

A Tutorial in Connectome Analysis (III): Topological and Spatial Features of Brain Networks



Dr Marcus Kaiser

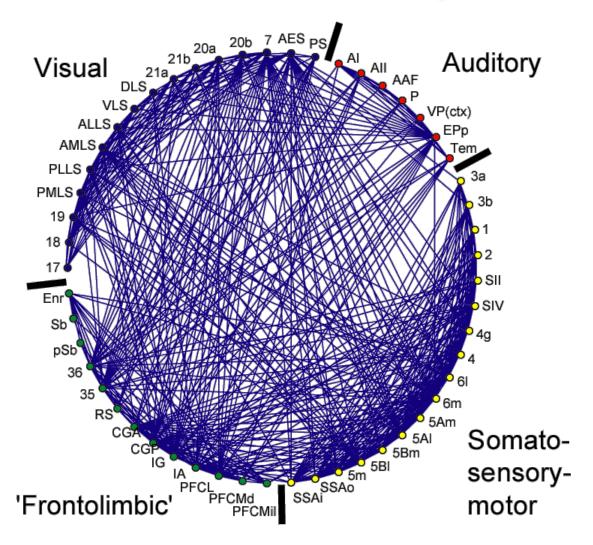
Professor of Neuroinformatics School of Computing Science / Institute of Neuroscience Newcastle University United Kingdom

http://www.dynamic-connectome.org

http://neuroinformatics.ncl.ac.uk/



Brain connectivity



Types of Brain Connectivity
Structural, functional, effective

Small-world

Neighborhood clustering Characteristic path length

Spatial

preference for short connections but more long-distance connections than expected

Structure->Function

Network changes lead to cognitive deficits (Alzheimer's disease, IQ)

Motifs

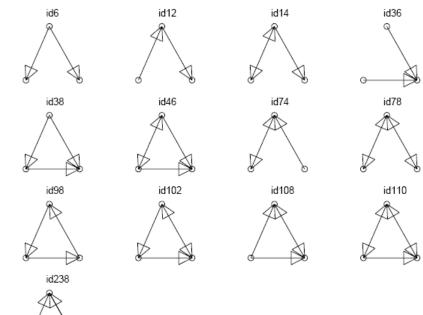
Motifs

Idea: determine building blocks of networks.

Hope: structural building blocks correspond to functional units.

Pattern: possible connection configuration for a k-node subgraph (see list of all 3-node configurations)

Motif: pattern that occurs significantly more often than for rewired benchmark networks (same number of nodes and edges and same degree distribution)



List of all 3-node patterns

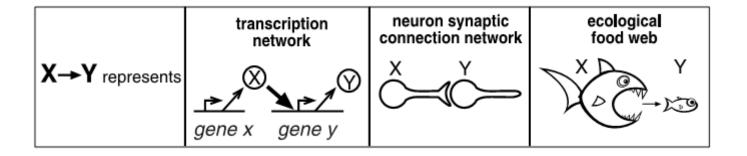
^{*} Milo et al. (2002) Science; http://www.weizmann.ac.il/mcb/UriAlon/groupNetworkMotifSW.html

Motif detection – algorithm

```
Network type: Directed
              Num of Nodes: 16 Num of Edges: 19
              Num of Nodes with edges: 16
              Maximal out degree (out-hub) : 3
              Maximal in degree (in-hub) : 3
              Roots num: 4 Leaves num: 4
              Single Edges num: 19 Mutual Edges num: 0
              Motif size searched 3
              Total number of 3-node subgraphs : 21
              Number of random networks generated: 100
              Random networks generation method: Switches
              Num of Switches range: 100.0-200.0,
                    Success switches Ratio: 0.652+0.01
        The following motifs were found:
        Criteria taken : Nreal Zscore > 2.00
                          Pval ignored (due to small number of random
        networks)
                          Mfactor > 1.10
Appearances
               Random
                          Uniqueness >= 4
                                            Uniqueness
                                                           Concentration
in the real
              networks:
                                                           X10-3
network
              mean+- SD
              Full list includes 1 motifs
        MOTIF NREAL NRAND
                                 NREAL
                                              NREAL
                                                          UNIO
                                                                 CREAL
                                                          VAL
                                                                 [MILI]
                    STATS
                                              PVAL
        ID
                                 ZSCORE
                    0.6+0.6
                                 6.93
        38
                                              0.000
                                                           4
                                                                 238.10
                        Motif
        0 1 1
                        Adjacency
        0 0 0
                        Matrix
```

Network name: network exmp.txt

Motif detection – results



Network	Nodes	Edges	$N_{\rm real}$	$N_{\rm rand} \pm {\rm SD}$	Z score	$N_{\rm real}$	$N_{\rm rand} \pm {\rm SD}$	Z score	$N_{\rm real}$	$N_{\rm rand} \pm {\rm SD}$	Z score
Gene regulat (transcriptio			>	Υ Ψ Ψ Σ	Feed- forward loop	X	√ W	Bi-fan			
E. coli	424	519	40	7 ± 3	10	203	47 ± 12	13			
S. cerevisiae*	685	1,052	70	11 ± 4	14	1812	300 ± 40	41			
Neurons			\	Υ Ψ Ψ Ζ	Feed- forward loop	X	√ W	Bi-fan	Y	x y v Z	Bi- parallel
C. elegans†	252	509	125	90 ± 10	3.7	127	55 ± 13	5.3	227	35 ± 10	20

Milo et al. Science, 2002

Motif detection – problems

Advantages:

Identify special network patterns which might represent functional modules

Disadvantages:

- Slow for large networks and unfeasible for large (e.g. 5-node) motifs (#patterns: 3-node – 13; 4-node – 199; 5-node: 9364; 6-node - 1,530,843)
- Rewired benchmark networks do not retain clusters;
 most patterns become insignificant for clustered benchmark networks*

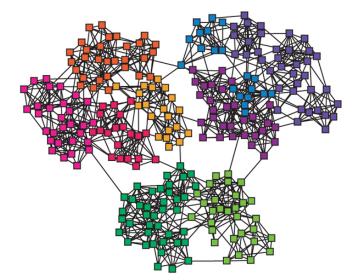
^{*} Kaiser (2011) Neuroimage

Clusters (or Modules or Communities)

Clusters

Clusters: nodes within a cluster tend to connect to nodes in the same cluster but are less likely to connect to nodes in other clusters

Quantitative measure: modularity Q (Newman & Girvan, Physical Review E, 2004)



important terms:

hierarchical (cluster, sub-cluster, ...)

overlapping or non-overlapping

(one node can only be member of one cluster)

predefined number of clusters

(e.g. k-means algorithm)

Potential time problem for large networks, O(k^N) Hundreds of algorithms for cluster detection!

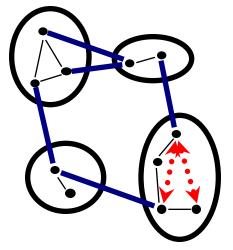


Cluster detection – example

Non-hierarchical, overlapping

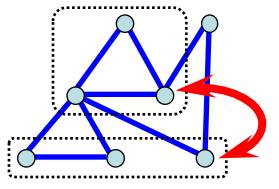


Genetic algorithm



- Have as few as possible connections between them
- Have as few as possible absent connections within them

Procedure



- Random starting configurations
- Evolution:

Mutation : Area relocation

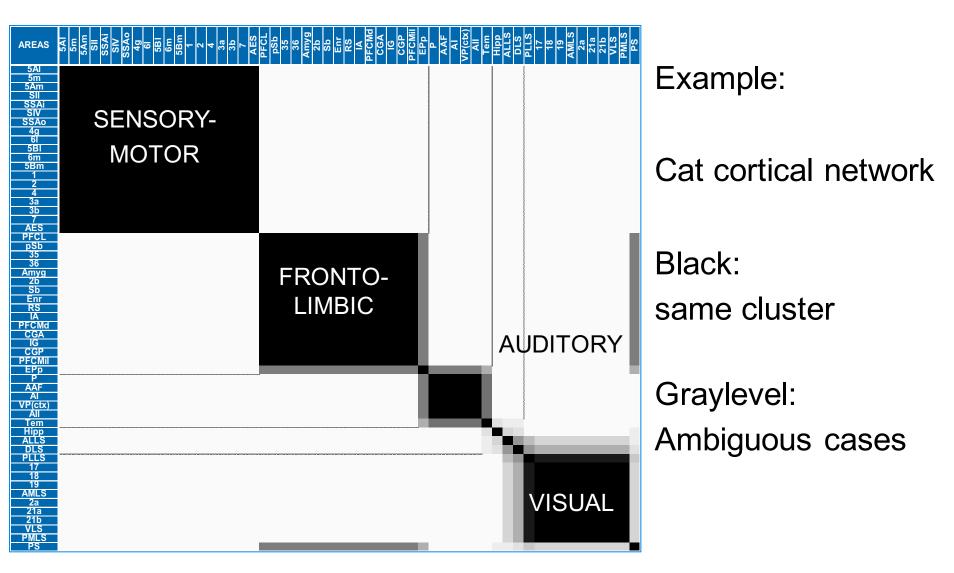
Evaluation : Cost function

Selection : Threshold

Validation

Hilgetag et al. (2000) Phil. Trans. Roy. Soc. Lond. B.

Cluster detection



Hilgetag et al. (2000) Phil Trans R Soc 355: 91

Random graphs

Preliminary: Degree distributions

Degree distributions

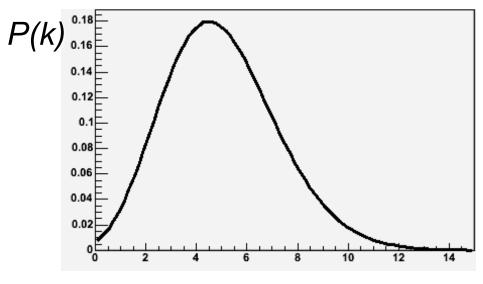
NORMAL TRIANGLE BETA LOG NORMAL

GAMMA
LEFT GAMMA
RIGHT

POISSON

POISSON

Theoretical (known properties): P(k) is the probability that a node with k edges exists in the network (probability distribution)

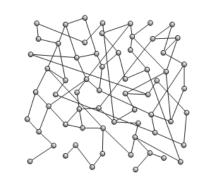


Node degree k

Degree distribution

Numerical (real-world network): use the number of occurrences of a node (histogram)

Random graphs



often called Erdős–Rényi* random graphs

Generation:

with probability p

For each potential edge (adjacency matrix element outside the diagonal), establish an edge

establish an edge (set that element of the adjacency matrix to 1) with probability
$$p$$

$$A = \begin{pmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}$$

^{*}Erdős, P.; Rényi, A. (1959). Publicationes Mathematicae 6: 290–297.

Properties of random graphs

- Edge density = p
- Binomial degree distribution (histogram of node degrees)

$$P(k) = \binom{n-1}{k} p^{k} (1-p)^{n-1-k}$$

Can be approximated as Poisson distribution

-> exponential *tail* (networks are therefore sometimes called *exponential networks*)

$$f(k; \lambda) = \frac{e^{-\lambda} \lambda^{k}}{k!} \qquad \lambda = n * p$$

$$0.10$$

$$0.08$$

$$0.06$$

$$0.04$$

$$0.02$$

$$0.00$$

$$1850$$

$$1900$$

$$1950$$

$$2000$$

$$2050$$

$$2100$$

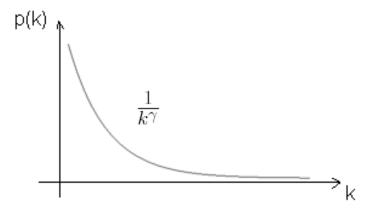
$$2150$$

Scale-free networks

Power-law degree distribution





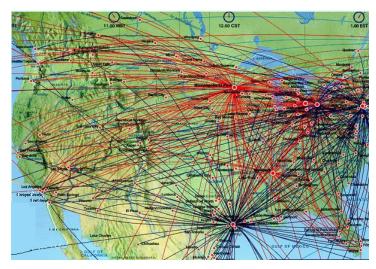


Barabasi & Albert, Science, 1999

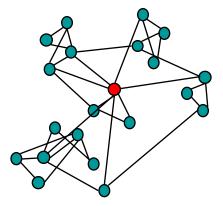
Power-law function:

$$f(x) = x^{-a} = 1/x^a$$

Scale-free = no characteristic scale



Airline network

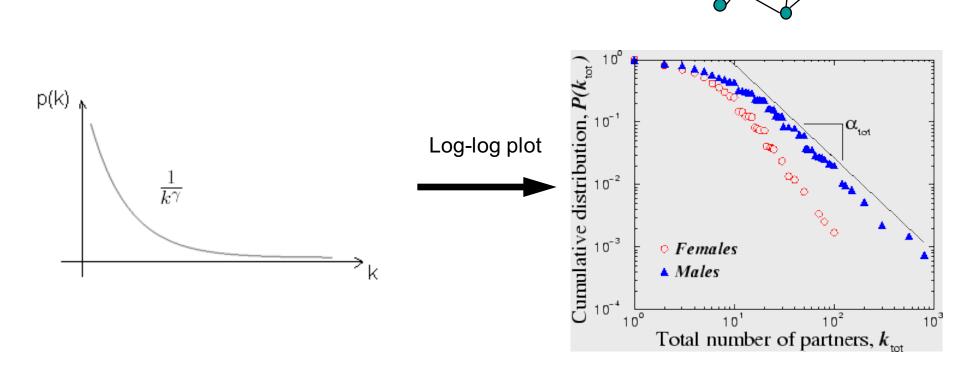


Hub =

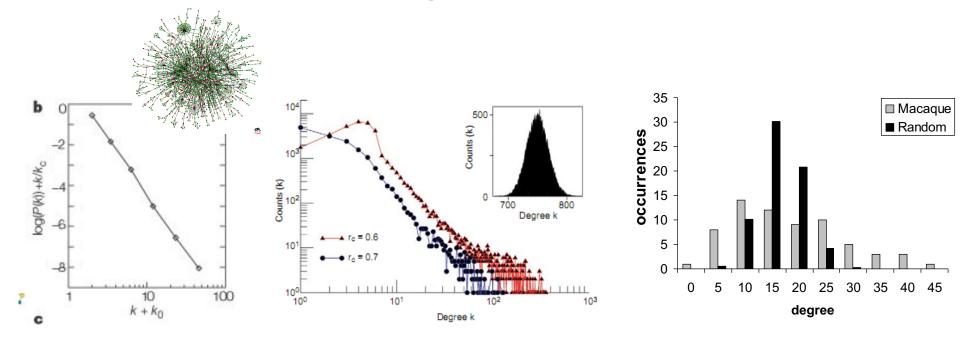
highly-connected node

(potentially important for the network)

Is your network scale-free?



Examples for biological scale-free networks



Protein-protein interaction network Correlation network between cortical tissue (fMRI voxels)

Cortical fibre tract network?

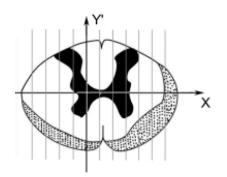
Jeong et al., Nature, 2001 Equiluz et al., Phys Rev Lett, 2005 Sporns et al., Trends Cogn Sci, 2004

Kaiser et al., Eur J Neurosci, 2007

Robustness

Neural robustness against network damage (lesions)

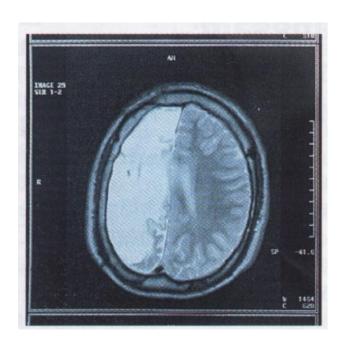
Rats: Spinal chord injury



large recovery possible with as few as 5% of remaining intact fibers

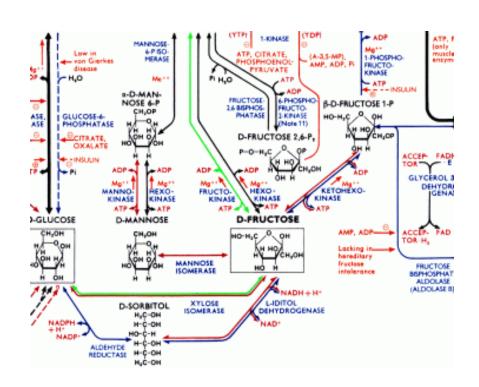
You et al., 2003

Human: Compensation for loss of one hemisphere at age 11



Cellular robustness against damage (gene knockouts)

- Mutations can be compensated by gene copies or alternative pathways*:
 ~70% of single-gene knockouts are non-lethal
- The metabolism can adjust to changes in the environment (e.g. switch between aerob and anaerob metabolism)



^{*} A. Wagner. Robustness against mutations in genetic networks of yeast. *Nature Genetics*, 24, 355-361 (2000).

Measures of structural integrity

How is the global topology of the network affected?

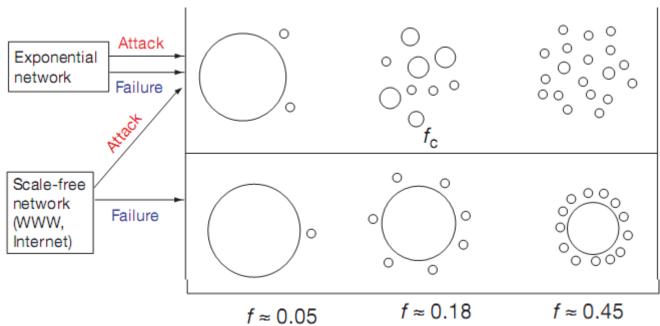
Idea: Changes in *structural* properties might indicate *functional* changes (like lower performance of the system)

Determined from ettermine to a contract

	Structural measure	Potential functional impact				
1	All-pairs shortest path	longer transmission time	Alzheimer			
1	Reachability Fragmentatio	n occurrence of isolated parts	s (components)			
1	Clustering coefficient	less interaction within modules Schizophrenia				

Example: fragmentation



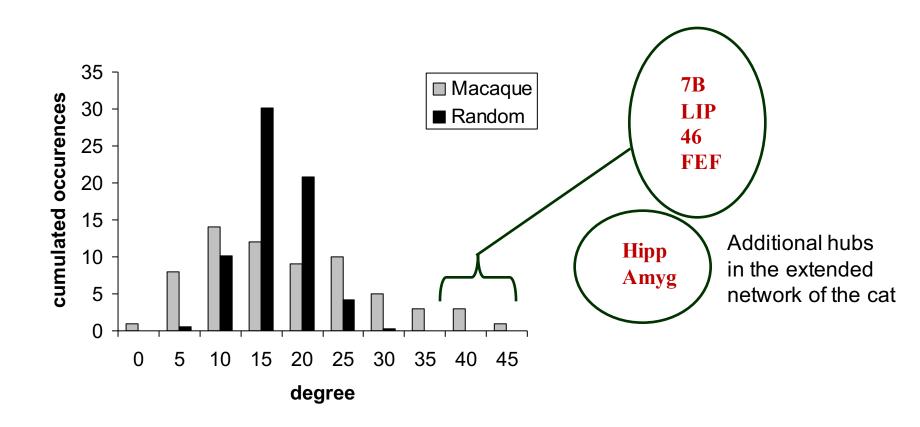


f: fraction of removed nodes

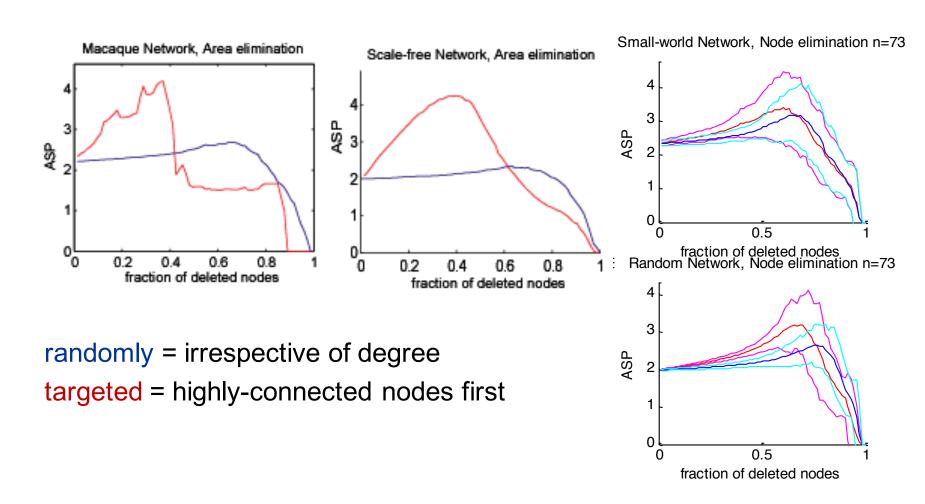
f_c: fraction where the network breaks into small fragments

Example: simulated brain lesions

Is the brain similar to a scale-free network?



Sequential removal of brain areas

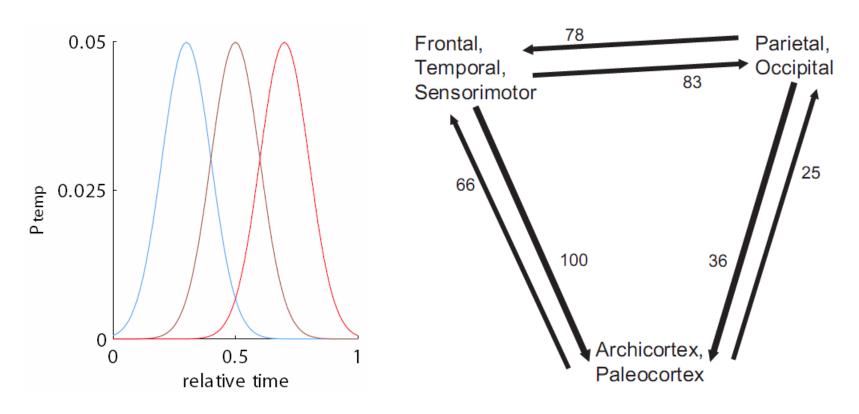


Kaiser et al. (2007) European Journal of Neuroscience 25:3185-3192

Where do 'hubs' come from?

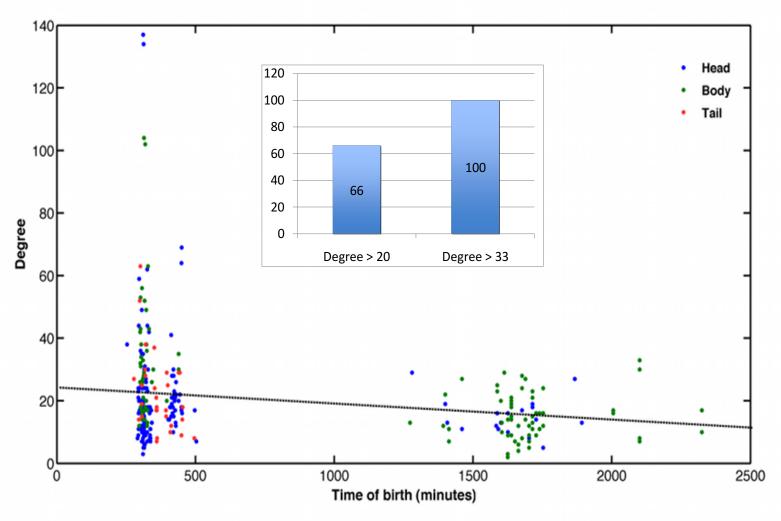
Not from preferential attachment...

During individual development, early-established nodes have more time to establish connections:



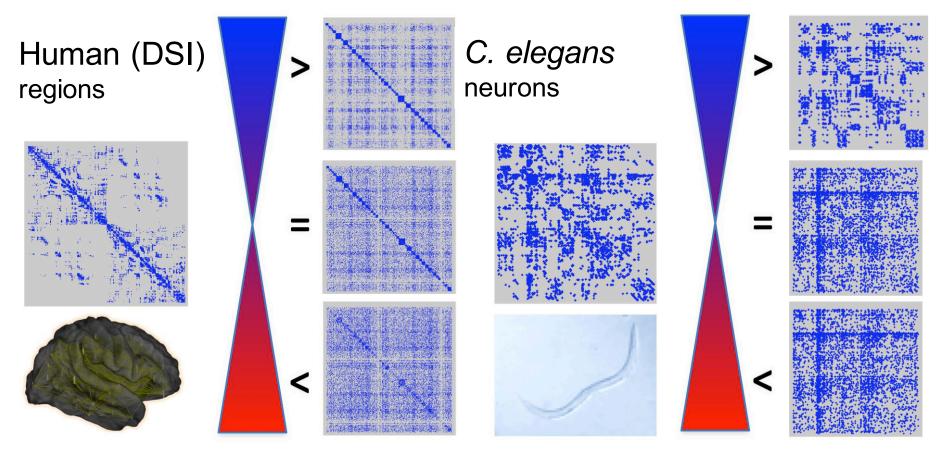
C. elegans network development: Varier & Kaiser (2011) PLoS Comput Biol Nisbach & Kaiser (2007) Eur Phys J B Kaiser et al. (2007) European Journal of Neuroscience 25:3185-3192

Hub neurons start early (old-gets-richer model)



Varier & Kaiser (2011) PLoS Computational Biology

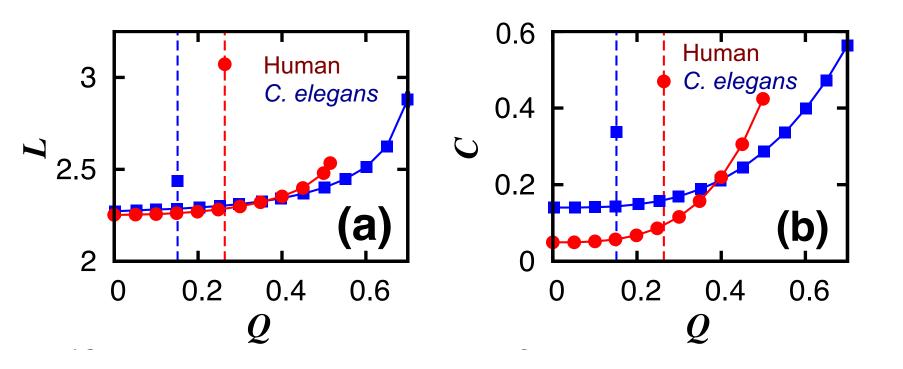
What is special about the modular organization of adult networks?



Increase or decrease of modularity Q

Kim & Kaiser (2014) Phil. Trans. R. Soc. B

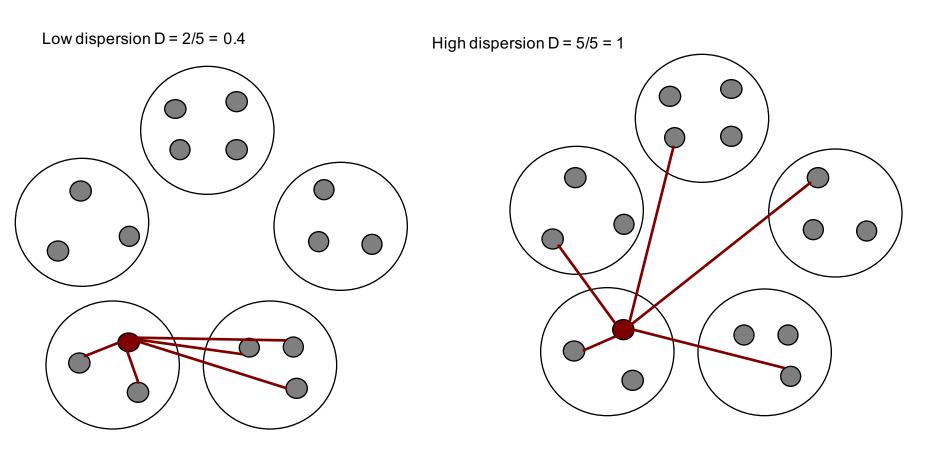
Higher characteristic path length and higher clustering coefficient



Lower dispersion D

For one node i: $D_i = R_i / R$

R_i the number of modules to which node i links to
R is the total number of modules (66 regions or 10 ganglia)

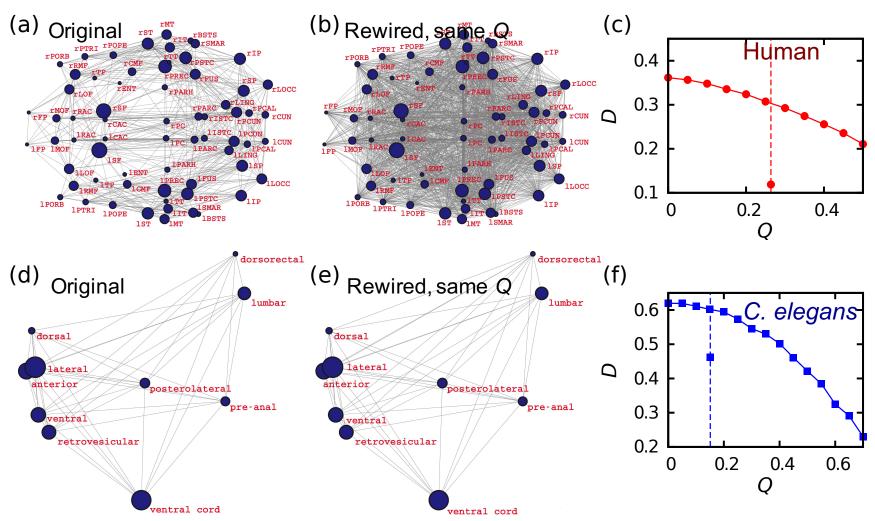


Kim & Kaiser (2014) Phil. Trans. R. Soc. B

Lower dispersion D

For one node i: $D_i = R_i / R$

R_i the number of modules to which node i links to R is the total number of modules (66 regions or 10 ganglia)



Kim & Kaiser (2014) Phil. Trans. R. Soc. B

Less information needed to grow the network

Algorithmic entropy: how much information is needed to encode for the network?

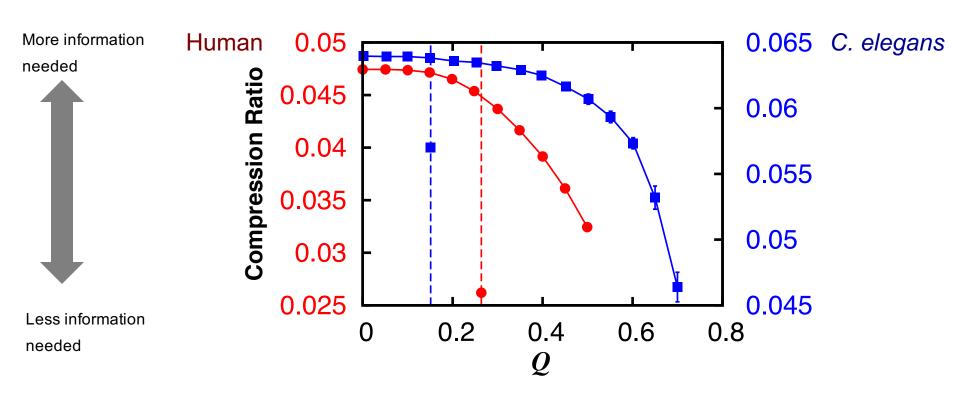
Compressed adjacency matrix = genetic information

Decompression algorithm = gene expression, Turing morphogenetic fields etc.

Decompressed = adult brain connectivity

Less information needed to grow the network

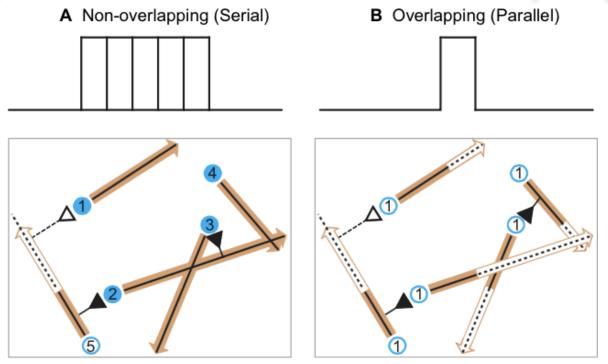
Algorithmic entropy: how much information is needed to encode for the network?



Compression ratio = size of compressed data / size of raw data

Kim & Kaiser (2014) Phil. Trans. R. Soc. B

Example growth rule: developmental time course - Axon growth time windows influence topology



Early starting neurons

- tend to become hubs
- have higher local efficiency
- have more long-distance connections

More bidirectional connections fewer long-distance connections

Model predictions are in agreement with C. elegans connectivity

Lim & Kaiser (2015) Biological Cybernetics

Summary

7. Macroscale:

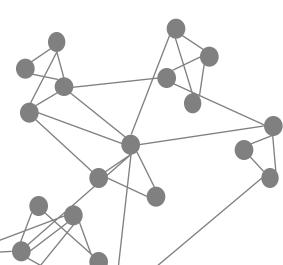
Degree distribution
 Random networks
 Scale-free networks

- Small-world networks

- Hierarchical networks

6. Mesoscale:

- Motifs
- Clusters/Modules



8. Robustness:

- Change of network properties after edge or node removal
- simulated brain lesions

9. Modular organisation

Preferential modularity: increased local clustering and global path length

→ better local integration and global separation of processing

Lower algorithmic entropy: less information needed to encode connectivity

→ fewer genes needed during brain development

Further readings



Costa et al. Characterization of Complex Networks

Advances in Physics, 2006



Ed Bullmore



Malcolm Young



Olaf Sporns

Kaiser et al. <u>Simulated Brain Lesions</u> (brain as scale-free network) *European Journal of Neuroscience, 2007*

Alstott et al. Modeling the impact of lesions in the human brain PLoS Computational Biology, 2009

Bullmore & Sporns. Complex Brain Networks

Nature Reviews Neuroscience, 2009