

Towards a transcriptogram



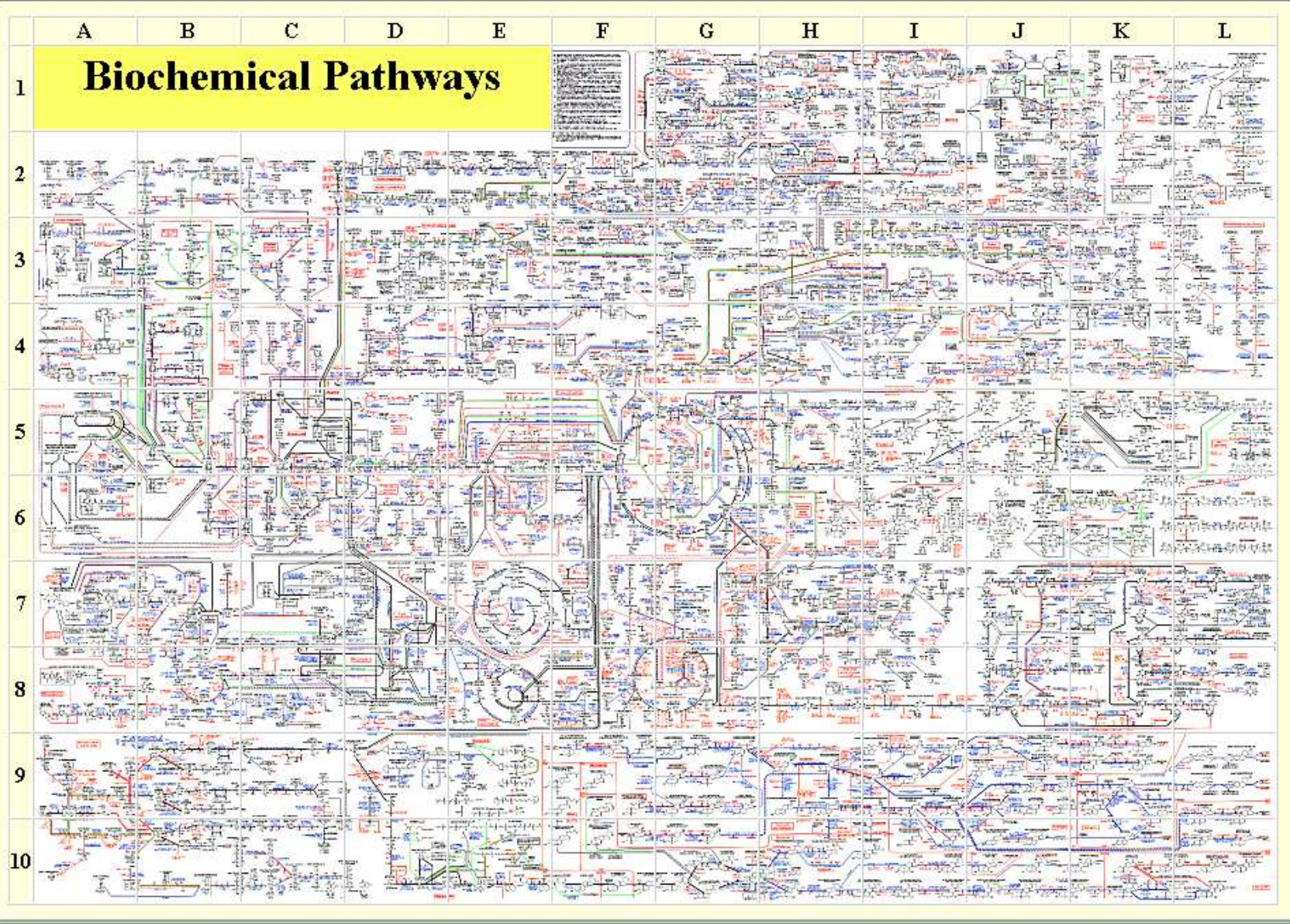
Instituto de Física UFRGS



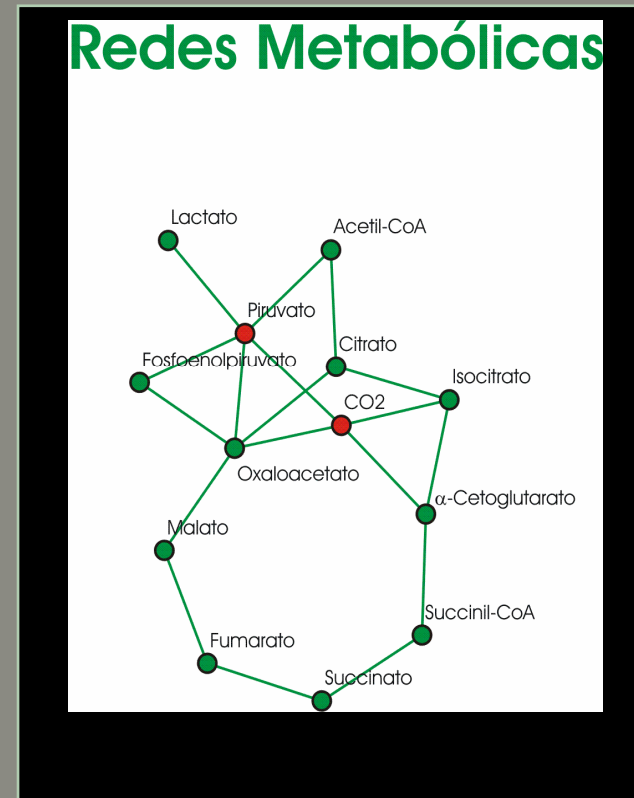
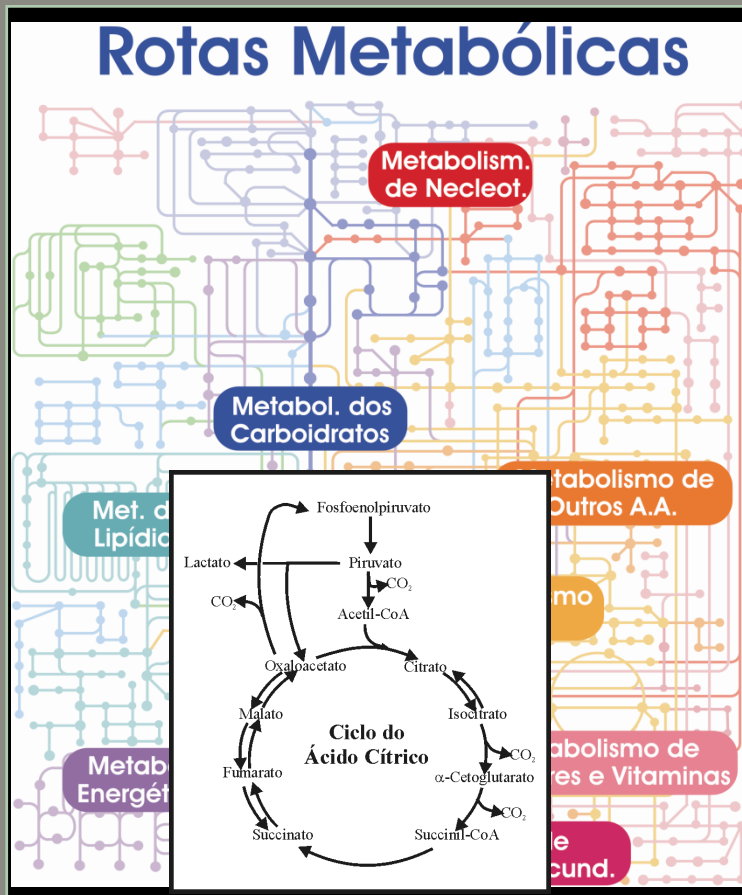
**INSTITUTO NACIONAL DE
CIÊNCIA E TECNOLOGIA DE
SISTEMAS COMPLEXOS**

Team

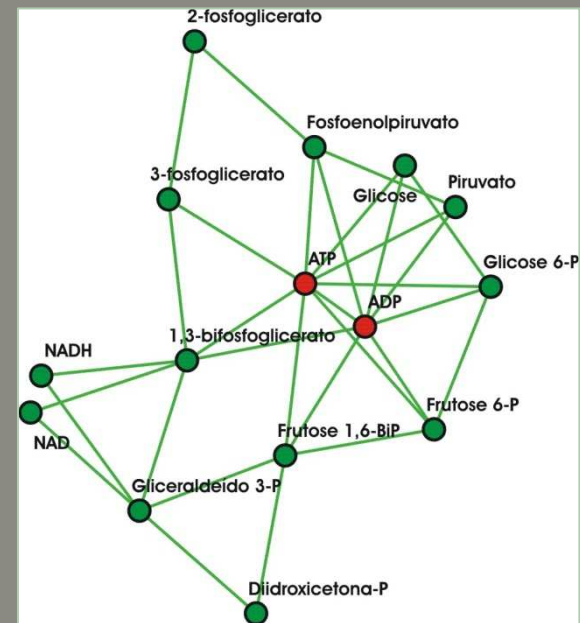
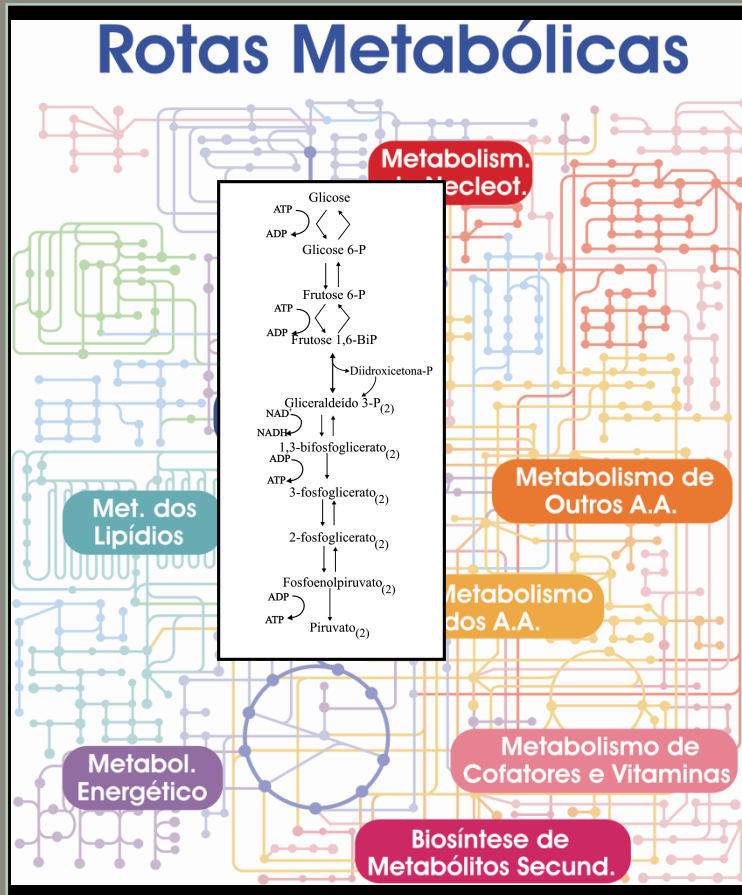
- ▶ José Cláudio Moreira (Biochemistry-UFRGS)
- ▶ Rita M. C. de Almeida (Physics-UFRGS)
- ▶ Leonardo Brunnet (Physics-UFRGS)
- ▶ José Carlos M. Mombach (Physics-UFSM)
- ▶ Mauro Castro (Cambridge, UK)
- ▶ Marialva Sinigaglia (Genetics-UFRGS)
- ▶ José Luiz Rybarczyk (Physics-UFRGS)
- ▶ Ricardo Mello (Physics-UFRGS)
- ▶ Rodrigo Dalmolin (Biochemistry-UFRGS)
- ▶ Gabriel Perrone (Physics-UFRGS)



Definitions



Definições



Gene Ontology Database

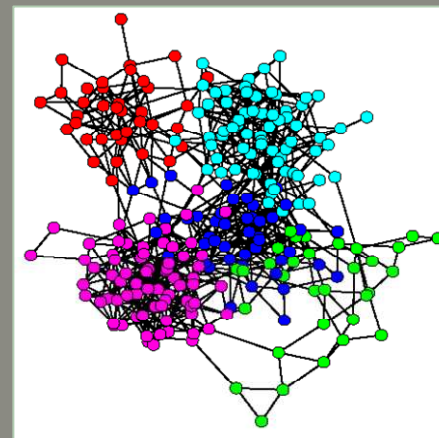
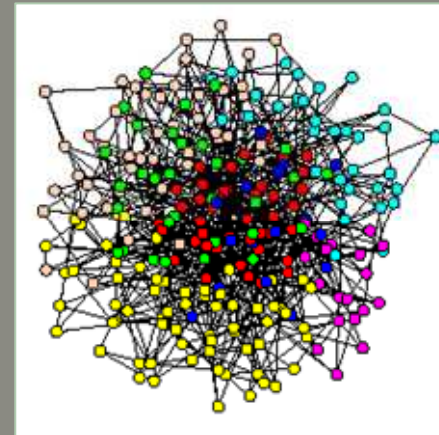
- 3 classifications - ontologies
 - Biologic Process
 - Cellular Component
 - Molecular molecular functions
- Hierarchical structure

Which one?

- Metabolic pathways → function based
- How isolate systems? How estimate errors?

Modularity

- Scale-free
- Modular



20 July 2011

INCT - Sistemas Complexos -CBPF

Ravasz E. *Phys. Rev. E*, 67: 026112 (2003)

How to choose the protein set?

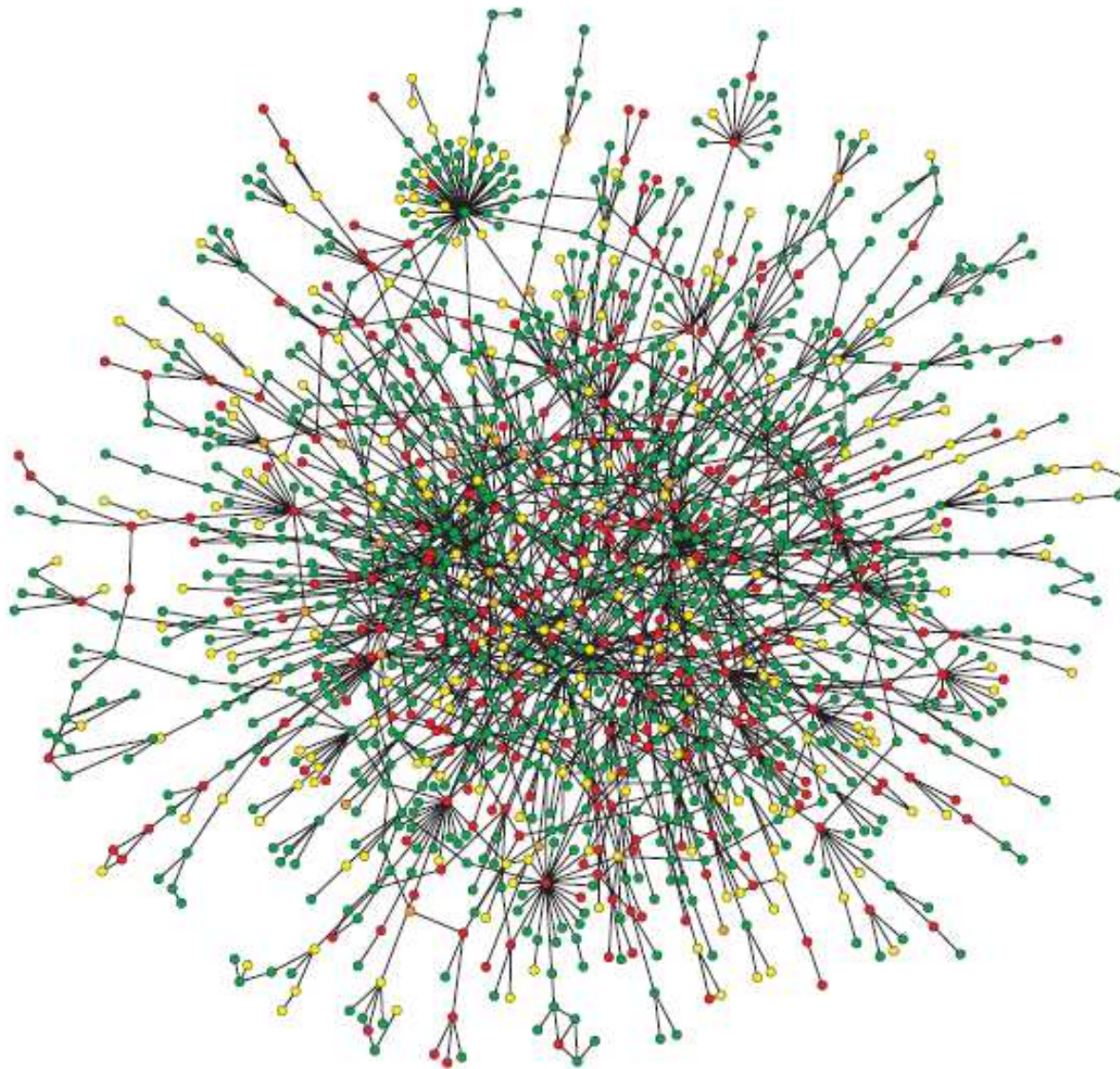
- Functions?
- Interactions?
- Can we define clusters?
- Error estimatives
- What about evolution?

The interaction matrix

- Enumerate the proteins in random list.
- Build an interaction matrix M_{ij} such that
 - $M_{ij}=1$ if i and j interact
 - $M_{ij}=0$ if i and j do not interact

STRING for interaction information

Aspergillus fumigatus e *Geophobomyces levisiae*



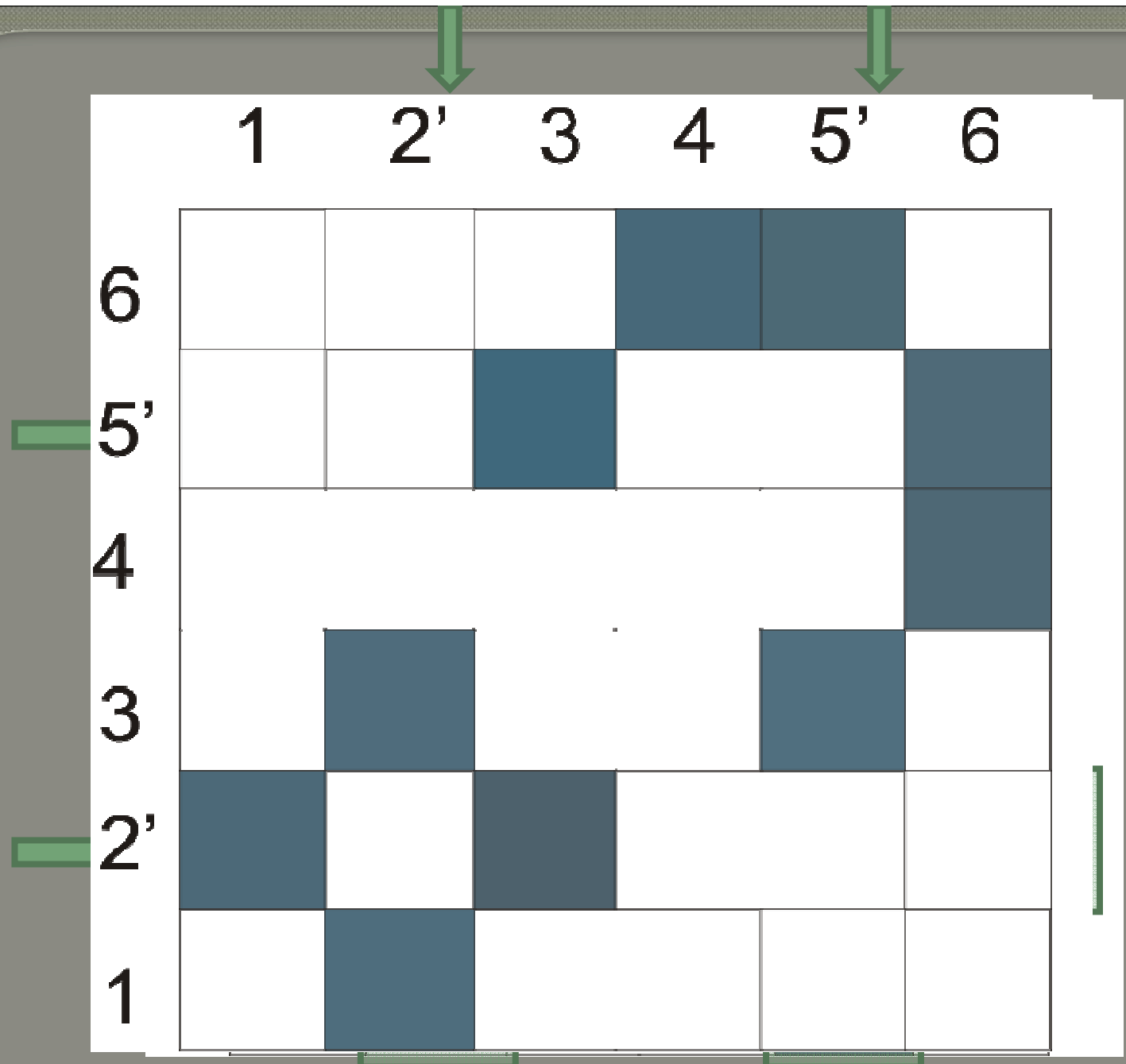
genes
tão
eatoriamente
denados.

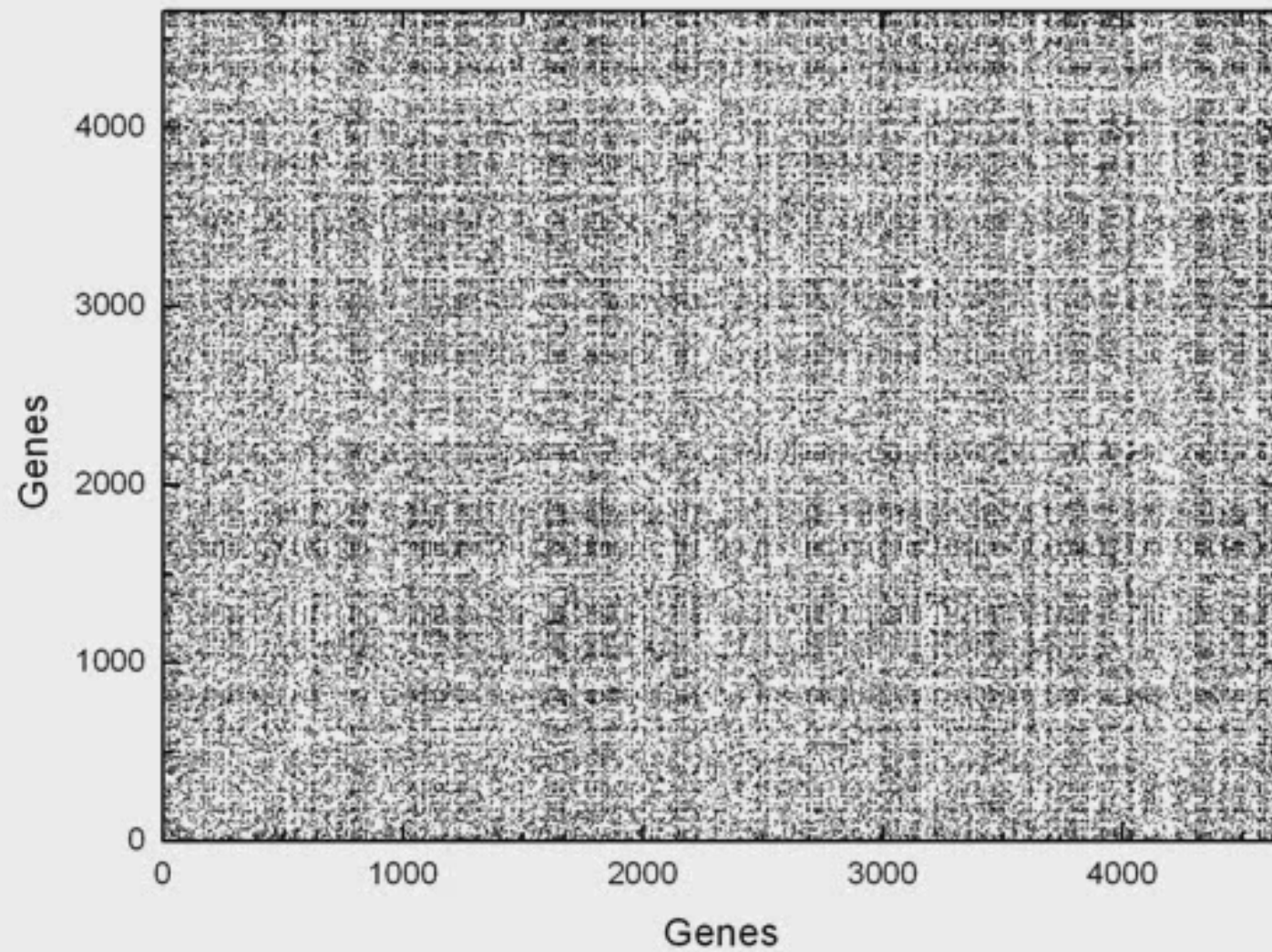
Strategy

- Energy of a matrix configuration:

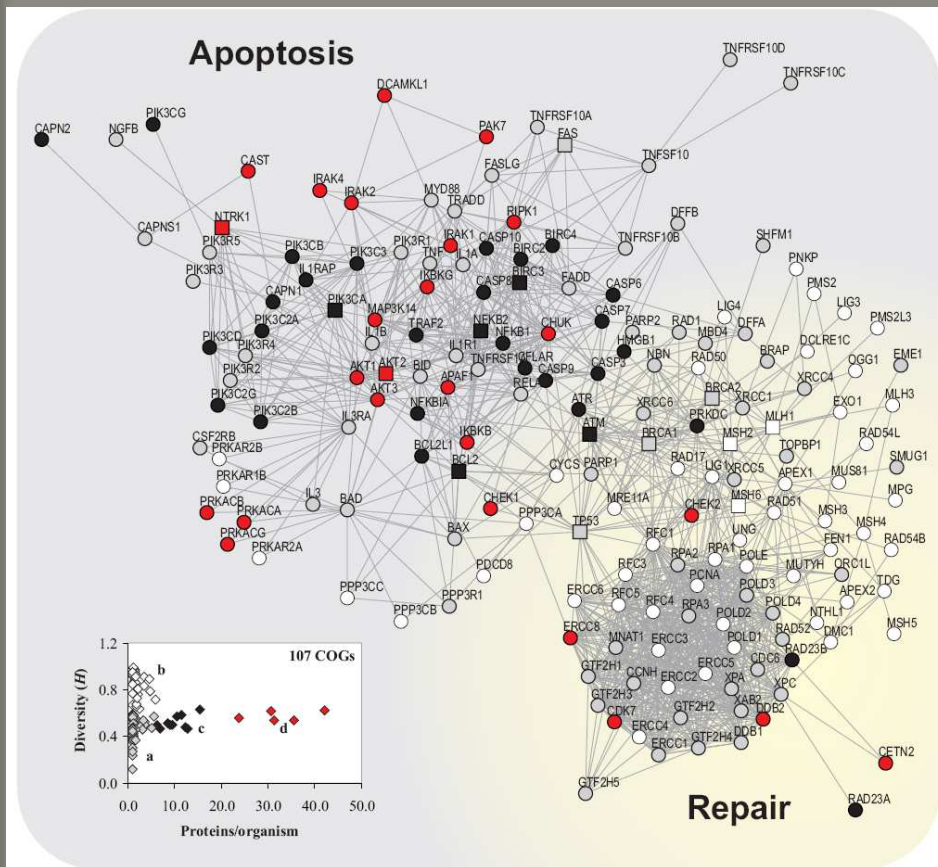
$$E = \sum_{i=1} \sum_{j=1} d_{ij} \{ |M_{i,j} - M_{i+1,j}| + |M_{i,j} - M_{i-1,j}| \\ + |M_{i,j} - M_{i,j+1}| + |M_{i,j} - M_{i,j-1}| \}$$

- Randomly choose two proteins, swap their positions and recalculate the energy.
- If the swapping lowers the energy, accept the change
- Repeat.





Modularity



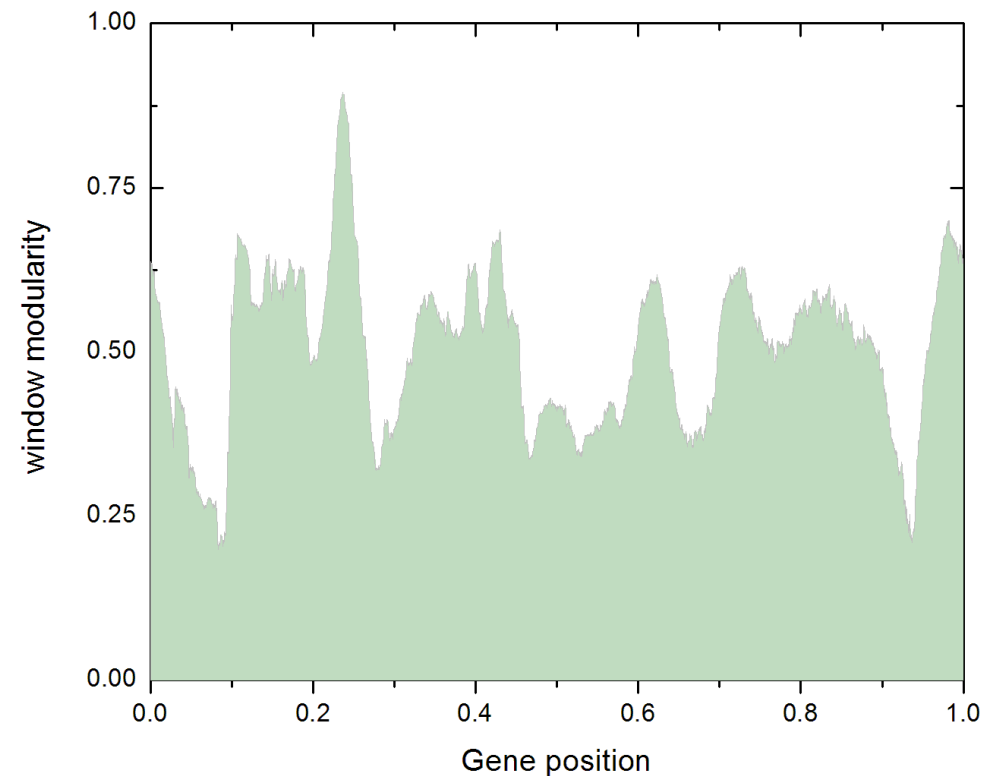
Given a gene set, Modularity is defined as the fraction

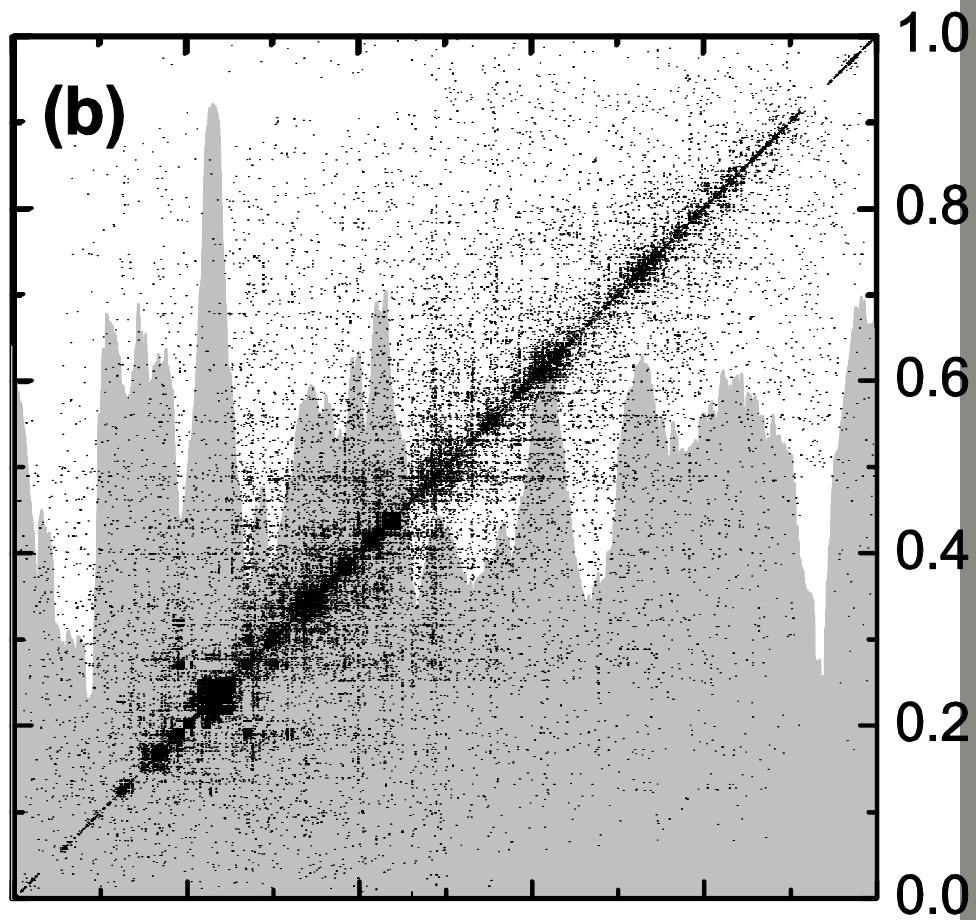
Number of links between two genes in the set

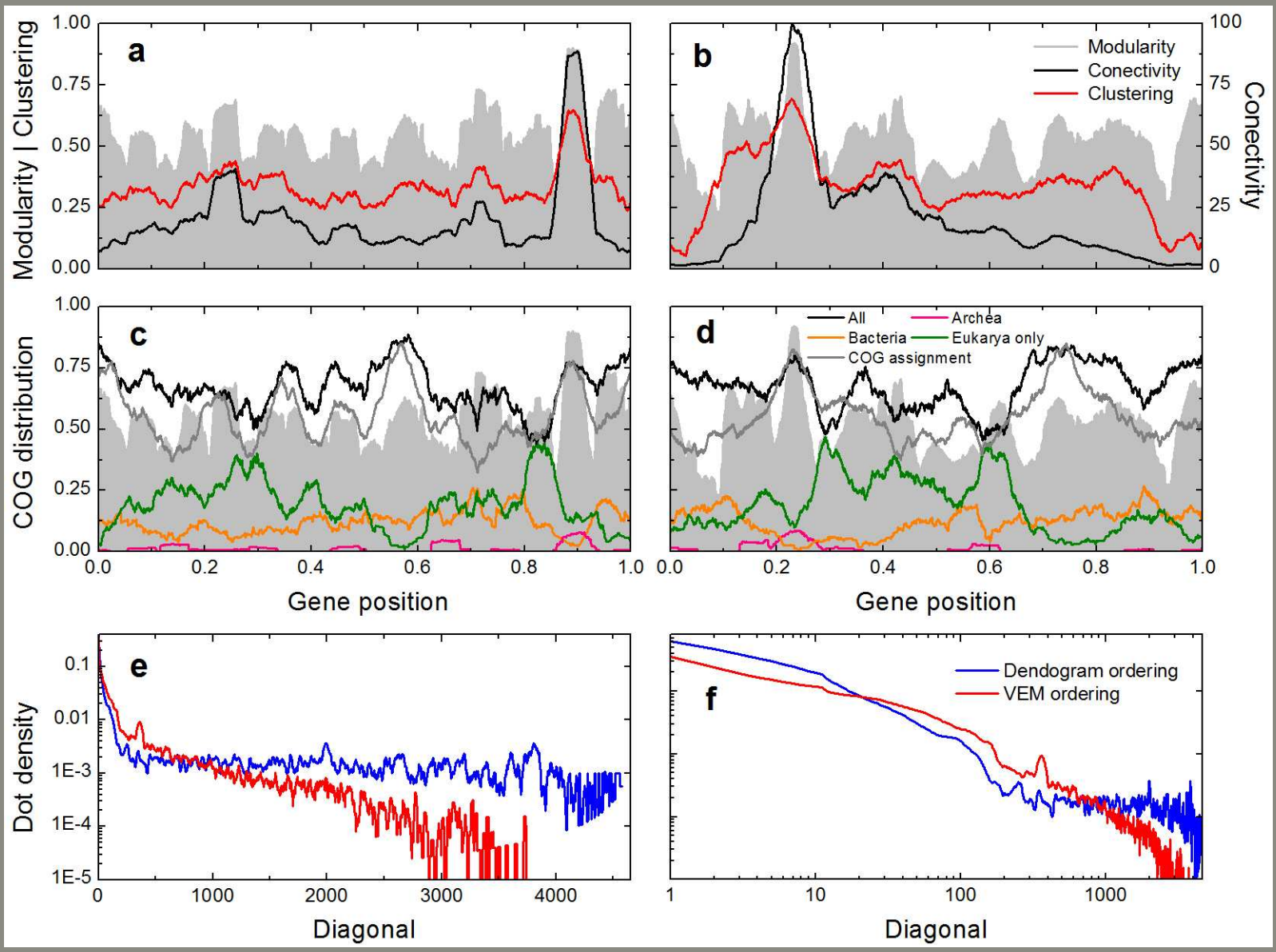
Number of links involving at least one gene in the set

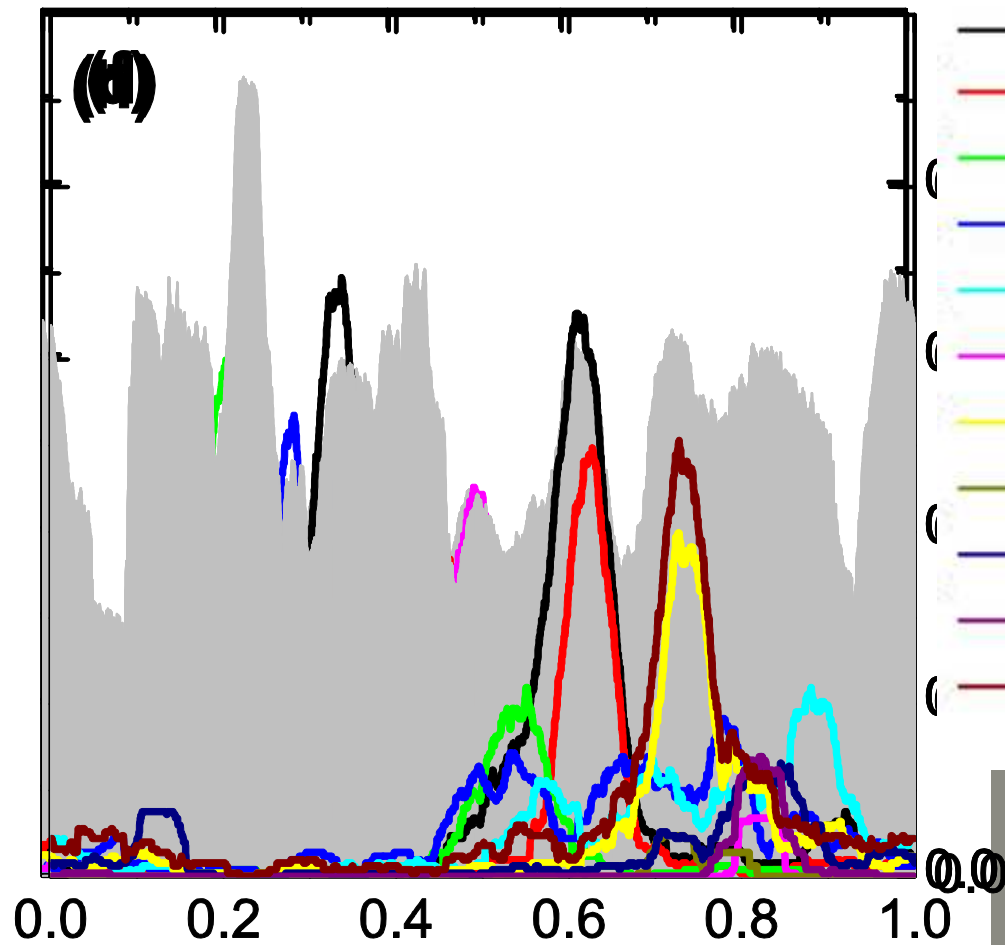
Window modularity

- The gene set is given by the $w/2$ neighbors to the right and to the left of each gene

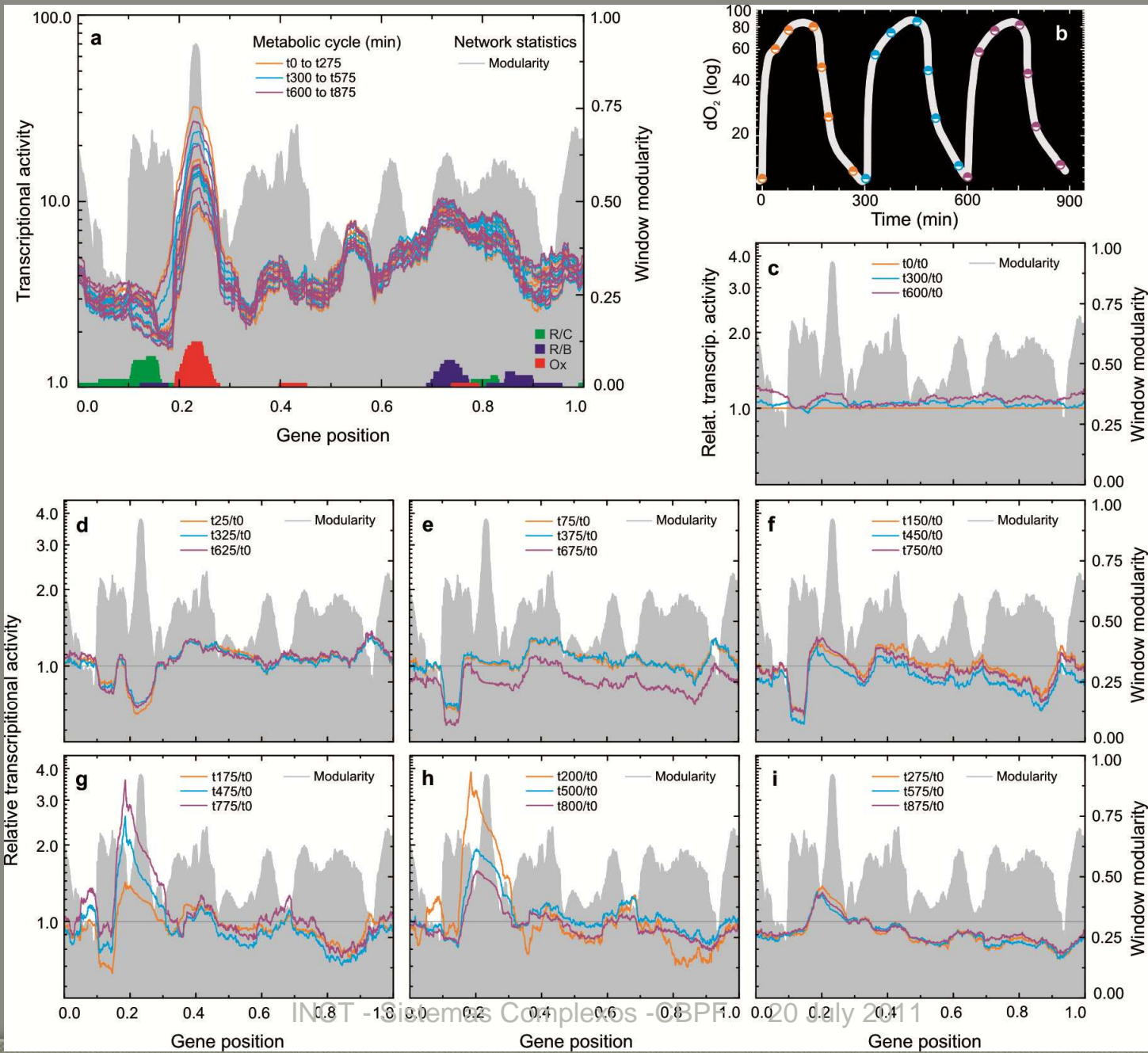


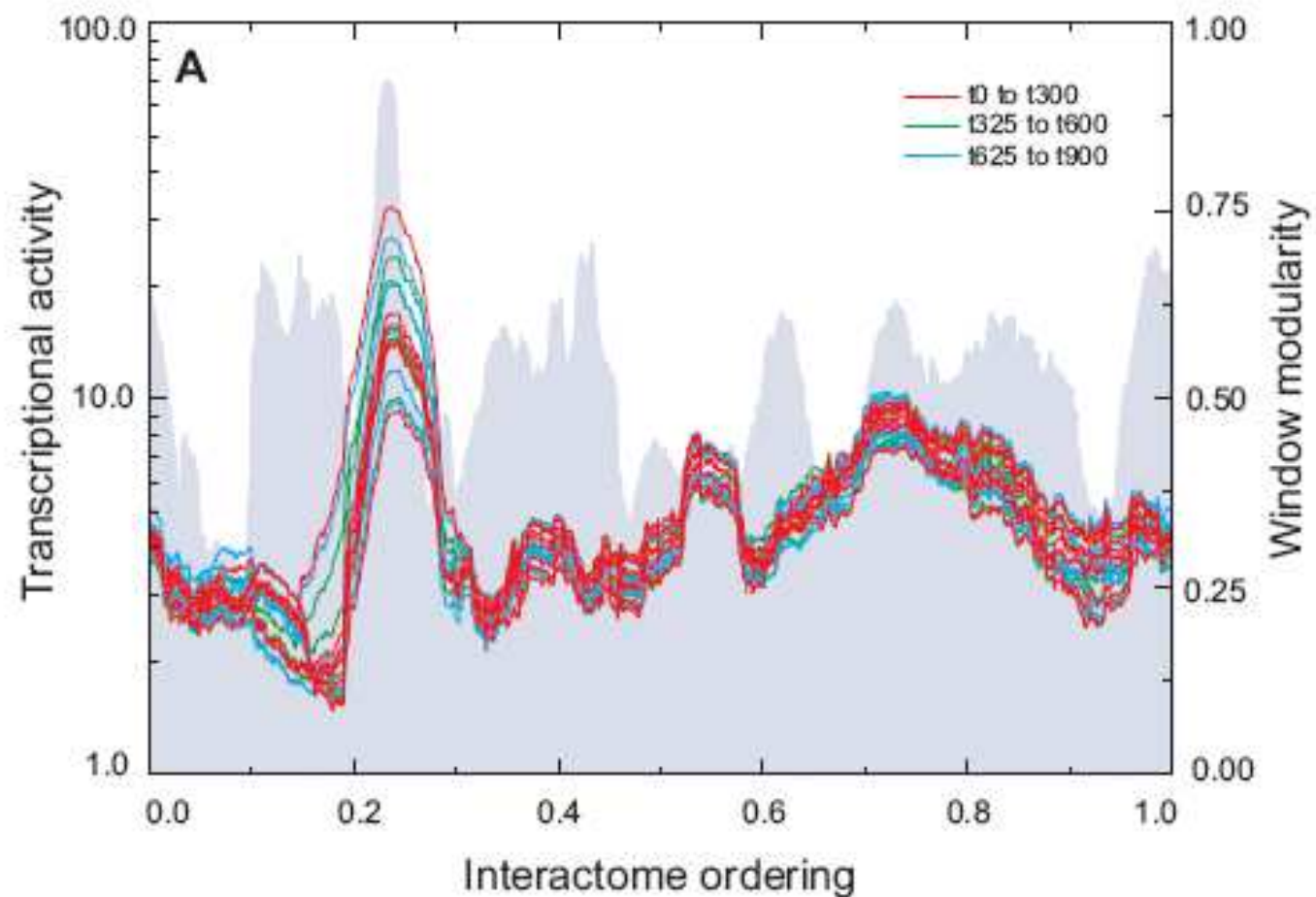


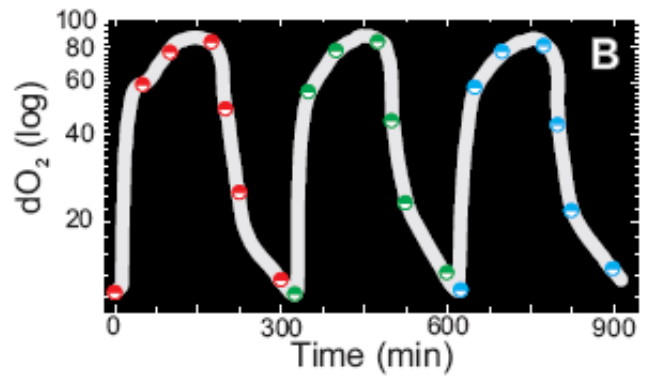




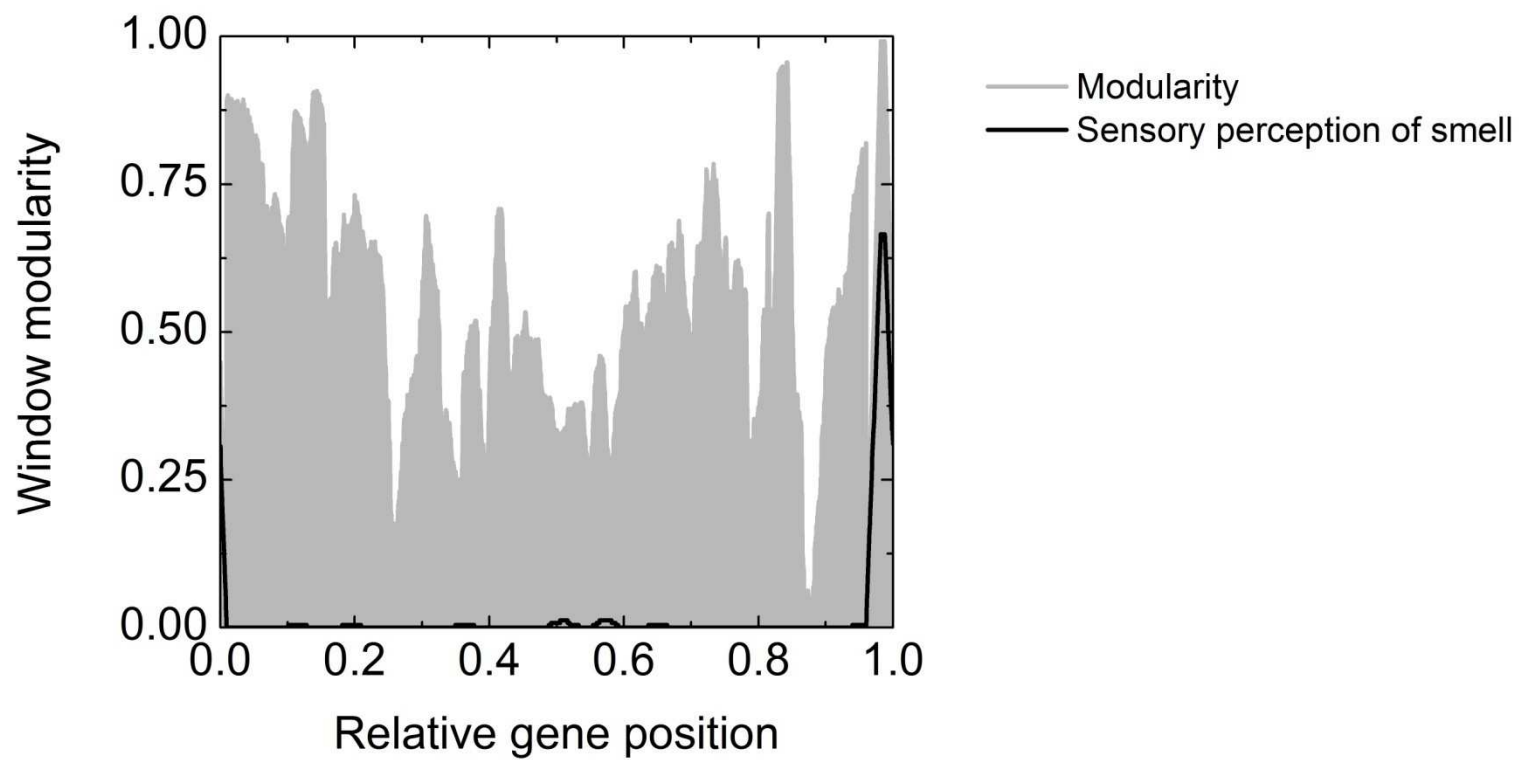
- DNA metabolic process
- vesicle mediated transport
- Golgi vesicle transport
- actin cytoskeleton org./biogen.
- carbohydrate met. proc.
- lipid met. proc.
- aminoacid / derivative met. proc.
- carboxylic acid met. proc.
- oxidative met. phosphorylation
- cellular respiration
- acetyl-CoA met. proc.
- ATP met. proc.

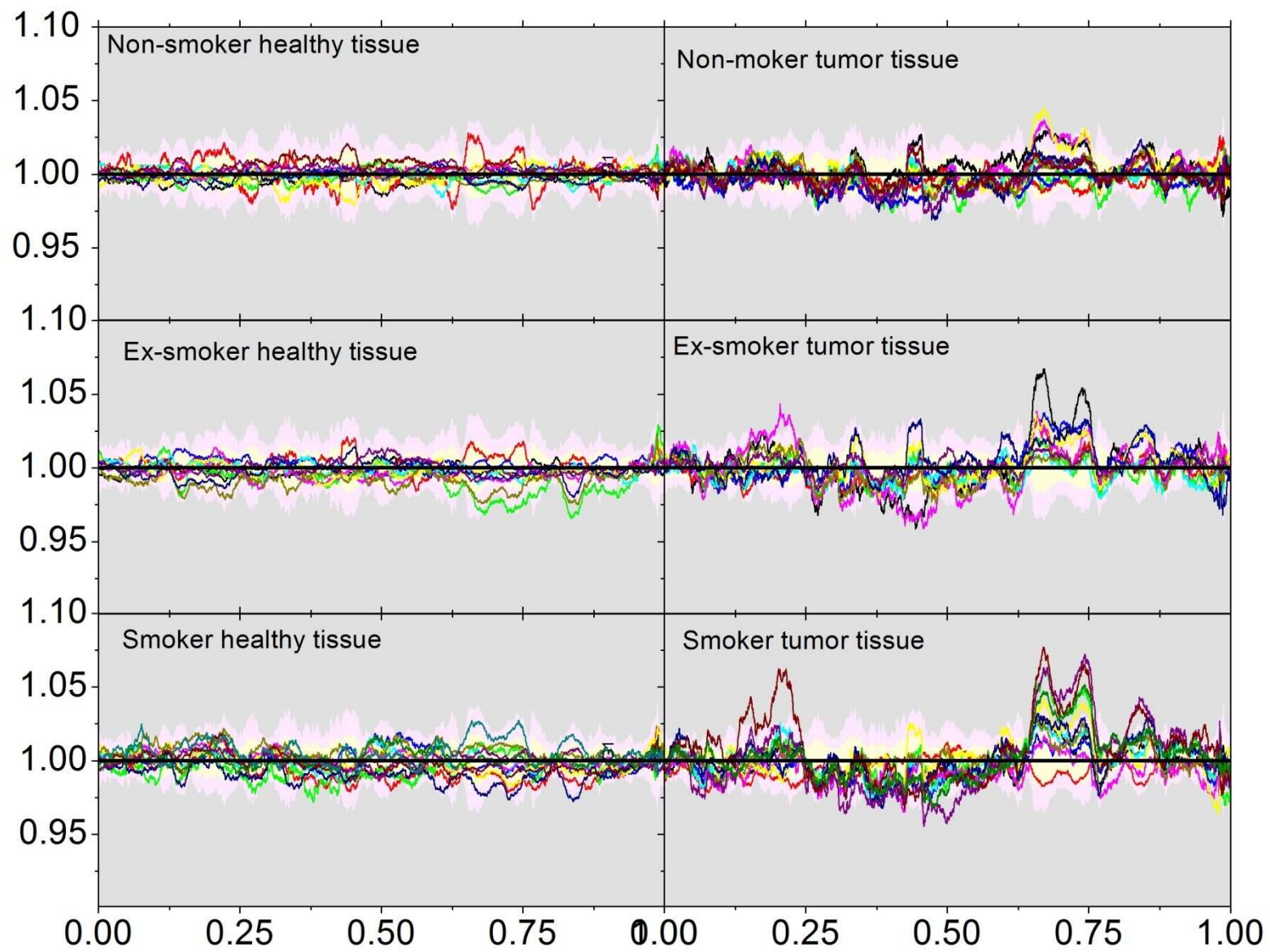


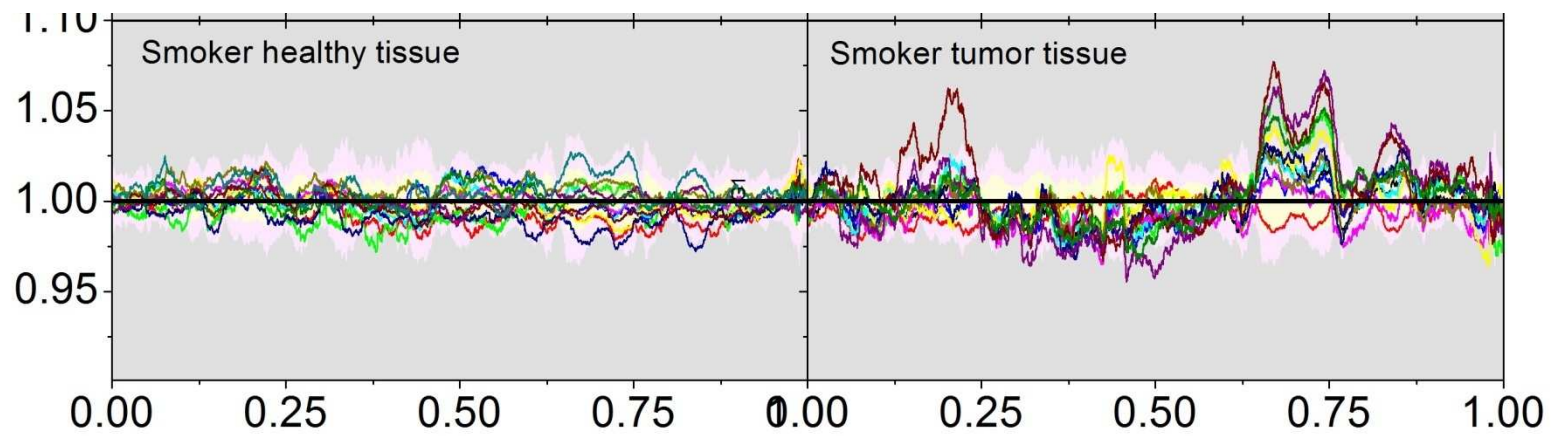
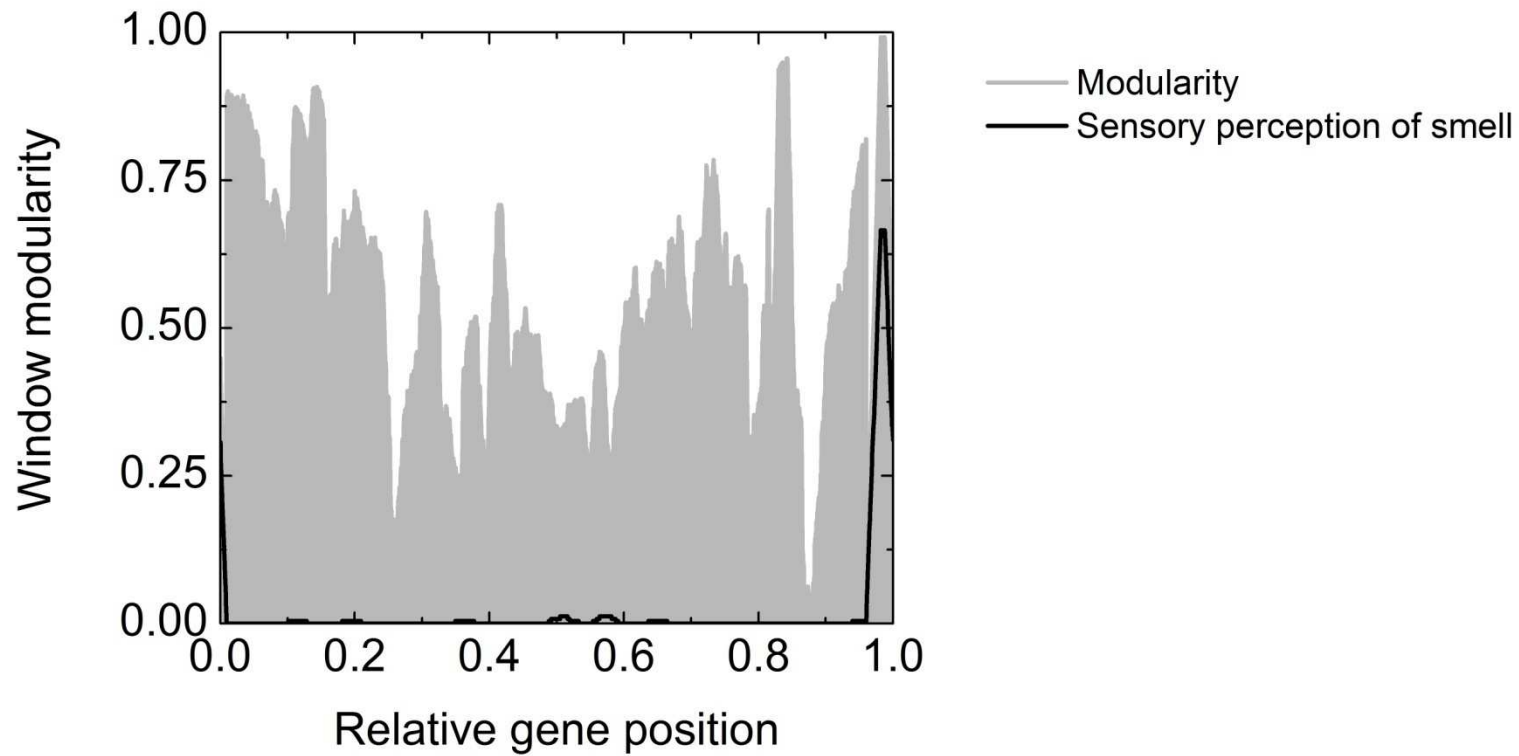





Tu, B.P., Kudlicki, A., Rowicka, M. & McKnight, S.L. Logic of the Yeast Metabolic Cycle: Temporal Compartmentalization of Cellular Processes. *Science* 310, 1152–1158 (2005).



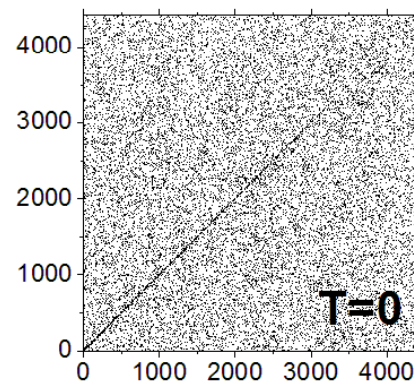
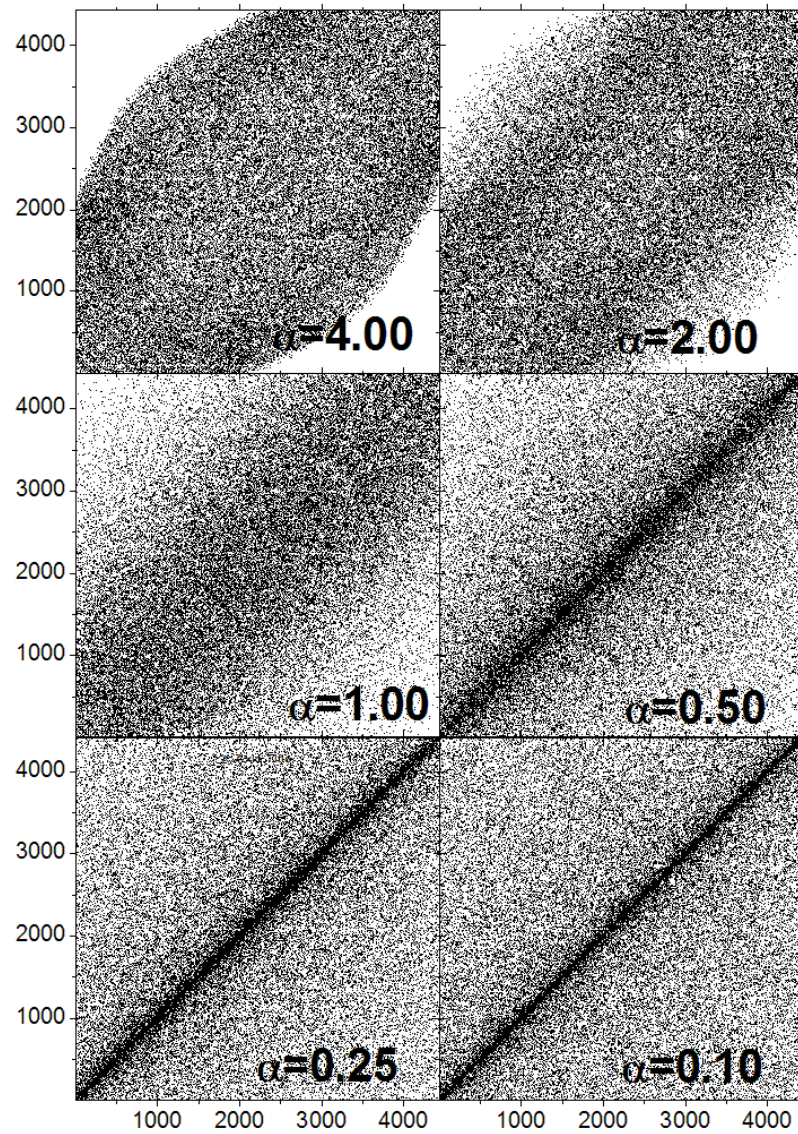




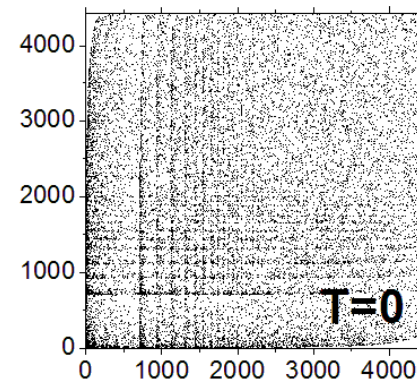
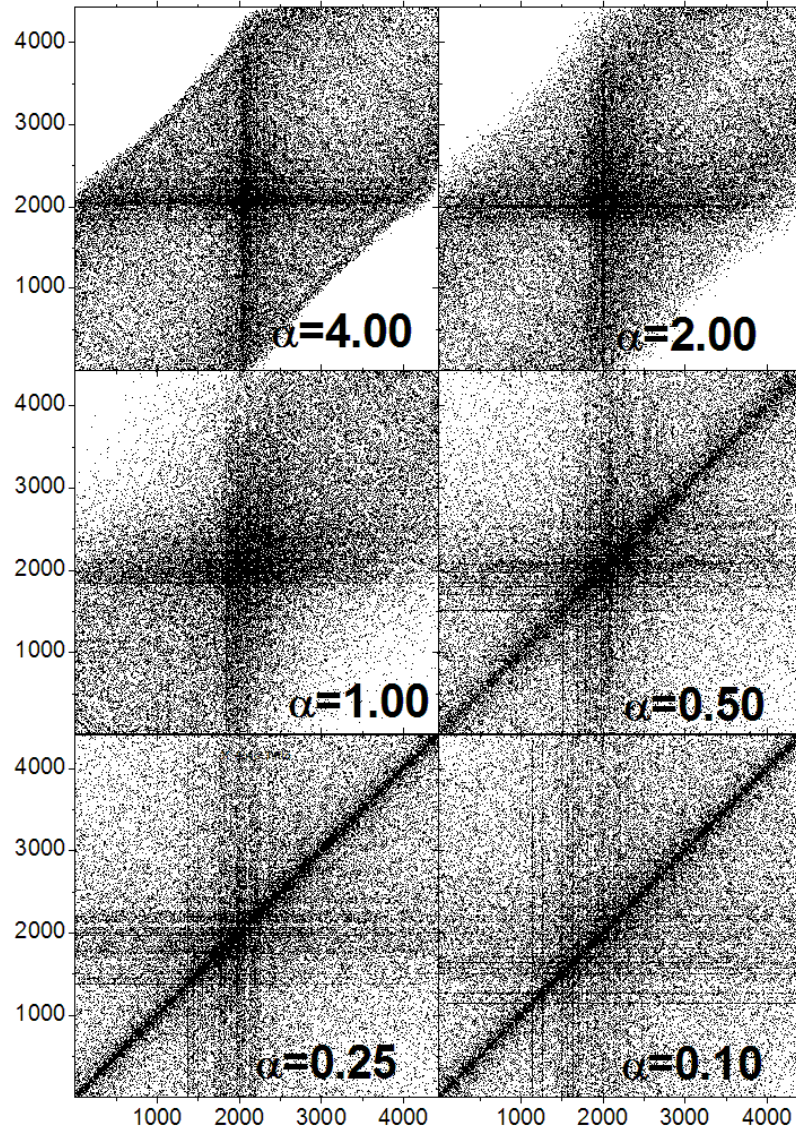
What's next?


$$E = \sum_{i=1} \sum_{j=1} d_{ij}^{\alpha} \left\{ \left| M_{i,j} - M_{i+1,j} \right| + \left| M_{i,j} - M_{i-1,j} \right| \right. \\ \left. + \left| M_{i,j} - M_{i,j+1} \right| + \left| M_{i,j} - M_{i,j-1} \right| \right\}$$

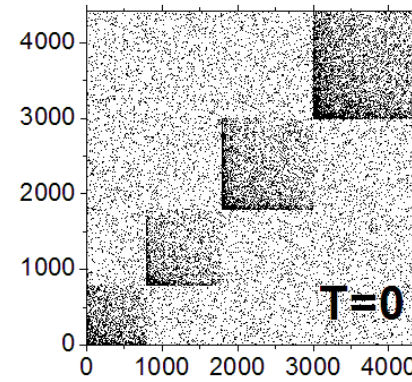
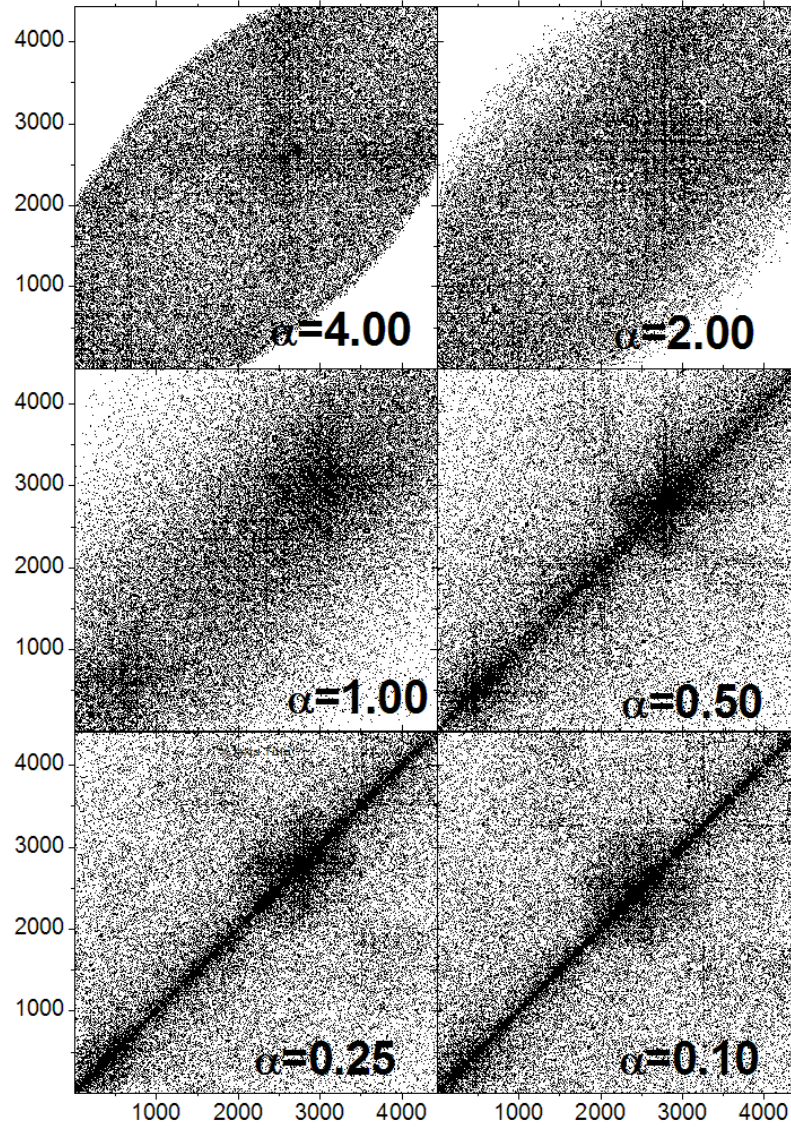
Random



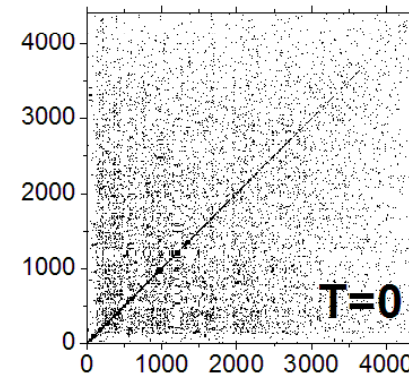
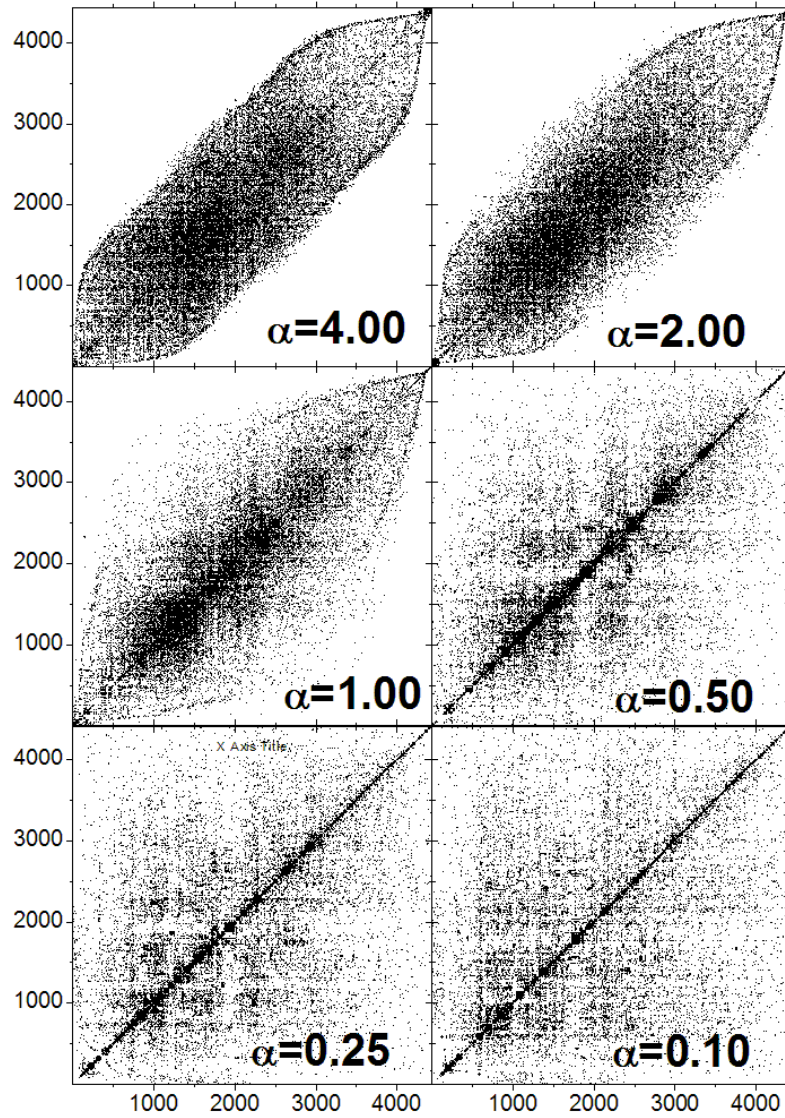
Barabasi



Barabasi-Randomico

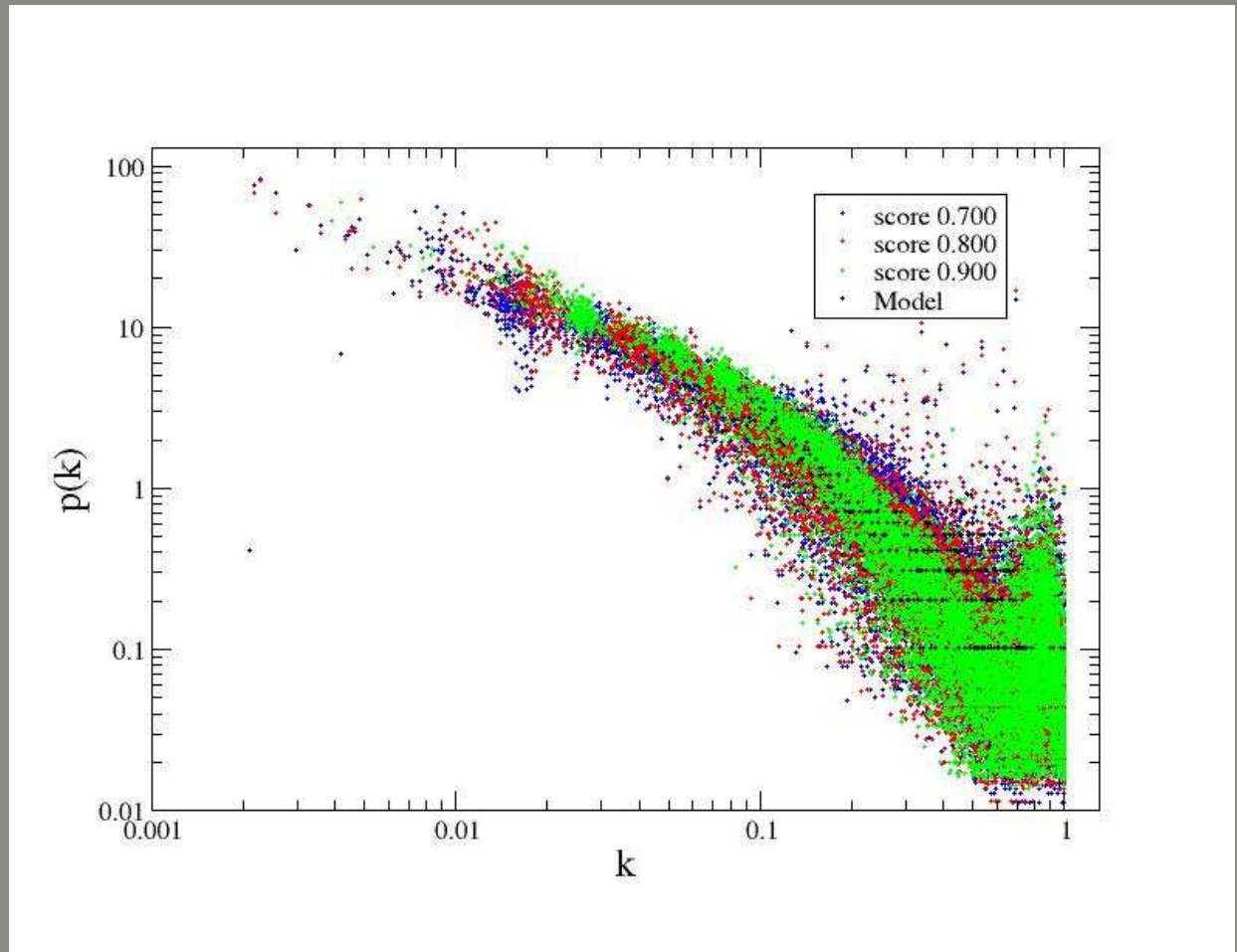


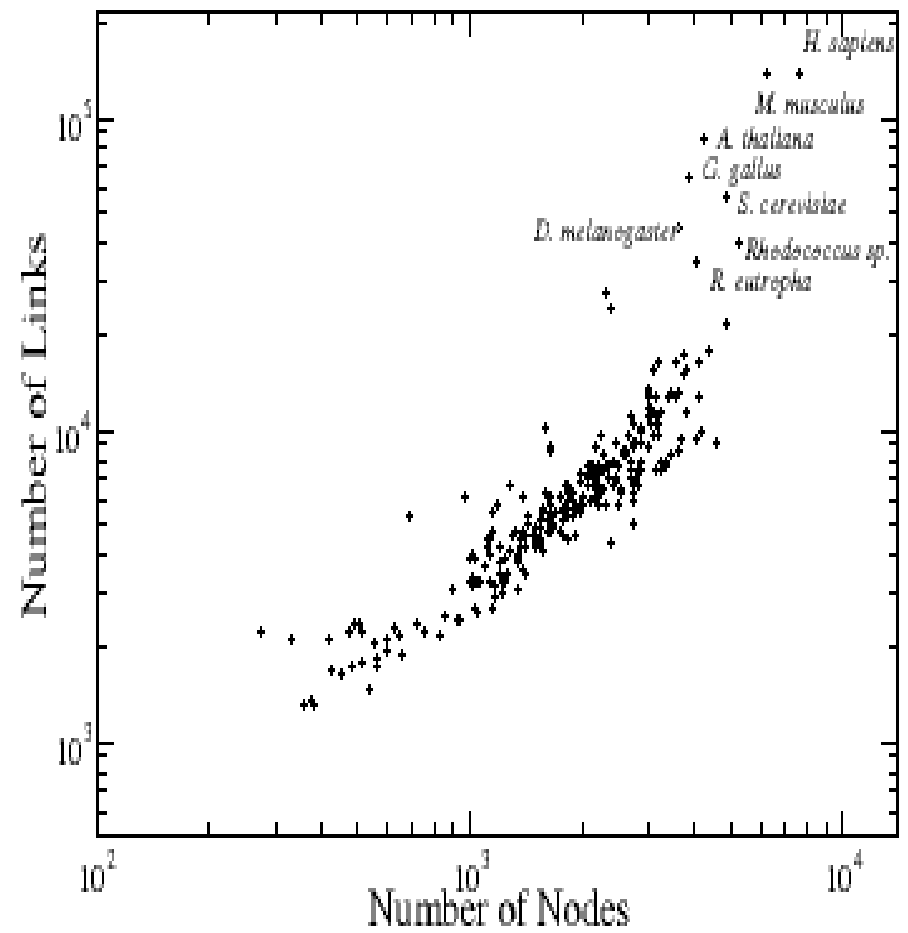
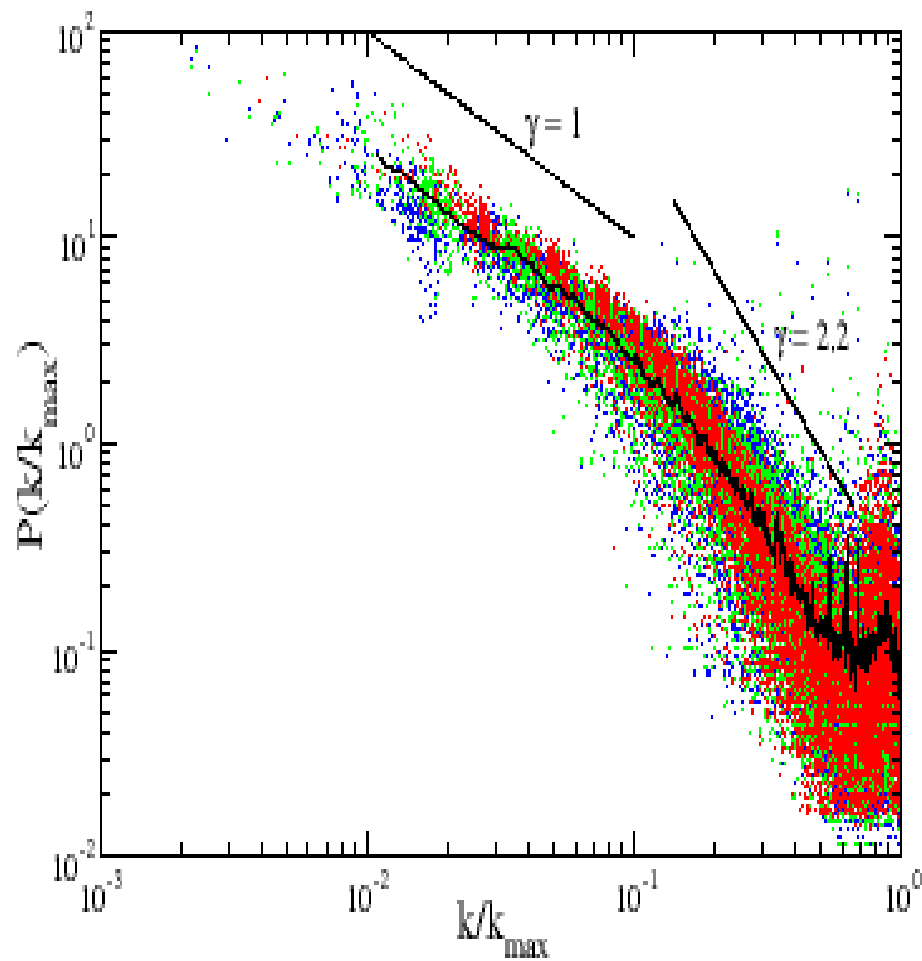
Prod-Saccharomyces

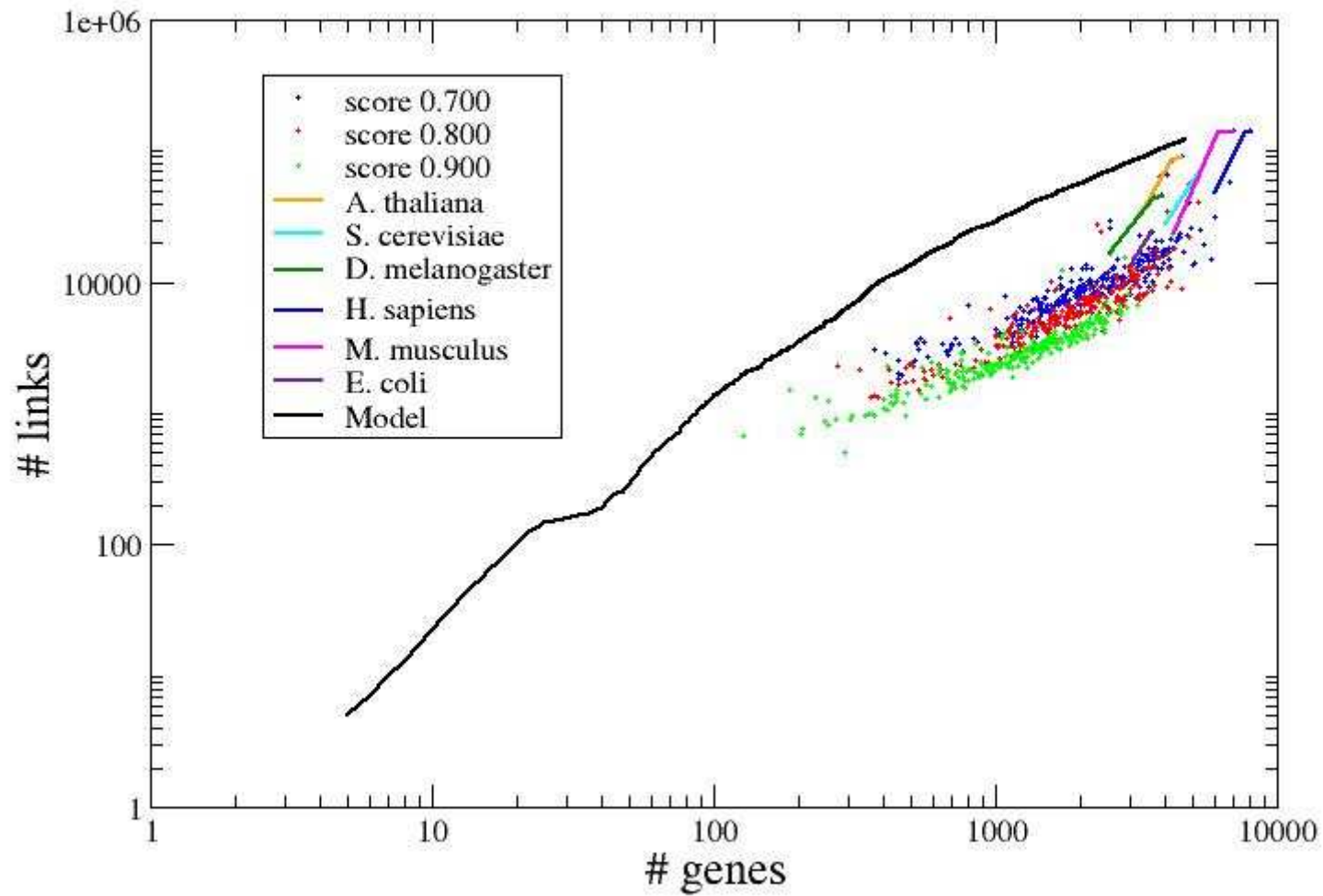


Modelos de construção de redes

- Barabasi-Albert: preferential attachment
- Vazquez: Duplicação-Divergência
- Duplicação e attachment.
- Probabilidade de duplicação: 90%



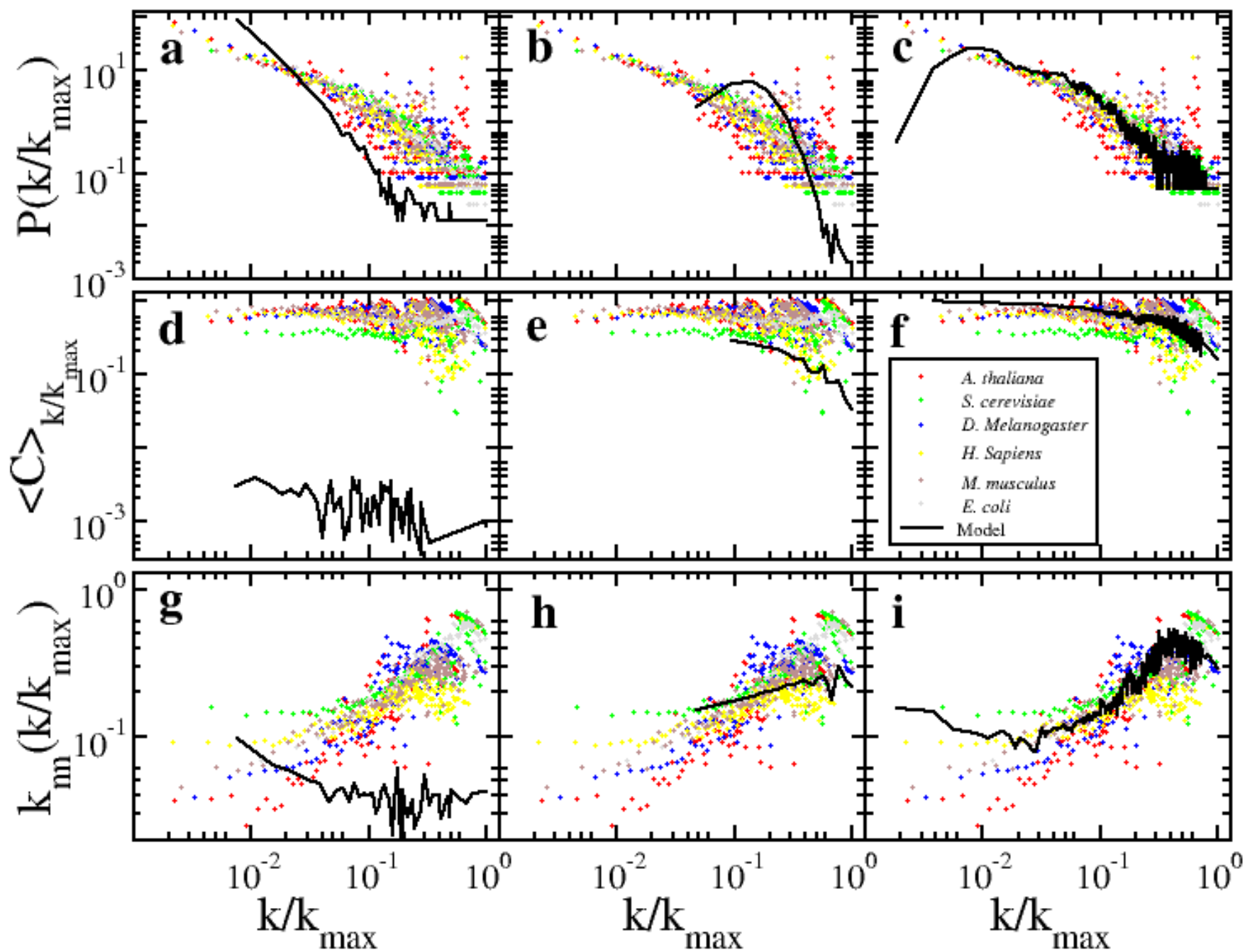




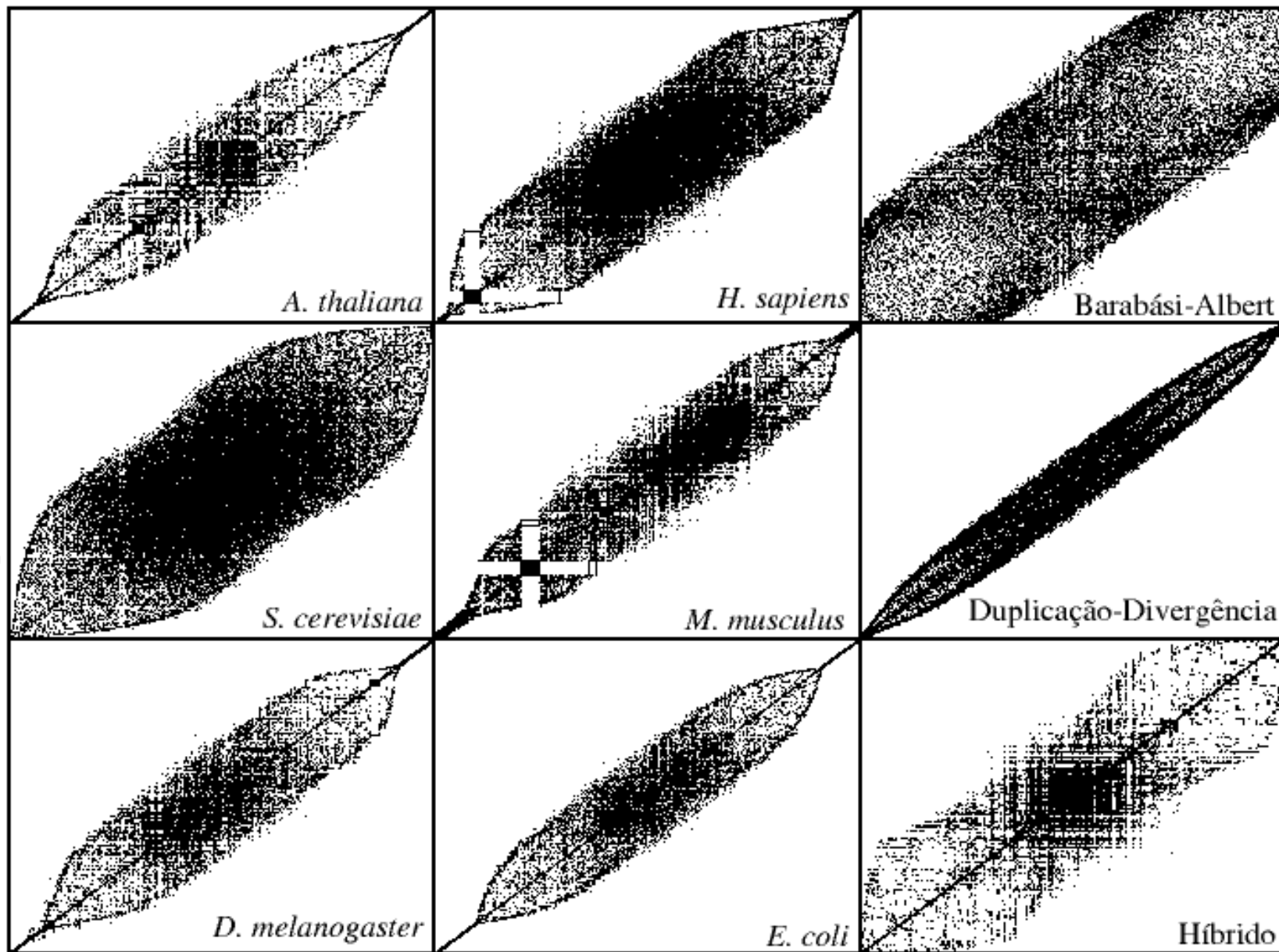
B-A Model

D-D Model

D-A Model



Posição dos Nós



Posição dos Nós

References

- ▶ Castro MAA, Onsten TTG, de Almeida RMC, Moreira JCF. *Journal of Theoretical Biology* 234:487-495. 2005.
- ▶ Mauro A.A. Castro; Verônica A. Grieneisen; Rita M. C.de Almeida, *Cell Biology International* v. 29, n. 11, p. 929-931 (2005)
- ▶ M. A. A. Castro, T. T. G. Onsten, J. C. F Moreira, and R. M. C de Almeida. *Mutation Research. Fundamental and Molecular Mechanisms of Mutagenesis*, v. 600, p. 150-164, 2006.
- ▶ Mauro A. A. Castro, José C. M. Mombach, Rita M. C. de Almeida, and José C. F. Moreira, *Nucleic Acids Res.* 2007; **35** (6):1859-67. Epub 2007 Mar 1.
- ▶ Mauro A. A. Castro^{1,3*}, Rodrigo J. S. Dalmolin^{1*}, José C. F. Moreira¹, José C. M. Mombach⁴ & Rita M. C. de Almeida² , *Evolutionary origins of human apoptosis and genome stability gene networks*, to appear.
- ▶ ViaComplex: software for landscape analysis of gene expression networks in genomic context, Mauro A. A. Castro, José L. Rybarczyk Filho, Rodrigo J. S. Dalmolin, Marialva Sinigaglia, José C. F. Moreira, José C. M. Mombach e Rita M. C. de Almeida, *Bionformatics*, accepted for publication (2009).
- ▶ *Rybarczyk et al. Nucl. Acids Res.* (2010) doi: 10.1093/nar/gkq1269 First published online: December 15, 2010