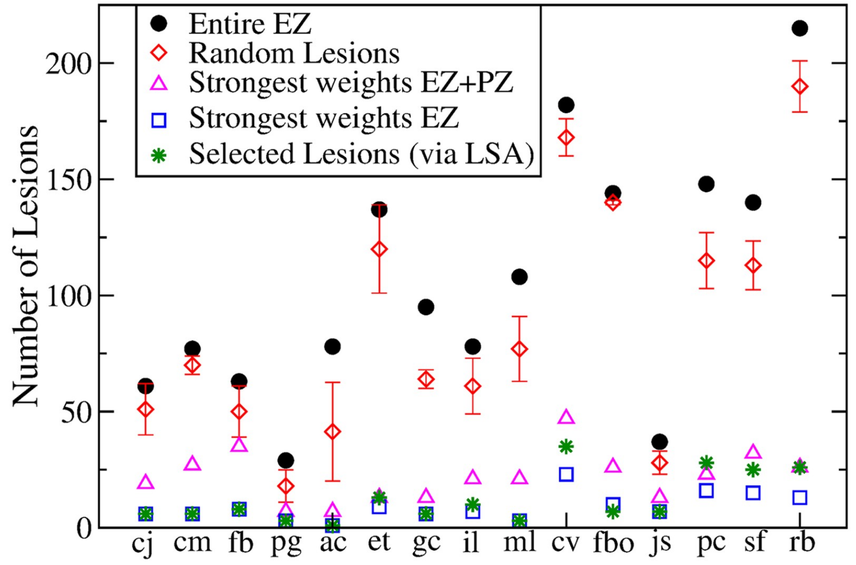


BOLD

THEVIRTUALBRAIN.

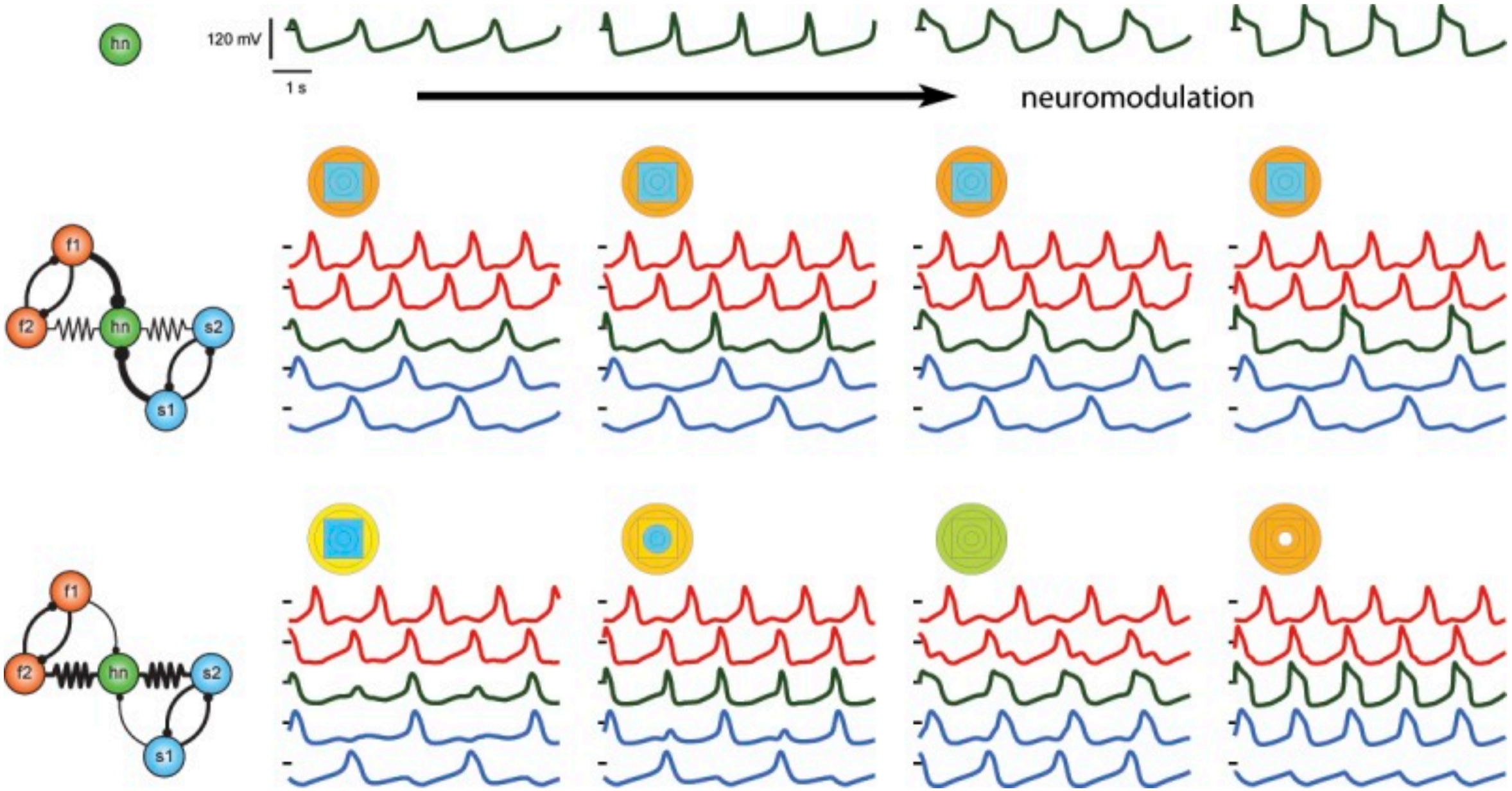




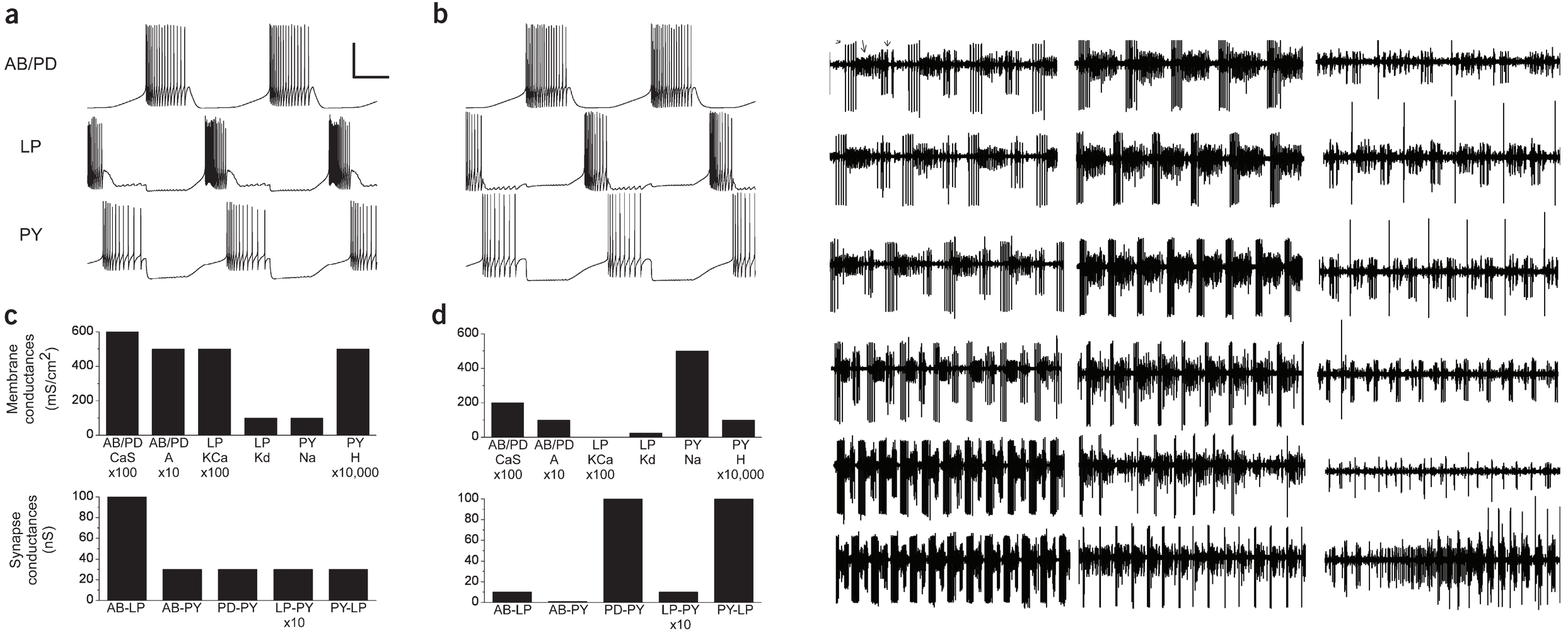


Olmi et al, 2018

But…

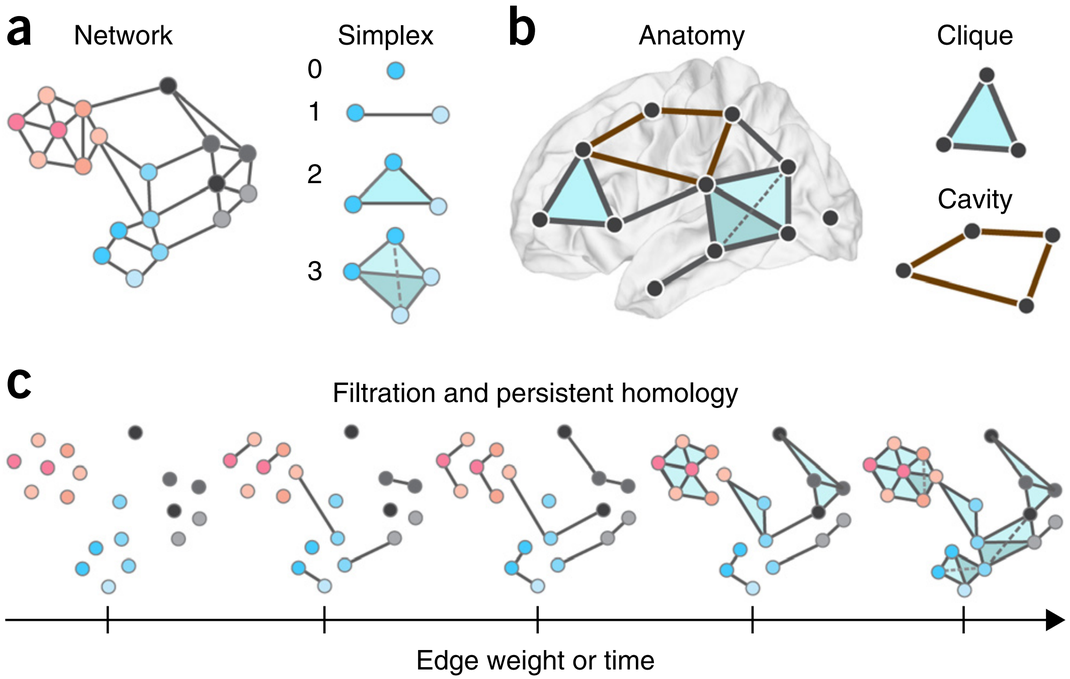


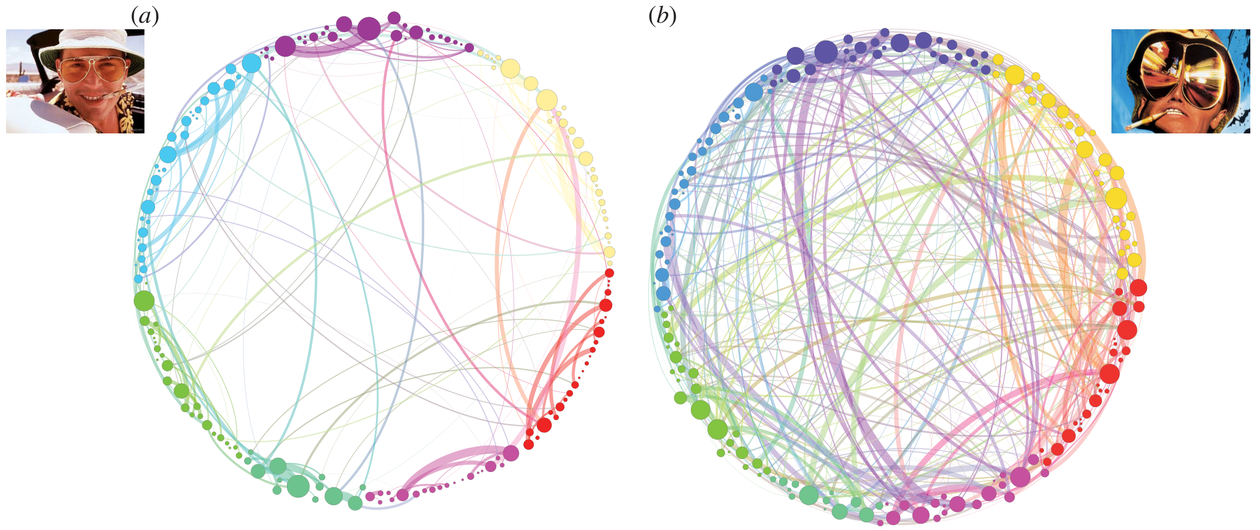
Gutierrez et al 2014

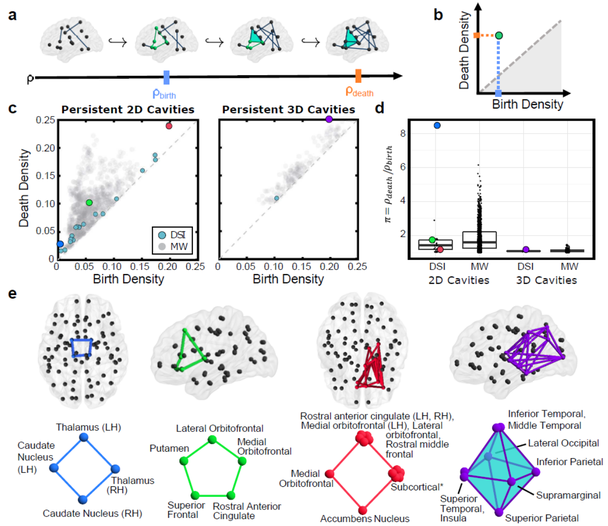


Prinz, Bucher, Marder 2004

Haddad and Marder 2017

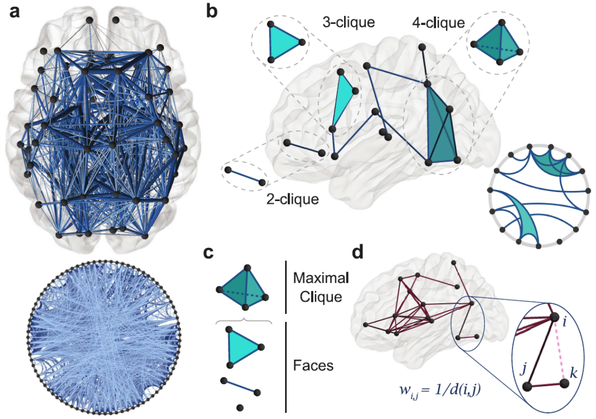


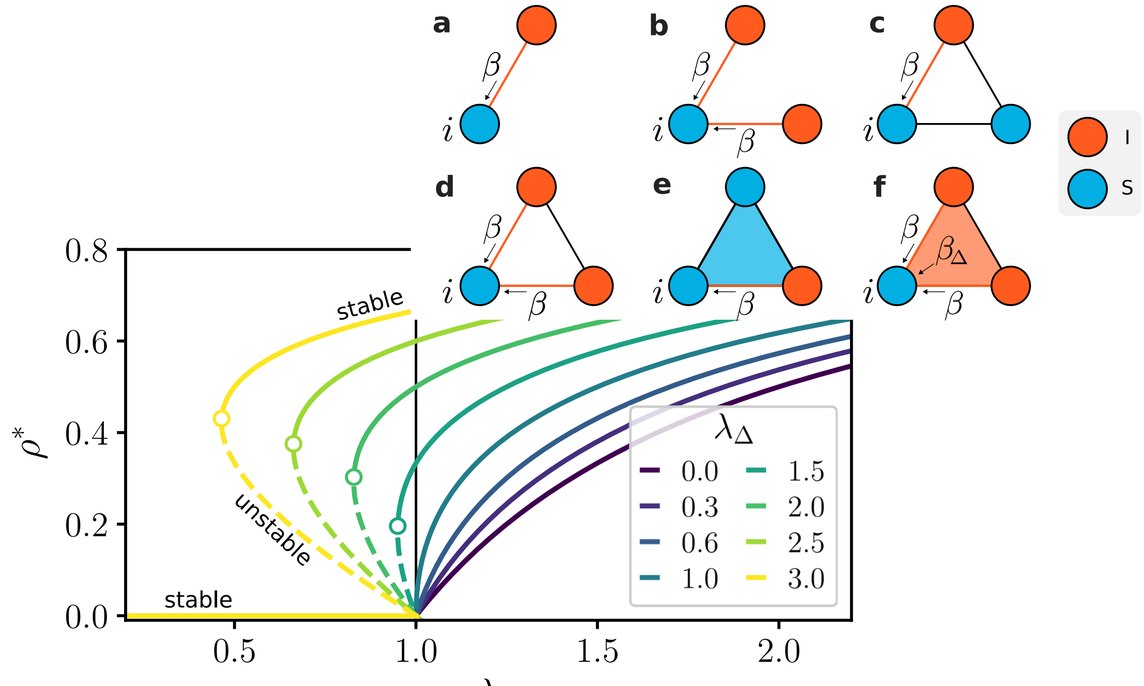




Structural brain cavities

Sizemore, Ann, et al. arXiv:1608.03520 (2016).





INTERPRETAZIONE

ANALISI/SISTEMA

DATI

LA MENTE SI PARLA: LA **COMPLESSITÀ** DELLE CONNESSIONI CEREBRALI

Big Theory versus Big Data, CNS 2018 : Eve Marder (with session intro)

How much ambiguity can each of you live with in your attempt to understand the brain...and what constitutes understanding?

Fictional quotes to explain the point:

“I am still not convinced in the role of large circuit networks, because when I ask they always give me small scale examples.”

Eve Marder,
High-density electroscope

“fMRI is crap, the only thing that I believe in theory-driven hypothesis to be tested with small scale EEG experiments”

My mom,
Old school electrophysiologist

“There is no hope we can reproduce or capture all connectivity/function, so let’s just fit HUGE models and predict”

Jack Gallant,
Bayesian modeller

“There is no way there is a single all-purpose circuit that we learn from data, so we need to look for a multitude of task primitives ”

Gary Marcus,
Famous cognitive DL expert

“I don’t care about tiny-weeny details of this or that receptor, I want normative theories of cognitive control, in simple graph-theoretical terms”

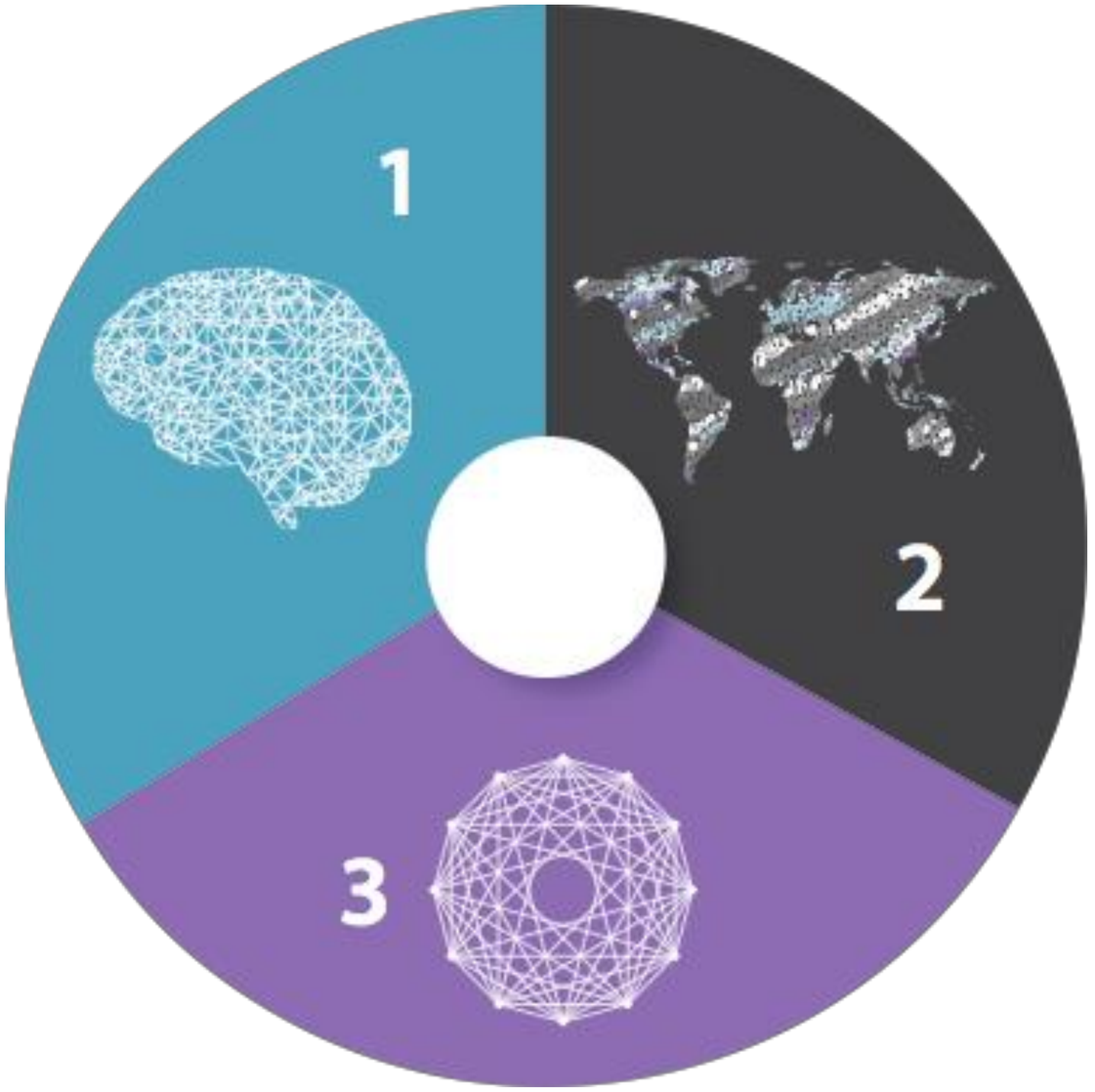
Jon Cohen,
Tsar of Cognitive Control

Take home

- Ci sono tante neuroscienze delle reti
- Feedback continuo fra dati/tecniche/teorie
- Le teorie dipendono dalla scala MA le scale interagiscono
- Shift da leggi a modelli computazionali
- Nuovo significato di “comprendere”

ISI

ISI Foundation
& ISI Global Science
Foundation



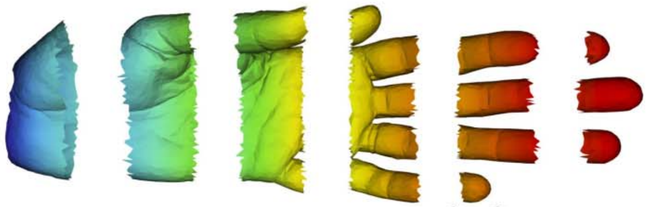
Domande?

Patania, Selvaggi, di Pasquale, Veronese, Expert, Petri (2019) “Topological gene-expression networks recapitulate brain anatomy and function”, in review Net. Neuroscience
https://www.biorxiv.org/content/10.1101/476382v1

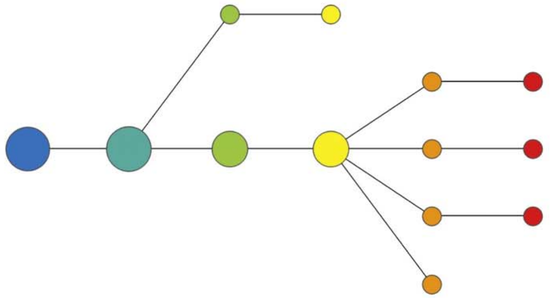
Point cloud

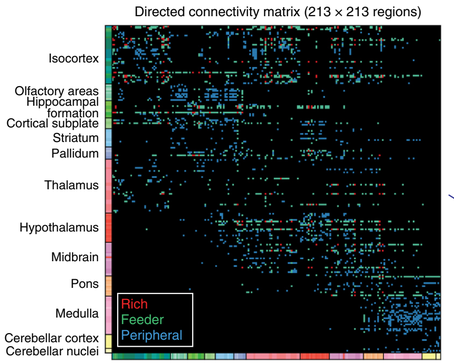
colouring (projecting) using geometric filters

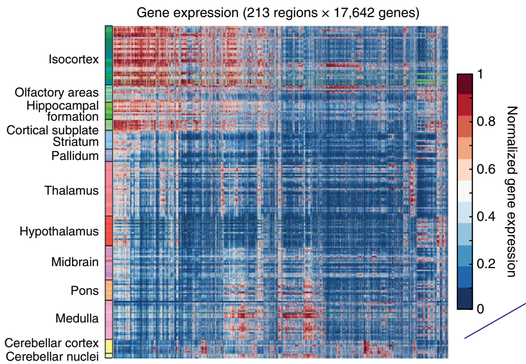
overlapped binning

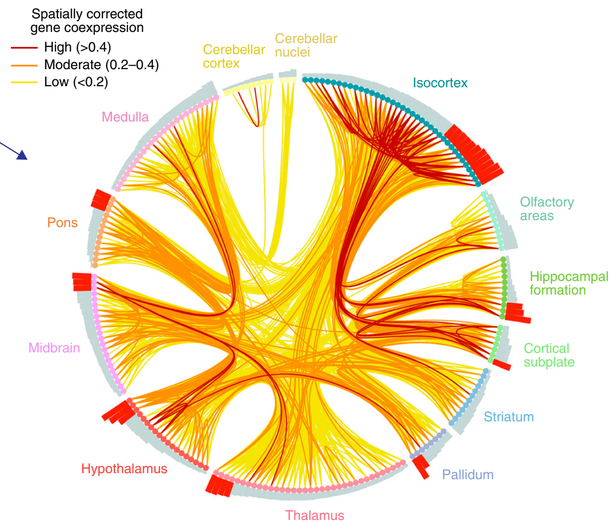


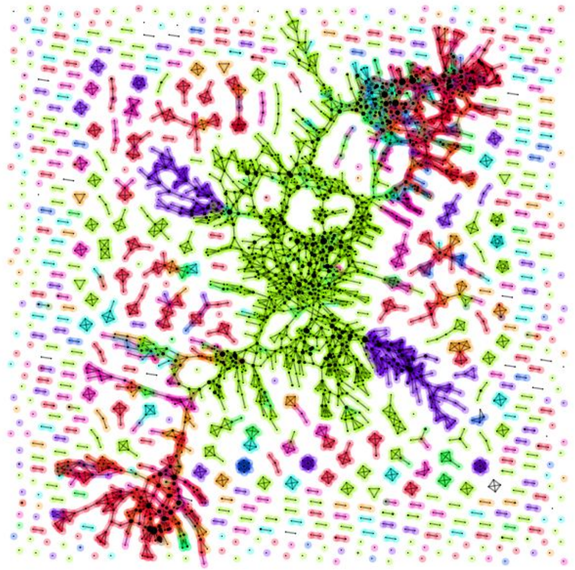
Clustering and network construction binning

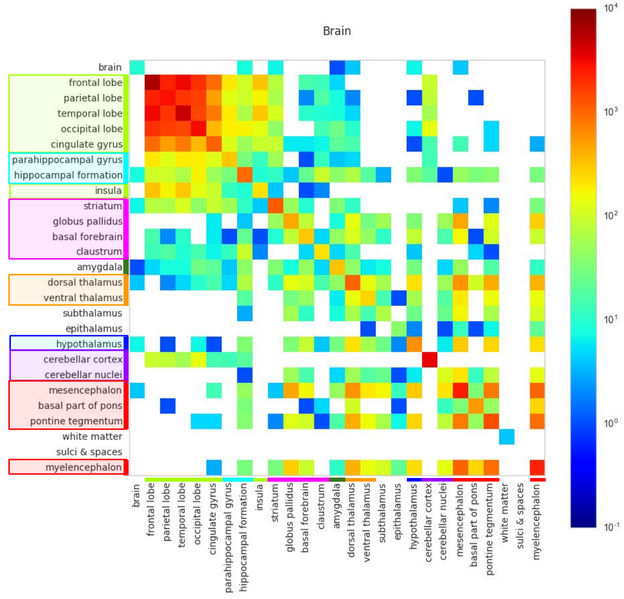


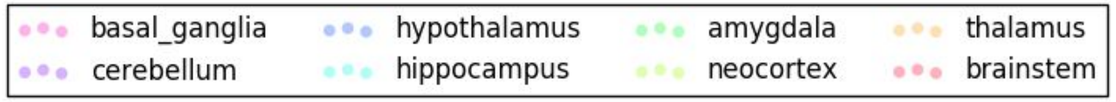




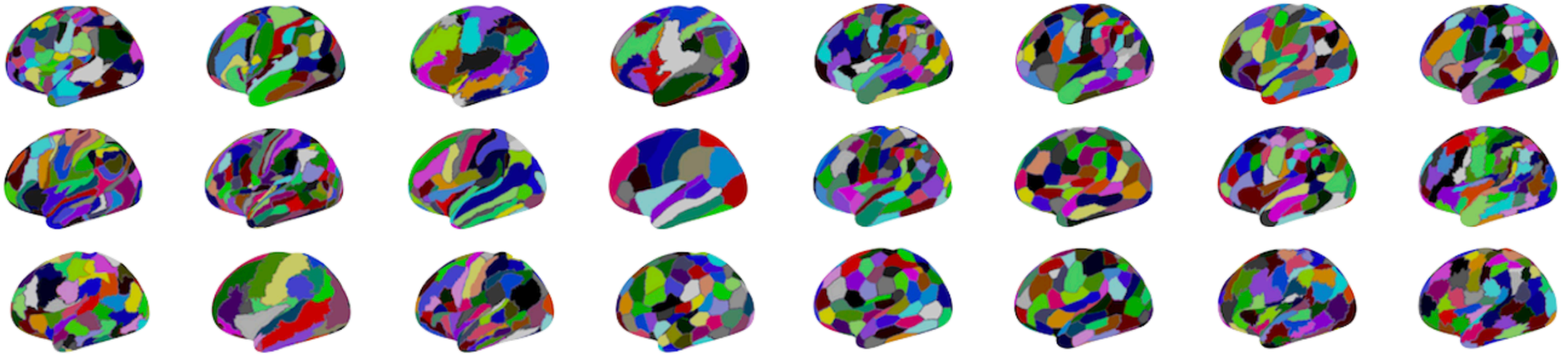








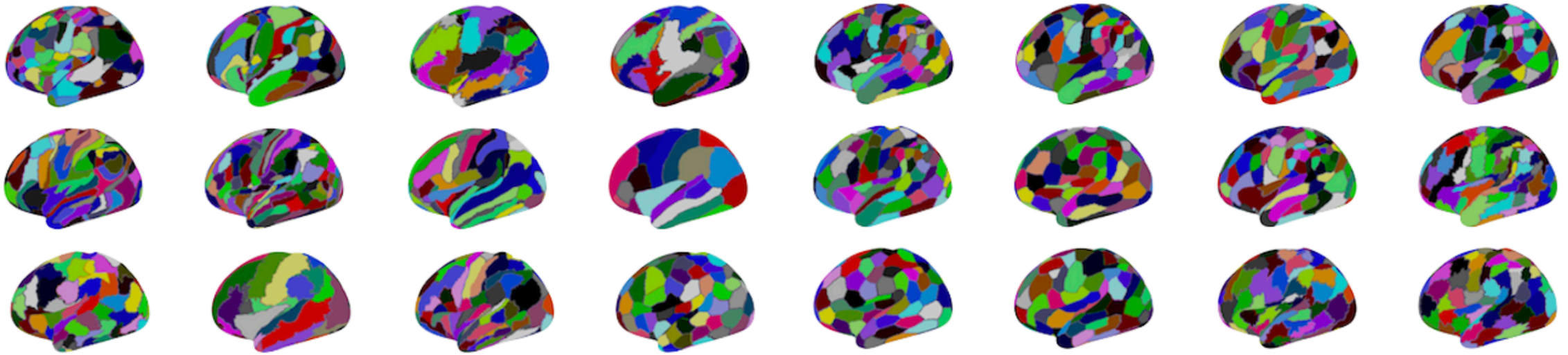
Brain Parcellation Survey



"Using resting-state functional MRI (rs-fMRI) data and several quantitative evaluation techniques, **10 subject-level** and **24 groupwise parcellation methods** are evaluated at different resolutions. The accuracy of parcellations is assessed from four different aspects: **(1) reproducibility across different acquisitions and groups**, (2) fidelity to the underlying connectivity data, (3) agreement with fMRI task activation, myelin maps, and cytoarchitectural areas, and (4) network analysis."

https://biomedia.doc.ic.ac.uk/brain-parcellation-survey/

Brain Parcellation Survey



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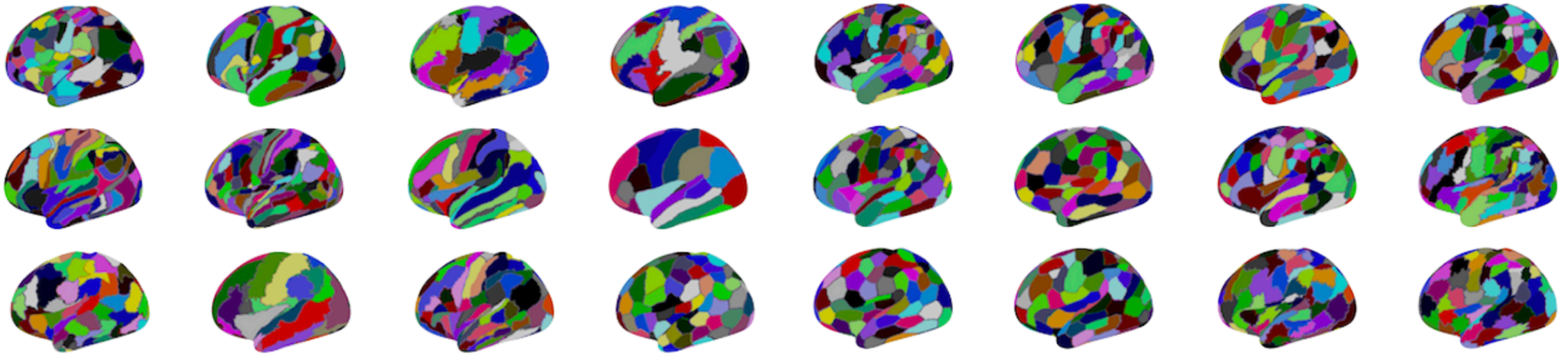

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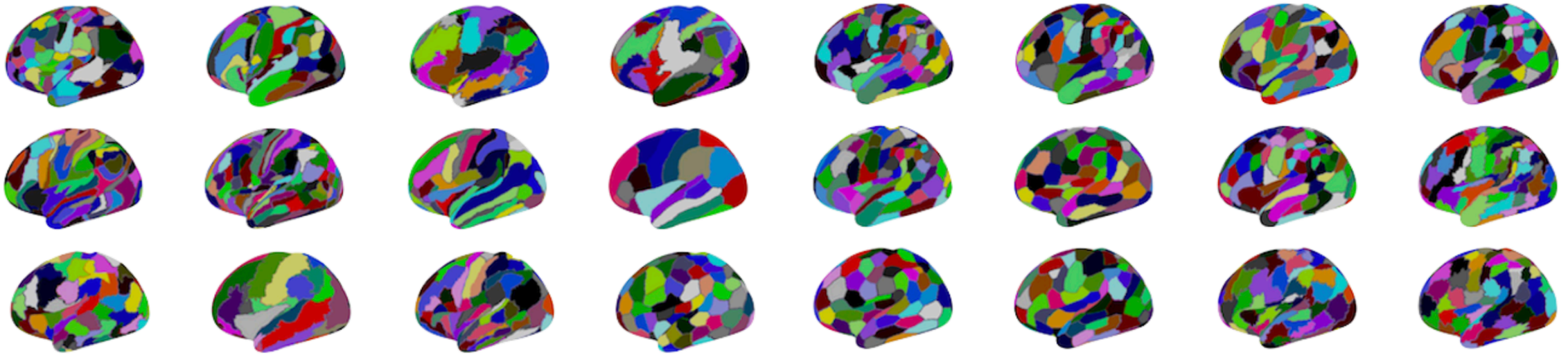

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