Beyond graph theory:

Alterations of the human structural and functional connectomes through aging

Demian Battaglia

Institut de Neurosciences des Systèmes

UMR1106 INSERM, Université Aix-Marseille, France

OLDER, SLOWER, HARDER, (BETTER?)

Demian Battaglia

Institut de Neurosciences des Systèmes

UMR1106 INSERM, Université Aix-Marseille, France

freely inspired to
"Harder, Better, Faster, Stronger"
world-famous French hit...

Viktor Jirsa
(INS, Marseille)

Enrique Hansen
(INS → FIAS, Frankfurt)

Thomas Boudou
(INS, Marseille & ENSTA ParisTech)

but much younger!

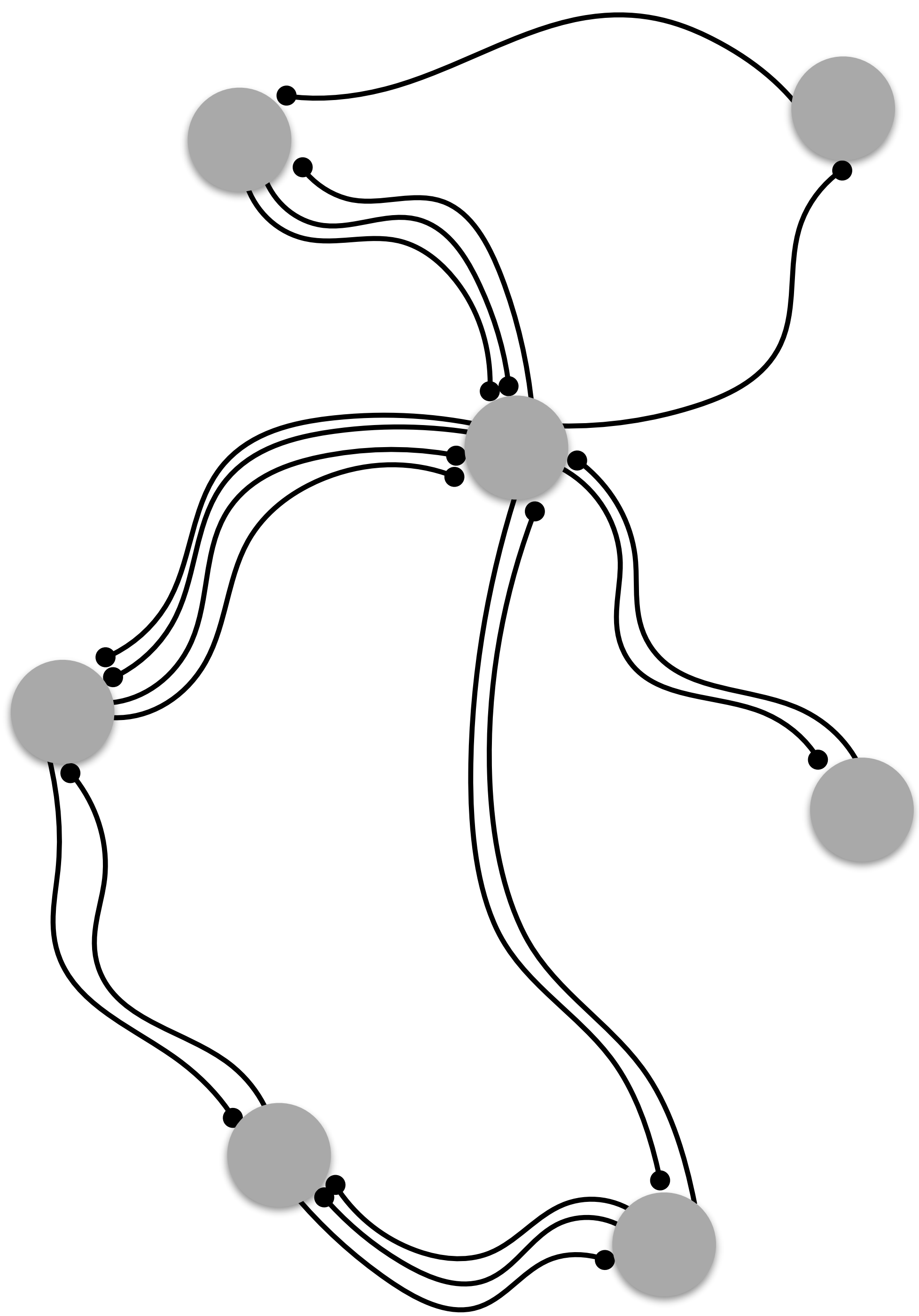
Petra Ritter
(Charité, Berlin)

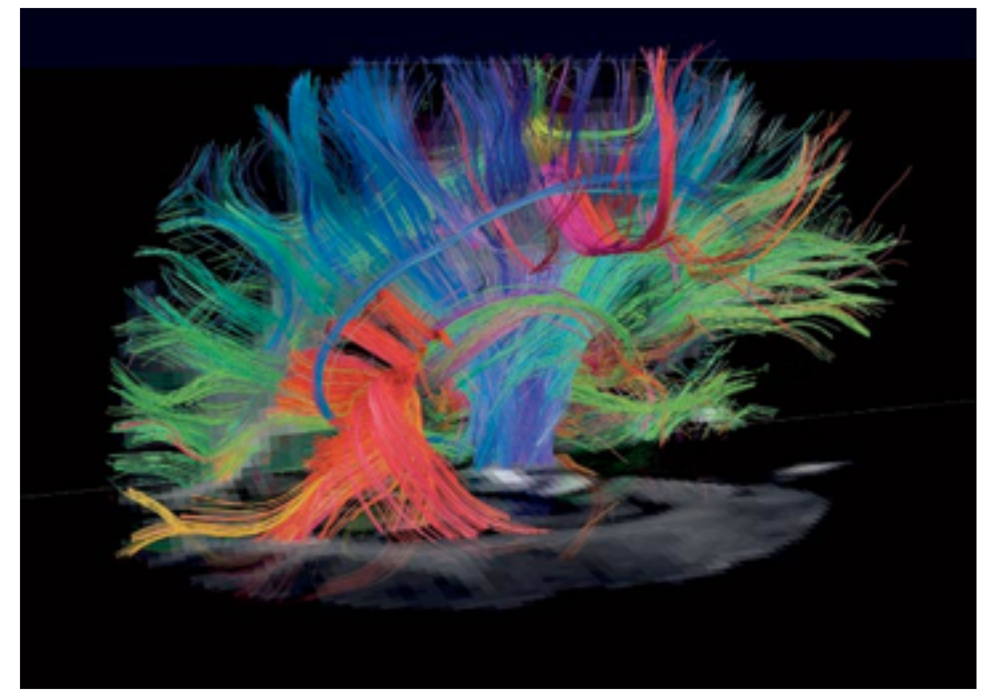
Francesco Vaccarino

Giovanni Petri

(ISI foundation, Turin)

Structural connectome

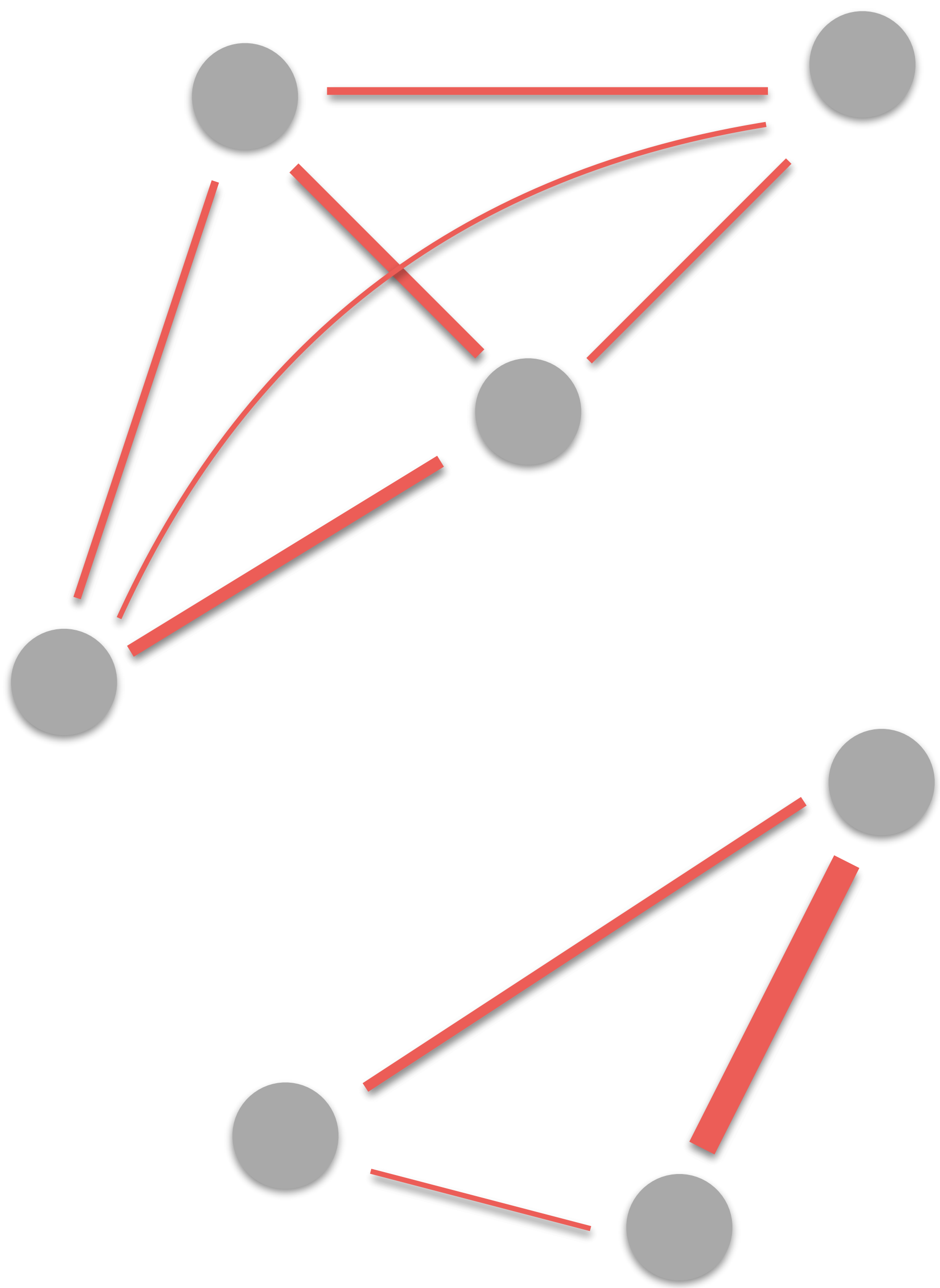


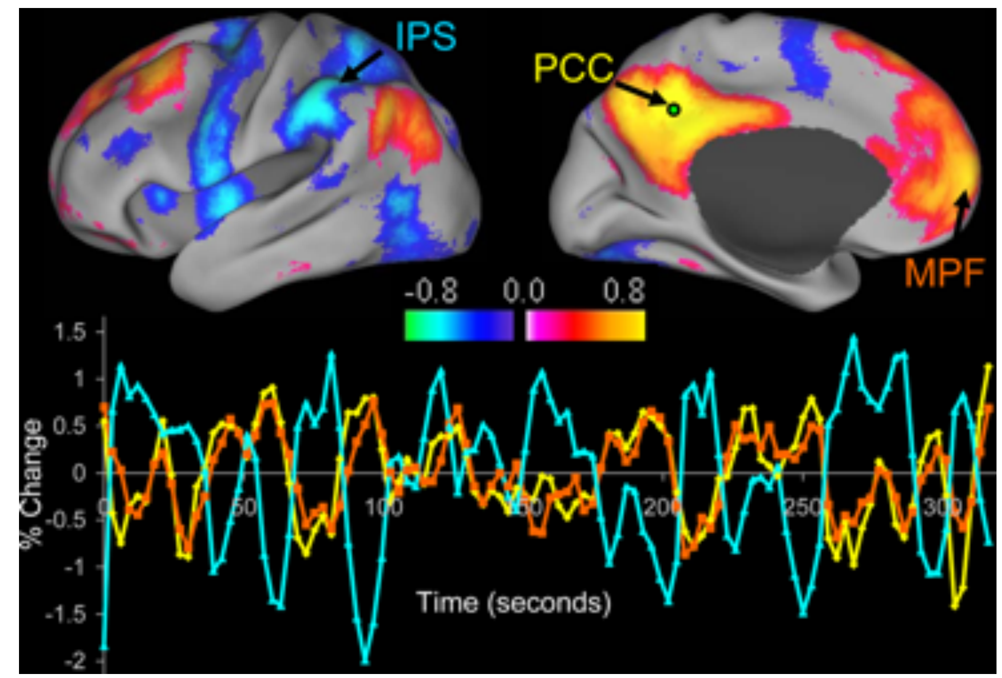


Brain tractography by DTI (Filler 2009)

Inter-areal anatomical connections (SC)

Functional connectome

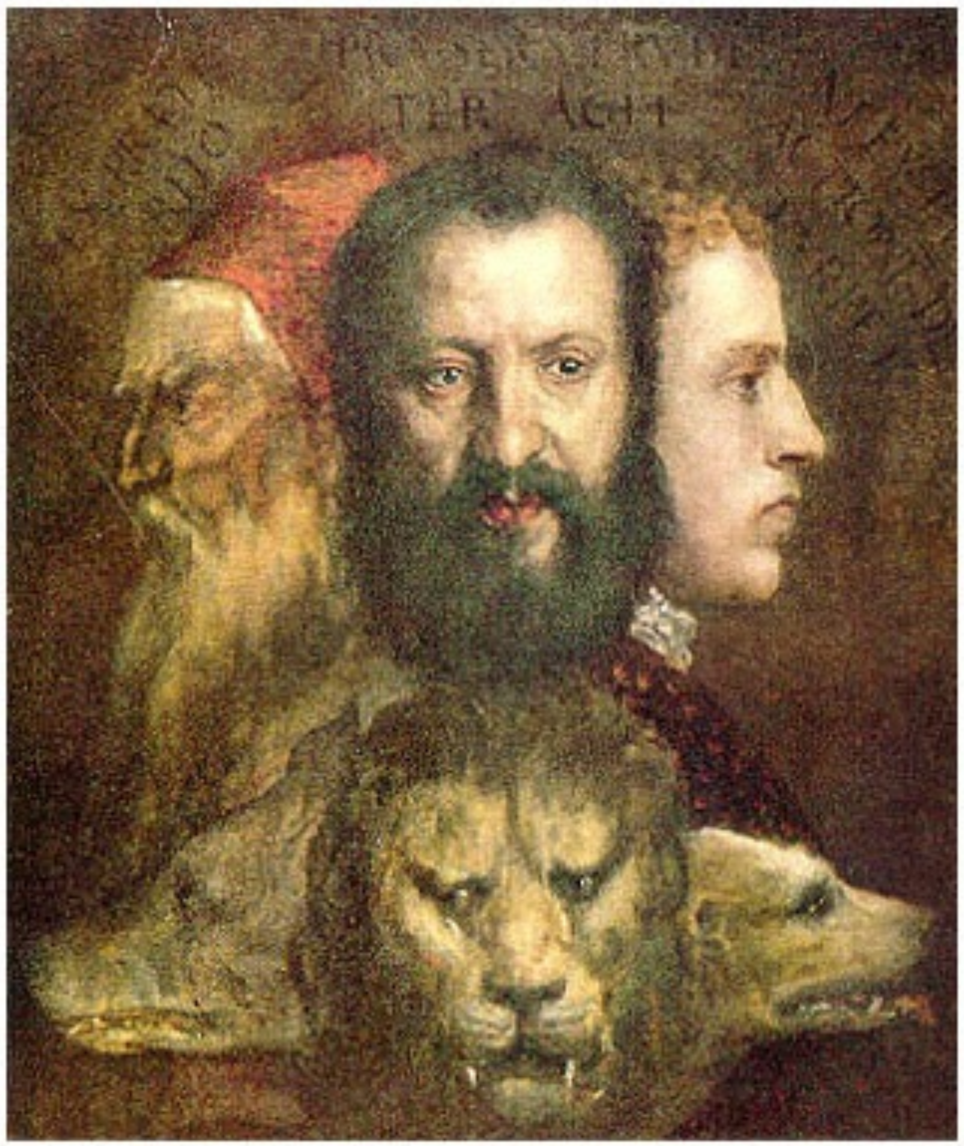




Resting state fluctuations (Fox & Greicius 2010)

Multi-areal activity correlation patterns (FC)

Aging



Tiziano, *Le Età dell'Uomo*

- Effects on cognitive performance and behavior…
  - ➡ *Selective attention, attention switching*
  - ➡ *Working memory content manipulation*
  - ➡ *Salthouse's theory of information processing slowing down*
- but also, **structural alterations**
  - ➡ *e.g., decreased path-efficiency, "disconnection"*
- Resting state **functional connectivity alterations**
  - ➡ *Within and between RSNs*

More Omes?

From the connectome to the "dynome"

(Kopell et al. 2014)

Connect
Gnome

Neuron

Perspective

Beyond the Connectome: The Dynome

Nancy J. Kopell,[1,*] Howard J. Gritton,[2] Miles A. Whittington,[3] and Mark A. Kramer[1]
[1]Department of Mathematics and Statistics, Boston University, Boston, MA 02215, USA
[2]Department of Biomedical Engineering, Boston University, Boston, MA 02215, USA
[3]The Hull York Medical School, University of York, Heslington, York YO10 5DD, UK
*Correspondence: nk@math.bu.edu
http://dx.doi.org/10.1016/j.neuron.2014.08.016

Dyn
Gnome

Chronnect
Gnome

From the "dynome" to the "chronnectome"

(Calhoun et al. 2014)

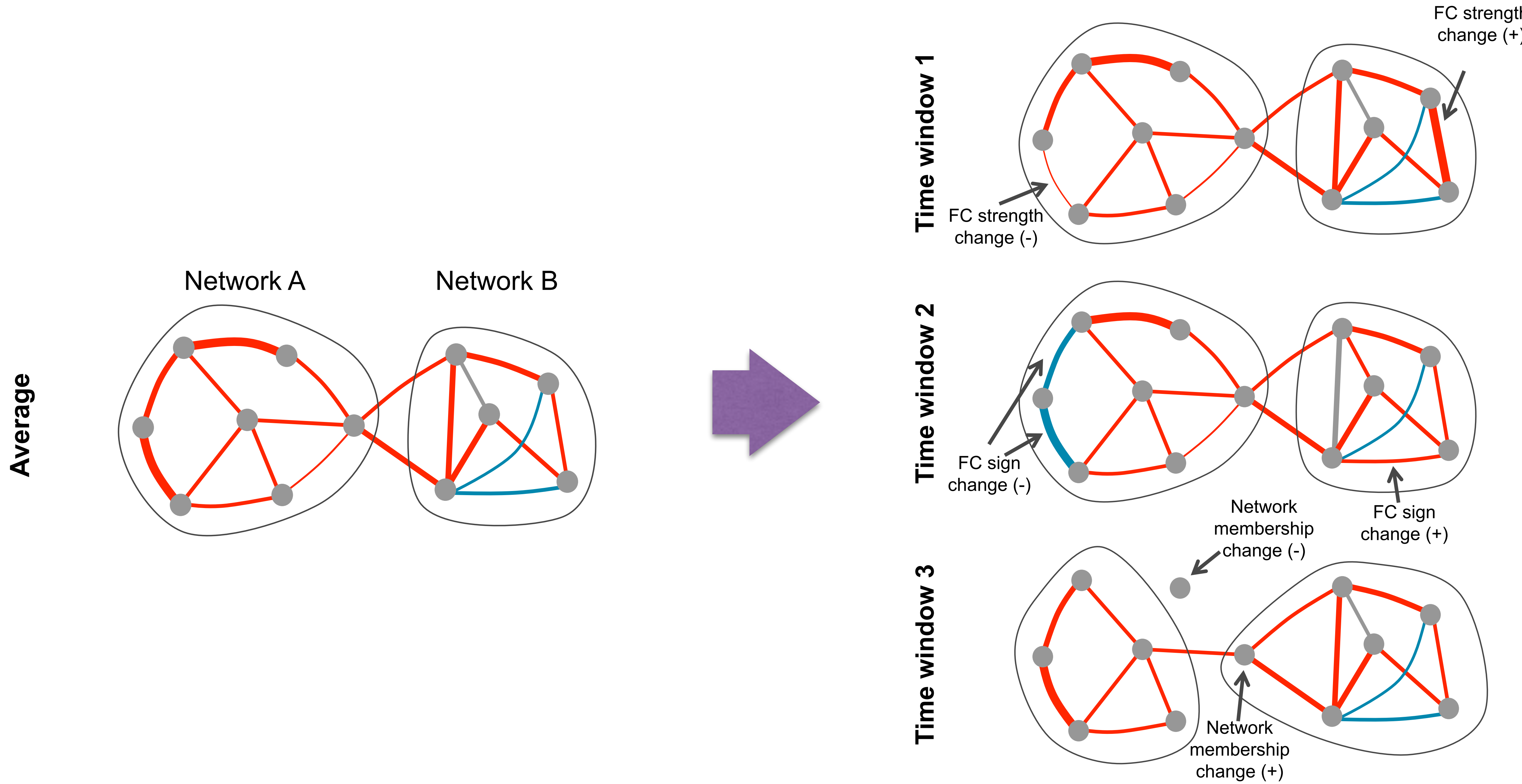
Connect
Gnome

The Chronnectome: Time-Varying Connectivity Networks as the Next Frontier in fMRI Data Discovery

Vince D. Calhoun,[1,2,*] Robyn Miller,[1] Godfrey Pearlson,[4] and Tulay Adalı[3]
[1]The Mind Research Network & LBERI, Albuquerque, NM 87106, USA
[2]Department of ECE, University of New Mexico, Albuquerque, NM 87131, USA
[3]Department of CSEE, University of Maryland, Baltimore County, Baltimore, MD 21250, USA
[4]Olin Neuropsychiatry Research Center, Hartford, CT 06114, USA
*Correspondence: vcalhoun@unm.edu

Dyn
Gnome

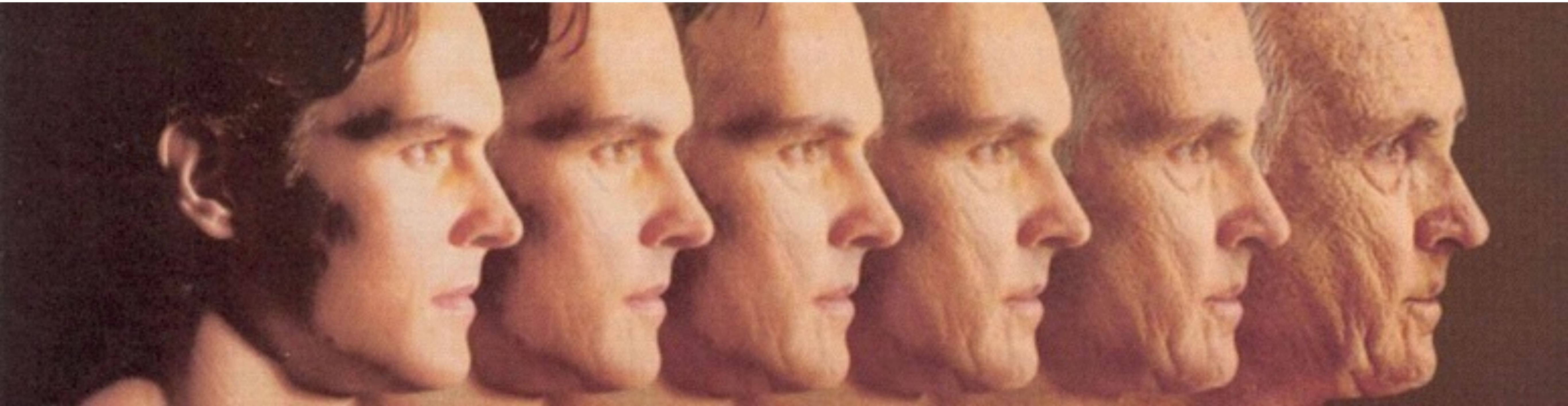
Time-varying FC

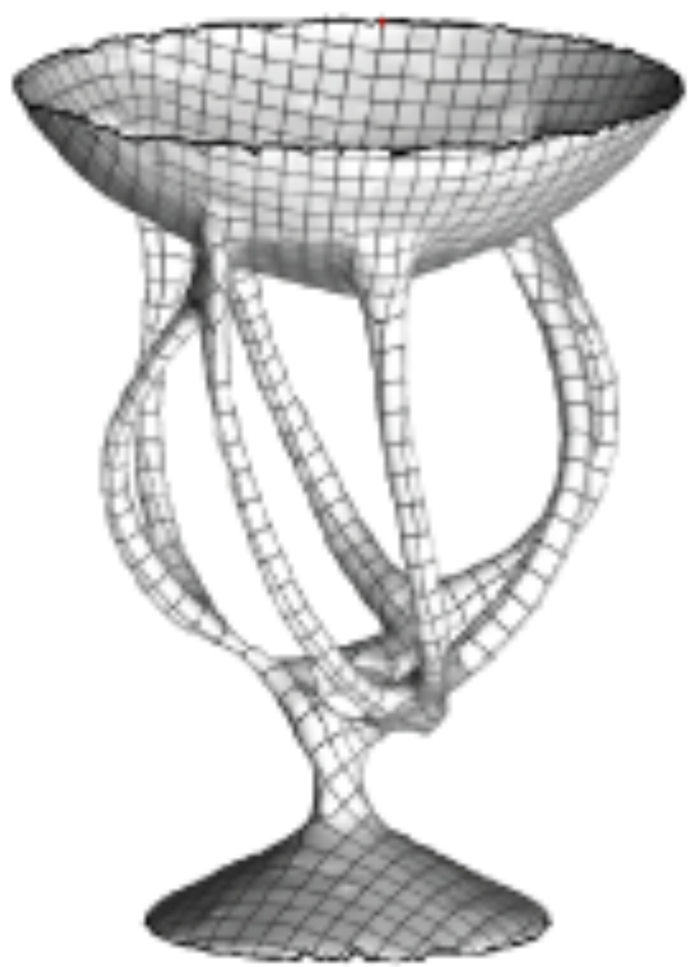


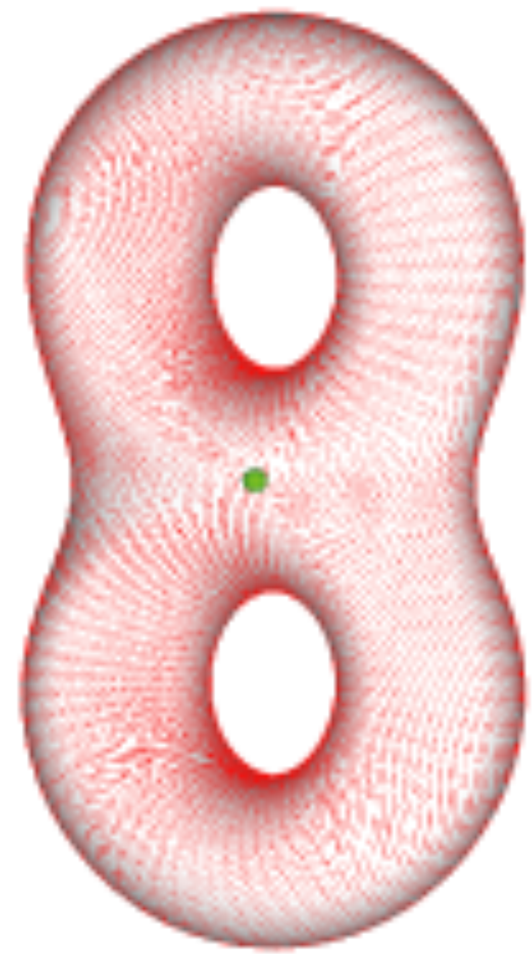
Functional Connectivity Dynamics, FCD

adapted from (Hutchison et al. 2013)

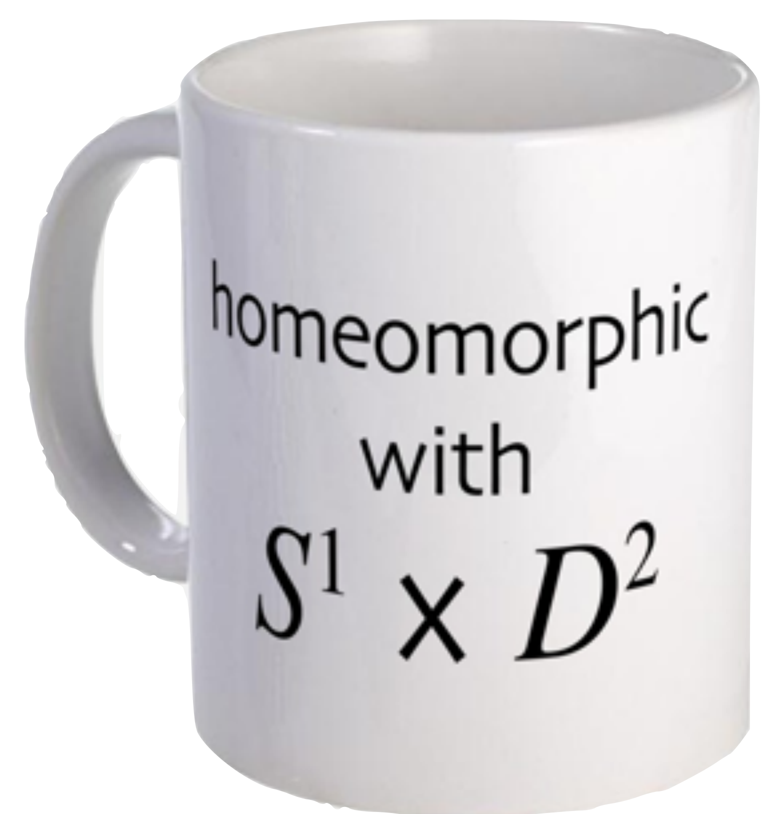
Does Functional Connectivity Dynamics provide better biomarkers of aging?

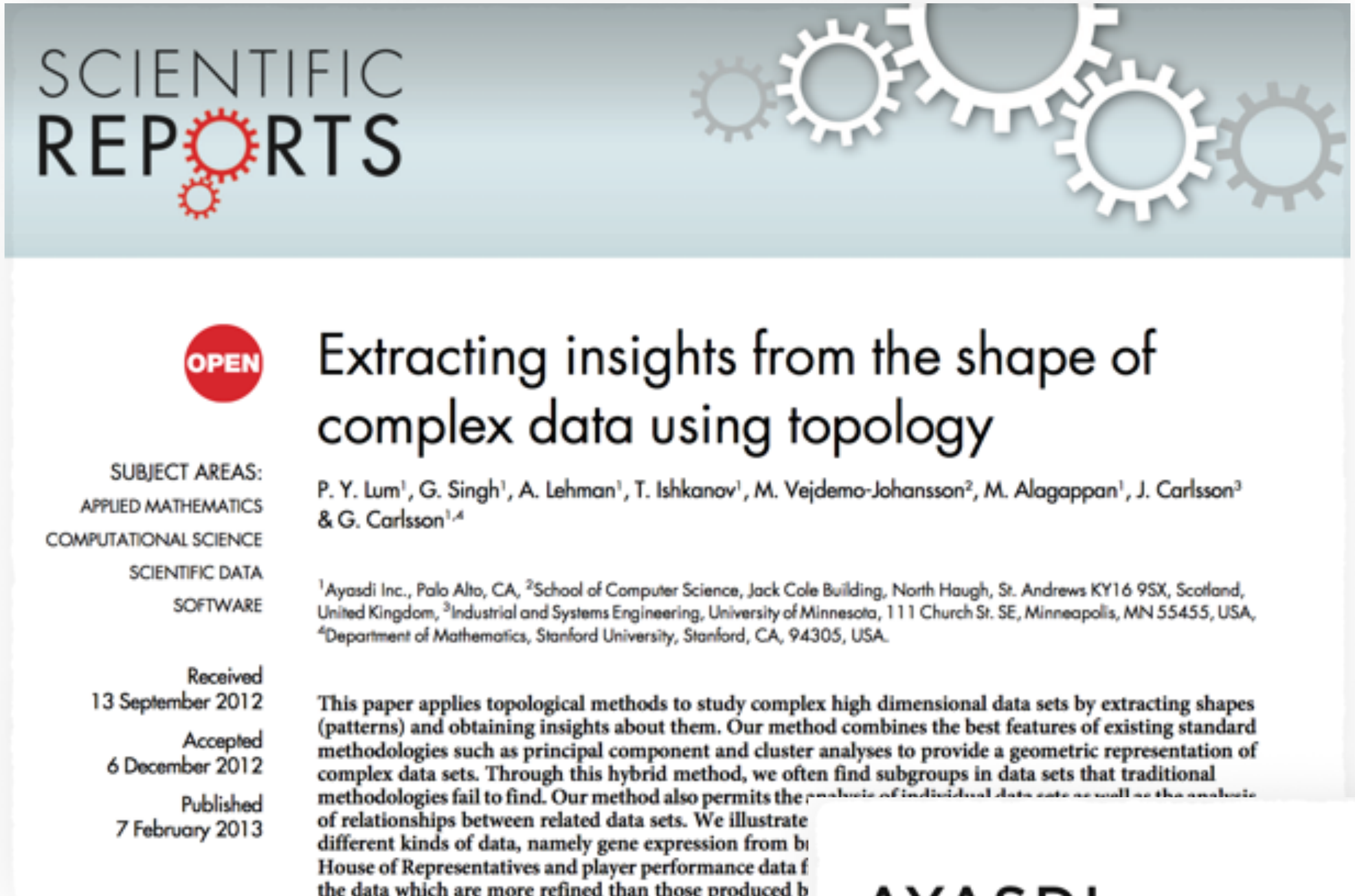






The topolome does not exist yet, but…




SCIENTIFIC REPORTS

OPEN

Extracting insights from the shape of complex data using topology

P. Y. Lum[1], G. Singh[1], A. Lehman[1], T. Ishkanov[1], M. Vejdemo-Johansson[2], M. Alagappan[1], J. Carlsson[3] & G. Carlsson[1,4]

[1]Ayasdi Inc., Palo Alto, CA, [2]School of Computer Science, Jack Cole Building, North Haugh, St. Andrews KY16 9SX, Scotland, United Kingdom, [3]Industrial and Systems Engineering, University of Minnesota, 111 Church St. SE, Minneapolis, MN 55455, USA, [4]Department of Mathematics, Stanford University, Stanford, CA, 94305, USA.

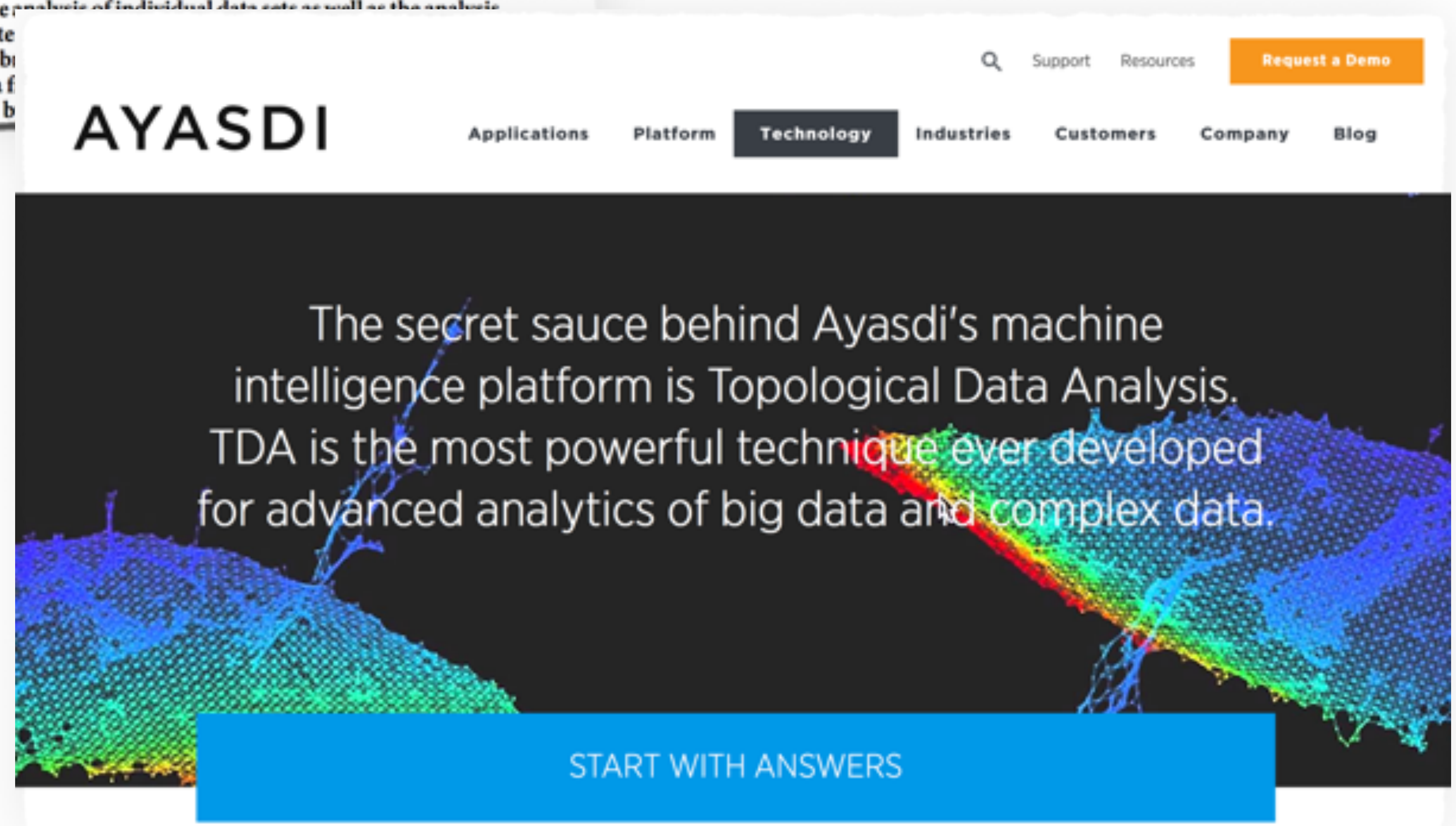
SUBJECT AREAS:
APPLIED MATHEMATICS
COMPUTATIONAL SCIENCE
SCIENTIFIC DATA
SOFTWARE

Received
13 September 2012
Accepted
6 December 2012
Published
7 February 2013

This paper applies topological methods to study complex high dimensional data sets by extracting shapes (patterns) and obtaining insights about them. Our method combines the best features of existing standard methodologies such as principal component and cluster analyses to provide a geometric representation of complex data sets. Through this hybrid method, we often find subgroups in data sets that traditional methodologies fail to find. Our method also permits the ... of relationships between related data sets. We illustrate ... different kinds of data, namely gene expression from ... House of Representatives and player performance data f... the data which are more refined than those produced b...

Lum et al., Scientific Reports 2013

Ayasdi company website



Clique topology reveals intrinsic geometric structure in neural correlations

Chad Giusti[a,b], Eva Pastalkova[c], Carina Curto[b,d,1], and Vladimir Itskov[b,d,1,2]

[a]Warren Center for Network and Data Science, Departments of Bioengineering and Mathematics, University of Pennsylvania, Philadelphia, PA 19104; [b]Department of Mathematics, University of Nebraska, Lincoln, NE 68588; [c]Janelia Research Campus, Howard Hughes Medical Institute, Ashburn, VA 20147; and [d]Department of Mathematics, The Pennsylvania State University, University Park, PA 16802

Edited by William Bialek, Princeton University, Princeton, NJ, and approved September 23, 2015 (received for review April 28, 2015)

Detecting meaningful structure in neural activity and connectivity data is challenging in the presence of hidden nonlinearities, where traditional eigenvalue-based methods may be misleading. We introduce a novel approach to matrix analysis, called clique topology, that extracts features of the data invariant under nonlinear monotone transformations. These features can be used to detect both random and geometric structure, and depend only on the relative ordering of matrix entries. We then analyzed the activity of pyramidal neurons in rat hippocampus, recorded while the animal was exploring a 2D environment, and confirmed that

should be invariant under matrix transformations of the following form:

$$C_{ij} = f(A_{ij}), \quad [1]$$

where f is a nonlinear monotonic function (Fig. 1*A*). In the case of hippocampal place cells, f captures the manner in which pairwise correlations C_{ij} decrease with distance between place field centers (3). In less studied contexts, the represented stimuli—and the function f—may be completely unknown.

frontiers in Systems Neuroscience

ORIGINAL RESEARCH
published: 08 November 2016
doi: 10.3389/fnsys.2016.00085

Insights into Brain Architectures from the Homological Scaffolds of Functional Connectivity Networks

Louis-David Lord[1], Paul Expert[2], Henrique M. Fernandes[1,3], Giovanni Petri[4], Tim J. Van Hartevelt[1,3], Francesco Vaccarino[4,5], Gustavo Deco[6,7], Federico Turkheimer[2] and Morten L. Kringelbach[1,3]*

[1] Hedonia Research Group, Department of Psychiatry, University of Oxford, Oxford, UK, [2] Department of Neuroimaging, Institute of Psychiatry, King's College London, London, UK, [3] Center for Music in the Brain, Aarhus University, Aarhus, Denmark, [4] Institute for Scientific Interchange (ISI Foundation), Torino, Italy, [5] Department of Mathematical Sciences, Politecnico di Torino, Torino, Italy, [6] Center for Brain and Cognition, Universitat Pompeu Fabra, Barcelona, Spain, [7] Instituci Catalana de la Recerca i Estudis Avanats, Universitat Pompeu Fabra, Barcelona, Spain

In recent years, the application of network analysis to neuroimaging data has provided useful insights about the brain's functional and structural organization in both health and disease. This has proven a significant paradigm shift from the study of individual brain regions in isolation. Graph-based models of the brain consist of vertices, which

JOURNAL OF THE ROYAL SOCIETY Interface

rsif.royalsocietypublishing.org

Research

Cite this article: Petri G, Expert P, Turkheimer F, Carhart-Harris R, Nutt D, Hellyer PJ, Vaccarino F. 2014 Homological scaffolds of brain functional networks. *J. R. Soc. Interface* **11**: 20140873.
http://dx.doi.org/10.1098/rsif.2014.0873

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]

[1]ISI Foundation, Via Alassio 11/c, 10126 Torino, Italy
[2]Centre for Neuroimaging Sciences, Institute of Psychiatry, Kings College London, De Crespigny Park, London SE5 8AF, UK
[3]Centre for Neuropsychopharmacology, Imperial College London, London W12 0NN, UK
[4]Computational, Cognitive and Clinical Neuroimaging Laboratory, Division of Brain Sciences, Imperial College London, London W12 0NN, UK
[5]Dipartimento di Scienze Matematiche, Politecnico di Torino, C.so Duca degli Abruzzi no 24, Torino 10129, Italy

Networks, as efficient representations of complex systems, have appealed to scientists for a long time and now permeate many areas of science, including neuroimaging (Bullmore and Sporns 2009 *Nat. Rev. Neurosci.* **10**, 186–198. (doi:10.1038/nrn2618)). Traditionally, the structure of complex networks has been studied through their statistical properties and metrics concerned with

J Comput Neurosci (2016) 41:1–14
DOI 10.1007/s10827-016-0608-6

Two's company, three (or more) is a simplex

Algebraic-topological tools for understanding higher-order structure in neural data

Chad Giusti[1,2] · Robert Ghrist[1,3] · Danielle S. Bassett[2,3]

Closures and Cavities in the Human Connectome

Ann Sizemore[1,2], Chad Giusti[1], Richard F. Betzel[1], and Danielle S. Bassett[1,3,*]

[1]Department of Bioengineering, University of Pennsylvania, Philadelphia, PA 19041 USA
[2]Broad Institute, Harvard University and the Massachusetts Institute of Technology, Cambridge, MA 02142 USA
[3]Department of Electrical & Systems Engineering, University of Pennsylvania, Philadelphia, PA 19041 USA
[*]To whom correspondence should be addressed: dsb@seas.upenn.edu

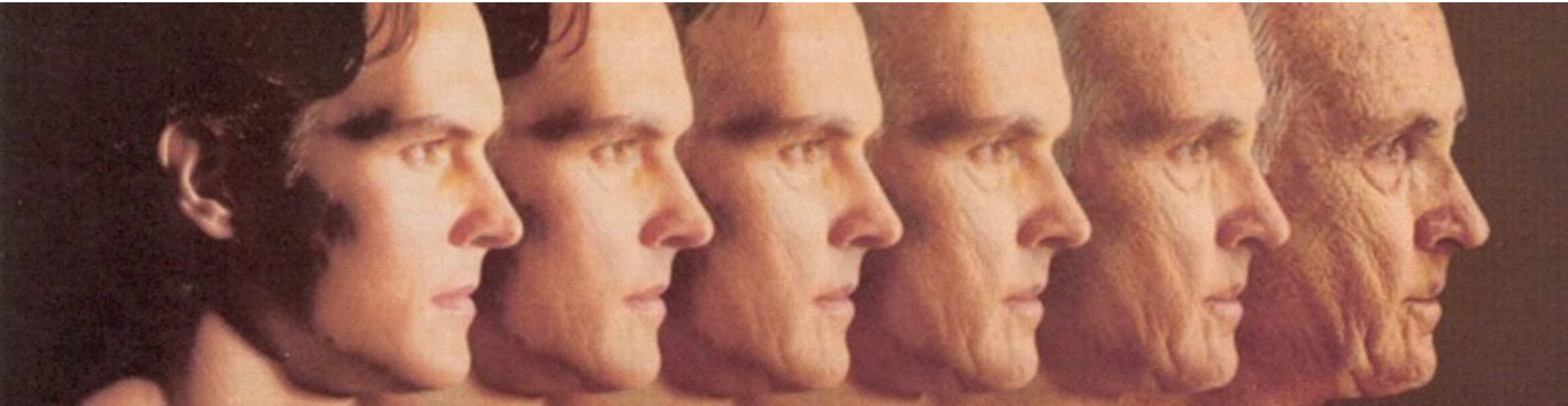
Biomedicine

How the Mathematics of Algebraic Topology Is Revolutionizing Brain Science

Nobody understands the brain's wiring diagram, but the tools of algebraic topology are beginning to tease it apart.

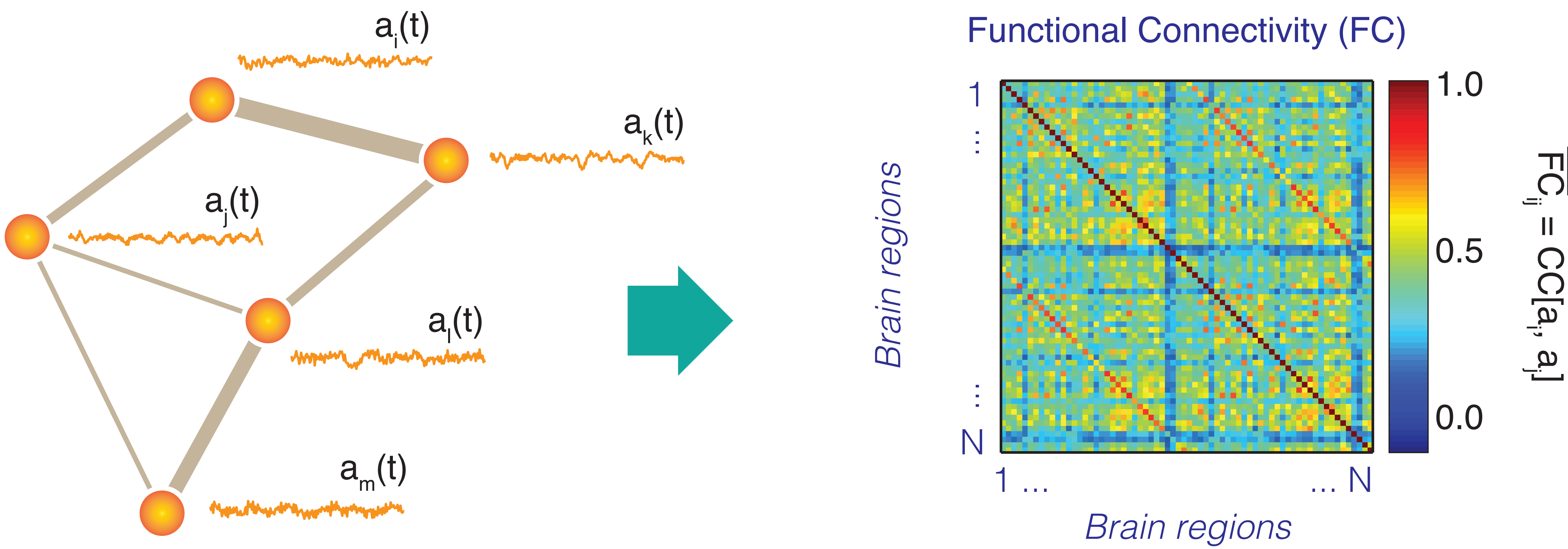
by Emerging Technology from the arXiv August 24, 2016

Does topological techniques provide better biomarkers of aging?



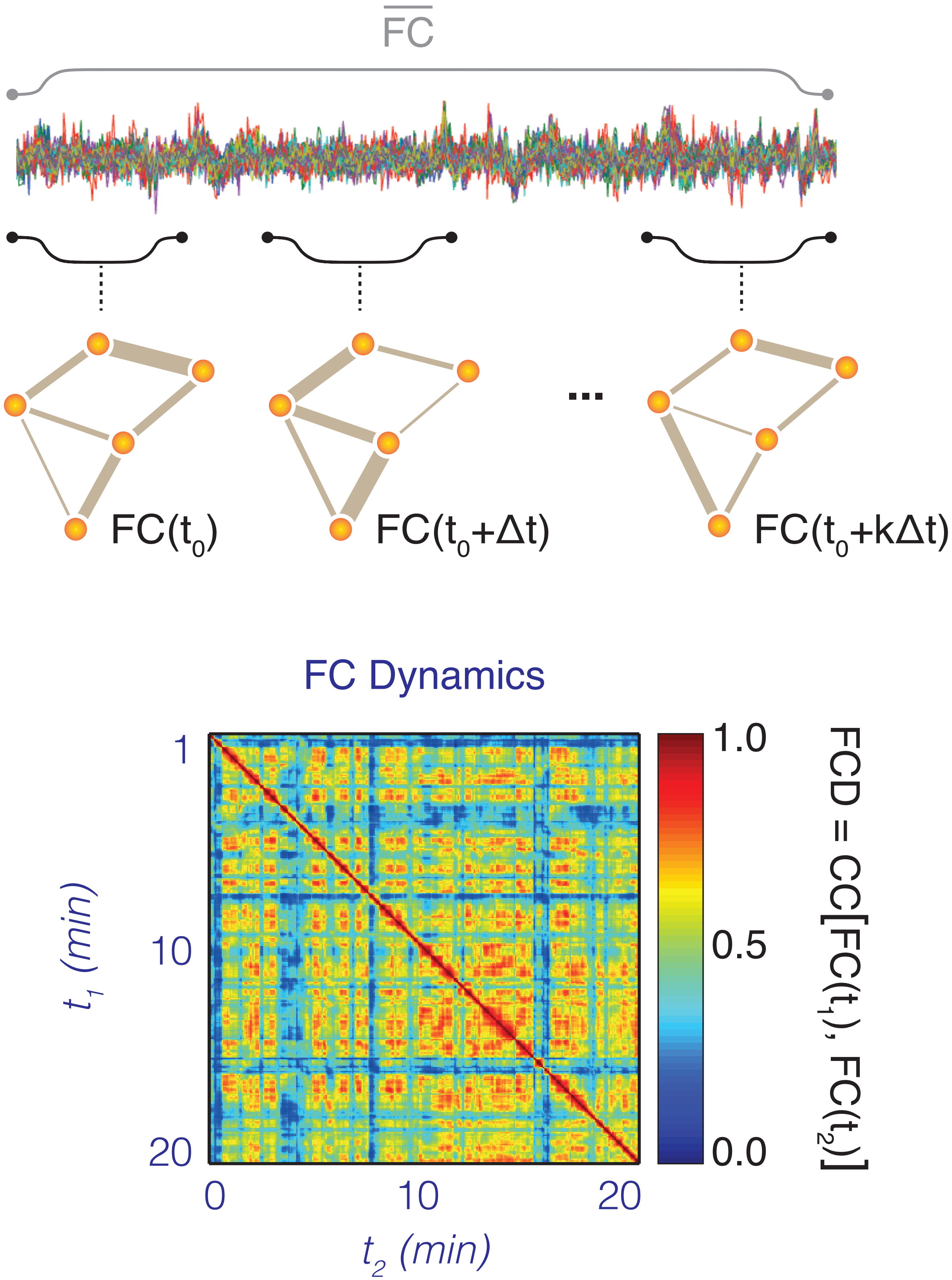
See later about the meaning of "better"…

Time-series of
***NODE** activity*
(e.g. resting-state BOLD)

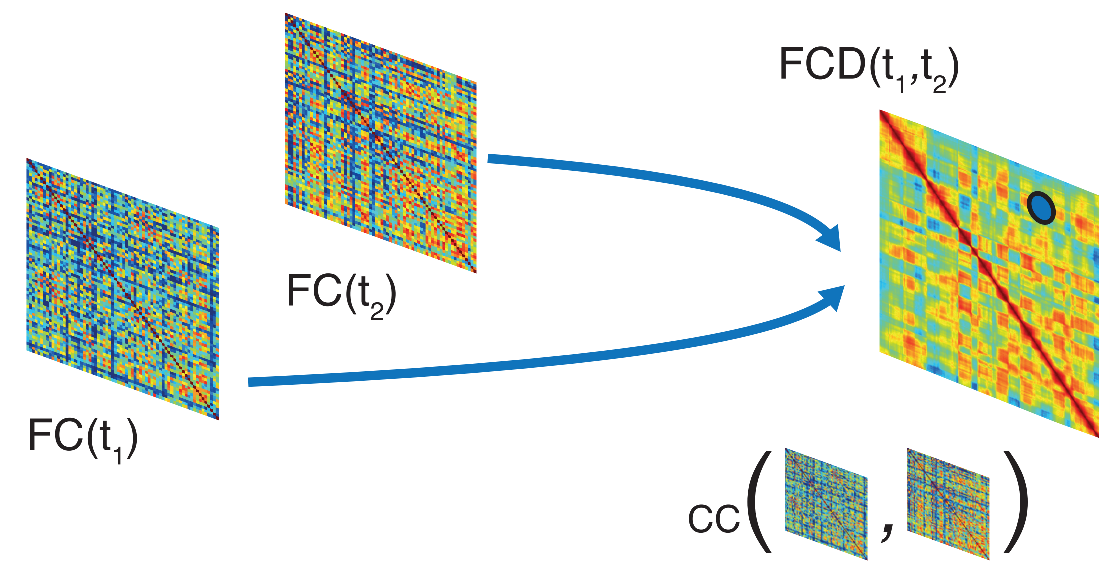


Link = correlation between node time-series

N x N matrix of inter-node correlations



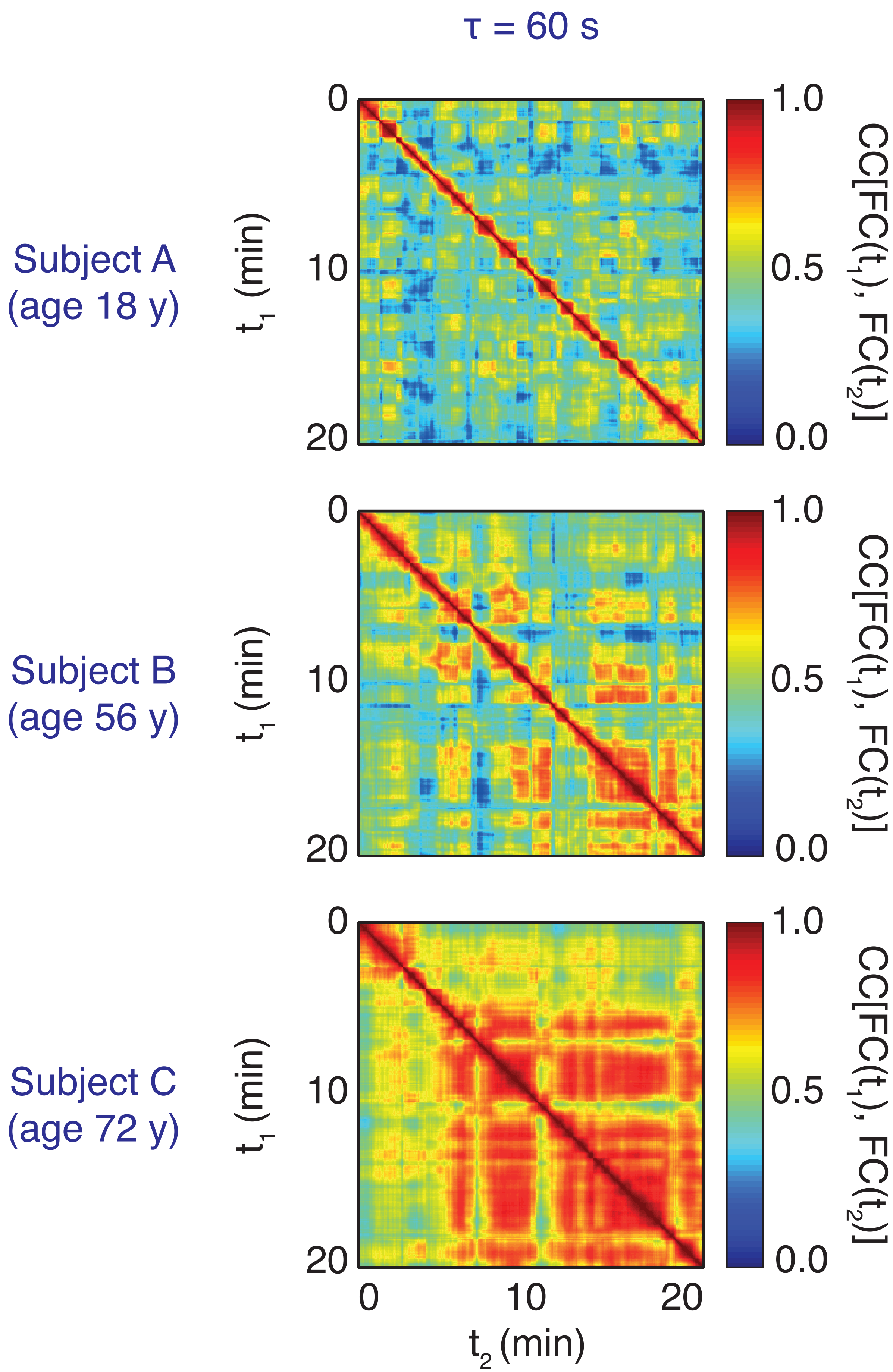
Time-series of
INTER-NODE CORRELATIONS



FUNCTIONAL CONNECTIVITY DYNAMICS
(FCD matrices)

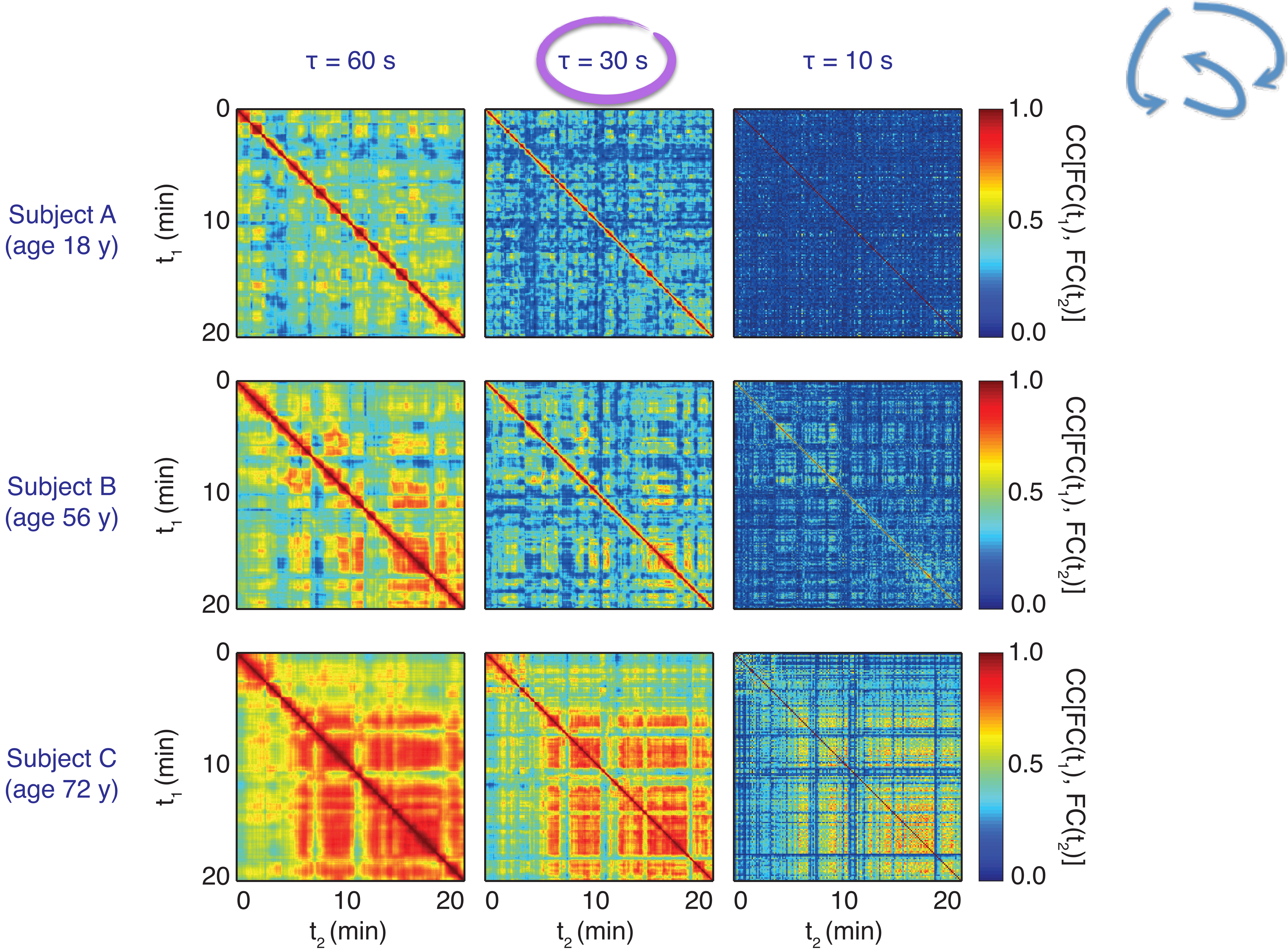
Correlation between networks at different times

OLDER...



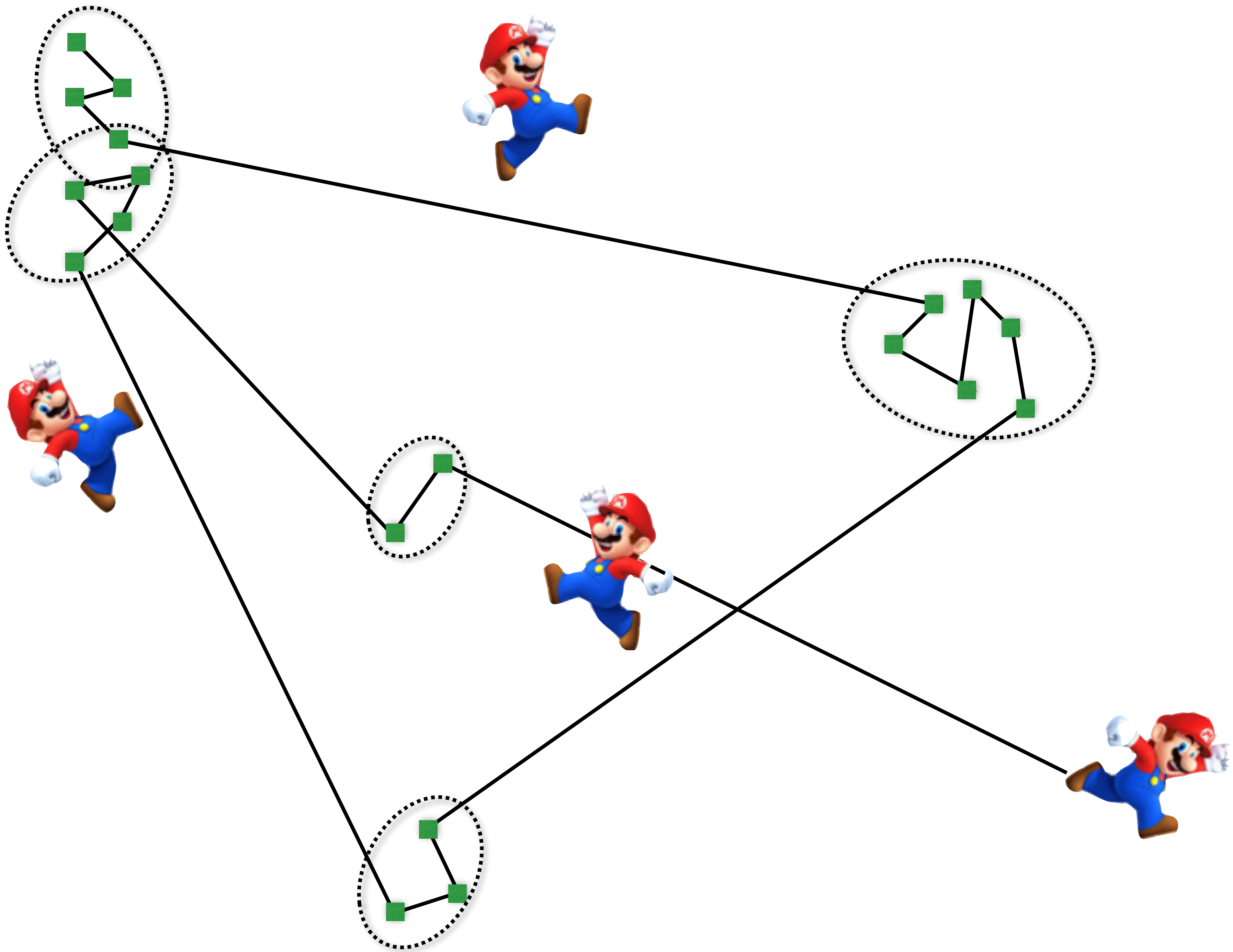
Petra Ritter
(Charité-BCCN, Berlin)

DSI structural connectivity,
20 min rs BOLD
and simultaneous EEG
for 50 human subjects
through the adult lifespan



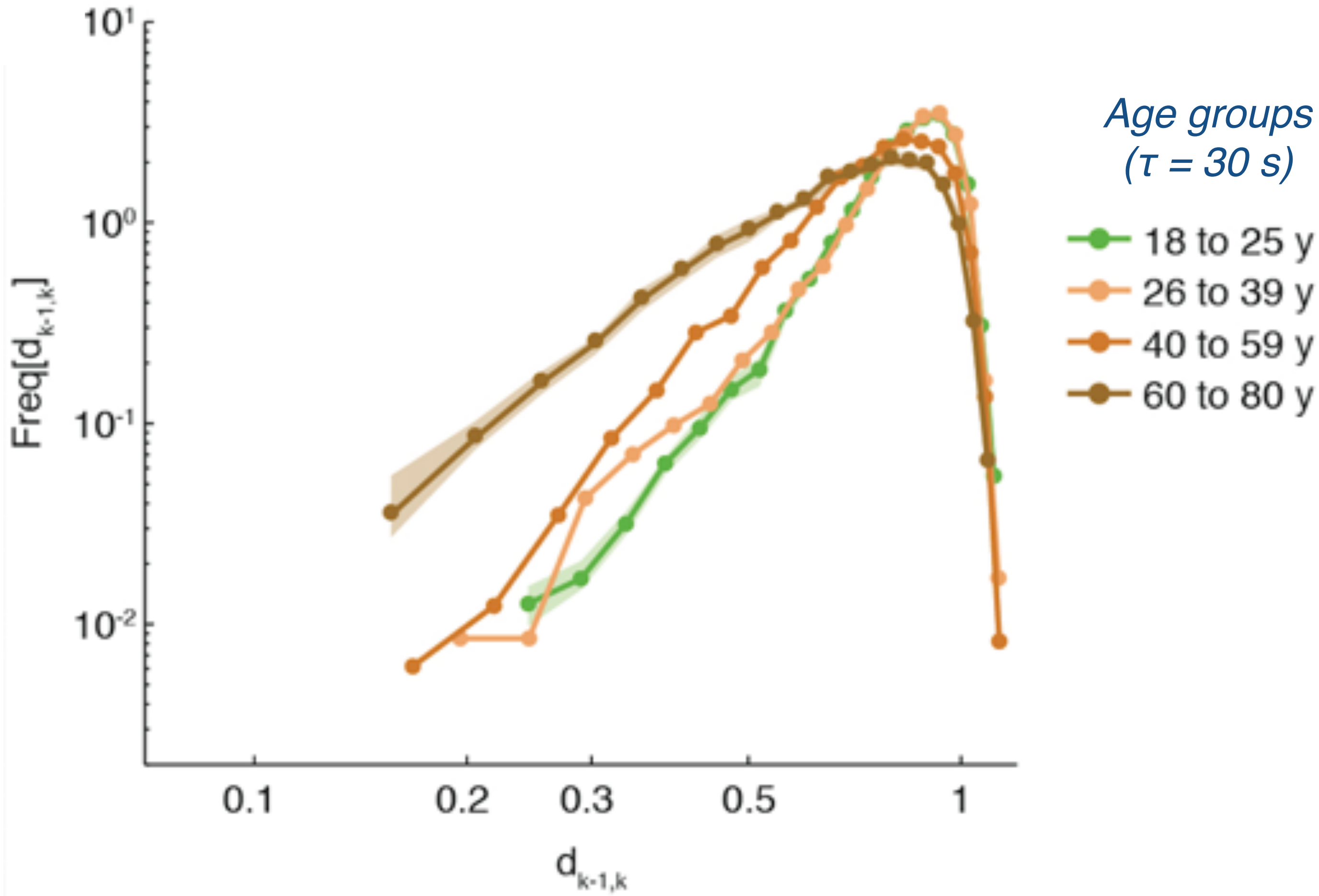
τ = 60 s
τ = 30 s
τ = 10 s
Subject A
(age 18 y)
Subject B
(age 56 y)
Subject C
(age 72 y)
t_1 (min)
t_2 (min)
0
10
20
1.0
0.5
0.0
CC[FC(t_1), FC(t_2)]

Let's quantify the reconfiguration of FC over time beyond visualization…

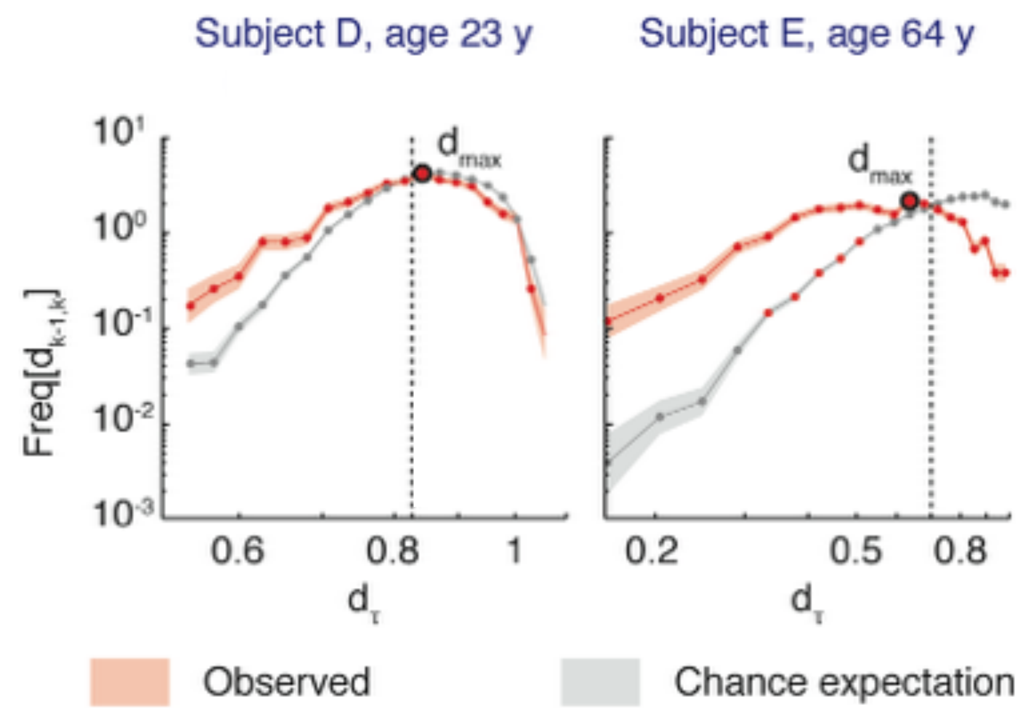


Steps in Functional Connectivity space!

JUMP LENGTH DISTRIBUTION
(for different age groups)

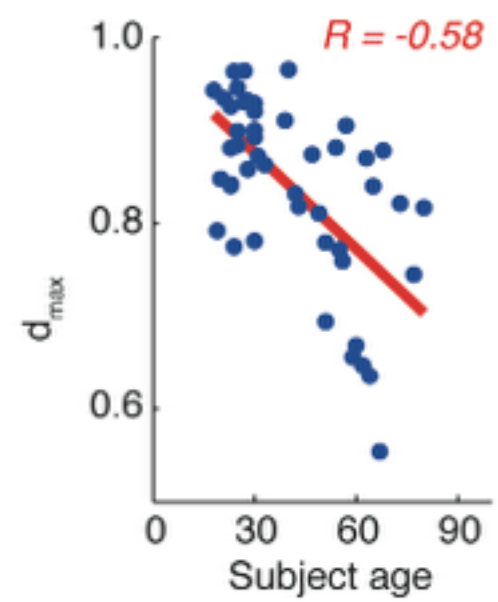


SINGLE-SUBJECT DISTRIBUTIONS



Step length distributions show a marked peak and (possibly) a "power-law" tail

TYPICAL STEP LENGTH

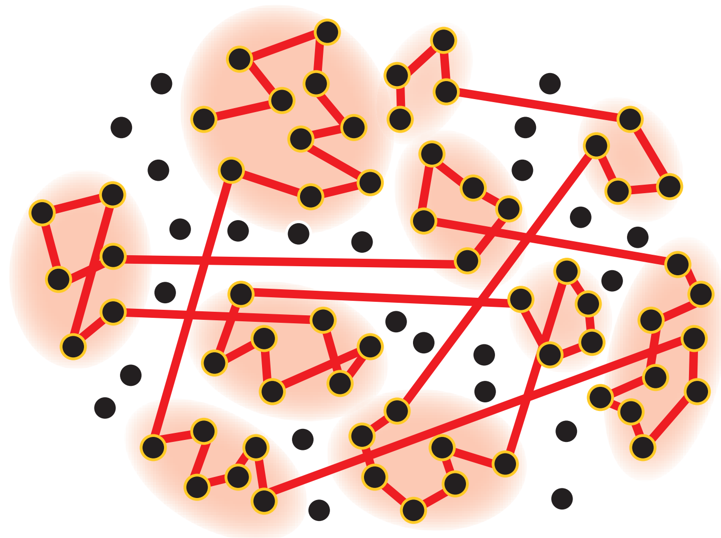


Typical step lengths anti-correlate with age

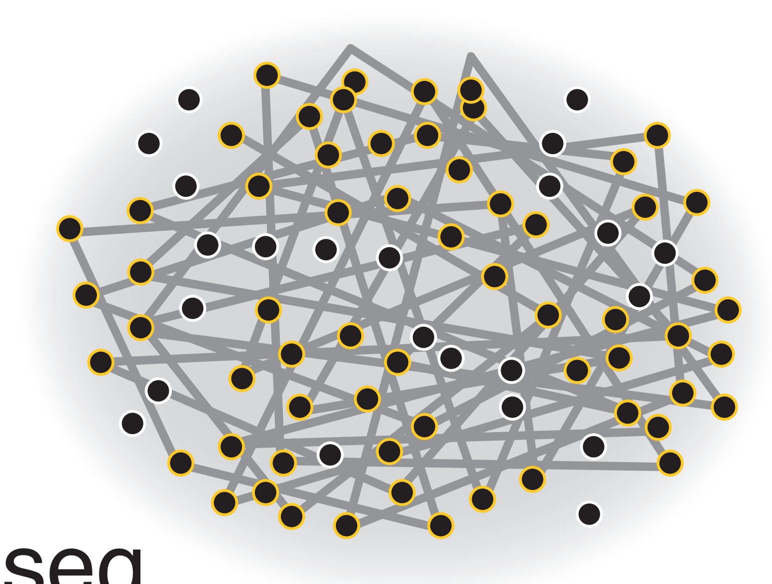
SLOWER...

Conclusion 1

FCD slows down
with aging

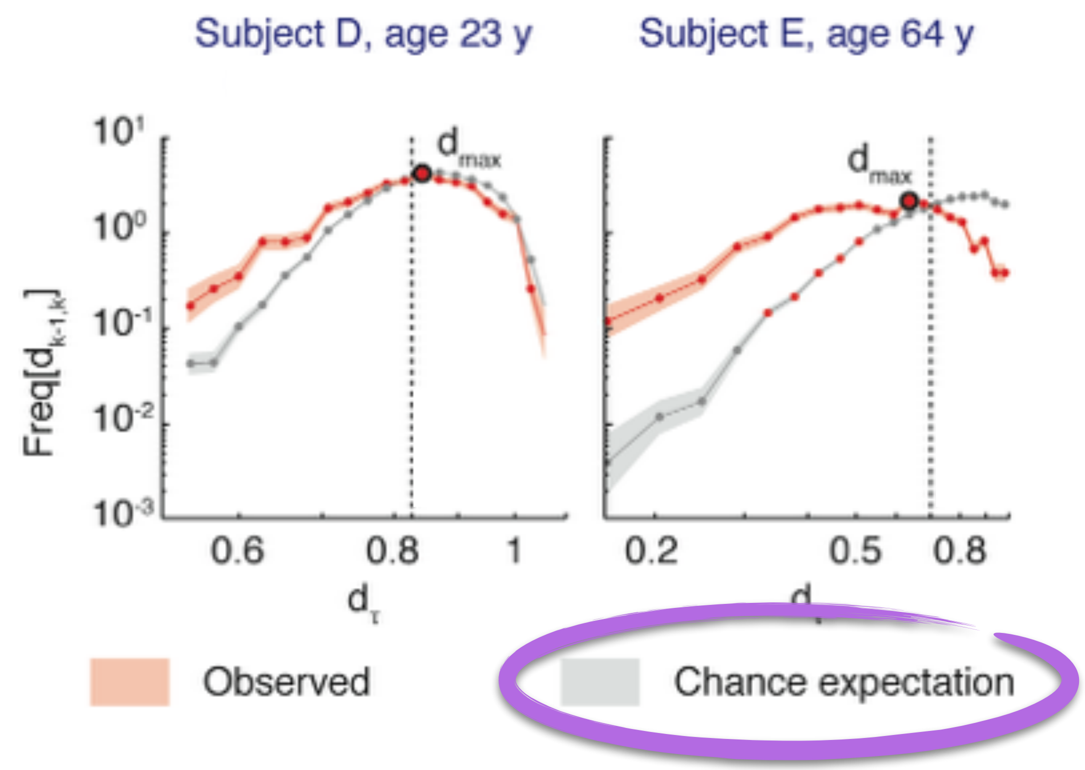


Empirical



No seq. correlations

SINGLE-SUBJECT DISTRIBUTIONS



FC observations preserved, but destroyed sequential correlations!

Detrended Fluctuation analysis

Detrended fluctuation analysis

From Wikipedia, the free encyclopedia

atistical self-a
lation functio
as mean and
ourier transfo

Given a bounded time series x_t of length N, where $t \in \mathbb{N}$, integration or summation first converts this into an unbounded process X_t:

$$X_t = \sum_{i=1}^{t} (x_i - \langle x \rangle)$$

X_t is called cumulative sum or profile. This process converts, for example, an i.i.d. white noise process into a random walk.

Next, X_t is divided into time windows of length n samples each, and a local least squares straight-line fit (the local trend) is calculated by minimising the least squared errors within each time window. Let Y_t be the series of straight line fits. Next, the root-mean-square deviation from the trend, the **fluctuation**, is calculated:

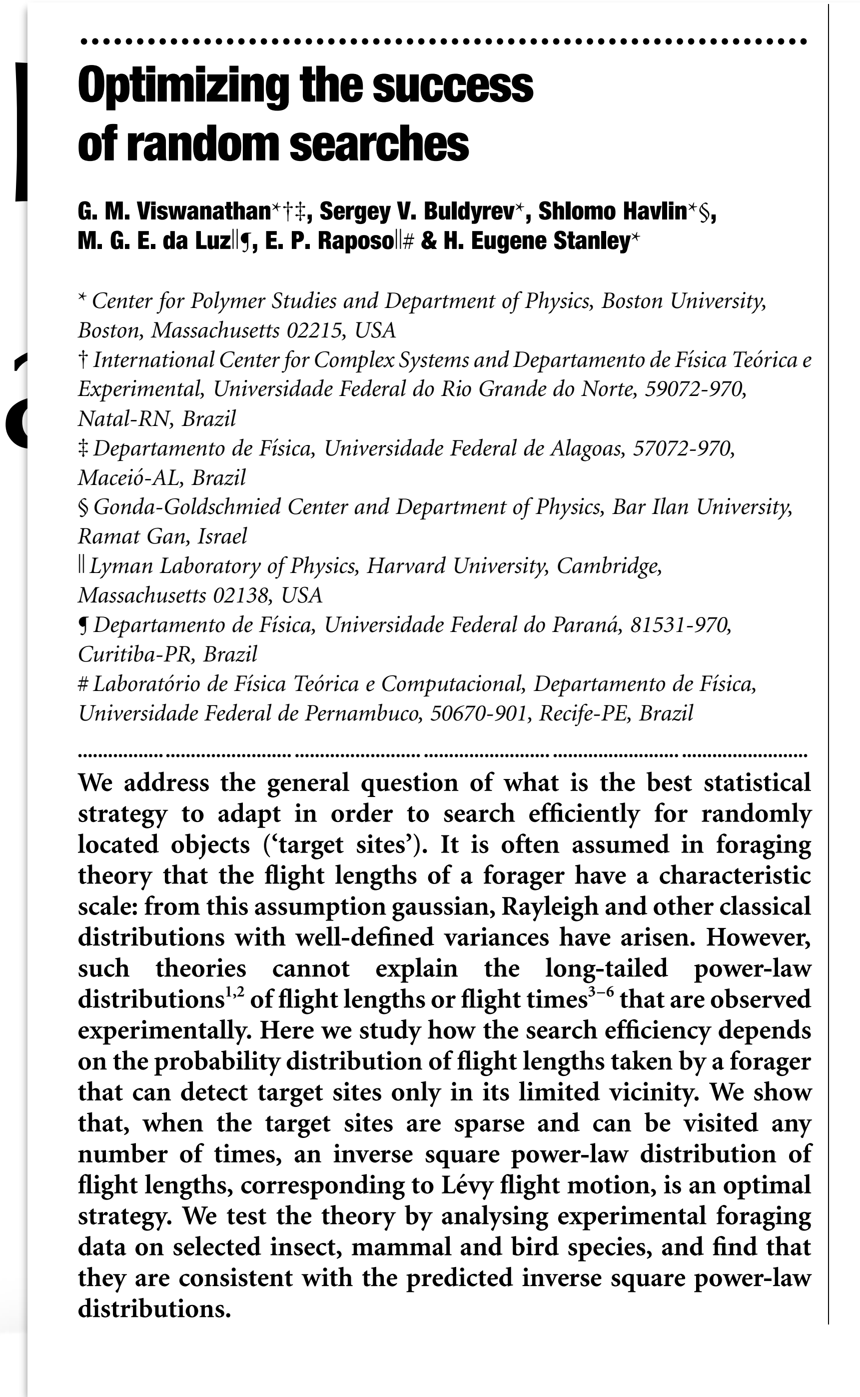
$$F(n) = \left[\frac{1}{N} \sum_{t=1}^{N} (X_t - Y_t)^2 \right]^{\frac{1}{2}}.$$

This detrending followed by fluctuation measurement process is repeated over a range of different window sizes n, and a log-log graph of n against $F(n)$ is constructed.

A straight line on this log-log graph indicates statistical self-affinity expressed as $F(n) \propto n^{\alpha}$. The scaling exponent α is calculated as the slope of a straight line fit to the log-log graph of n against $F(n)$ using least-squares. This exponent is a generalization of the Hurst exponent. Because the expected displacement in an uncorrelated random walk of length N grows like $\sqrt{N}$, an exponent of $\frac{1}{2}$ would correspond to uncorrelated white noise. When the exponent is between 0 and 1, the result is Fractional Brownian motion, with the precise value giving information about the series self-correlations:

- $\alpha < 1/2$: anti-correlated
- $\alpha \simeq 1/2$: uncorrelated, white noise
- $\alpha > 1/2$: correlated
- $\alpha \simeq 1$: 1/f-noise, pink noise
- $\alpha > 1$: non-stationary, unbounded
- $\alpha \simeq 3/2$: Brownian noise

d Fluctuation



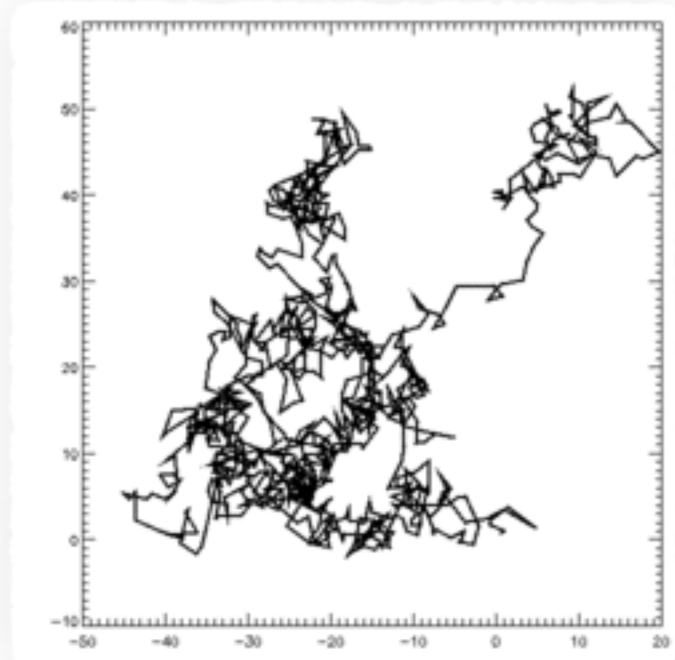
Optimizing the success of random searches

G. M. Viswanathan*†‡, Sergey V. Buldyrev*, Shlomo Havlin*§, M. G. E. da Luz‖¶, E. P. Raposo‖# & H. Eugene Stanley*

* *Center for Polymer Studies and Department of Physics, Boston University, Boston, Massachusetts 02215, USA*
† *International Center for Complex Systems and Departamento de Física Teórica e Experimental, Universidade Federal do Rio Grande do Norte, 59072-970, Natal-RN, Brazil*
‡ *Departamento de Física, Universidade Federal de Alagoas, 57072-970, Maceió-AL, Brazil*
§ *Gonda-Goldschmied Center and Department of Physics, Bar Ilan University, Ramat Gan, Israel*
‖ *Lyman Laboratory of Physics, Harvard University, Cambridge, Massachusetts 02138, USA*
¶ *Departamento de Física, Universidade Federal do Paraná, 81531-970, Curitiba-PR, Brazil*
\# *Laboratório de Física Teórica e Computacional, Departamento de Física, Universidade Federal de Pernambuco, 50670-901, Recife-PE, Brazil*

We address the general question of what is the best statistical strategy to adapt in order to search efficiently for randomly located objects ('target sites'). It is often assumed in foraging theory that the flight lengths of a forager have a characteristic scale: from this assumption gaussian, Rayleigh and other classical distributions with well-defined variances have arisen. However, such theories cannot explain the long-tailed power-law distributions[1,2] of flight lengths or flight times[3–6] that are observed experimentally. Here we study how the search efficiency depends on the probability distribution of flight lengths taken by a forager that can detect target sites only in its limited vicinity. We show that, when the target sites are sparse and can be visited any number of times, an inverse square power-law distribution of flight lengths, corresponding to Lévy flight motion, is an optimal strategy. We test the theory by analysing experimental foraging data on selected insect, mammal and bird species, and find that they are consistent with the predicted inverse square power-law distributions.

- $\alpha \simeq 1/2$: uncorrelated, white noise
- $\alpha > 1/2$: correlated
- $\alpha \simeq 1$: 1/f-noise, pink noise
- $\alpha > 1$: non-stationary, unbounded
- $\alpha \simeq 3/2$: Brownian noise



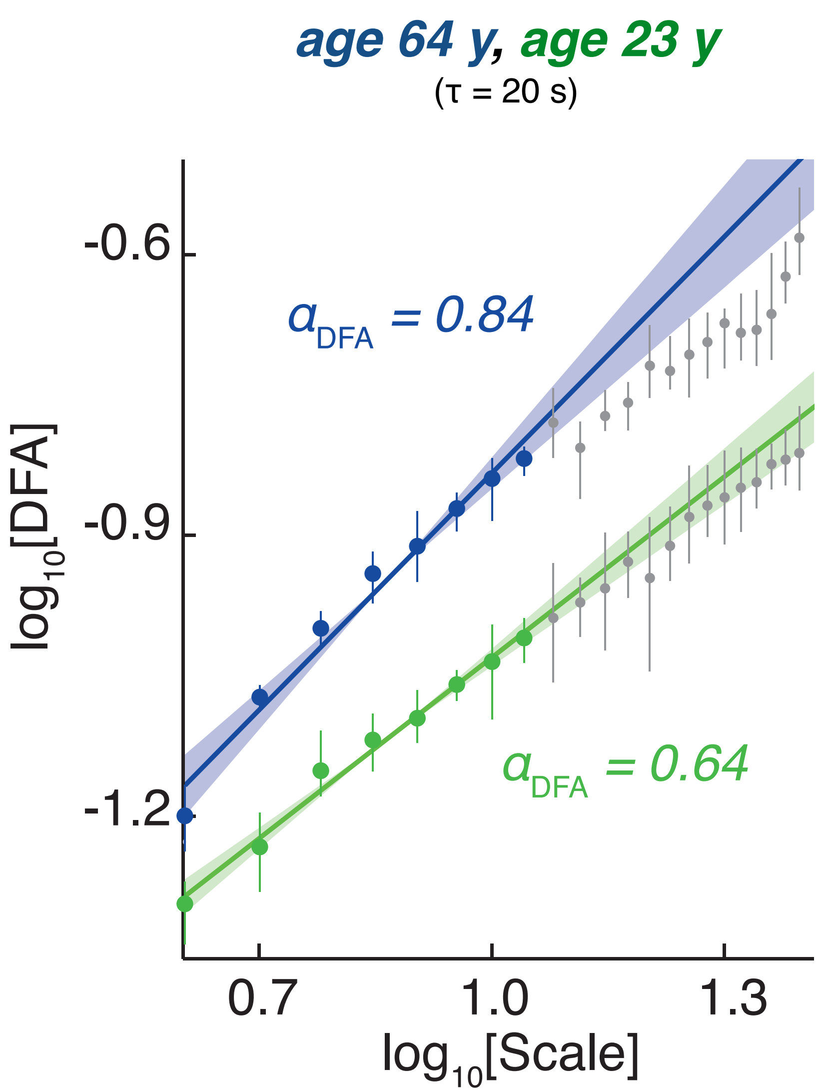
"Classic" gaussian random walk

Levy-type walk

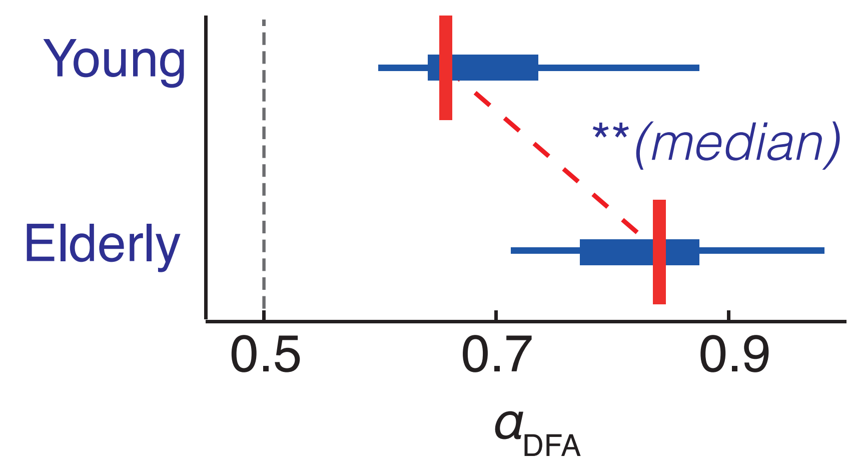
"Black death" in middle age

Contemporary epidemics

DFA of FCD and aging

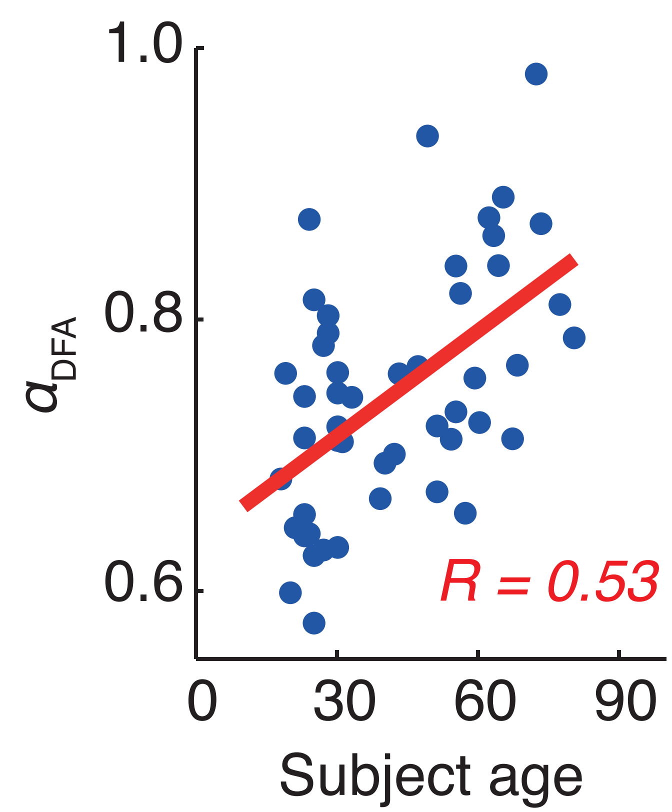


Single-subject DFA of FCD



Inter-group comparison

Thomas Boudou

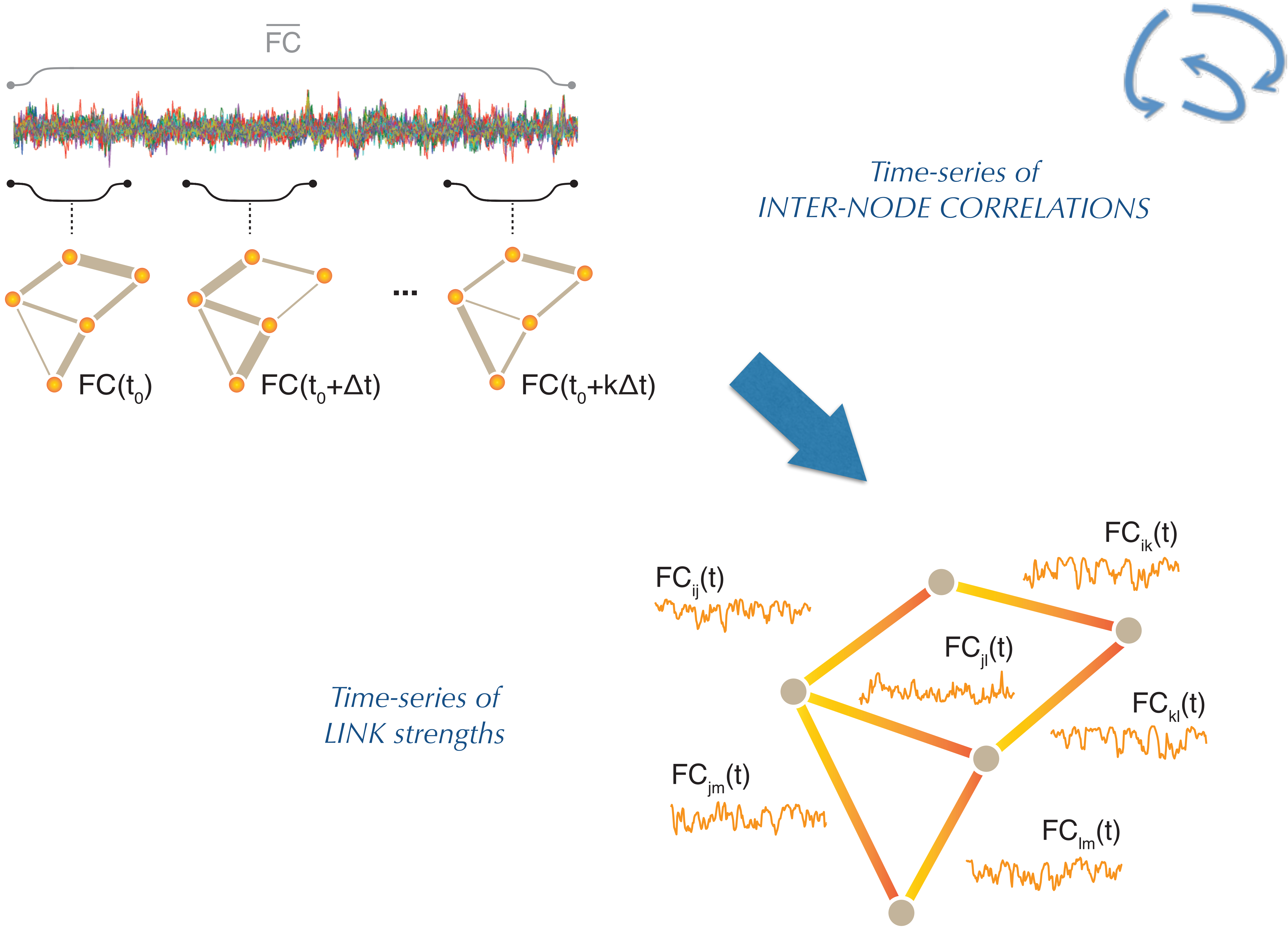


Correlation between DFA of FCD exponent and age

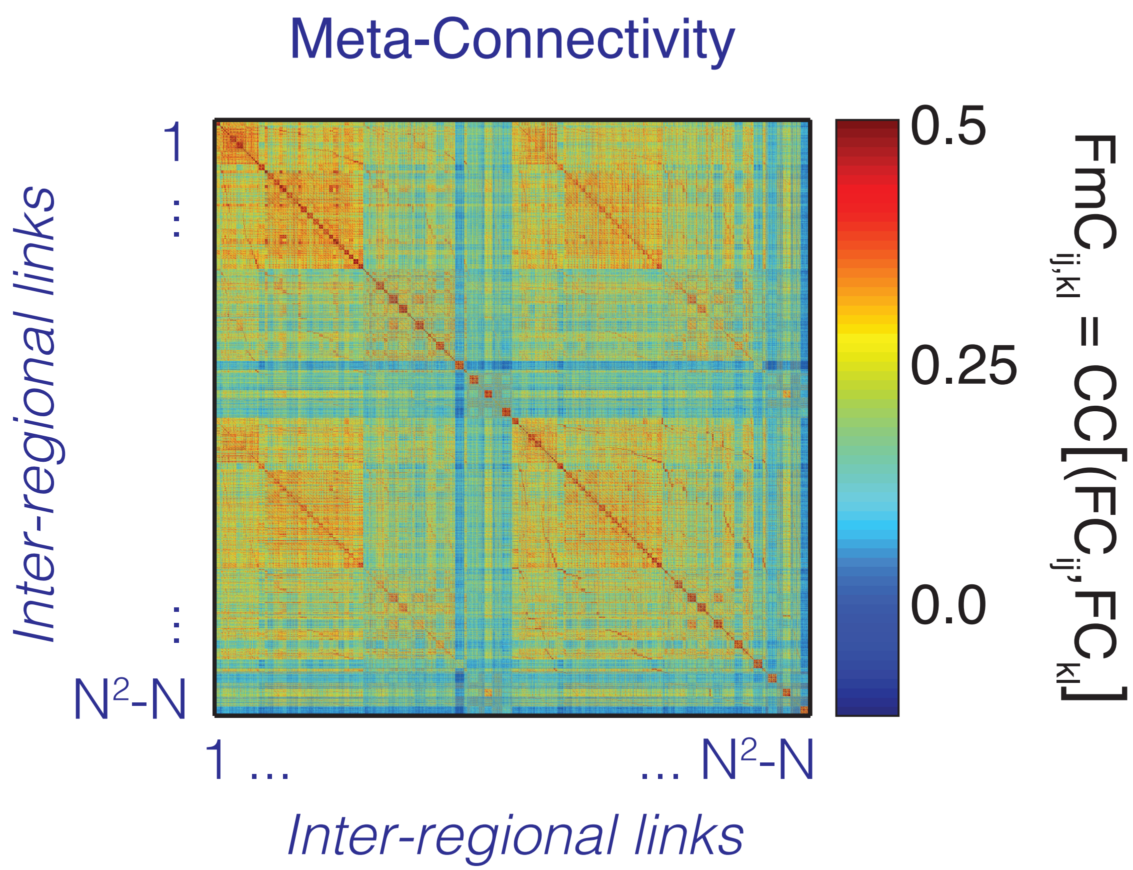
Conclusion 1b

FCD become “less brownian” and “more Levy” with aging

Let's now introduce
an alternative description of FCD…



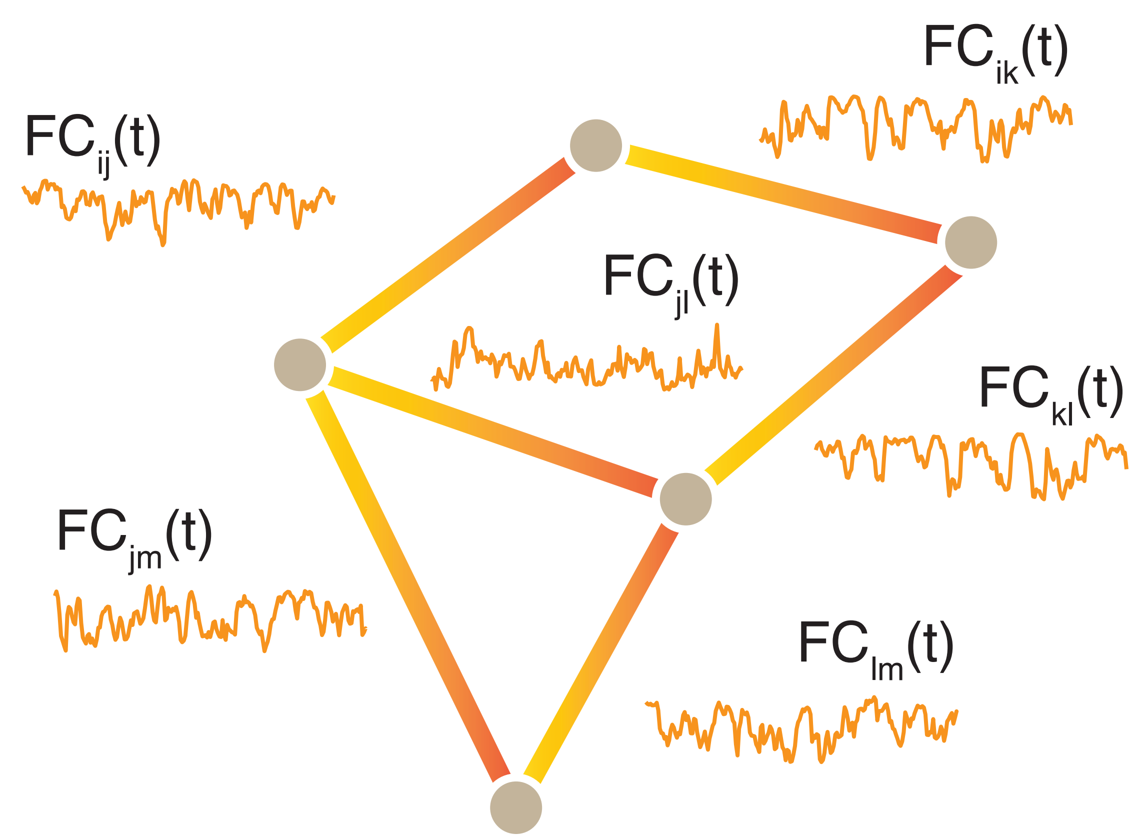
$\overline{FC}$
FC(t0)
FC(t0+Δt)
...
FC(t0+kΔt)
Time-series of
INTER-NODE CORRELATIONS
Time-series of
LINK strengths
FCij(t)
FCik(t)
FCjl(t)
FCkl(t)
FCjm(t)
FClm(t)



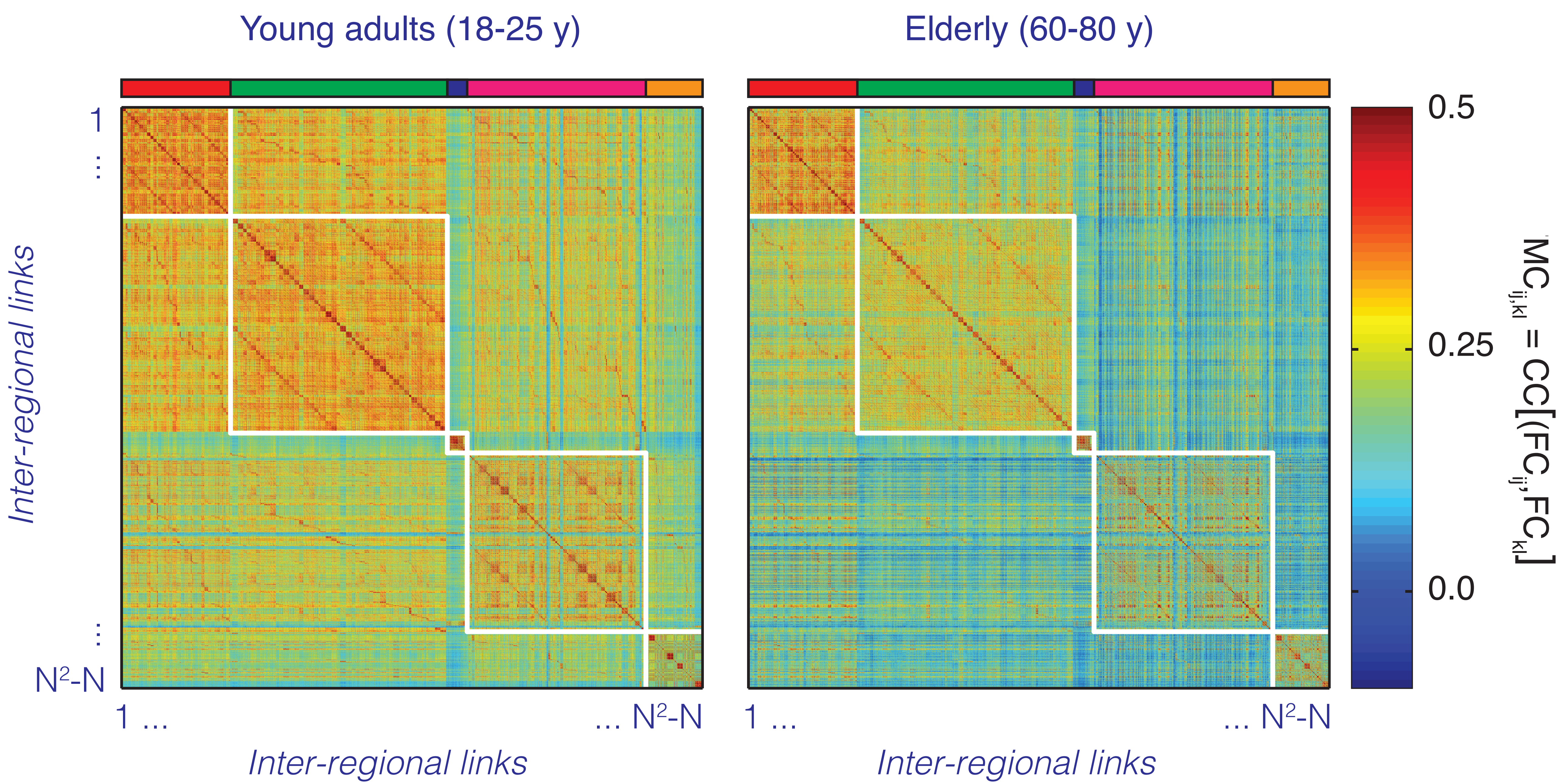
FUNCTIONAL META-CONNECTIVITY
(FMC matrices)

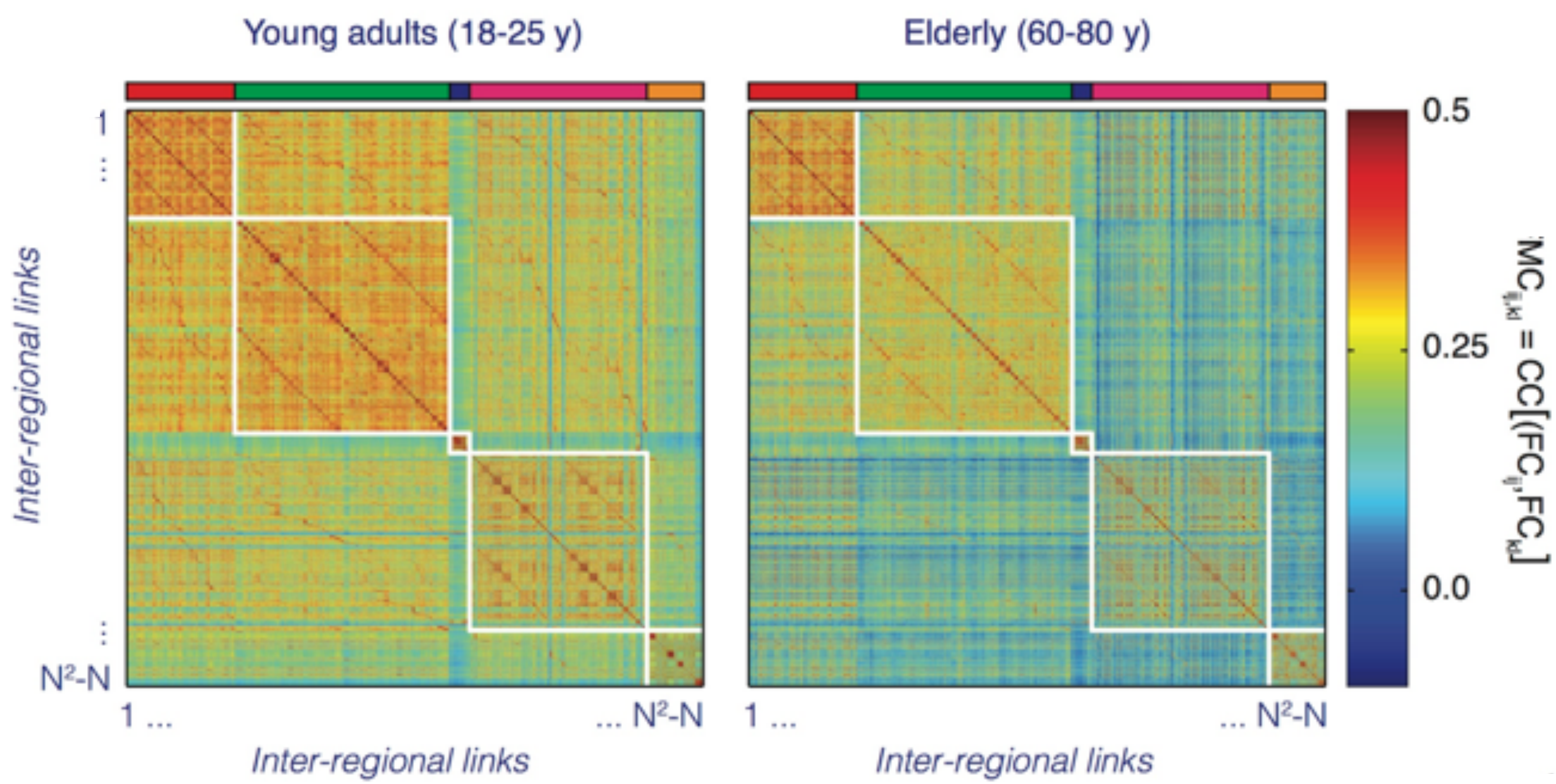
N(N-1) x N(N-1) matrix of
inter-link correlations

Time-series of
LINK strengths



Aging alters Meta-connectivity too!



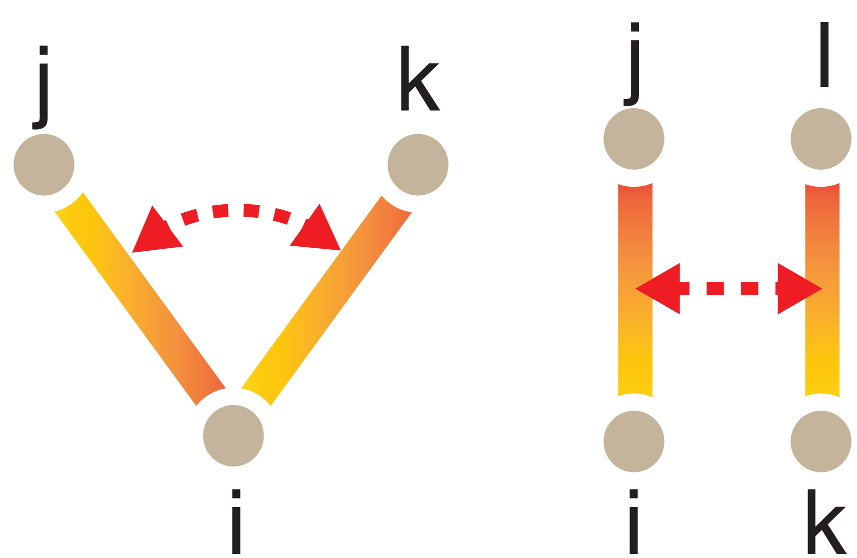


Communities of co-modulated links

$$\{MC_{ij,kl}\}$$

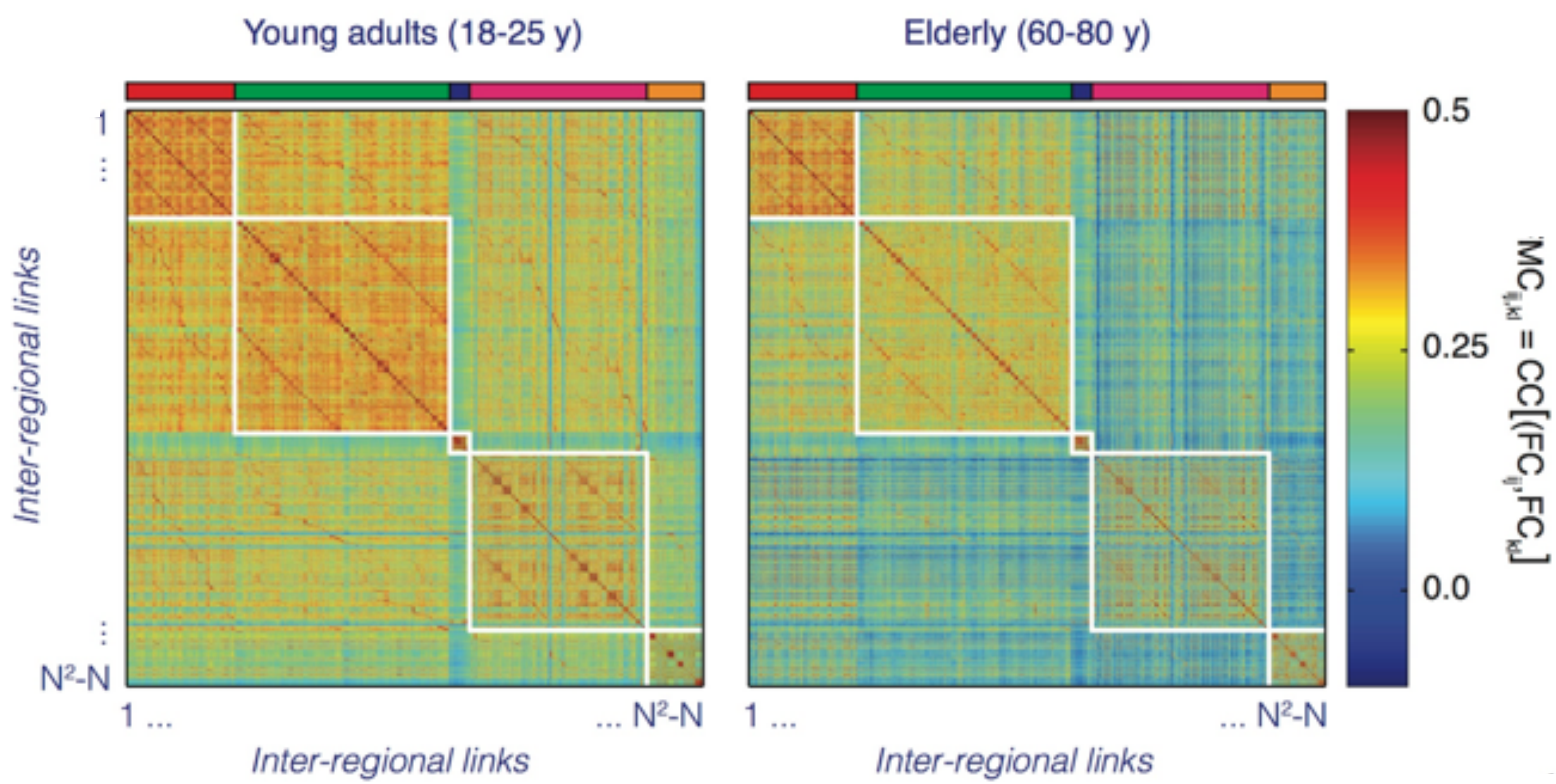
$$\cup$$

$$\{MC_{ij,ik}\}$$



"Trimers" *"Tetramers"*

$$MC(i) = \sum_{j,k} MC_{ij,ik}$$

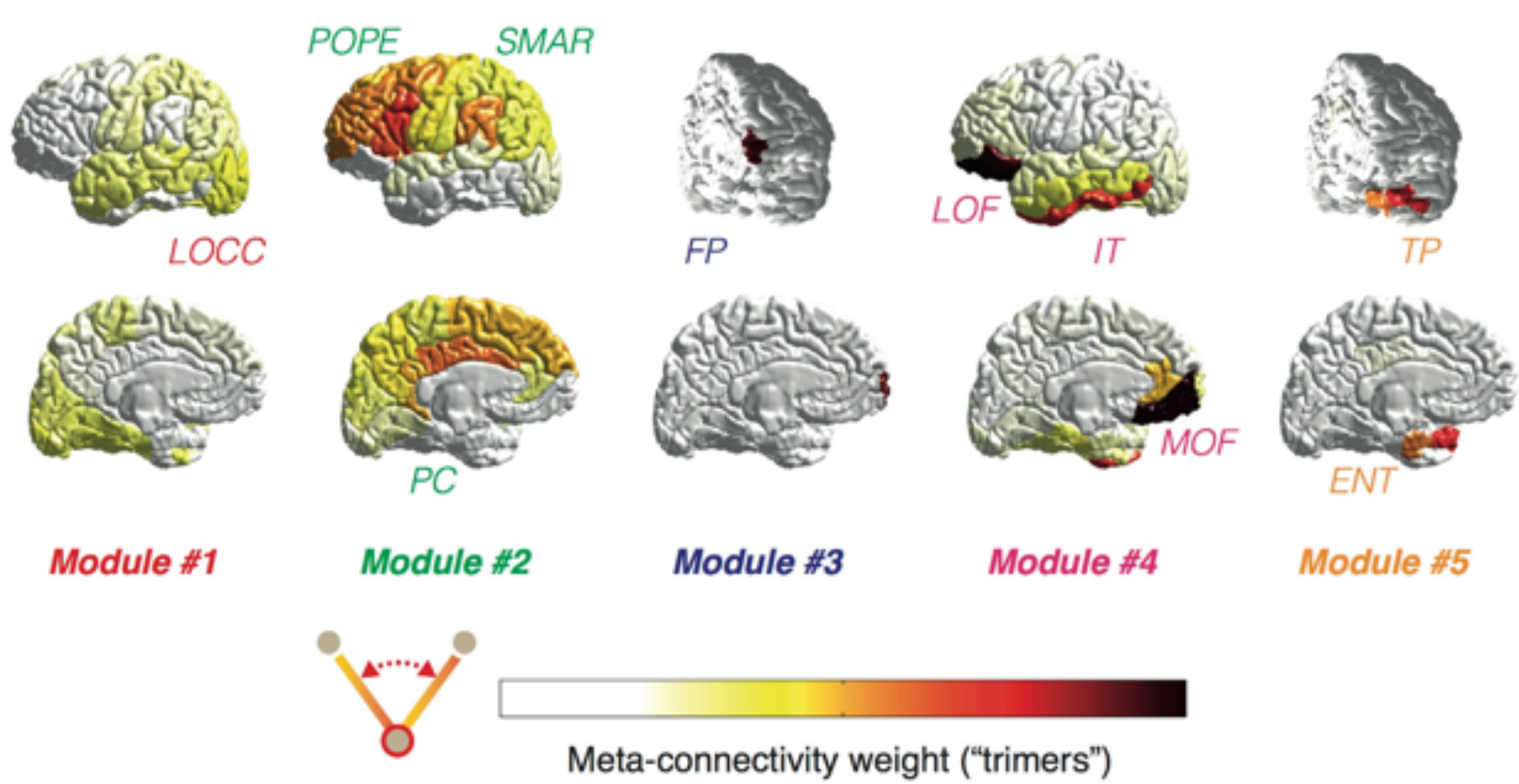


Communities of
co-modulated links

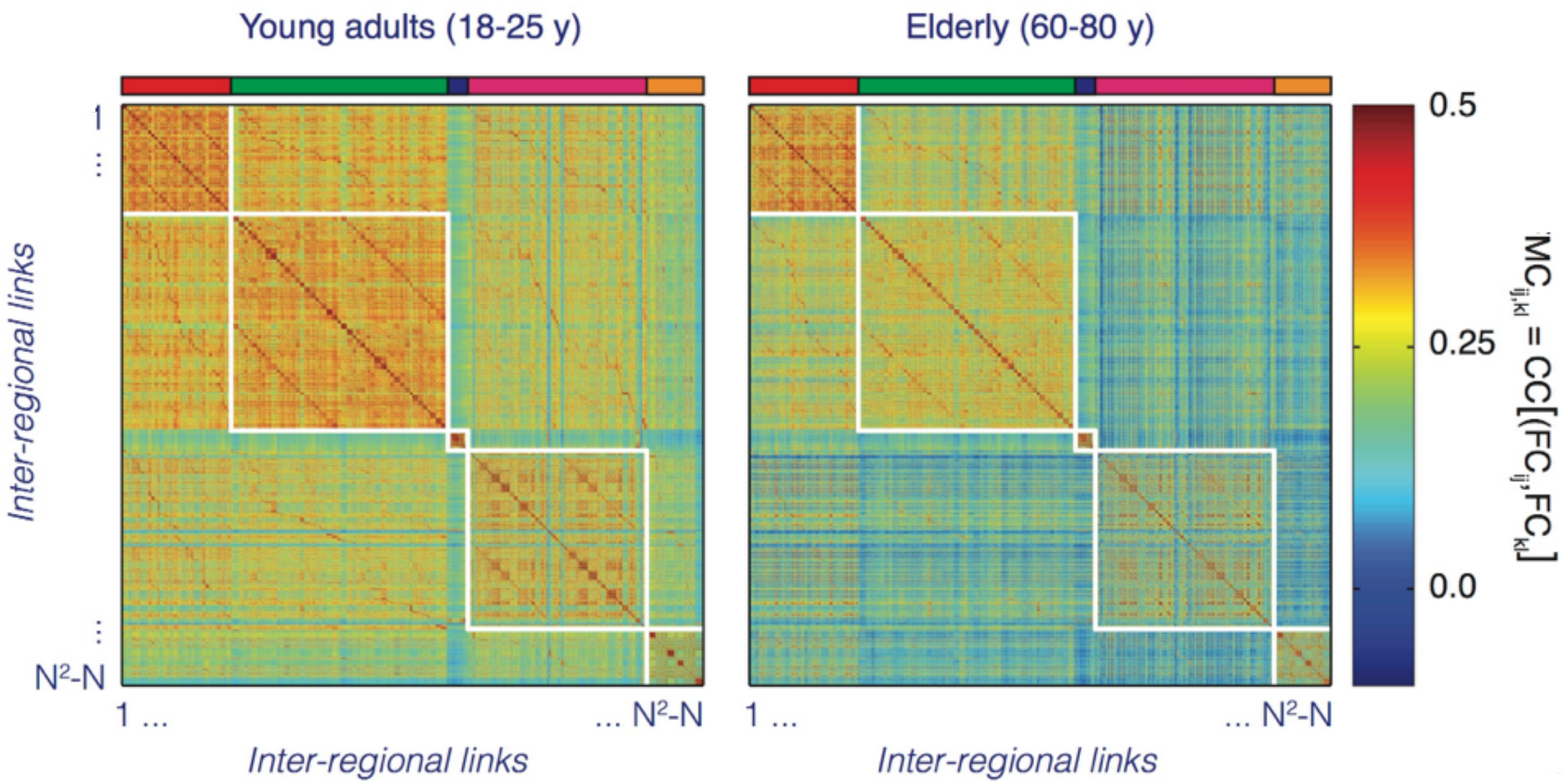
$$\{MC_{ij,kl}\}$$

$$\cup$$

$$\{MC_{ij,ik}\}$$



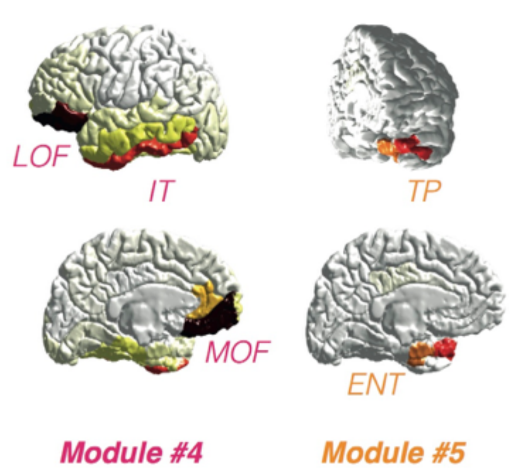
$$MC(i) = \sum_{j,k} MC_{ij,ik}$$

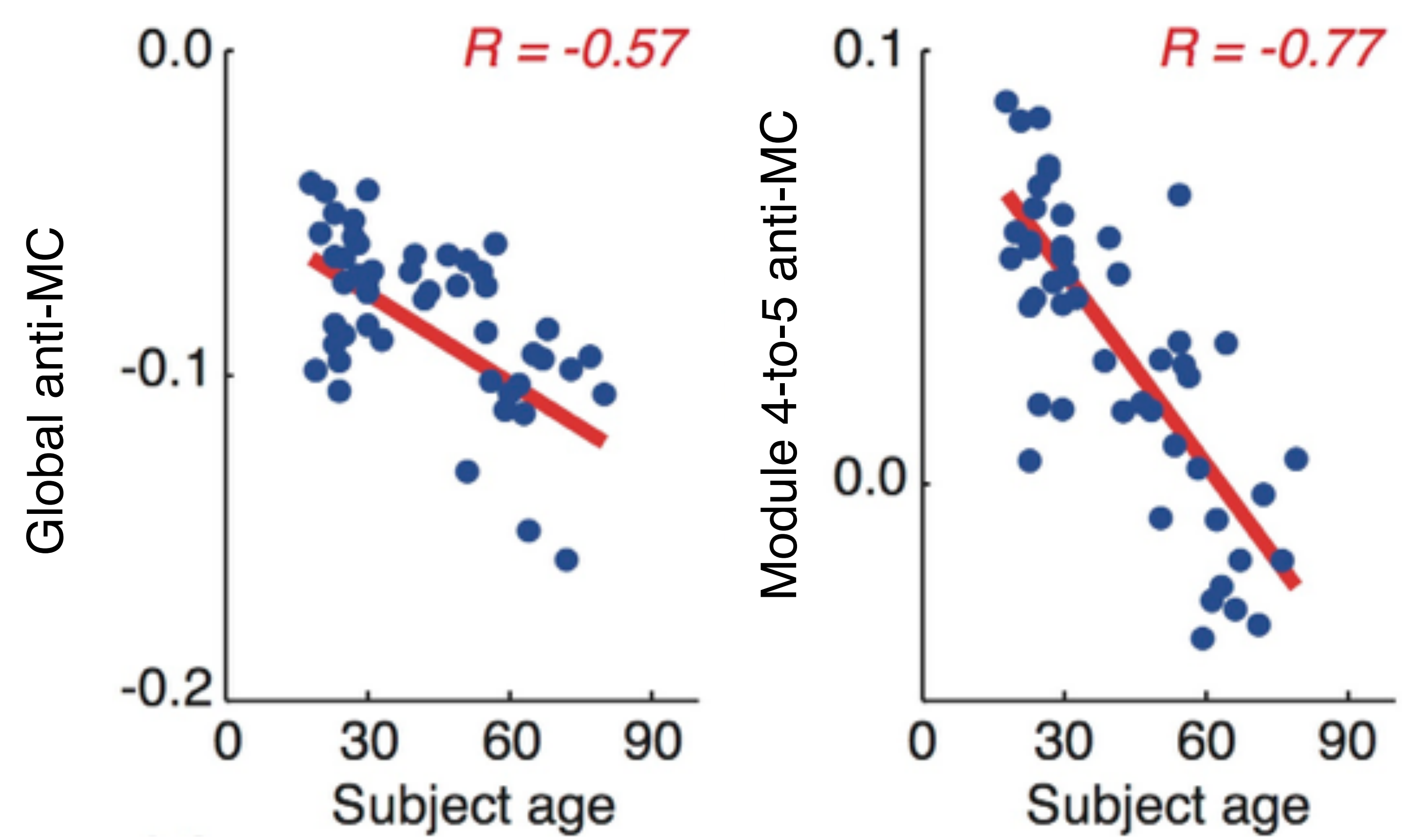


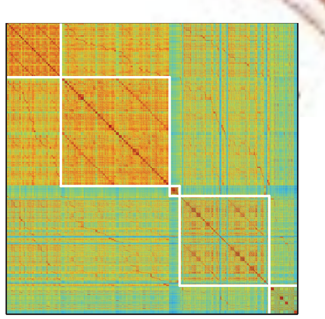
Communities of co-modulated links

Negative meta-connectivity develops with aging

("frustration")

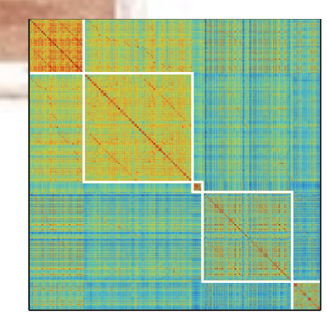






Young

Elderly



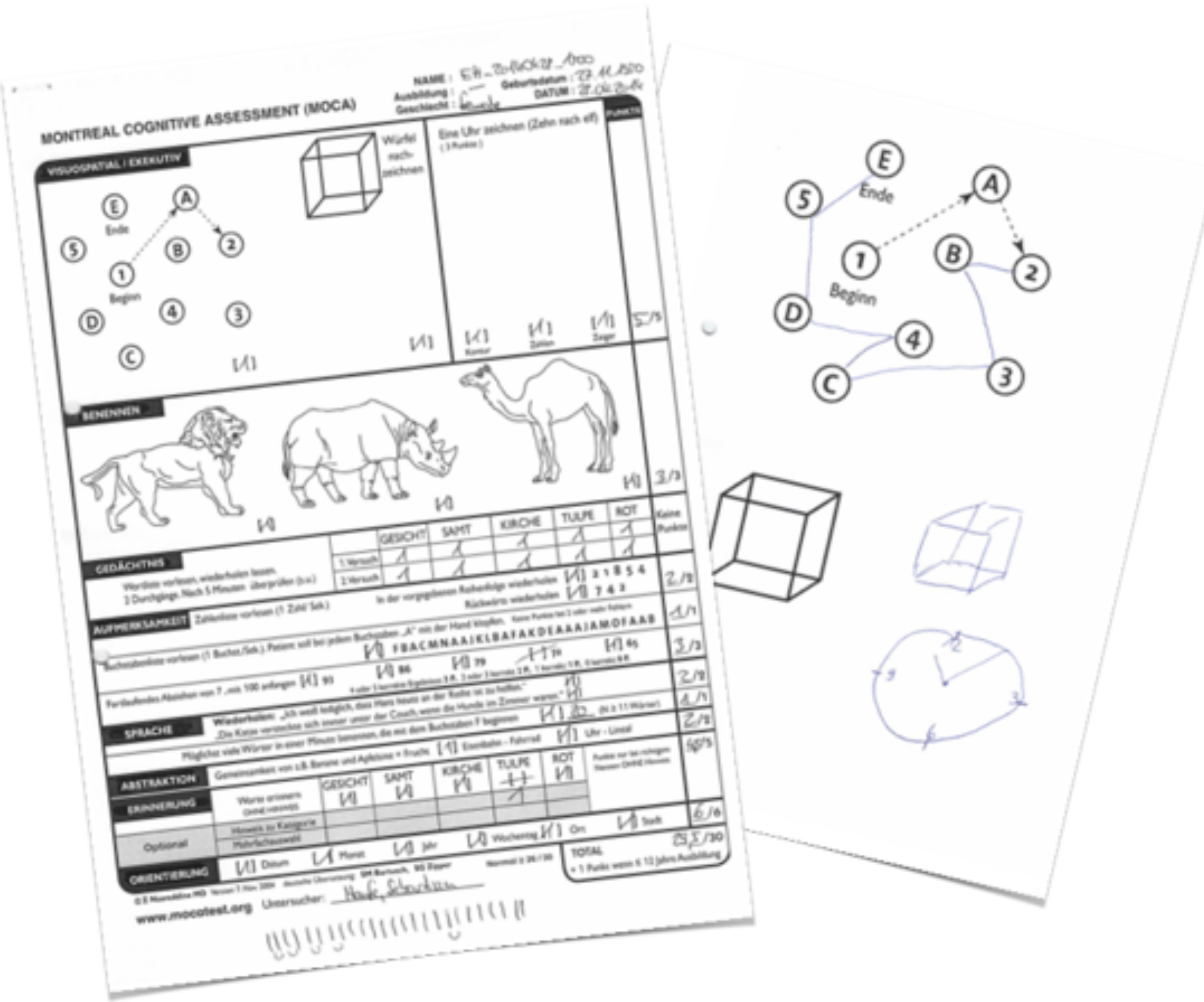
HARDER...

Conclusion 2

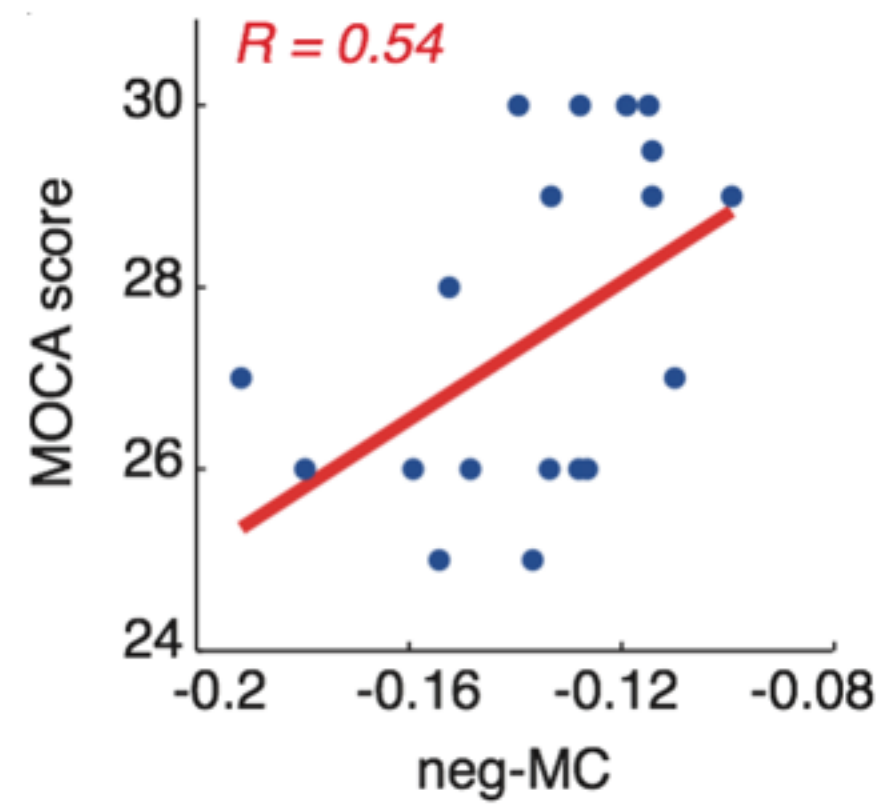
FCD "choreography" becomes more constrained, less fluent

(increased competition)

FCD (seems to) correlate with cognitive performance

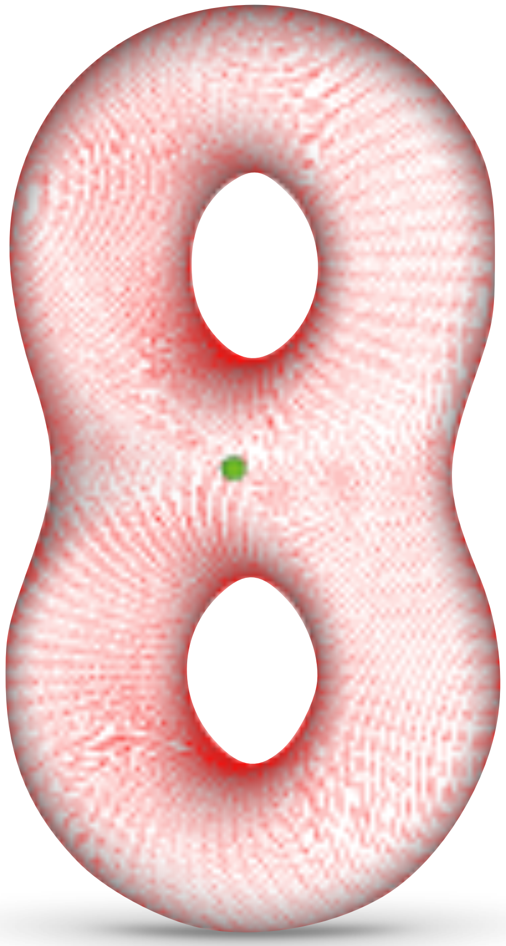


Cognitive Assessment scores…



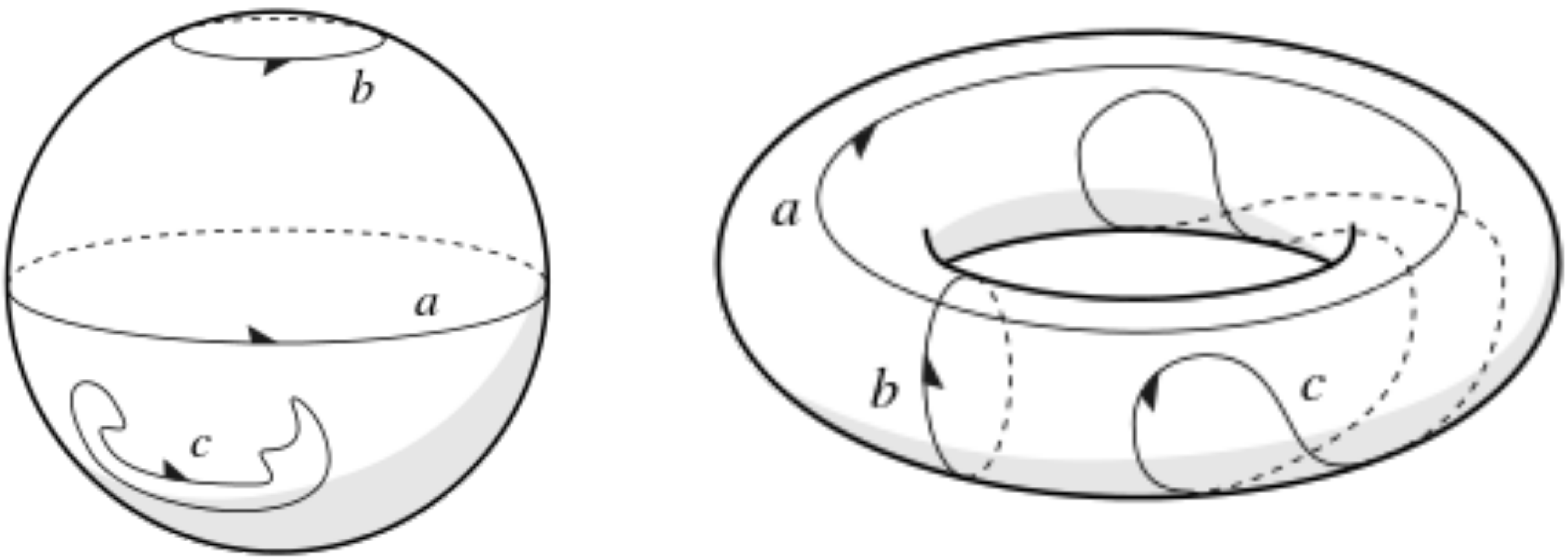
… correlate with MC frustration

CC(neg-MC, MOCA | Age) = 0.51 (**)
CC(neg-MC, MOCA-wm | Age) = 0.65 (***)

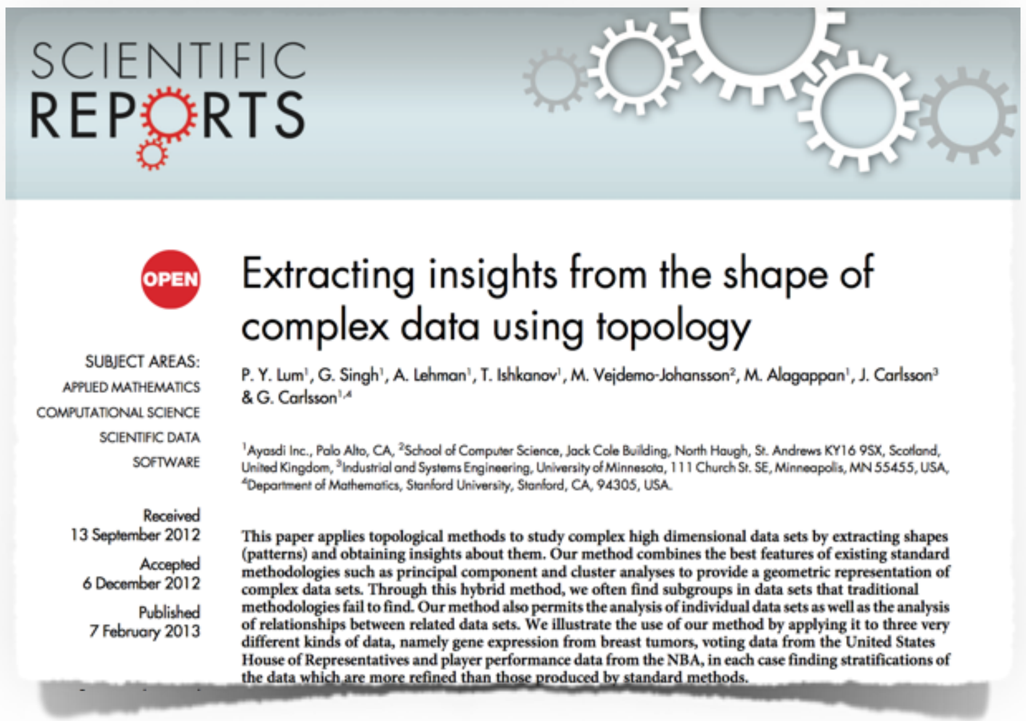


Topolome and aging!

Homology



Persistent homology


SCIENTIFIC REPORTS

OPEN

Extracting insights from the shape of complex data using topology

P. Y. Lum[1], G. Singh[1], A. Lehman[1], T. Ishkanov[1], M. Vejdemo-Johansson[2], M. Alagappan[1], J. Carlsson[3] & G. Carlsson[1,4]

[1]Ayasdi Inc., Palo Alto, CA, [2]School of Computer Science, Jack Cole Building, North Haugh, St. Andrews KY16 9SX, Scotland, United Kingdom, [3]Industrial and Systems Engineering, University of Minnesota, 111 Church St. SE, Minneapolis, MN 55455, USA, [4]Department of Mathematics, Stanford University, Stanford, CA, 94305, USA.

SUBJECT AREAS:
APPLIED MATHEMATICS
COMPUTATIONAL SCIENCE
SCIENTIFIC DATA
SOFTWARE

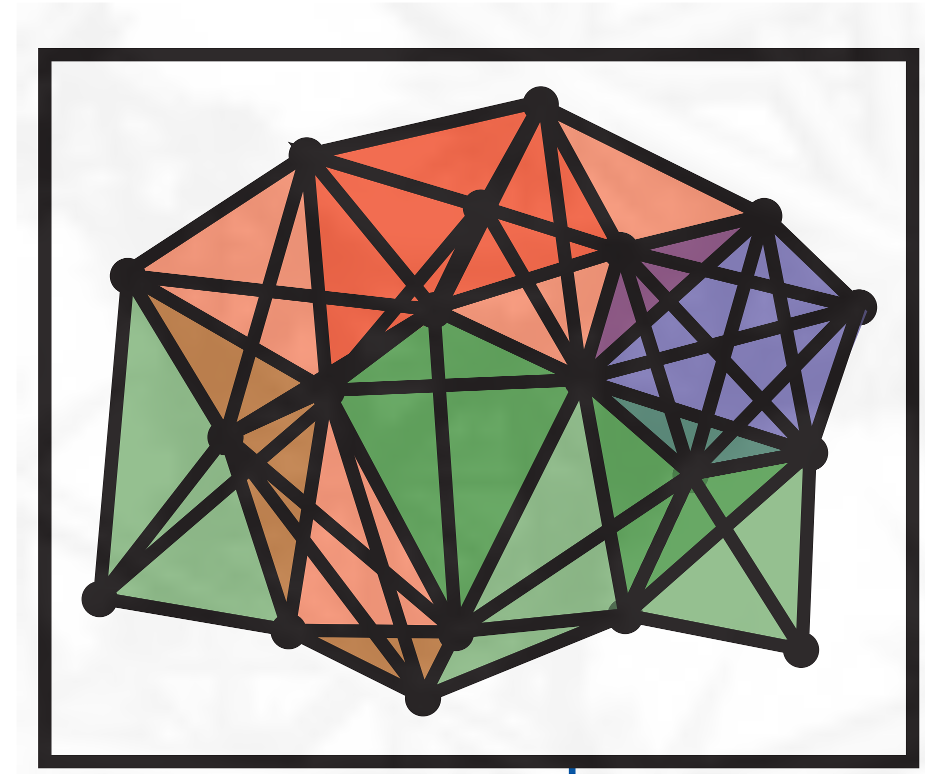
Received
13 September 2012

Accepted
6 December 2012

Published
7 February 2013

This paper applies topological methods to study complex high dimensional data sets by extracting shapes (patterns) and obtaining insights about them. Our method combines the best features of existing standard methodologies such as principal component and cluster analyses to provide a geometric representation of complex data sets. Through this hybrid method, we often find subgroups in data sets that traditional methodologies fail to find. Our method also permits the analysis of individual data sets as well as the analysis of relationships between related data sets. We illustrate the use of our method by applying it to three very different kinds of data, namely gene expression from breast tumors, voting data from the United States House of Representatives and player performance data from the NBA, in each case finding stratifications of the data which are more refined than those produced by standard methods.

?

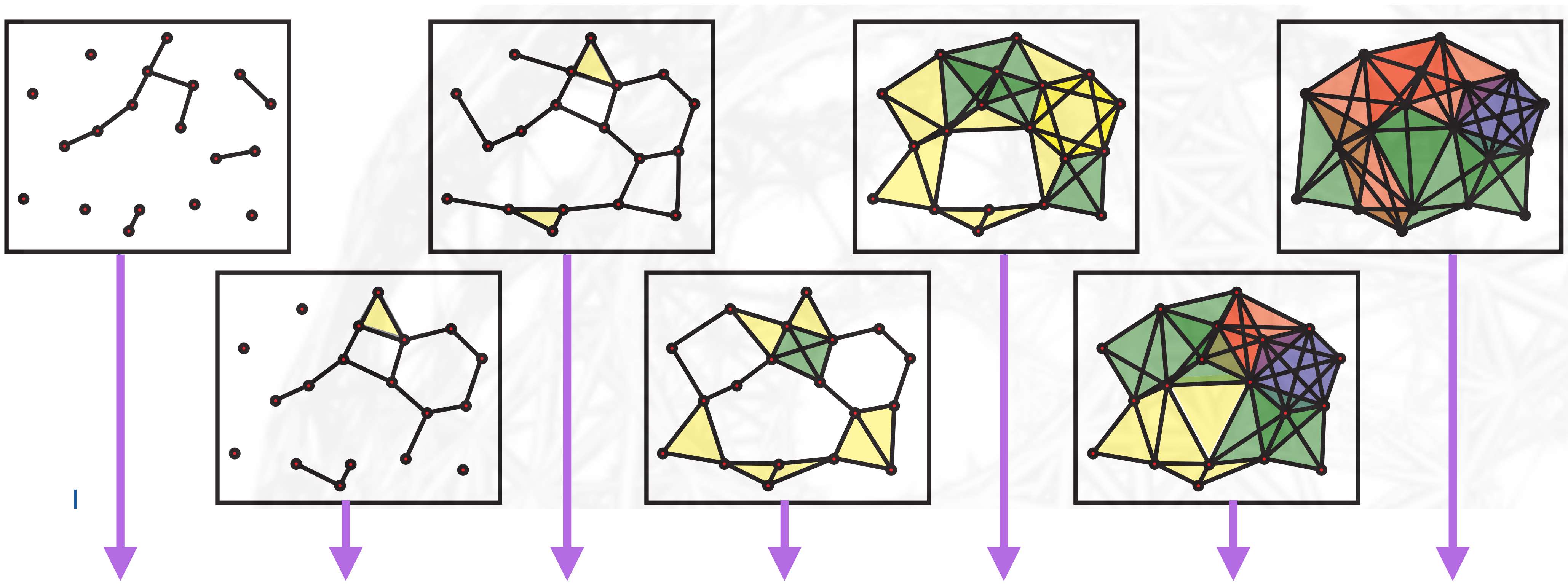


Francesco Vaccarino

Giovanni Petri

WARNING!
Ask my pals mathematicians
for details!

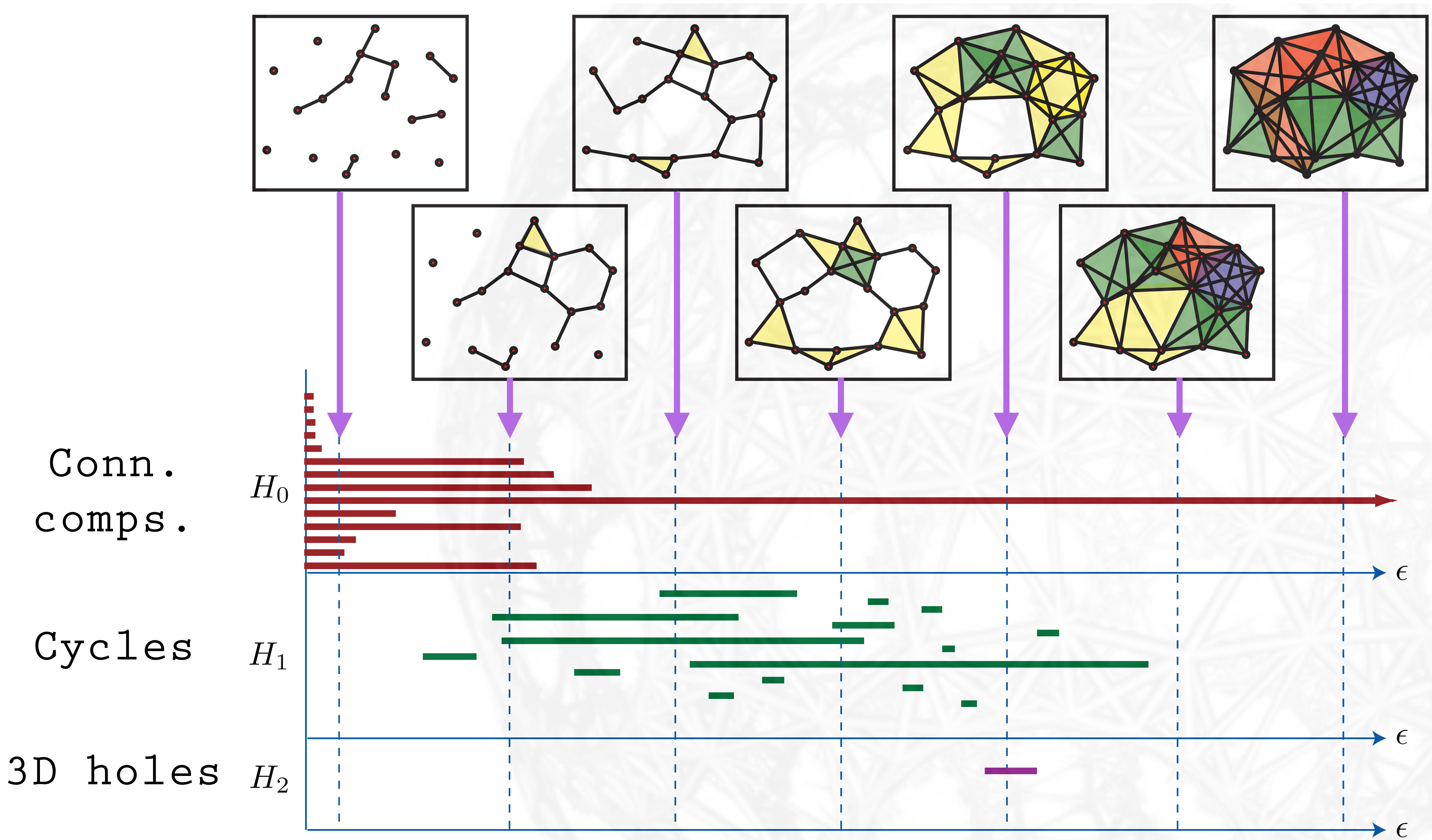
Persistent homology



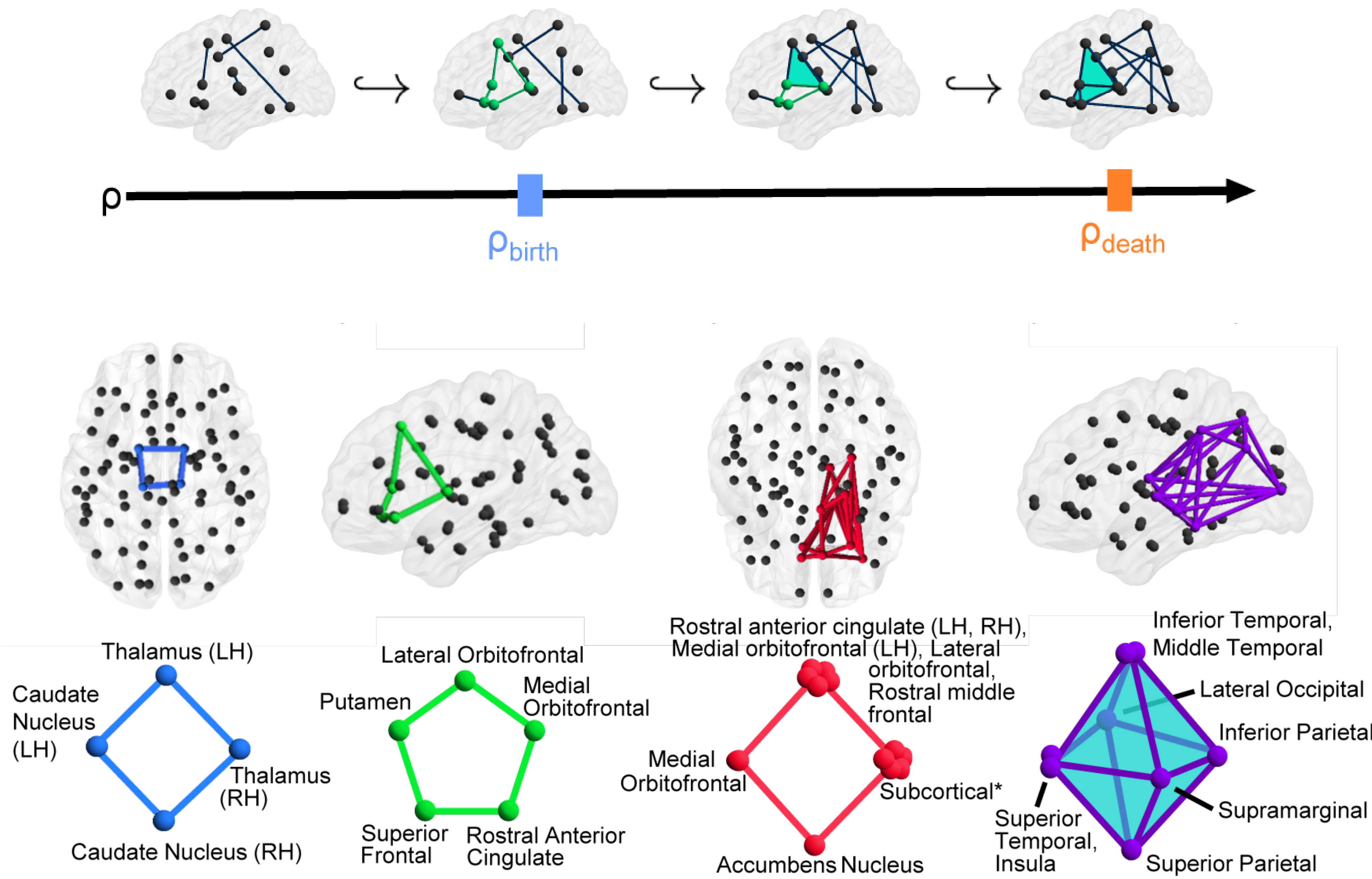
"Filtration"

Let's add (or remove) gradually nodes, e.g. in order of decreasing strength

Persistent homology



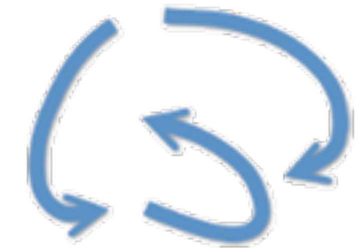
Cycles and "cavities"



The most persistent cicles and holes

Adapted from
Sizemore, Giusti, Bassett,
arXiV (2016)

Persistence homology scaffold



JOURNAL OF THE ROYAL SOCIETY Interface

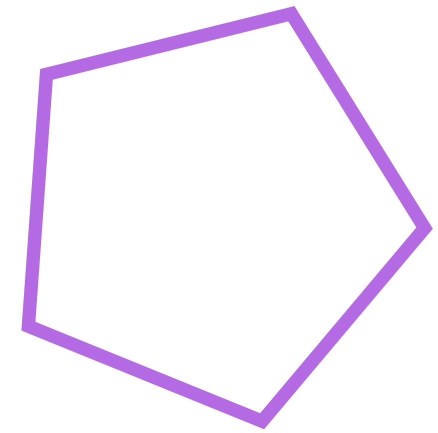
rsif.royalsocietypublishing.org

Homological scaffolds of brain functional networks

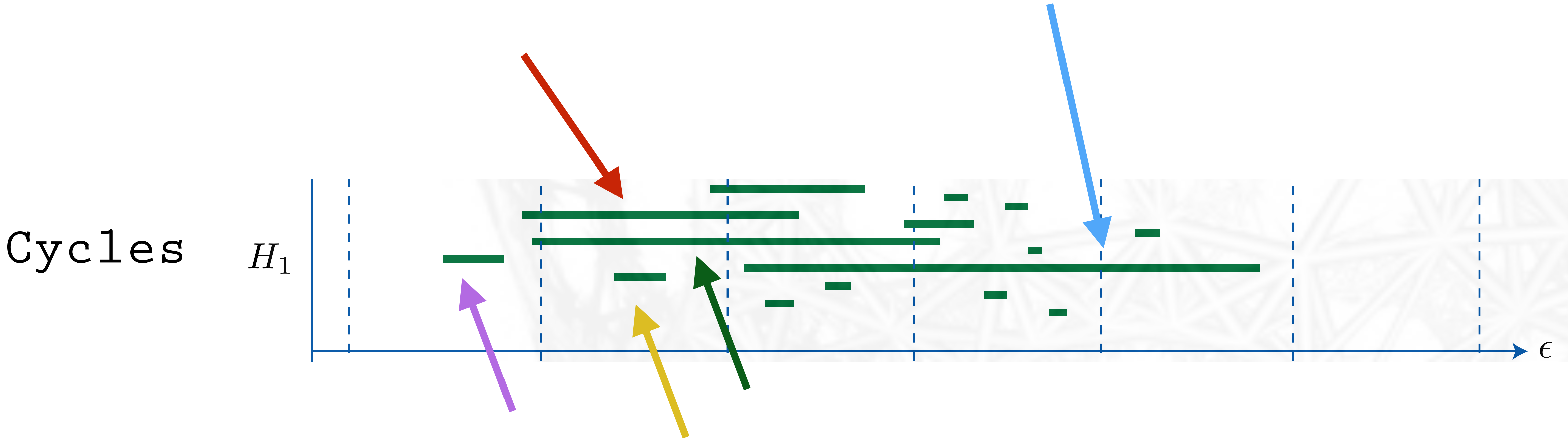
G. Petri[1], P. Expert[2], F. Turkheimer[2], R. Carhart-Harris[3], D. Nutt[3], P. J. Hellyer[4] and F. Vaccarino[1,5]

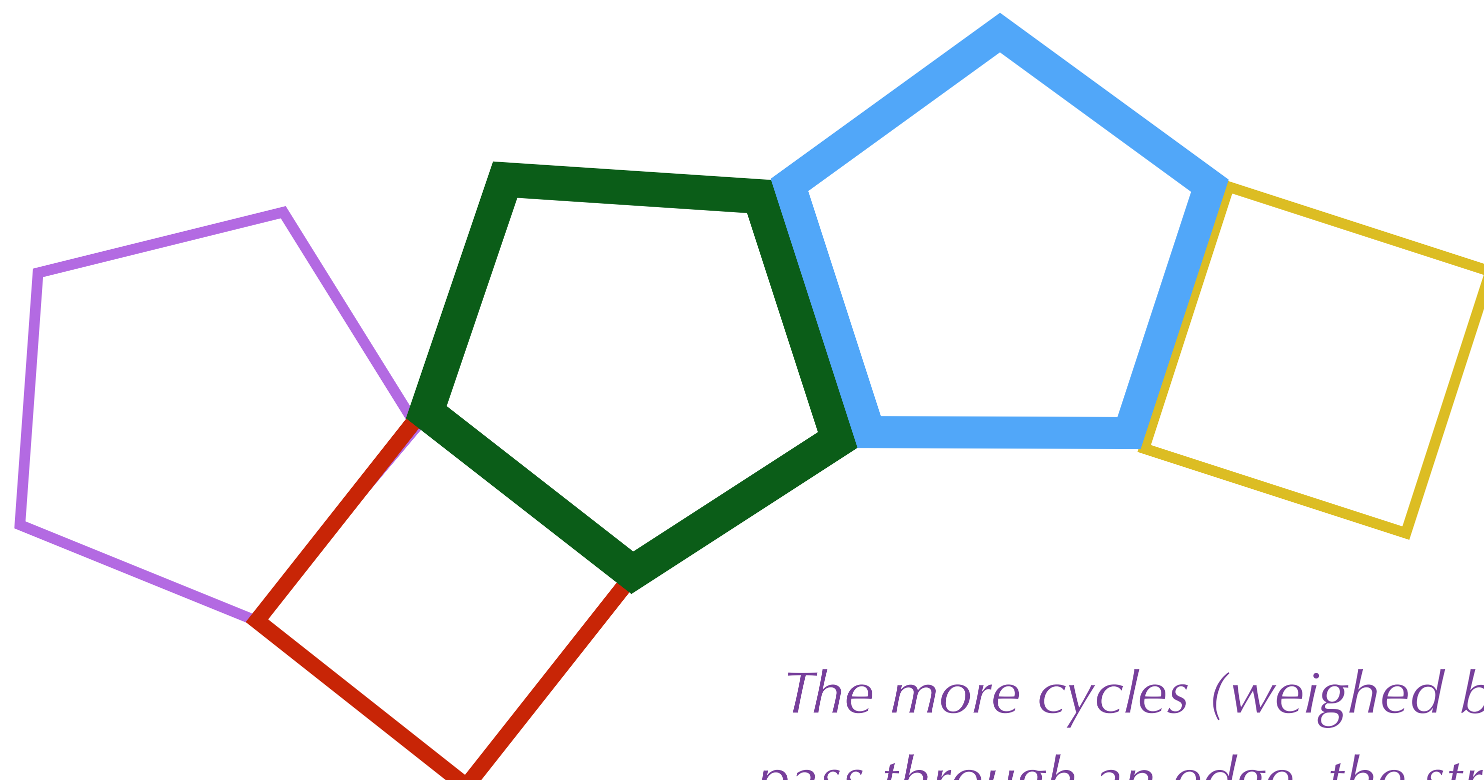
We exploit this to define two new objects, the *persistence* and the *frequency homological scaffolds* $\mathscr{H}^{p}_{G}$ and $\mathscr{H}^{f}_{G}$ of a graph G. The *persistence homological scaffold* is the network composed of all the cycle paths corresponding to generators weighted by their persistence. If an edge e belongs to multiple cycles $g_0, g_1, \ldots, g_s$, its weight is defined as the sum of the generators' persistence:

$$\omega_e^{\pi} = \sum_{g_i | e \in g_i} \pi_{g_i}. \tag{4.1}$$



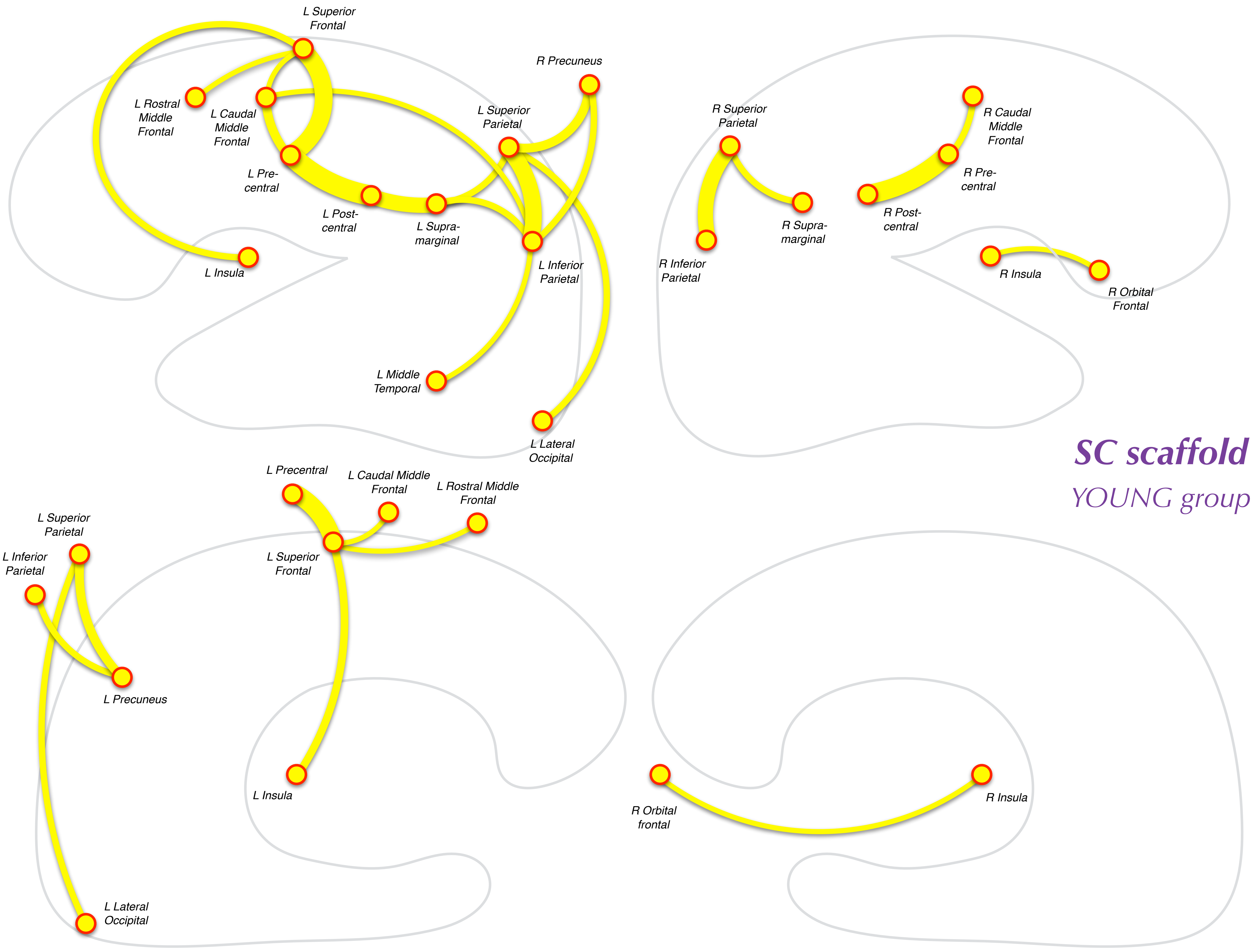
Persistence homology scaffold

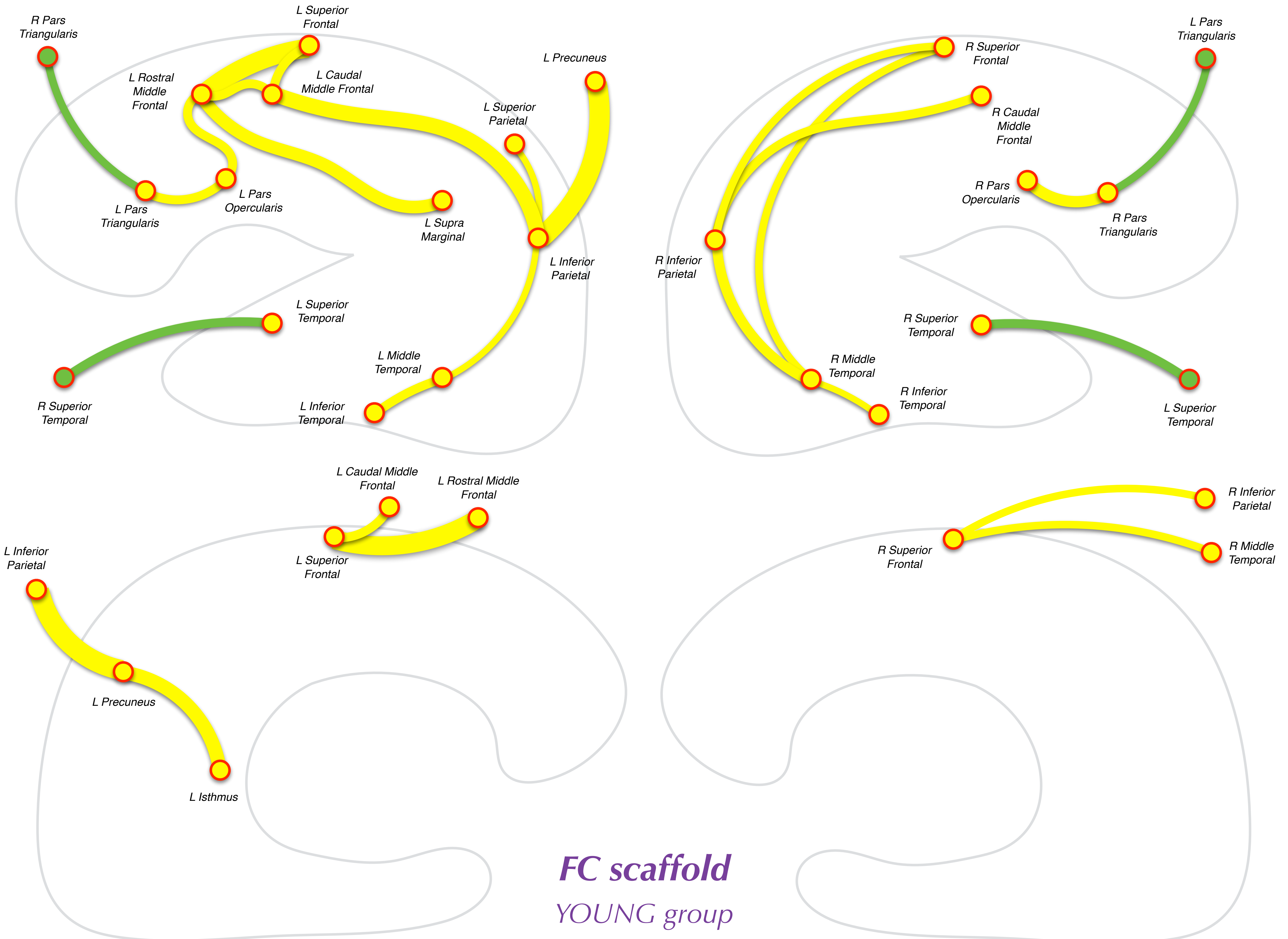




$$\omega_e^{\pi} = \sum_{g_i | e \in g_i} \pi_{g_i}.$$

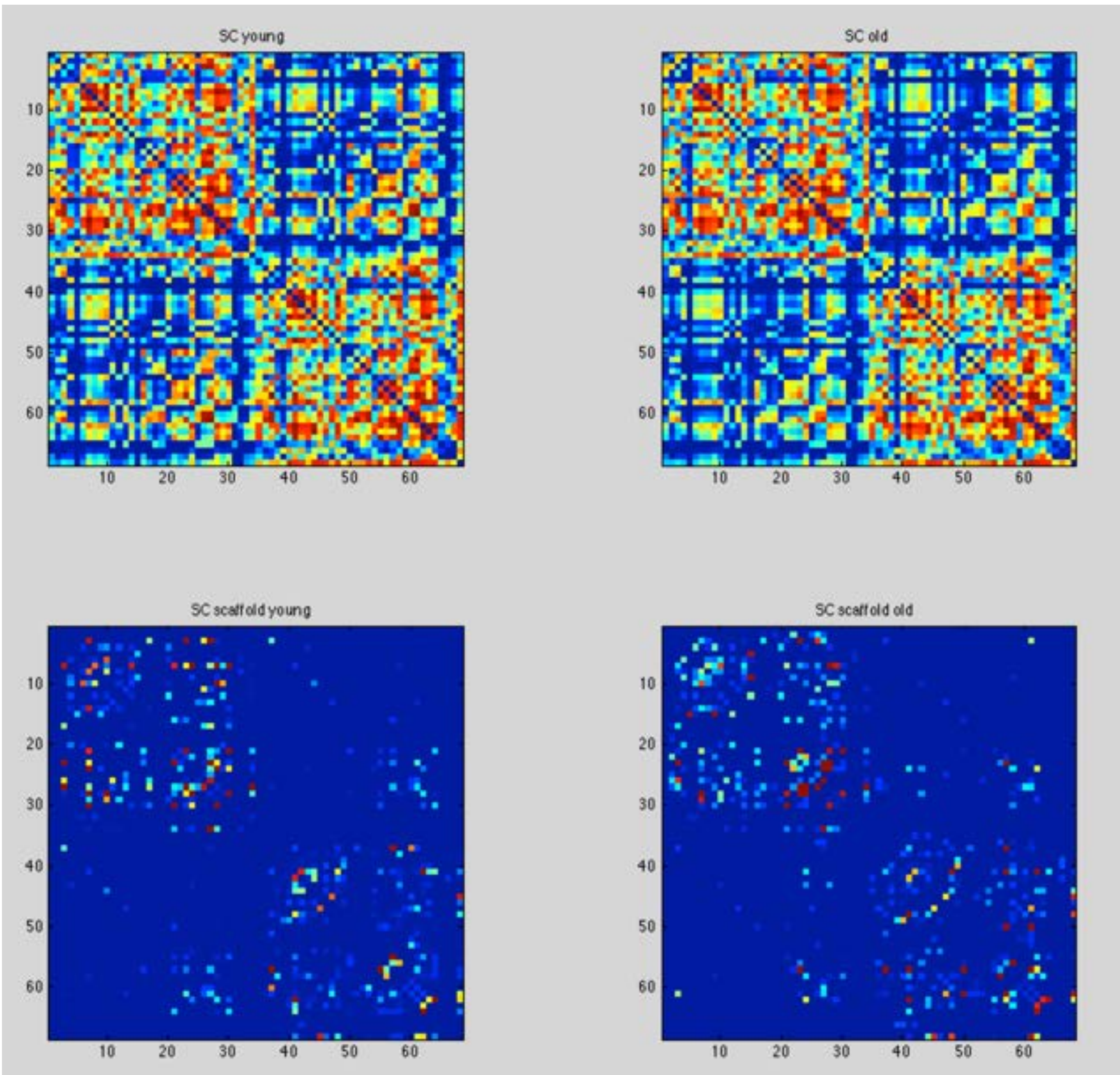
The more cycles (weighed by persistence) pass through an edge, the stronger this edge will be in the scaffold


L Superior Frontal
L Rostral Middle Frontal
L Caudal Middle Frontal
L Pre-central
L Post-central
L Supra-marginal
L Superior Parietal
R Precuneus
L Inferior Parietal
L Insula
L Middle Temporal
L Lateral Occipital
R Superior Parietal
R Inferior Parietal
R Supra-marginal
R Caudal Middle Frontal
R Pre-central
R Post-central
R Insula
R Orbital Frontal
SC scaffold
YOUNG group
L Precentral
L Caudal Middle Frontal
L Rostral Middle Frontal
L Superior Frontal
L Superior Parietal
L Inferior Parietal
L Precuneus
L Insula
L Lateral Occipital
R Orbital frontal
R Insula


R Pars Triangularis
L Superior Frontal
L Rostral Middle Frontal
L Caudal Middle Frontal
L Precuneus
L Superior Parietal
L Pars Triangularis
L Pars Opercularis
L Supra Marginal
L Inferior Parietal
L Superior Temporal
R Superior Temporal
L Middle Temporal
L Inferior Temporal
R Superior Frontal
L Pars Triangularis
R Caudal Middle Frontal
R Pars Opercularis
R Pars Triangularis
R Inferior Parietal
R Superior Temporal
R Middle Temporal
R Inferior Temporal
L Superior Temporal
L Caudal Middle Frontal
L Rostral Middle Frontal
L Superior Frontal
L Inferior Parietal
L Precuneus
L Isthmus
R Inferior Parietal
R Superior Frontal
R Middle Temporal
FC scaffold
YOUNG group

Scaffolds are diluted!

YOUNG *OLD*



Full SC graph

SC scaffold graph

Some results

- Structural connectome:
  - *Average persistence maintained*
  - *cycle length increases ("drying sponge")*
- Functional connectome:
  - *Average persistence and length maintained!*
- In other words: nothing changes too much! ➠ **Homology is conserved through aging**

Some results

- Comparison with null models
  - *We generate surrogate SC and FC by fitting trends with age of the strength of each link…*
  - *… but each link is independently decreasing (or increasing)!*
- Data vs model
  - ***There is matching for structural connectome****: "drying sponge effect" can be simply explained by the individual disconnection rates*
  - ***There is NOT matching for functional connectome****: in the model the Betti number is exploding, the persistence is dropping, the length is reducing… nothing works!*
- ➠ **Homology conservation in FC is a non trivial result!**

Some results

- The actual scaffolds are changing…
- … in ways compatible with known hypotheses (“HAROLD”, “PASA”…)
- So holes and cycles relocate… but to build an object with the same homology!
- ➠ **Compensatory effects?**
- **Go to pathological cohorts…** *in the future*


WORK
IN PROGRESS

BETTER ?

On the meaning of “better”…

Or better say different!

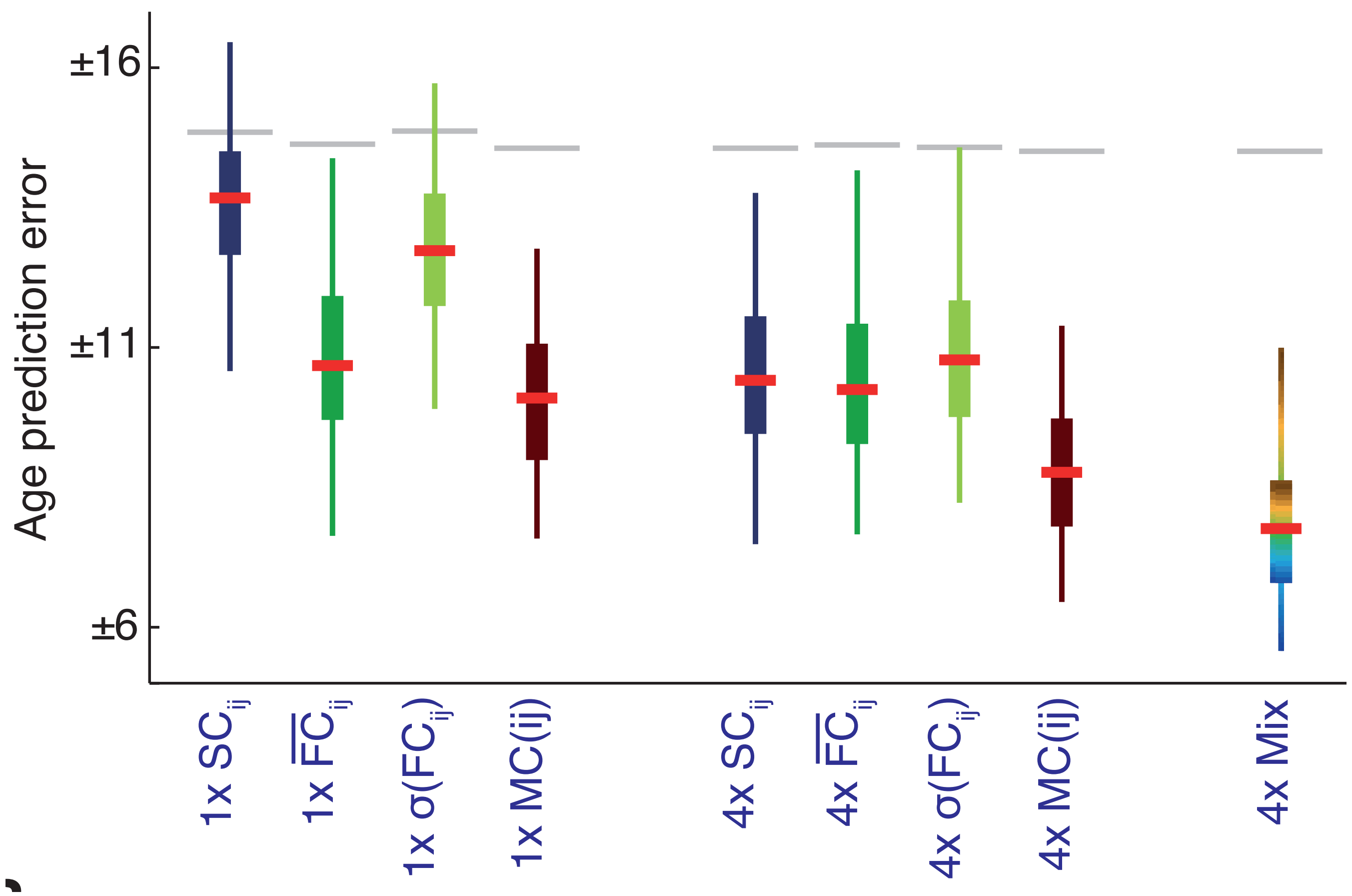
"Better" we don't know yet…

Functional Connectivity Dynamics (FCD) as biomarker

- Closer to the dynamic nature of the brain!
    - *What is altered may be the dynamics, not the networks!*
- Avoids misinterpreting temporal variability as inter-subject variability!

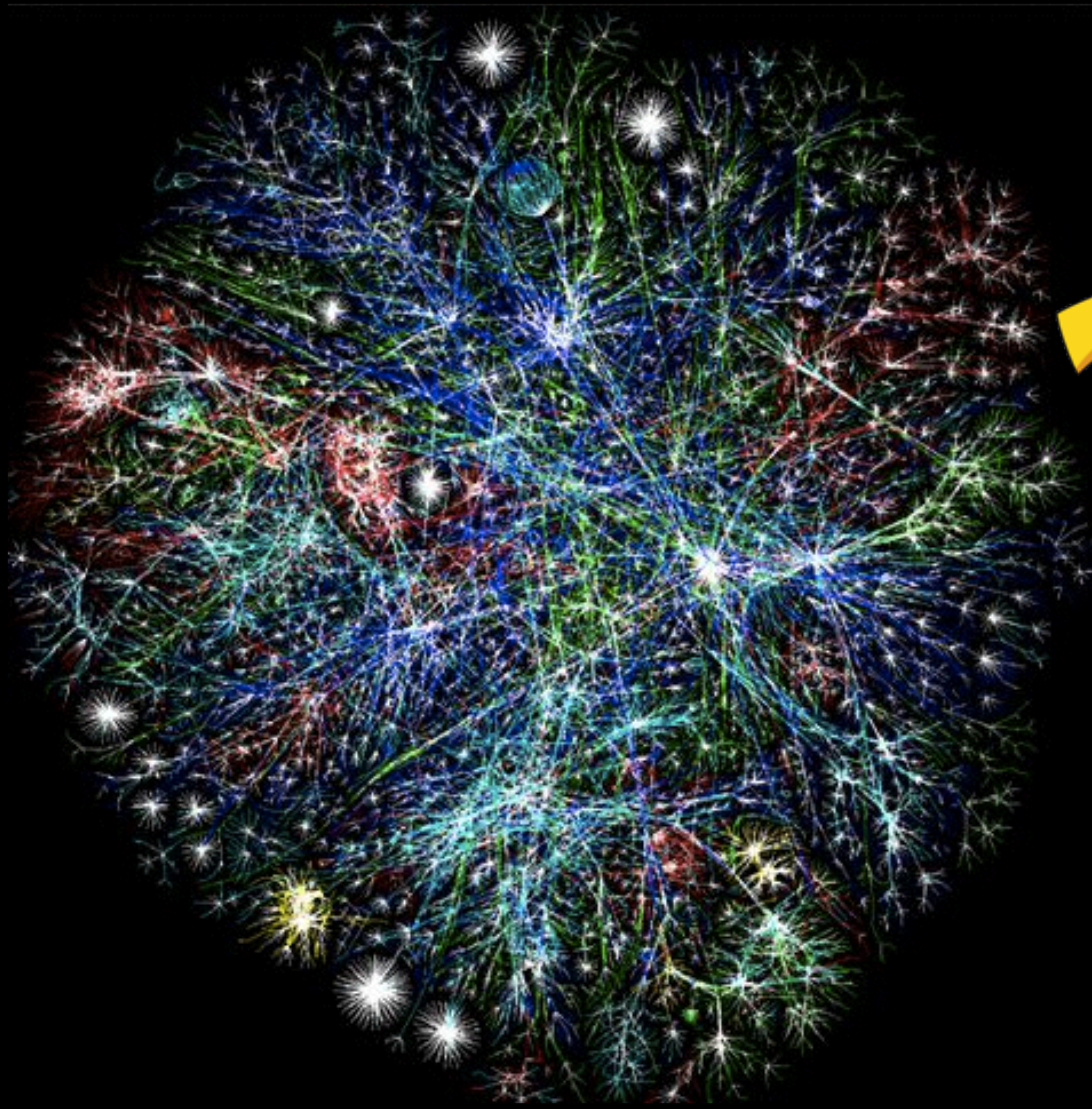
- Closer to the dynamic nature of the brain!
    - *What is altered may be the dynamics, not the networks!*
- Avoids misinterpreting temporal variability as inter-subject variability!

Predicting age



SYNERGY!

Crappy linear prediction



Let's go beyond graphs!

Institut de Neurosciences des Systèmes

Thanks!

Nintendo

bccn göttingen