



COARSE-GRAINING BIOLOGICAL NETWORKS THROUGH SYMMETRIES AND SYNCHRONIZATION

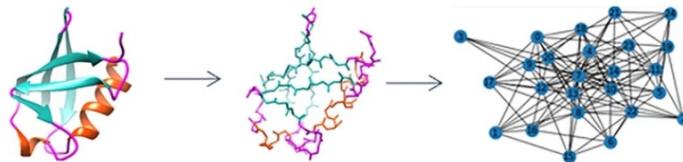
TOMMASO GILI

*Networks Days : Bridging **micro** with **macro***

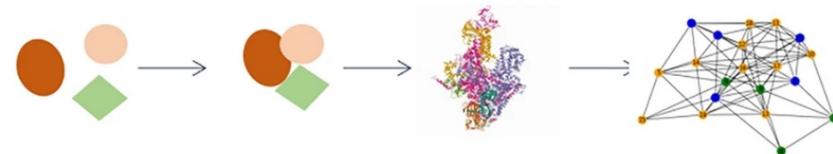
Padua, 25th October 2024

NETWORKS@IMT

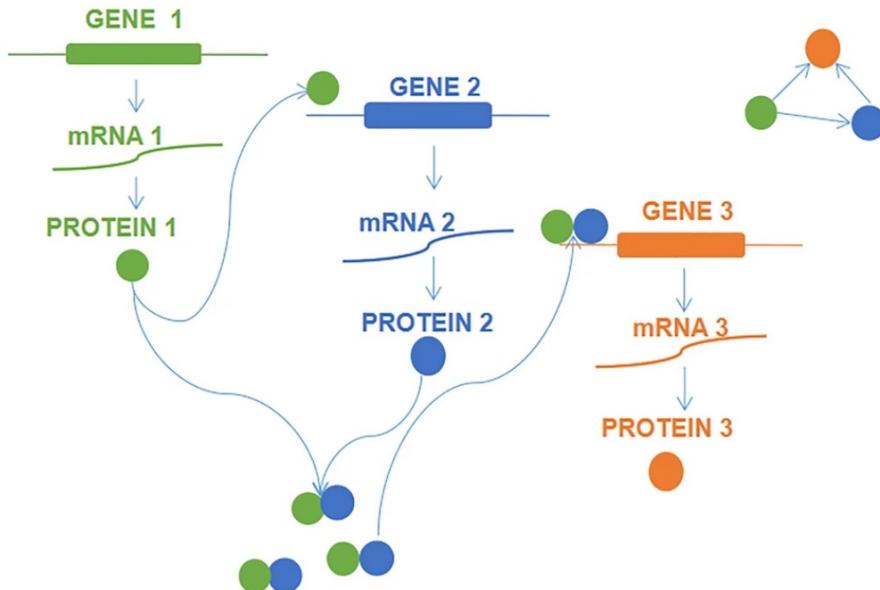
Biological Complex Systems and Networks



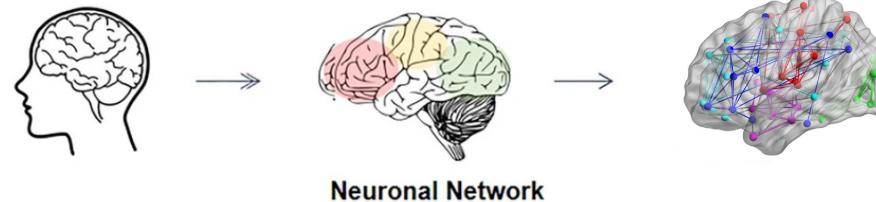
Protein Contact Network



Protein-Protein Interaction Network



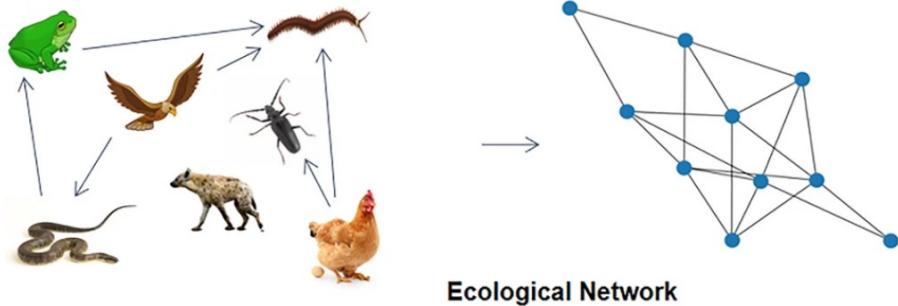
Gene Regulatory Network



Neuronal Network



Signal Transduction Network

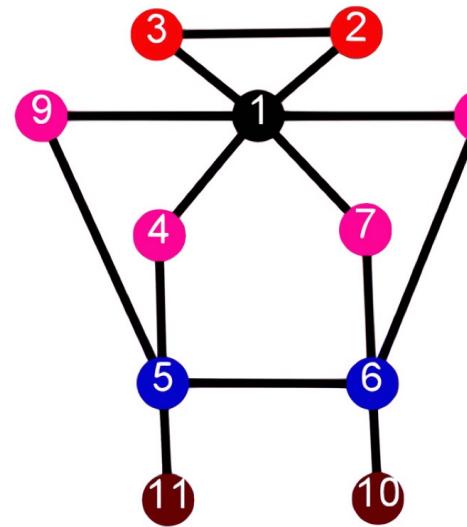


Ecological Network

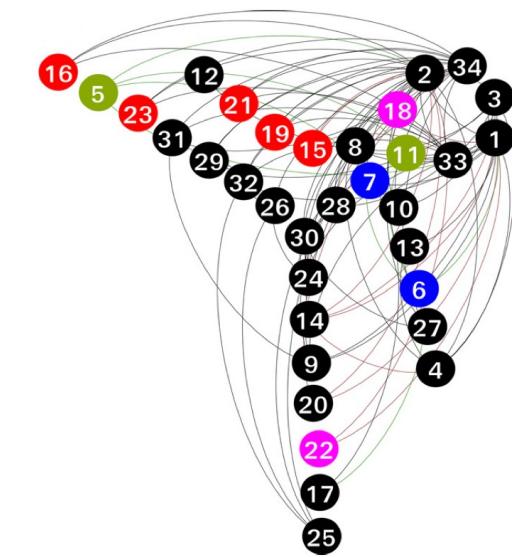
Group Symmetries

Network symmetries (applied to the adjacency matrix) that leave the dynamics of the network unchanged

$$\dot{x}_i = \mathbf{F}(x_i) + \sigma \sum_j A_{ij} \mathbf{H}(x_j)$$



Toy Model



Zachary's Karate Club

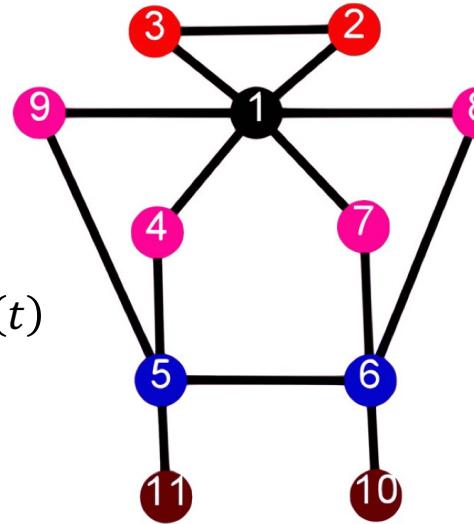
Arenas A et al., Phys. Rep., 469: 93, 2008

Pecora LM et al., Nat. Commun, 5: 4079, 2014

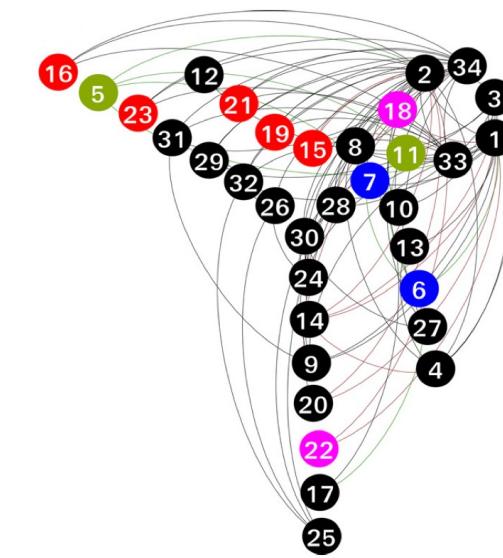
Khanra P et al., Chaos Soliton Fract, 155: 111703, 2022

Global Synchronisation, in which all nodes follow the same trajectory in state space, is a well-studied effect, the conditions for which are related to the network structure and its Group Symmetries.

$$\dot{\theta}_i = \omega_i + K \sum_{j=1}^N A_{ij} \sin[\theta_j(t) - \theta_i(t)] + \sigma \eta_i(t)$$



Toy Model



Zachary's Karate Club

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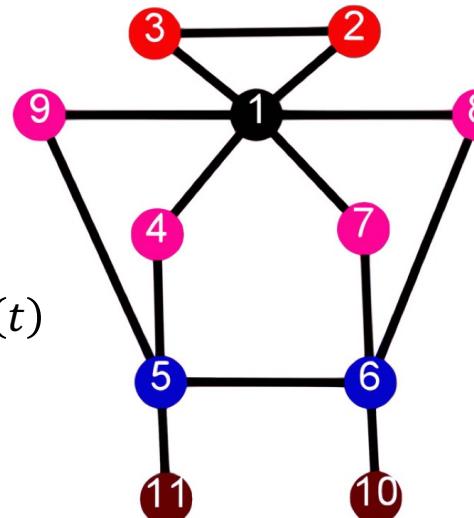
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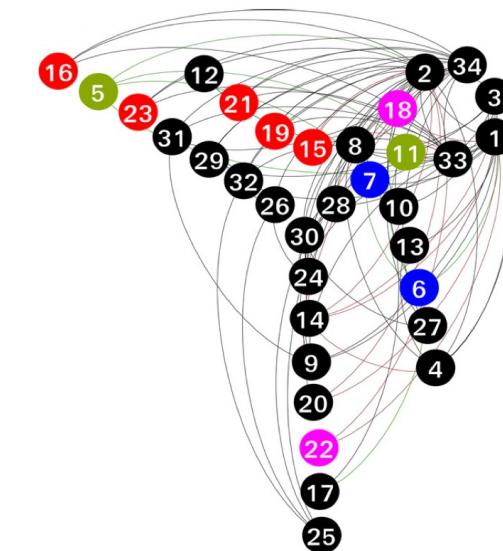
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$$\dot{\theta}_i = \omega_i + K \sum_{j=1}^N A_{ij} \sin[\theta_j(t) - \theta_i(t)] + \sigma \eta_i(t)$$

$$\dot{\theta}_i \sim -K \sum_{j=1}^N L_{ij} \theta_j(t)$$



Toy Model



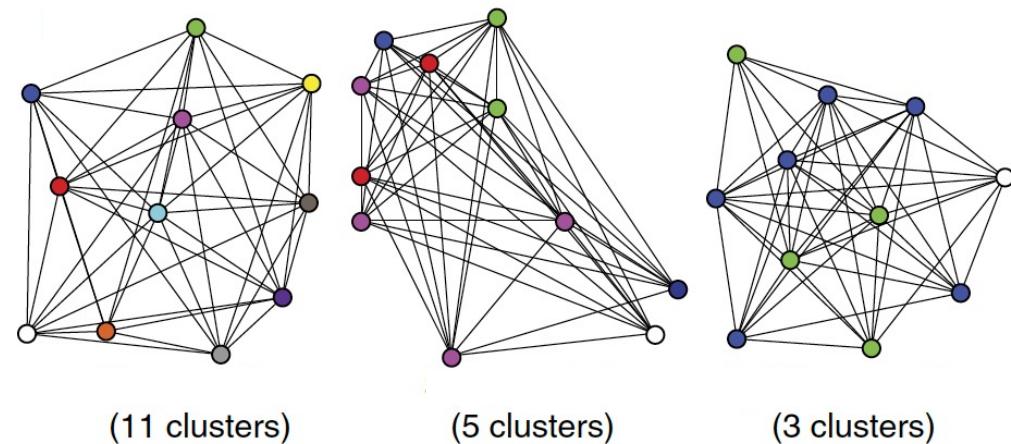
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Equally important, and perhaps more ordinary, is Cluster Synchronization, in which patterns or sets of synchronized elements emerge.



$$A = \begin{bmatrix} & & \\ & & \\ & & \end{bmatrix}$$

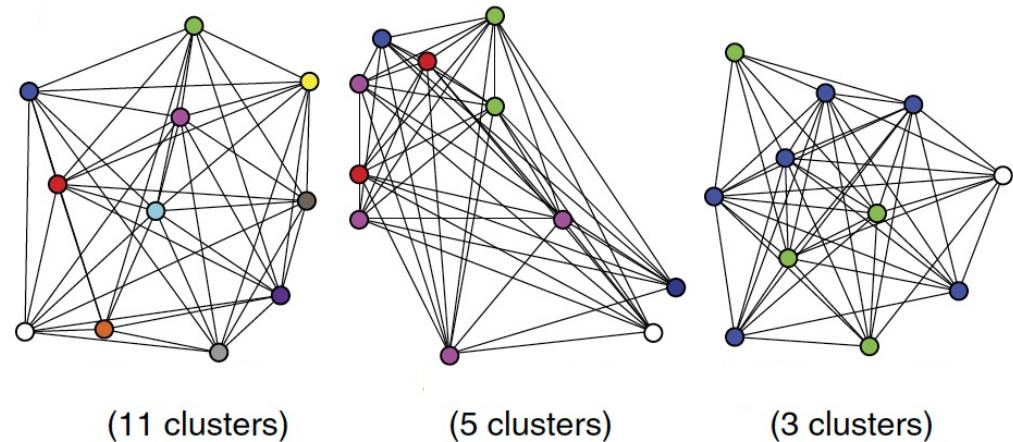
$$A = \begin{bmatrix} & & \\ & & \\ & & \end{bmatrix}$$

$$B = \begin{bmatrix} \textcolor{blue}{\bullet} & & & & \\ \textcolor{green}{\circ} & \textcolor{black}{\blacksquare} & & & \\ \textcolor{yellow}{\times} & & \textcolor{black}{\blacksquare} & & \\ \textcolor{red}{\circ} & & & \textcolor{black}{\blacksquare} & \\ \textcolor{orange}{\circ} & & & & \textcolor{black}{\blacksquare} \\ & \textcolor{white}{\circ} & & & \\ & & \textcolor{grey}{\circ} & & \\ & & & \textcolor{cyan}{\circ} & \\ & & & & \textcolor{purple}{\bullet} \\ & & & & & \textcolor{brown}{\circ} \\ & & & & & & \textcolor{violet}{\bullet} \end{bmatrix}$$

Zhou C and Kurths J, Chaos, 16: 015104, 2006.
Pecora LM et al., Nat. Commun, 5: 4079, 2014
Sorrentino F et al., Sci. Adv., 2(4):e1501737.17, 2016

Equally important, and perhaps more ordinary, is Cluster Synchronization, in which patterns or sets of synchronized elements emerge.

Many real-world networks, such as biological networks, do not admit Group Symmetries but show Cluster Synchronization



$$A = \begin{bmatrix} & & \\ & & \\ & & \end{bmatrix}$$

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$B =$

Zhou C and Kurths J, Chaos, 16: 015104, 2006

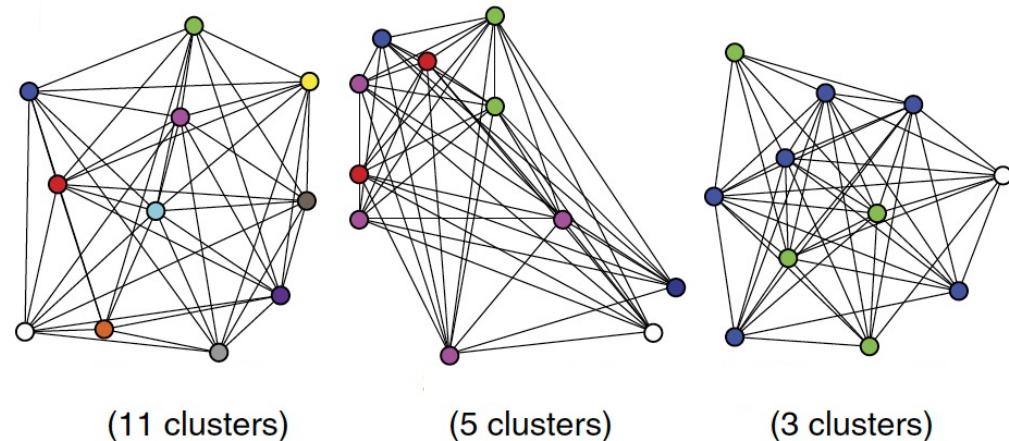
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Equally important, and perhaps more ordinary, is Cluster Synchronization, in which patterns or sets of synchronized elements emerge.

Many real-world networks, such as biological networks, do not admit Group Symmetries but show Cluster Synchronization

*In such networks
Cluster Synchronization is
guaranteed by
Fibration Symmetries*



$$A = \begin{bmatrix} & \\ & \end{bmatrix}$$

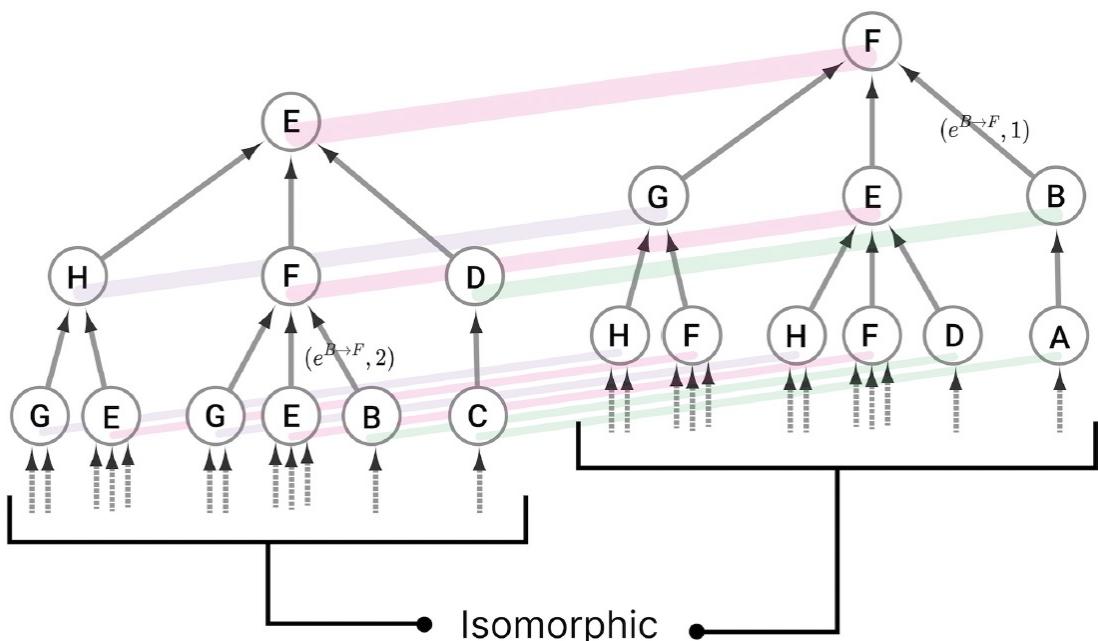
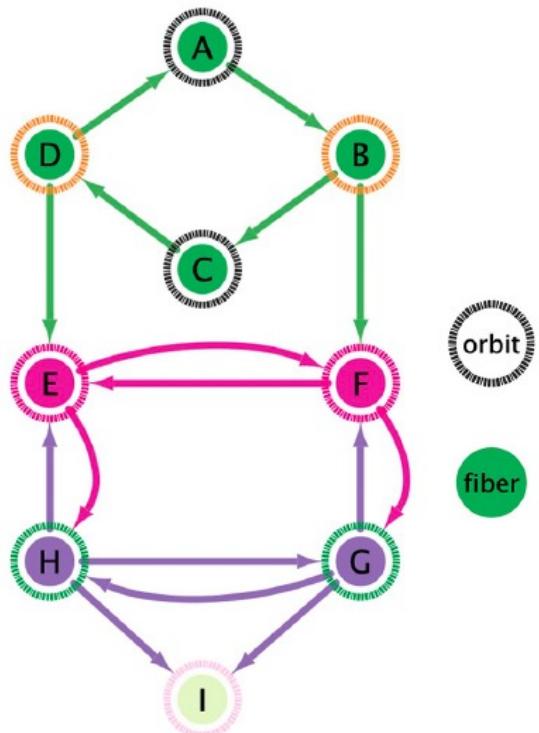
$$B = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{bmatrix}$$

Morone F, and Makse H, Nat Commun, 10 (1): 4961, 2019

Morone F, Leifer I, Makse H, PNAS, 17 (15): 8306-8314, 2020

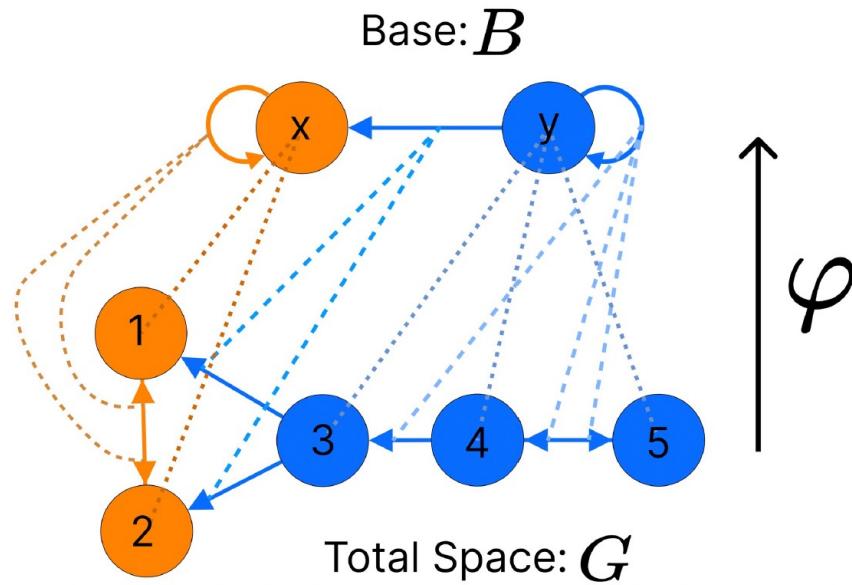
I Leifer, et al., J. Stat. Mech.: Theory Exp, (7): 073403, 2022

Fibration Symmetries are morphisms between networks that identify clusters of synchronized nodes (called fibers) with isomorphic input trees.



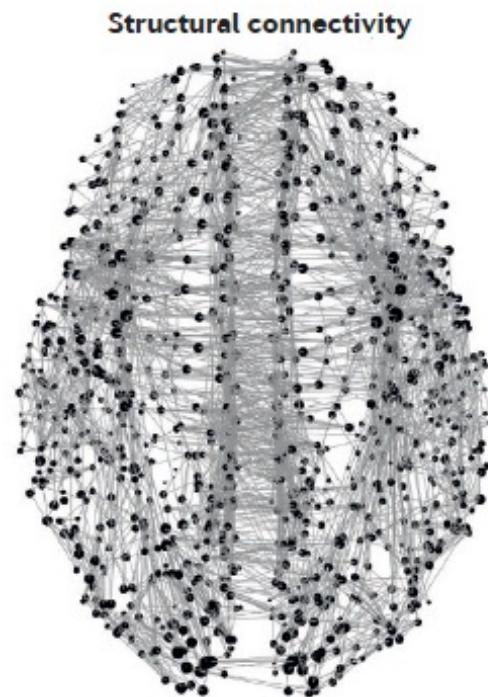
Boldi, P. and Vigna, S. Discrete Math. 243, 21–66, 2002
Avila B et al., Plose One, Plos one 19 (4), e0297669, 2024

Nodes in a fiber can be collapsed by a symmetry fibration into a single representative node called the base.

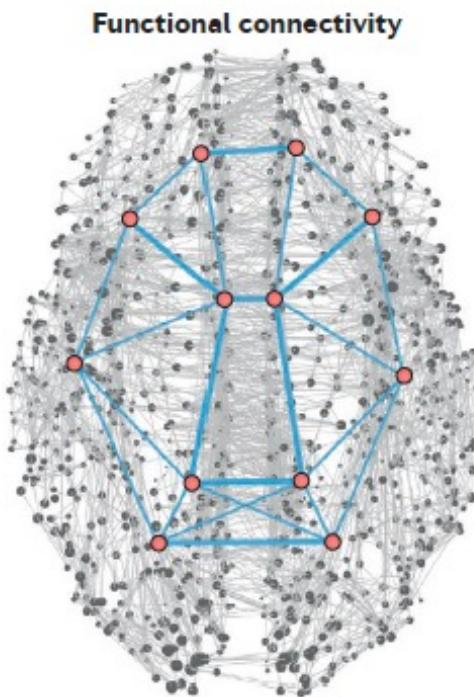


The fibers are then the synchronized building blocks of the network and symmetry fibrations are transformations that preserve the dynamics of information flow in the network.

Communication in the brain



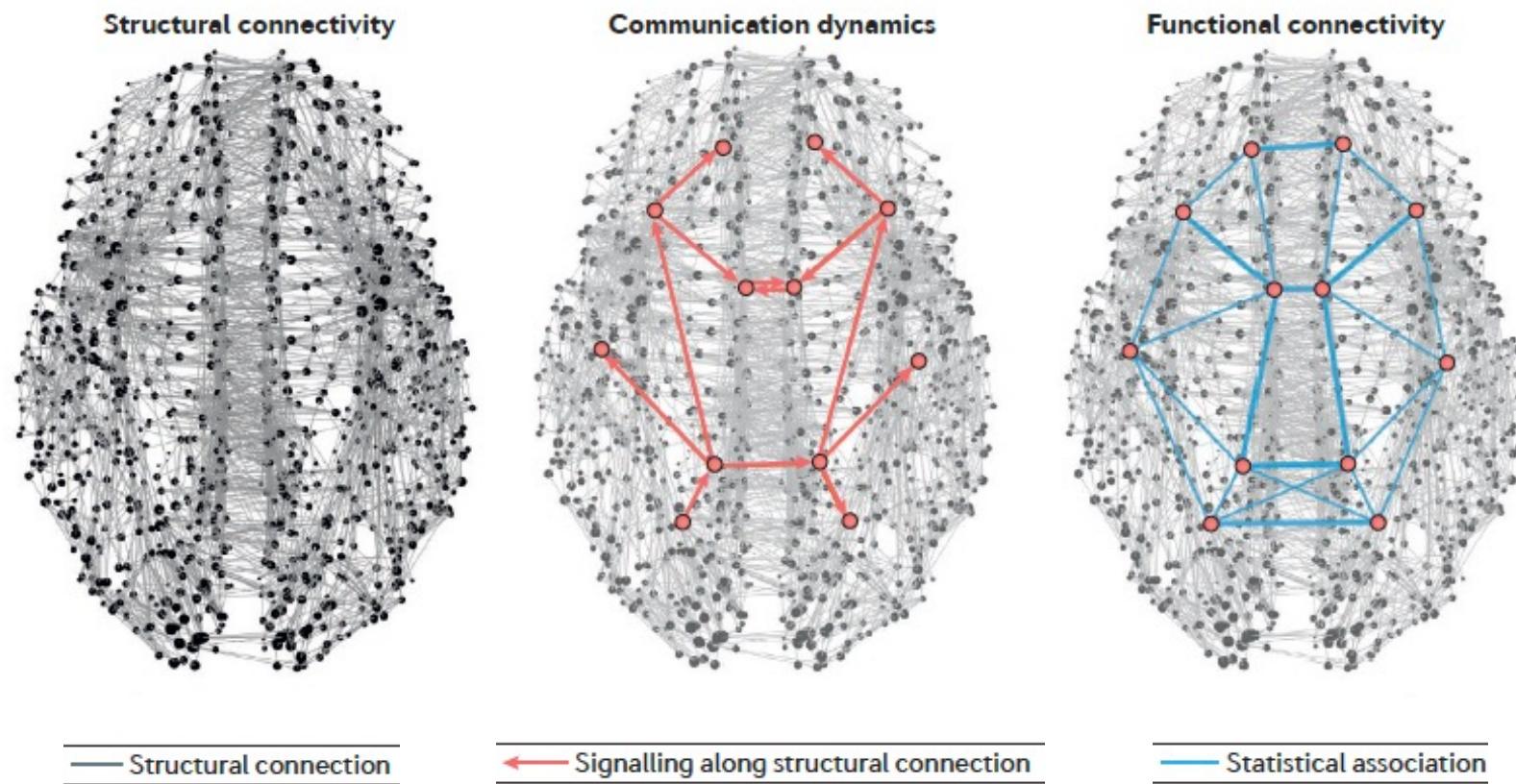
— Structural connection



— Statistical association

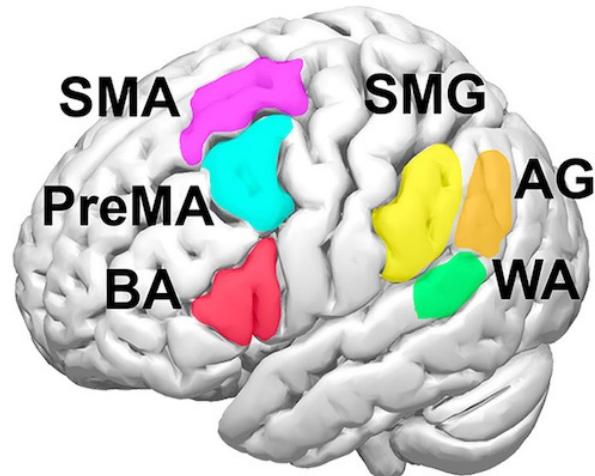
Park H-J & Friston K. Structural and functional brain networks: from connections to cognition. Science 342: 1238411 (2013)

Communication in the brain

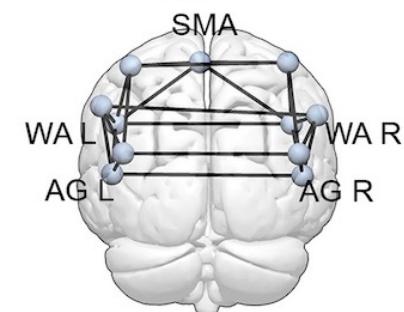
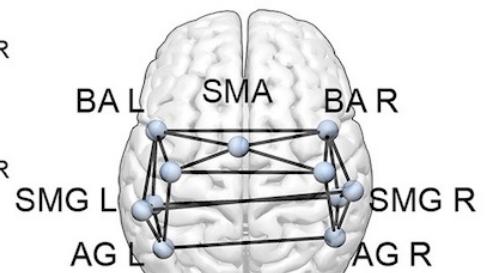
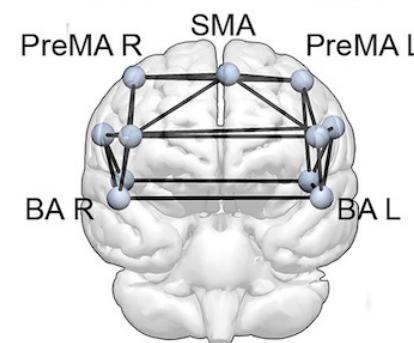
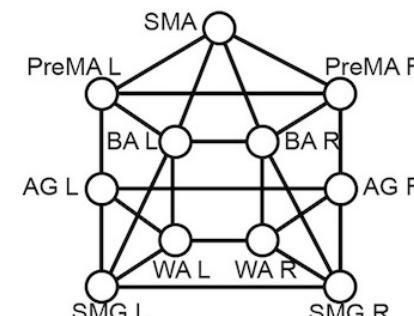


Park H-J & Friston K. Structural and functional brain networks: from connections to cognition. Science 342: 1238411 (2013)

DORSAL STREAM MODEL



LANGUAGE NETWORK

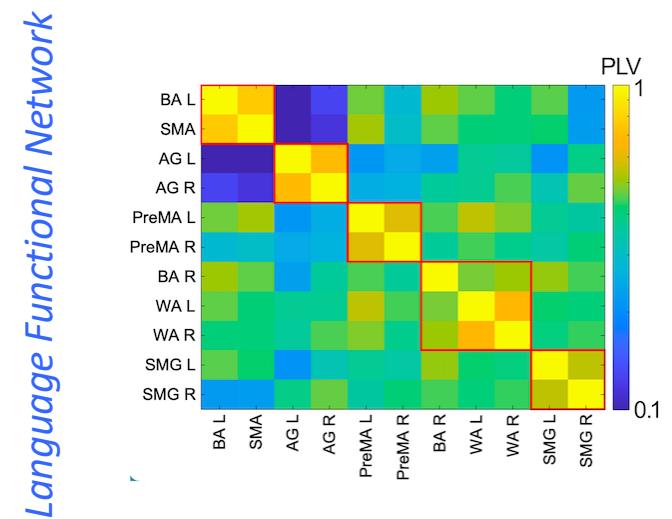
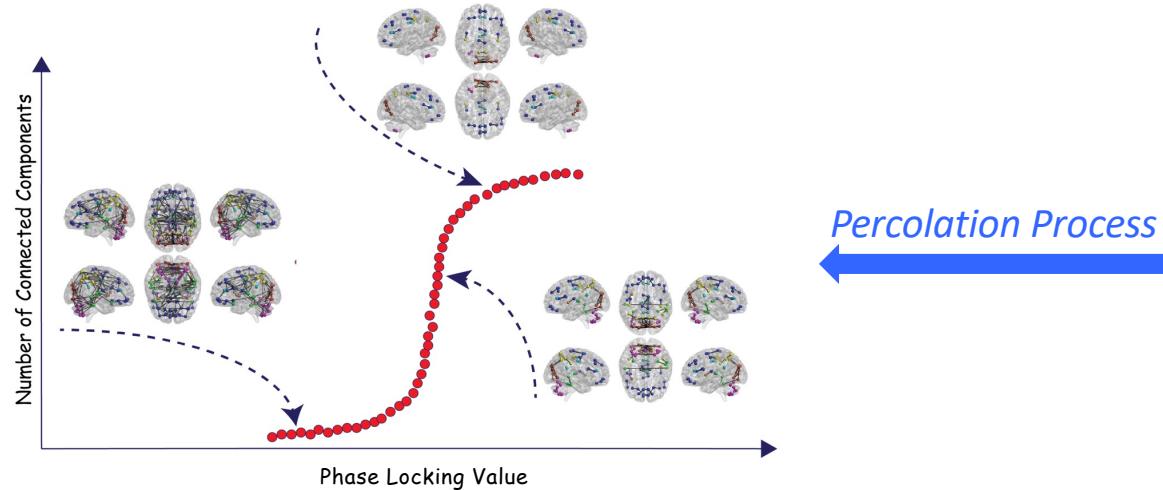
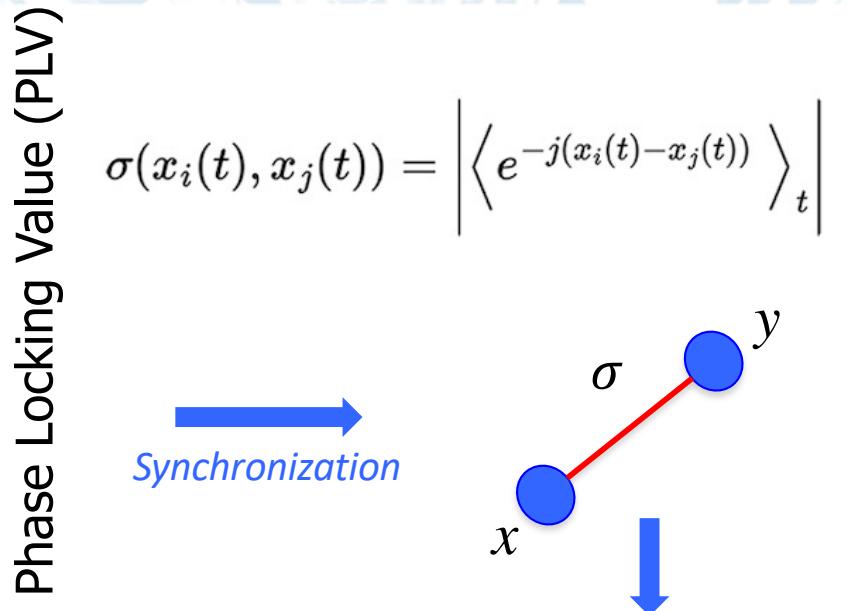
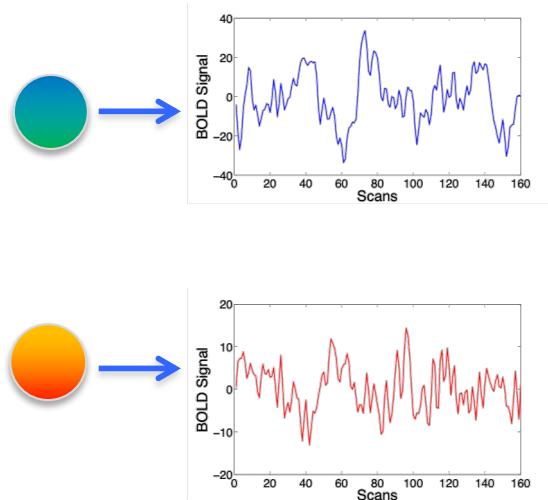


Brain Network Synchronization

RESTING STATE VERB GENERATION PHONEMIC FLUENCY

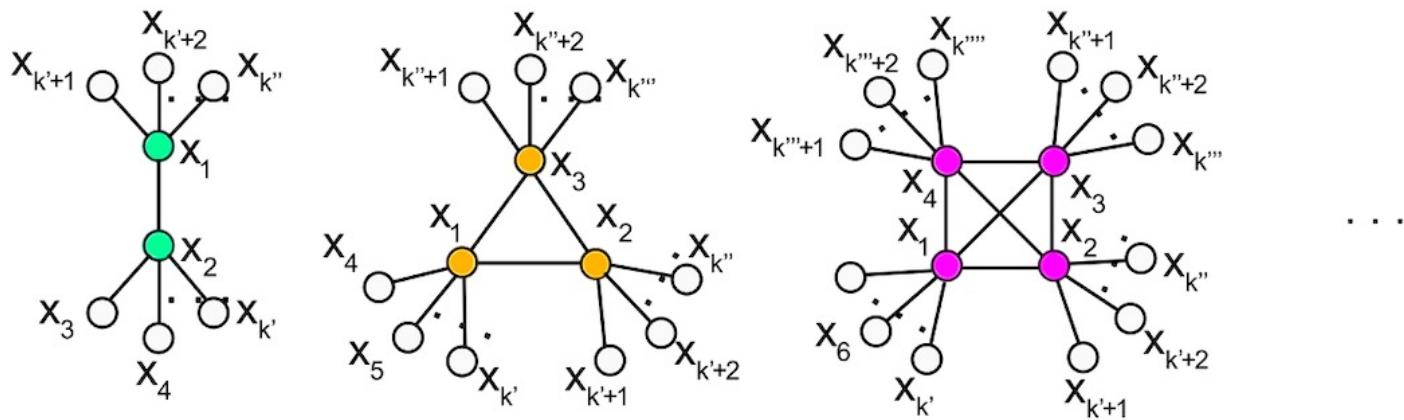
fMRI timeseries from anatomical regions of interest

- Angular Gyrus L (AG L)
Angular Gyrus R (AG R)
Broca's Area L (BA L)
Broca's Area R (BA R)
Premotor Area L (PreMA L)
Premotor Area R (PreMA R)
Supplementary Motor Area (SMA)
Supramarginal Gyrus L (SMG L)
Supramarginal Gyrus R (SMG R)
Wernicke's Area L (WA L)
Wernicke's Area R (WA R)



Cluster Synchronization Cliques

Cluster Synchronization Cliques

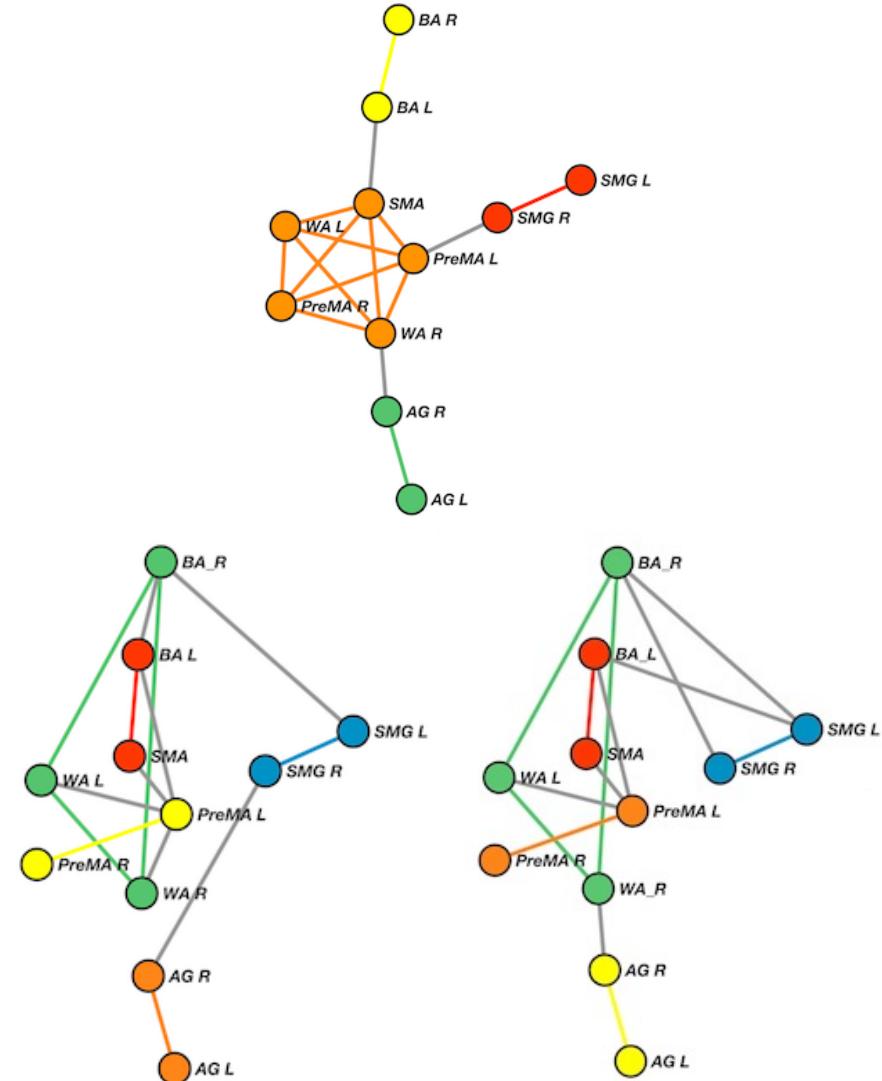
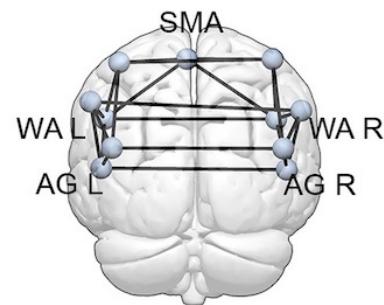
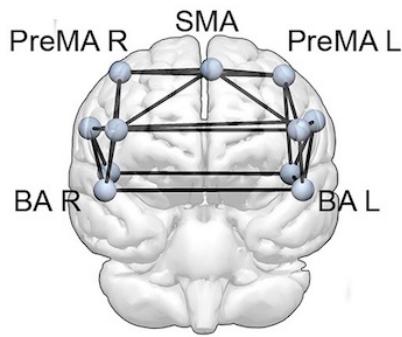
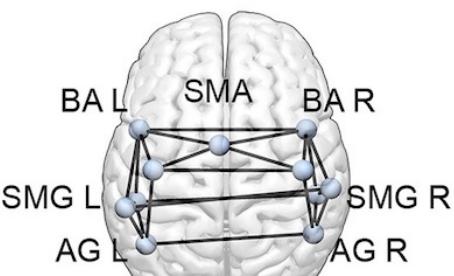
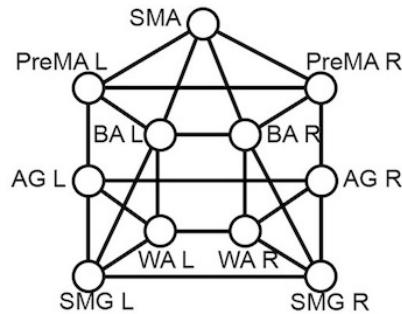


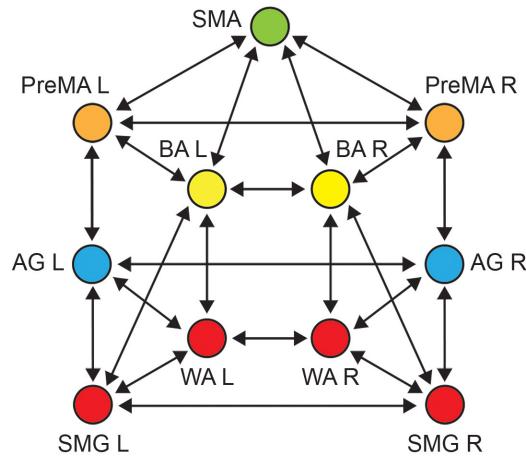
$\{x_k\}$ forms a CS N-clique if and only if

$$\sum_{i < j}^{1,N} \sigma(x_i(t), x_j(t)) \geq \frac{N(N-1)}{2} \sigma(x_k(t), x_{k'}(t)) \quad \forall k = 1, \dots, N \text{ and } k' \in \mathcal{M}_k$$

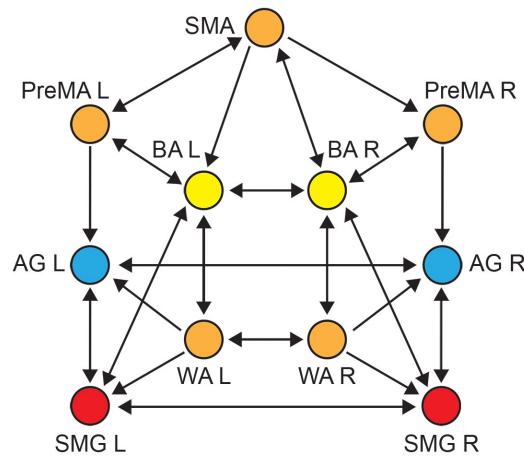
SYNCHRO COLOURING

LANGUAGE NETWORK

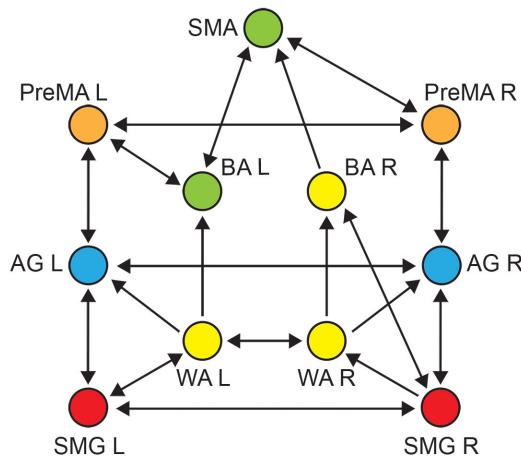


a) Baseline Connectome

Fibration Symmetry
and
Group Symmetry

b) Resting State

Fibration Symmetry
and
Broken Group Symmetry

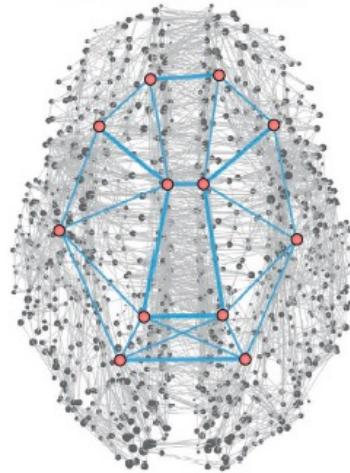
c) Task

Broken Fibration Symmetry
and
Broken Group Symmetry

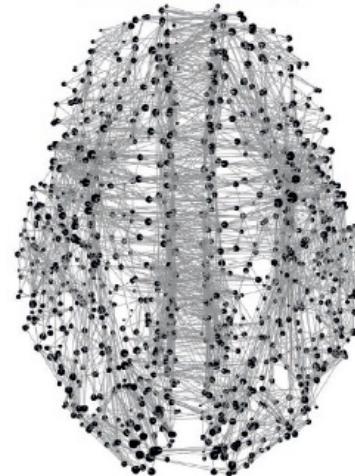
PreMA L: Premotor Left BA L: Broca's Area Left AG L: Angular Gyrus Left WA L: Wernicke's Area Left SMG L: Supramarginal Gyrus Left
PreMA R: Premotor Right BA R: Broca's Area Right AG R: Angular Gyrus Right WA R: Wernicke's Area Right SMG R: Supramarginal Gyrus Right
SMA: Supplementary Motor Area

Take Home Message

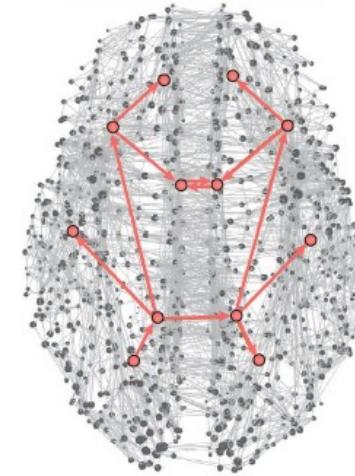
Functional connectivity



Structural connectivity

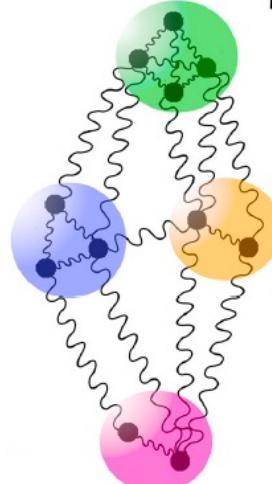


Communication dynamics

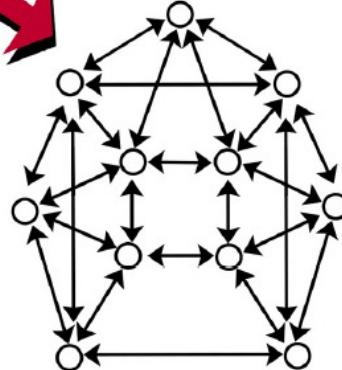


Take Home Message

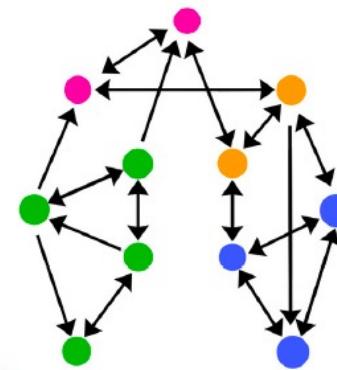
CS CLIQUES



INFERRED FIBRATION
STRUCTURAL NETWORK



BASELINE
CONNECTOME





SCHOOL
FOR ADVANCED
STUDIES
LUCCA



Memorial Sloan Kettering
Cancer Center

Thanks to



Hernan Makse



Università
Ca' Foscari
Venezia



Andrea Gabrielli



Guido Caldarelli



UNIVERSITÀ
DEGLI STUDI
DI MILANO



Paolo Boldi



David Phillips

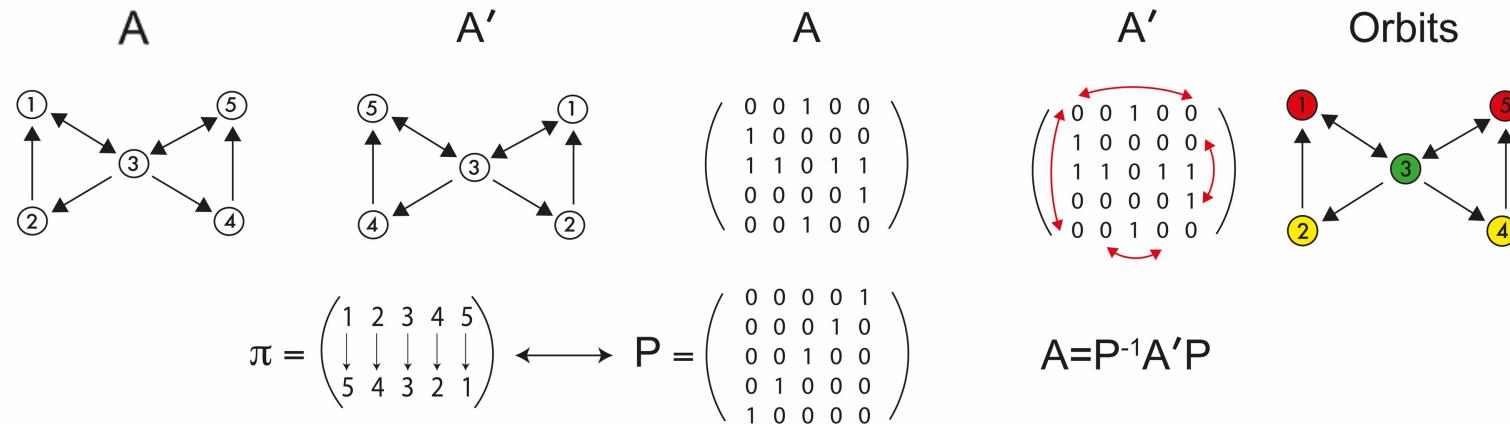


Andrei Holodny

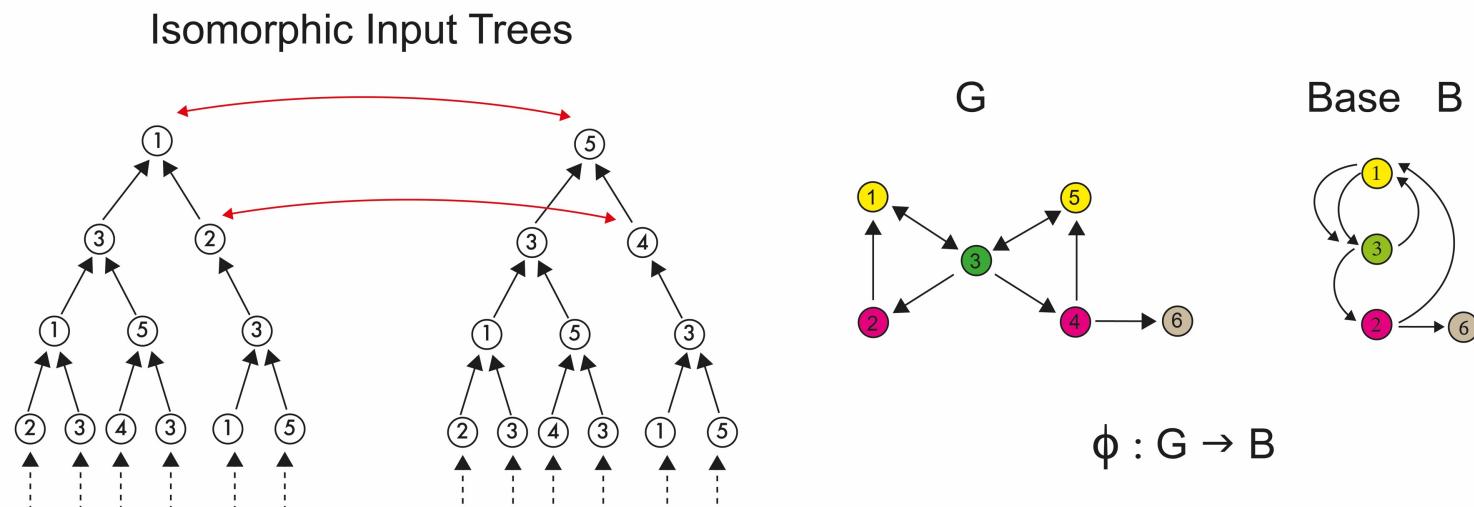


Manuel Zimmer

Network with a symmetry group



Network with no symmetry group and a fibration symmetry



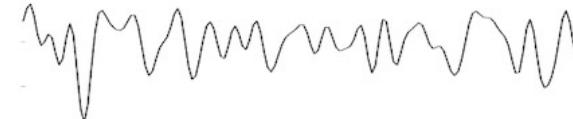
Cluster Synchronization Cliques

Hilbert Transform

$n_i(t)$



$n_j(t)$



$$\hat{n}_i(t) = \frac{1}{\pi} p.v. \int_{-\infty}^{\infty} \frac{n_i(\tau)}{t - \tau} d\tau$$

$$\hat{n}_j(t) = \frac{1}{\pi} p.v. \int_{-\infty}^{\infty} \frac{n_j(\tau)}{t - \tau} d\tau$$

$$x_i(t) = \arg(n_i(t) + j\hat{n}_i(t))$$

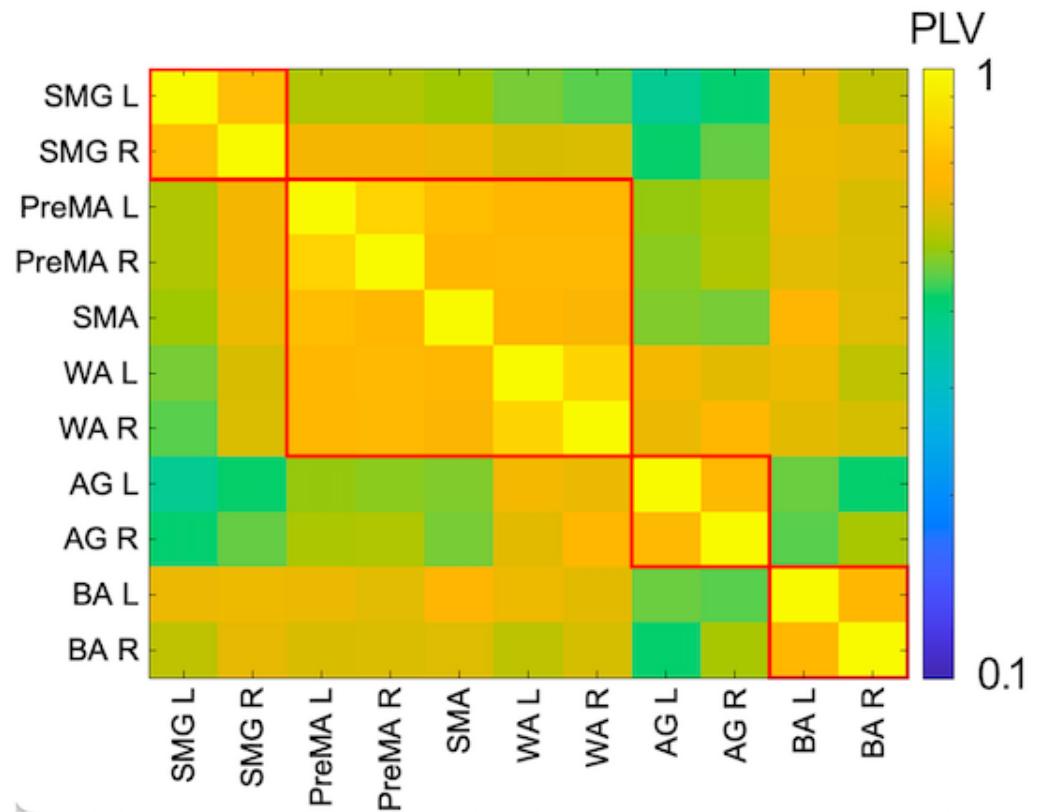
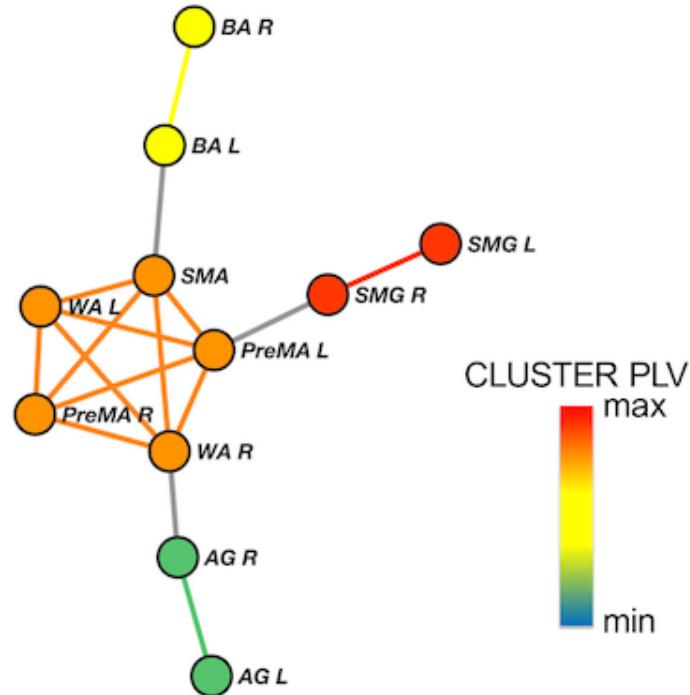
$$x_j(t) = \arg(n_j(t) + j\hat{n}_j(t))$$

Phase Coupling

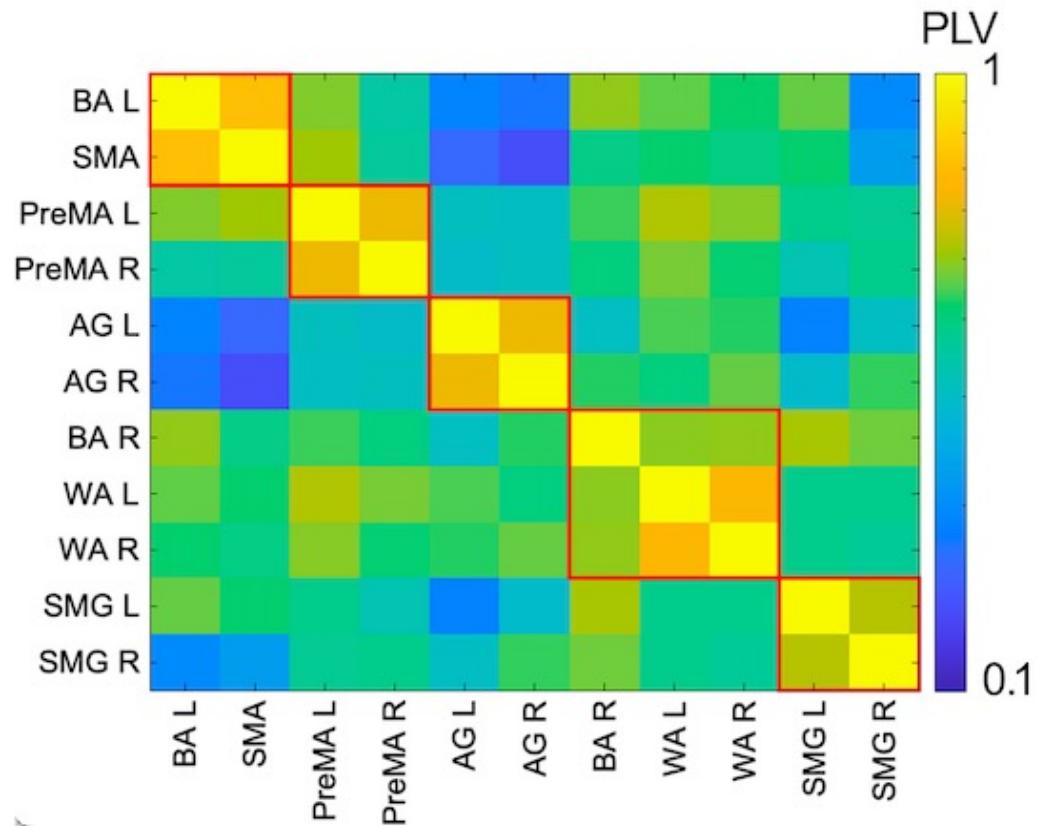
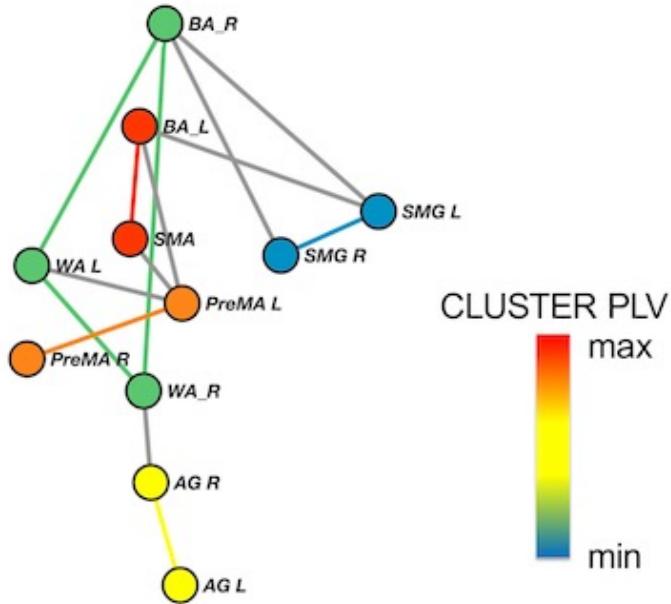


$$\sigma(x_i(t), x_j(t)) = \left| \left\langle e^{-j(x_i(t) - x_j(t))} \right\rangle_t \right|$$

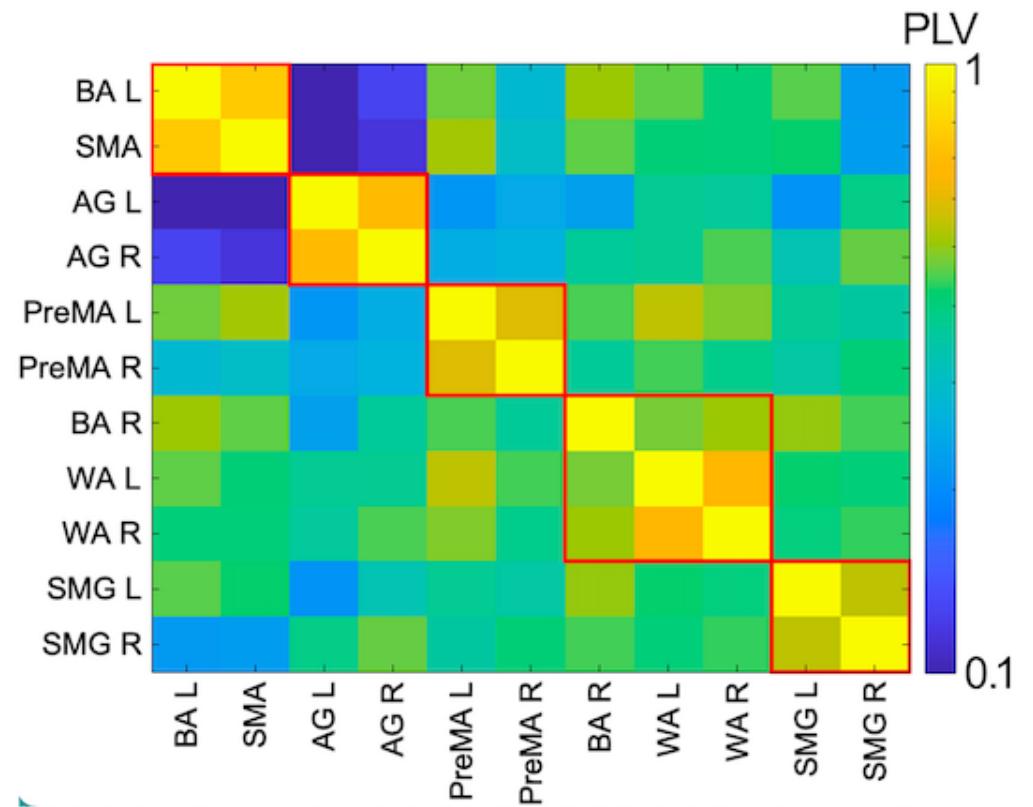
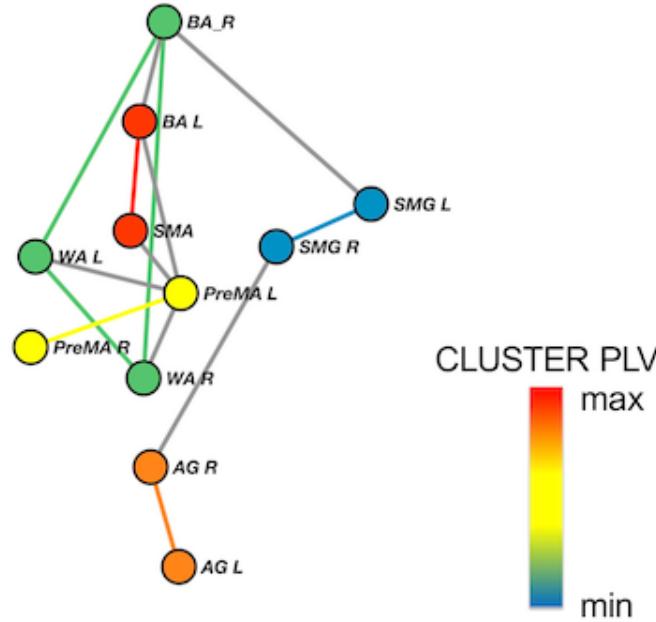
RESTING STATE



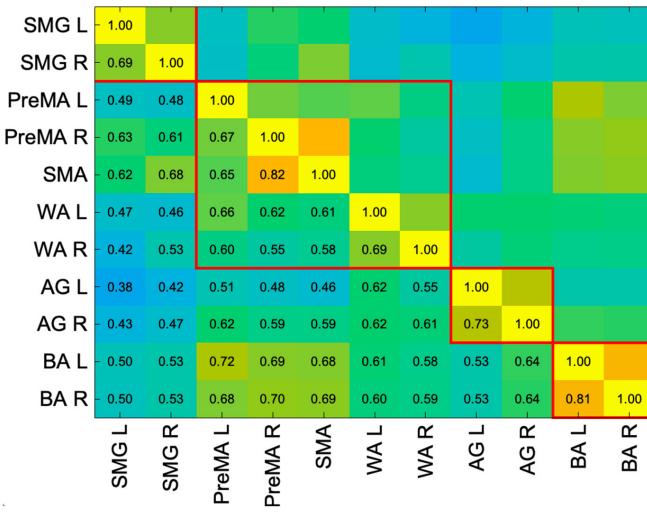
VERB GENERATION TASK



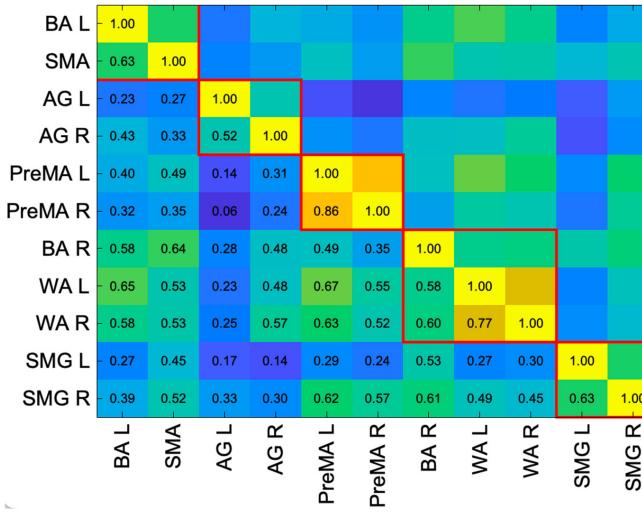
PHONEMIC FLUENCY TASK



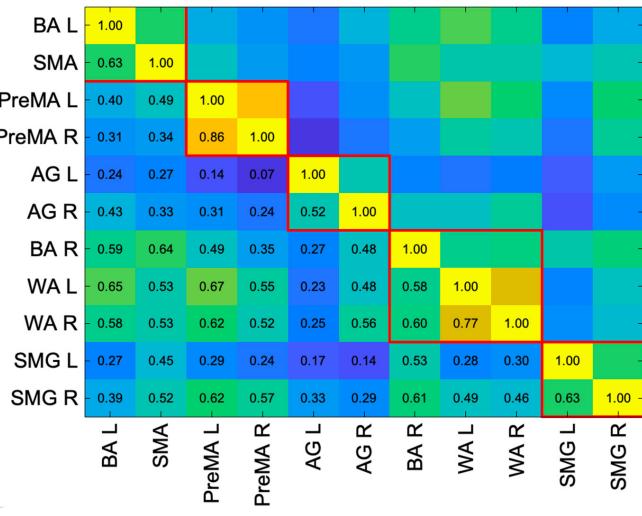
Resting State



Phonemic Fluency Task

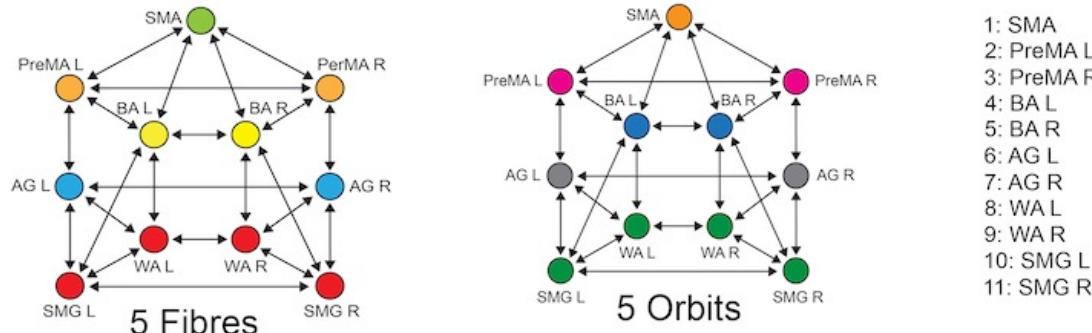


Verb Generation Task



Symmetry analysis of dorsal stream baseline connectome

Fibration symmetry = Group symmetry

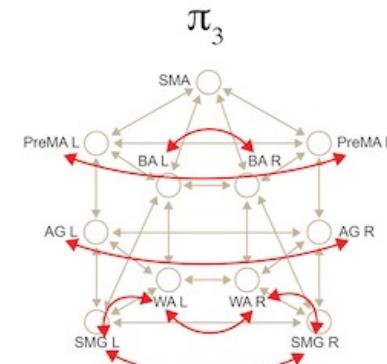
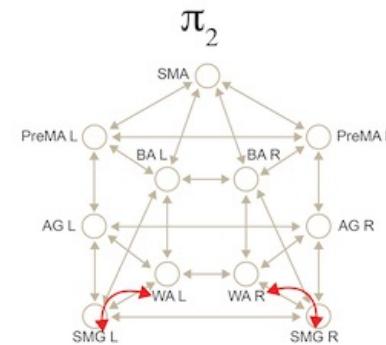
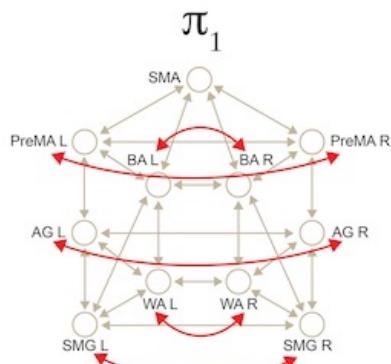


Automorphisms

$$\pi_1 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 3 & 2 & 5 & 4 & 7 & 6 & 9 & 8 & 11 & 10 \end{pmatrix}$$

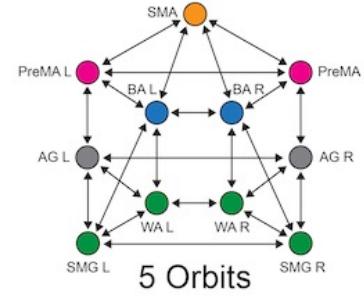
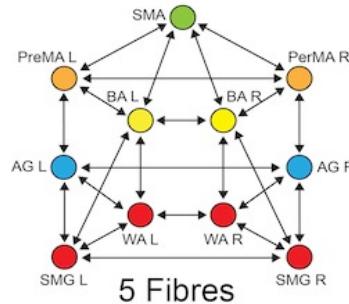
$$\pi_2 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 10 & 11 & 8 & 9 \end{pmatrix}$$

$$\pi_3 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 3 & 2 & 5 & 4 & 7 & 6 & 11 & 10 & 9 & 8 \end{pmatrix}$$



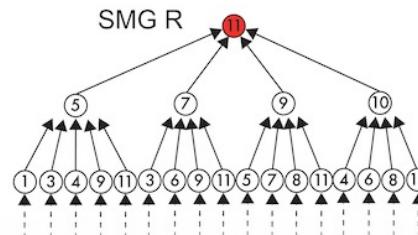
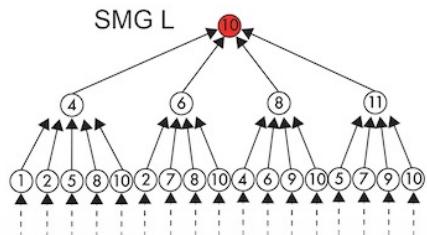
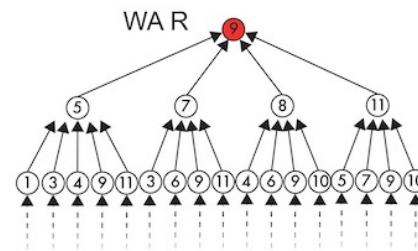
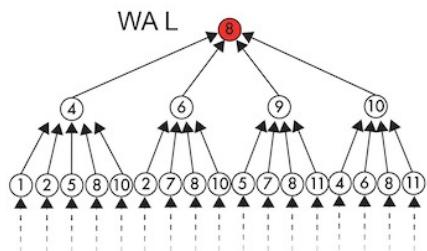
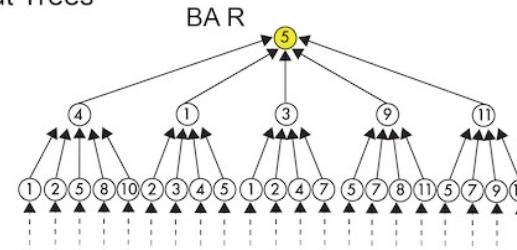
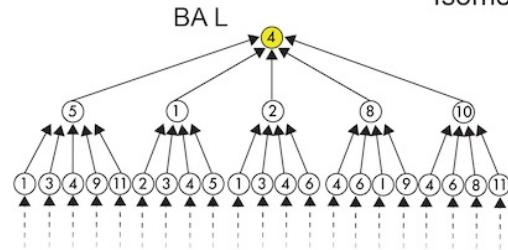
Symmetry analysis of dorsal stream baseline connectome

Fibration symmetry = Group symmetry

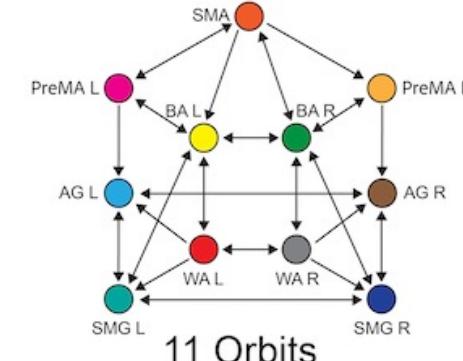
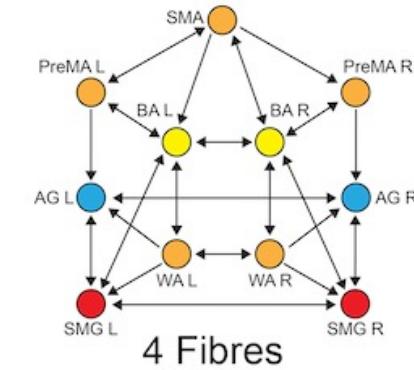
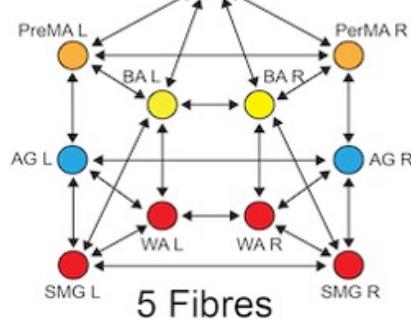


- 1: SMA
- 2: PreMA L
- 3: PreMA R
- 4: BA L
- 5: BA R
- 6: AG L
- 7: AG R
- 8: WAL
- 9: WAR
- 10: SMG L
- 11: SMG R

Isomorphic Input Trees



Symmetry analysis of inferred resting state structural network

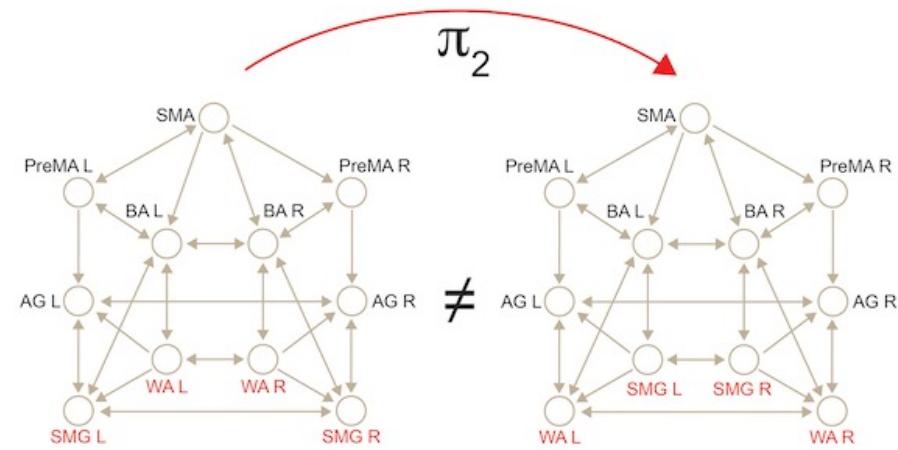
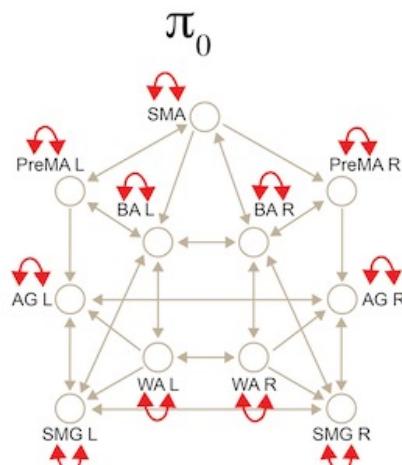
BASELINE
CONNECTOME

- 1: SMA
- 2: PreMA L
- 3: PreMA R
- 4: BA L
- 5: BA R
- 6: AG L
- 7: AG R
- 8: WA L
- 9: WA R
- 10: SMG L
- 11: SMG R

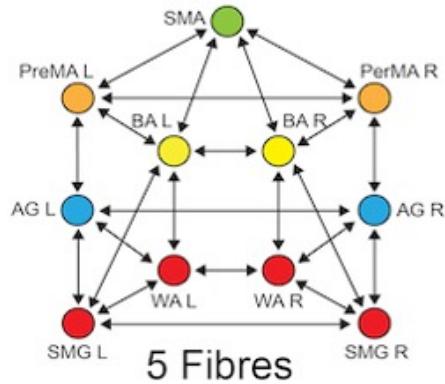
Automorphisms

$$\pi_0 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \end{pmatrix}$$

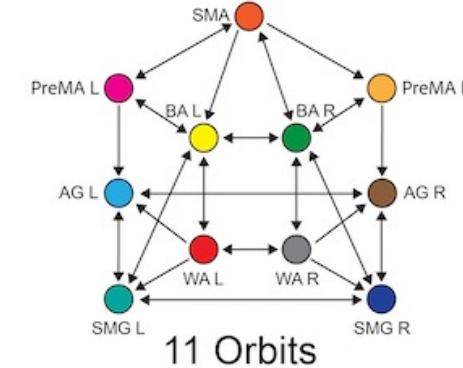
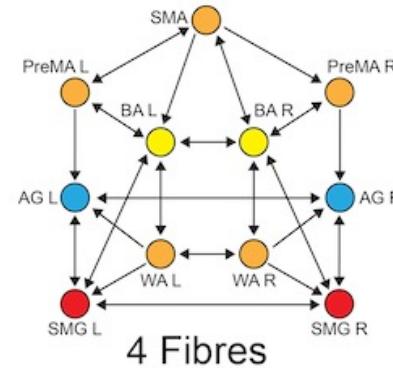
$$\pi_2 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 10 & 11 & 8 & 9 \end{pmatrix}$$



BASELINE CONNECTOME

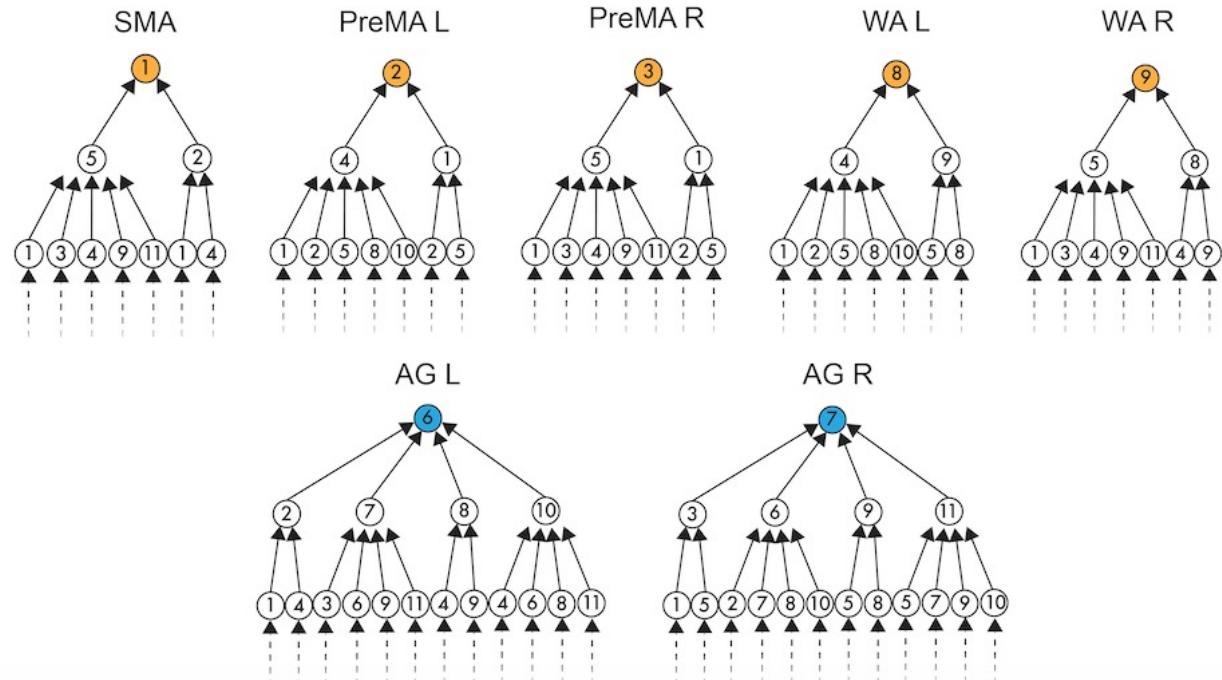


Fibration symmetry \neq Group symmetry



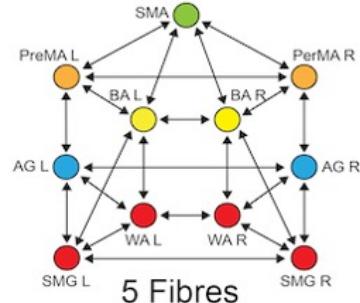
- 1: SMA
- 2: PreMA L
- 3: PreMA R
- 4: BA L
- 5: BA R
- 6: AG L
- 7: AG R
- 8: WA L
- 9: WA R
- 10: SMG L
- 11: SMG R

Isomorphic Input Trees

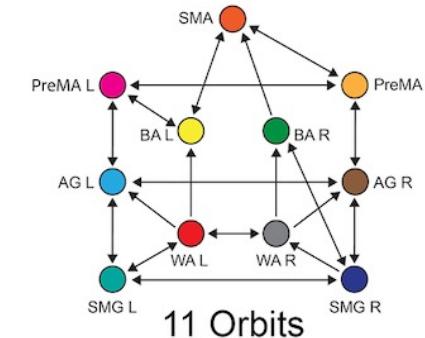
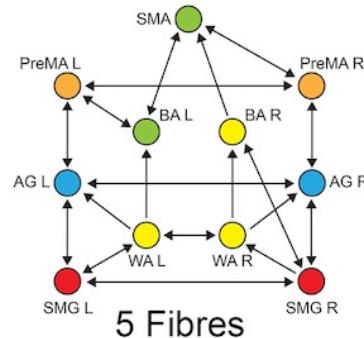


Symmetry analysis of inferred language structural network

BASELINE CONNECTOME



Fibration symmetry \neq Group symmetry

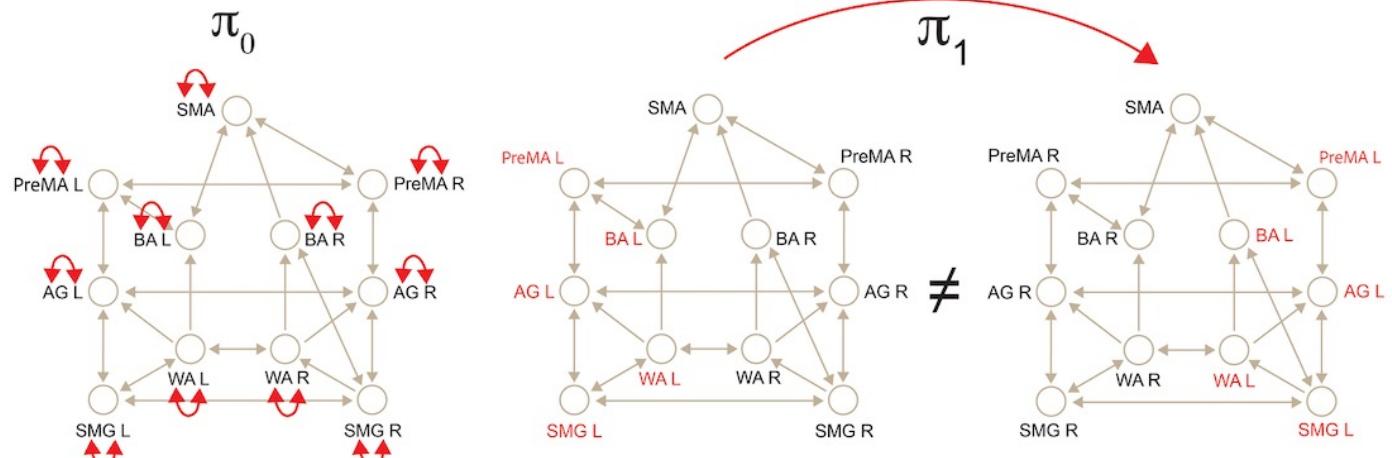


- 1: SMA
- 2: PreMA L
- 3: PreMA R
- 4: BA L
- 5: BA R
- 6: AG L
- 7: AG R
- 8: WA L
- 9: WA R
- 10: SMG L
- 11: SMG R

Automorphisms

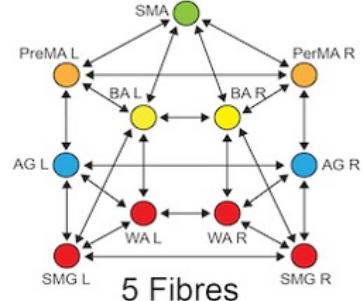
$$\pi_0 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \end{pmatrix}$$

$$\pi_1 = \begin{pmatrix} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\ \downarrow & \downarrow \\ 1 & 3 & 2 & 5 & 4 & 7 & 6 & 9 & 8 & 11 & 10 \end{pmatrix}$$

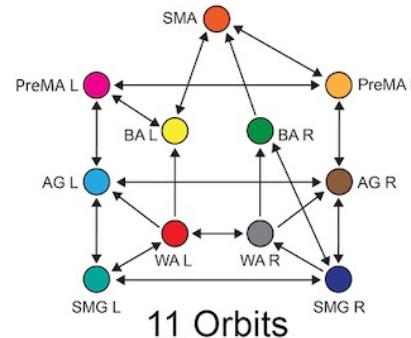
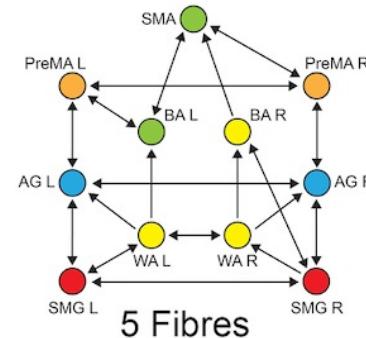


Symmetry analysis of inferred language structural network

BASELINE CONNECTOME



Fibration symmetry \neq Group symmetry



- 1: SMA
- 2: PreMA L
- 3: PreMA R
- 4: BA L
- 5: BA R
- 6: AG L
- 7: AG R
- 8: WAL
- 9: WAR
- 10: SMG L
- 11: SMG R

Isomorphic Input Trees

