

# Artificial networks

- Random: for  $N$  genes, randomly choose  $M$  pairs  $(i,j)$  of genes.
- Barabasi-Albert: start with  $N_0$  genes connected with one another. Complete  $M$  interaction by choosing the interacting genes with a probability that goes as its connectivity.

# A matriz de interações

- Enumeram-se as proteínas
- Constrói-se a matriz de interações  $M_{ij}$  de tal maneira que

$M_{ij}=1$  se  $i$  e  $j$  interagem

$M_{ij}=0$  se  $i$  e  $j$  não interagem

# Objetivos

- Encontrar sistemas  $\rightarrow$  diagonal por blocos.
- Sem blocos, mas com a maior região possível sem interações.

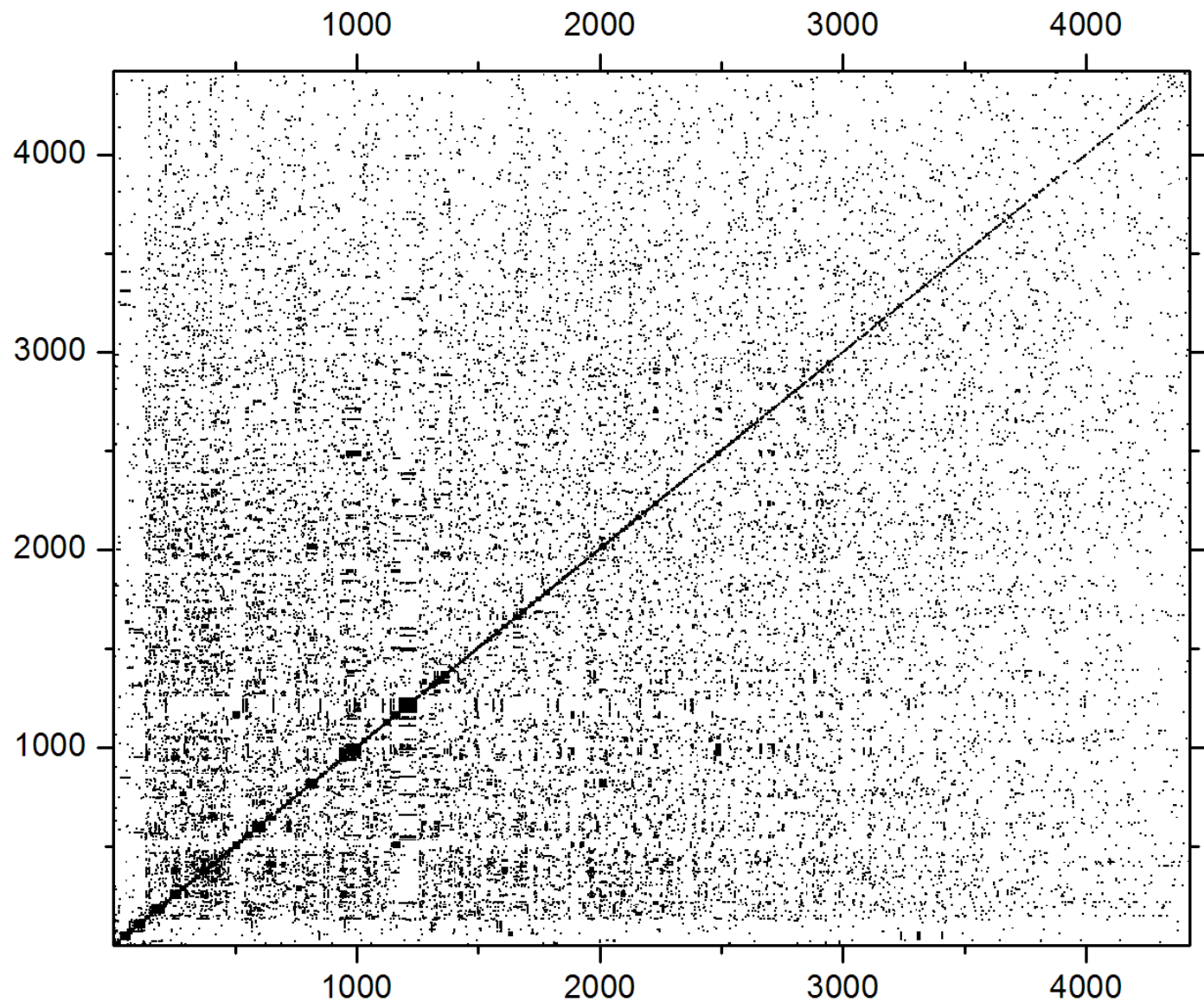
# Estratégias

- Associamos uma energia a cada configuração da matriz:

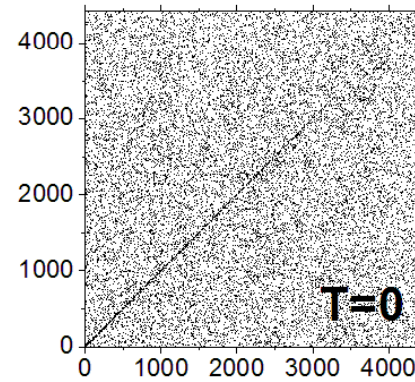
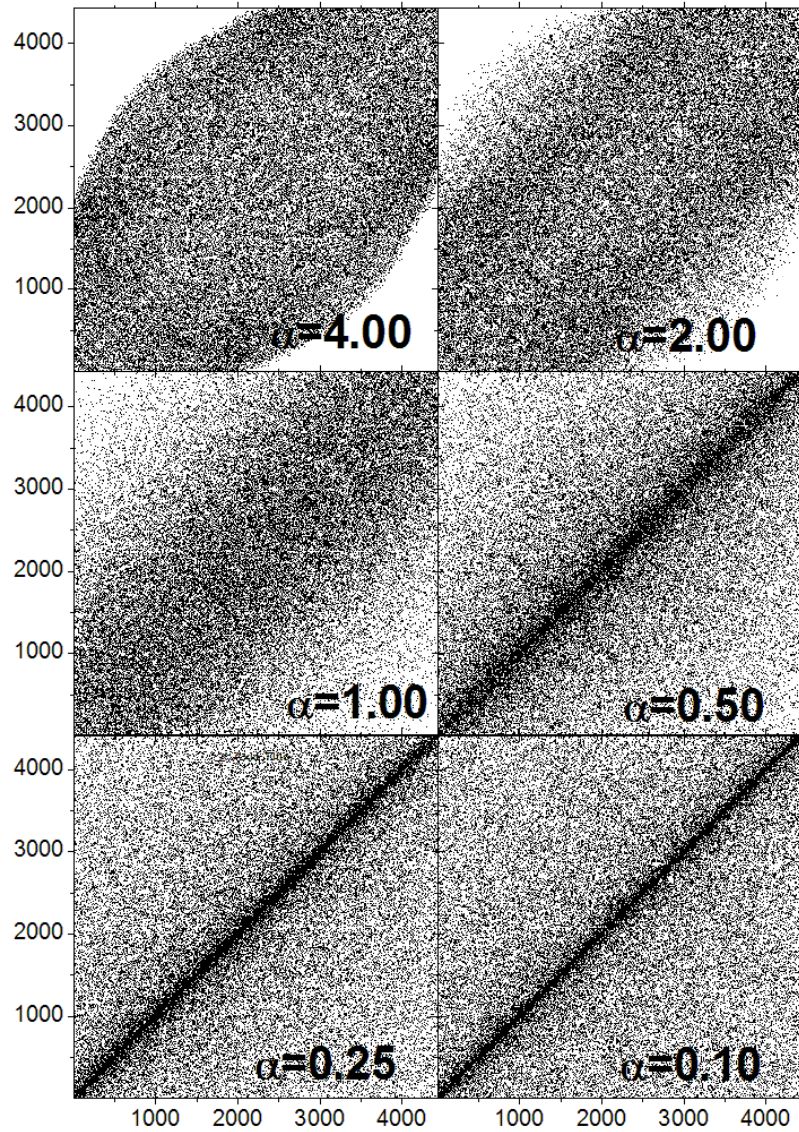
$$E = \sum_{ij}^N (i^2 - j^2)^\alpha [4 - \delta(S_{i,j} - S_{i+1,j}) - \delta(S_{i,j} - S_{i-1,j}) - \delta(S_{i,j} - S_{i,j+1}) - \delta(S_{i,j} - S_{i,j-1})]$$

- Escolhemos dois rótulos ao acaso, trocamos as proteínas de lugar, reobtemos a matriz e sua energia.
- Se a nova energia é menor a troca é aceita
- Caso contrário, volta-se à configuração inicial
- Repete-se o procedimento

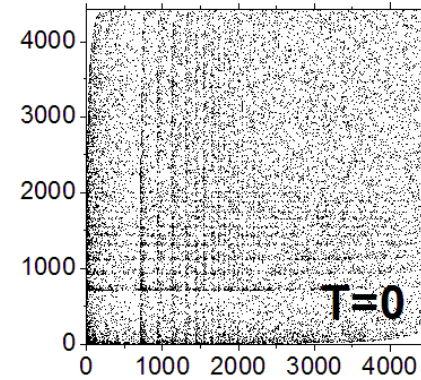
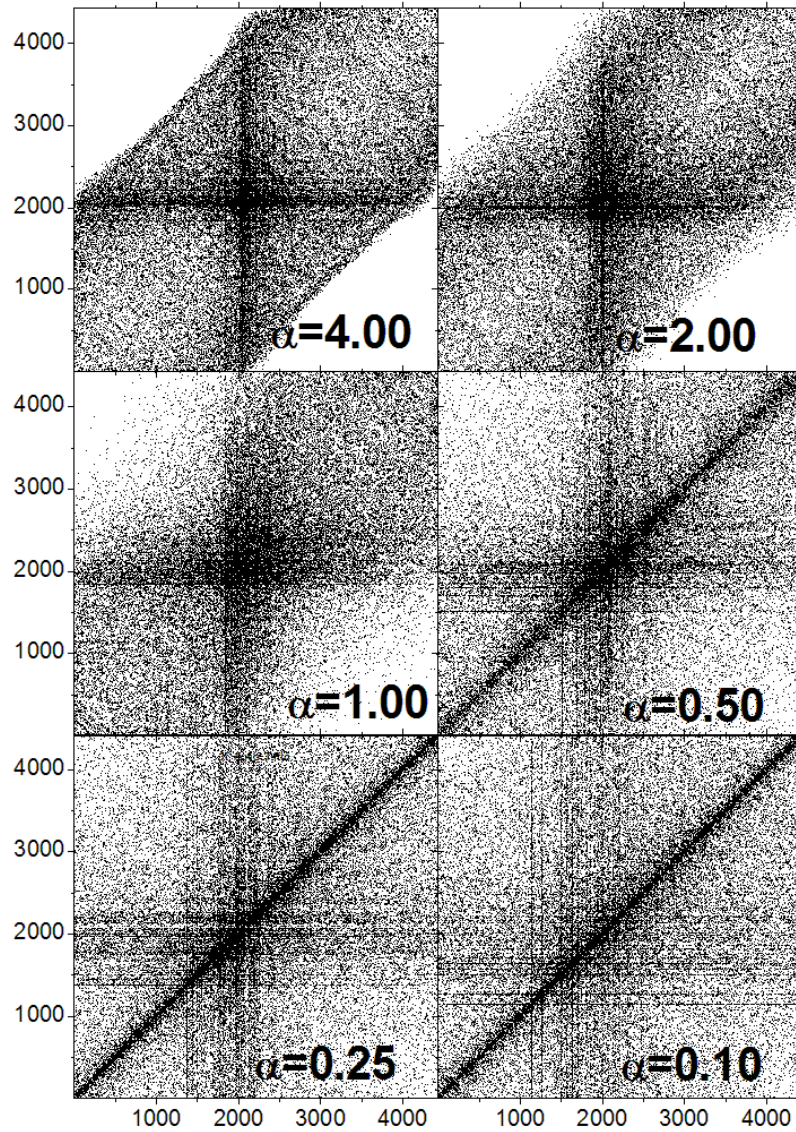
Como rotas foram escolhidas? Não haveria outras?



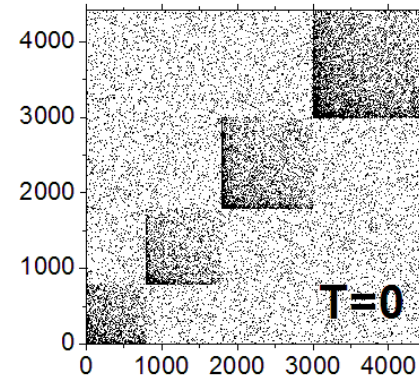
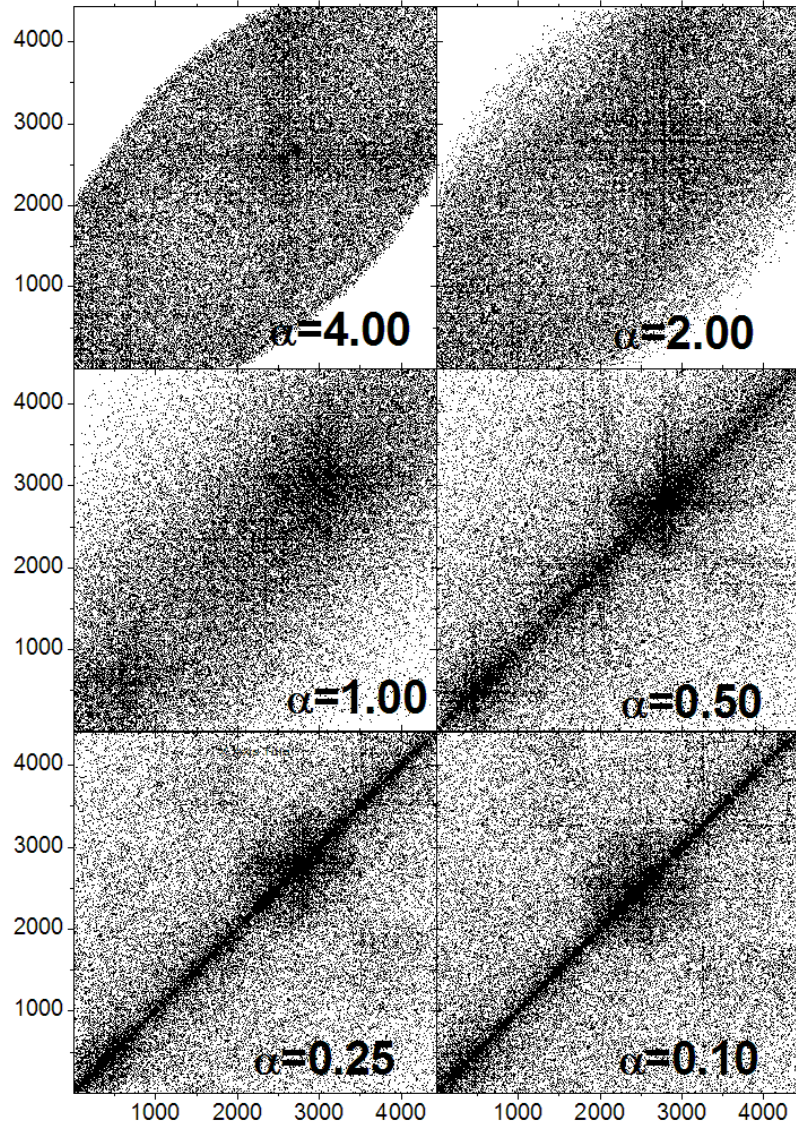
# Random



# Barabasi

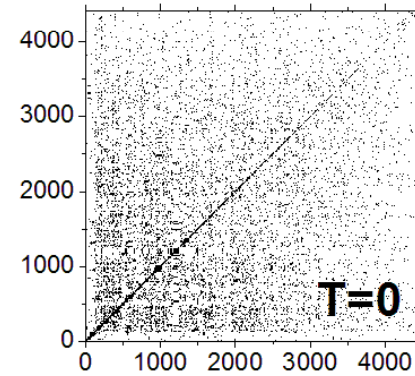
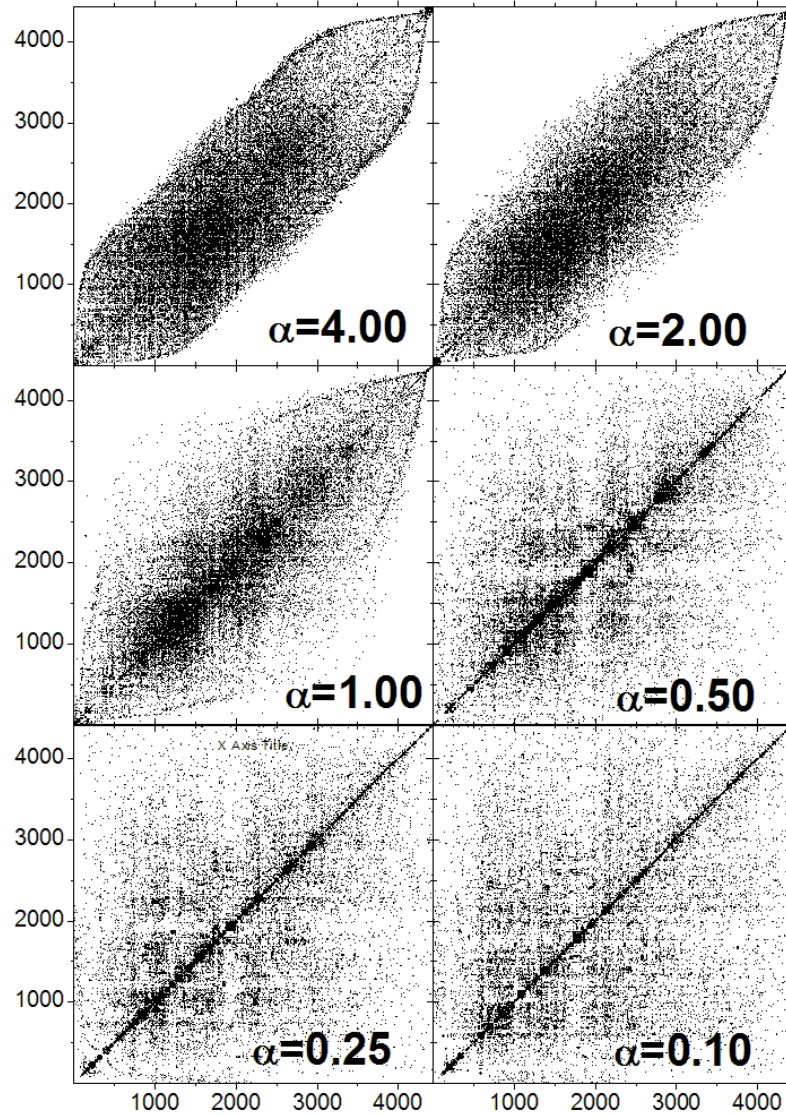


# Barabasi-Randomico

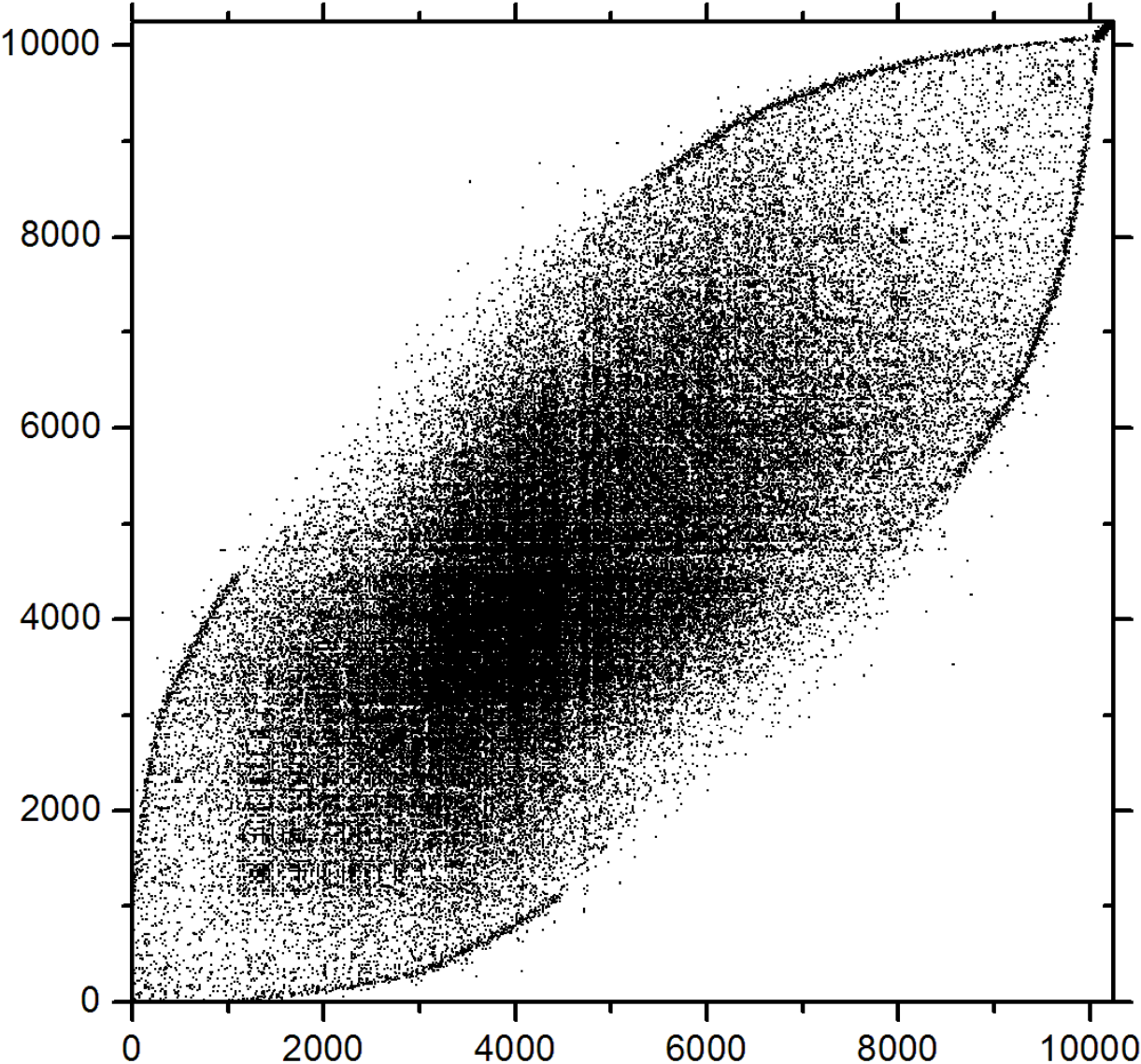




# Prod-Saccharomyces



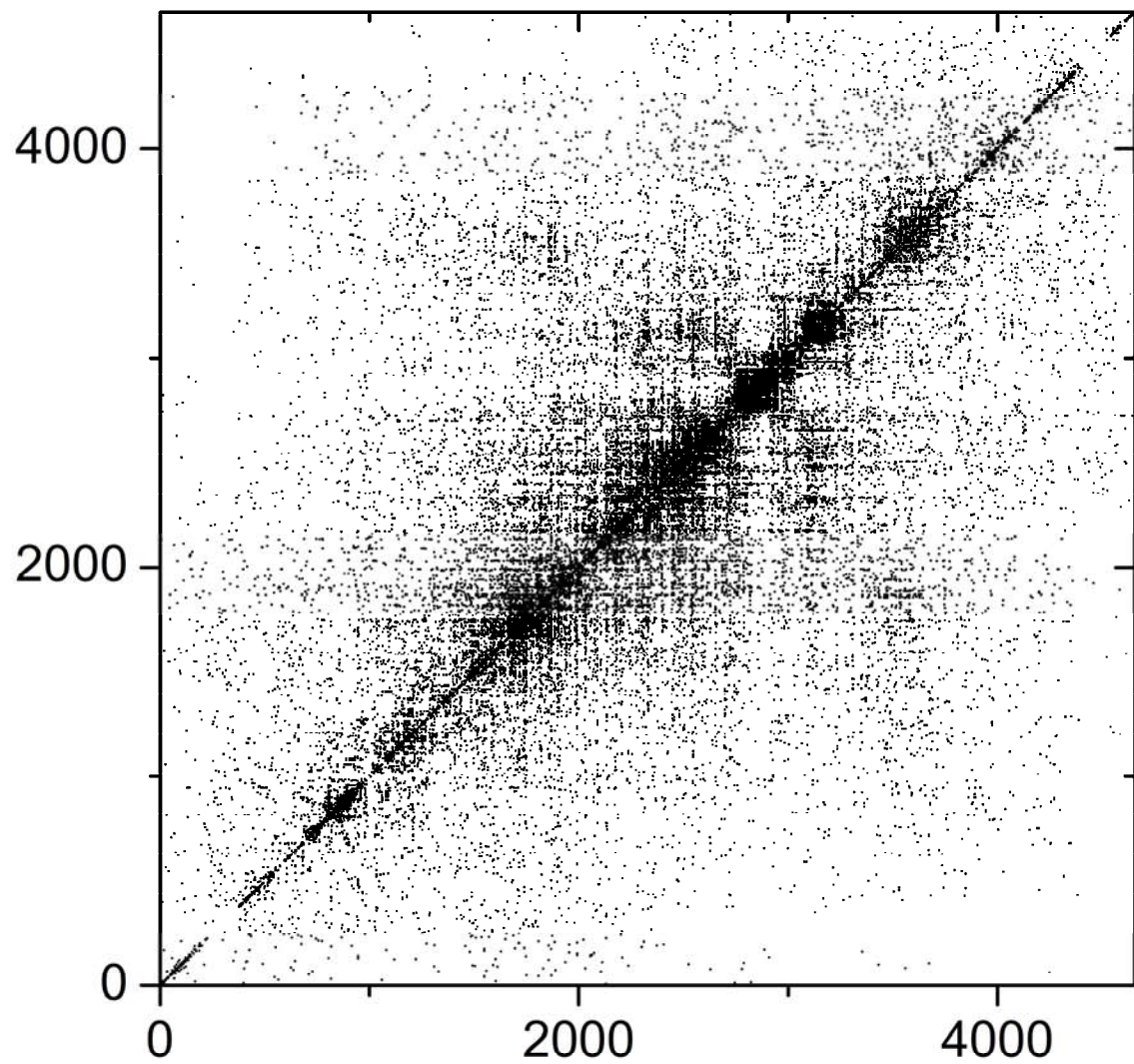
Homo sapiens



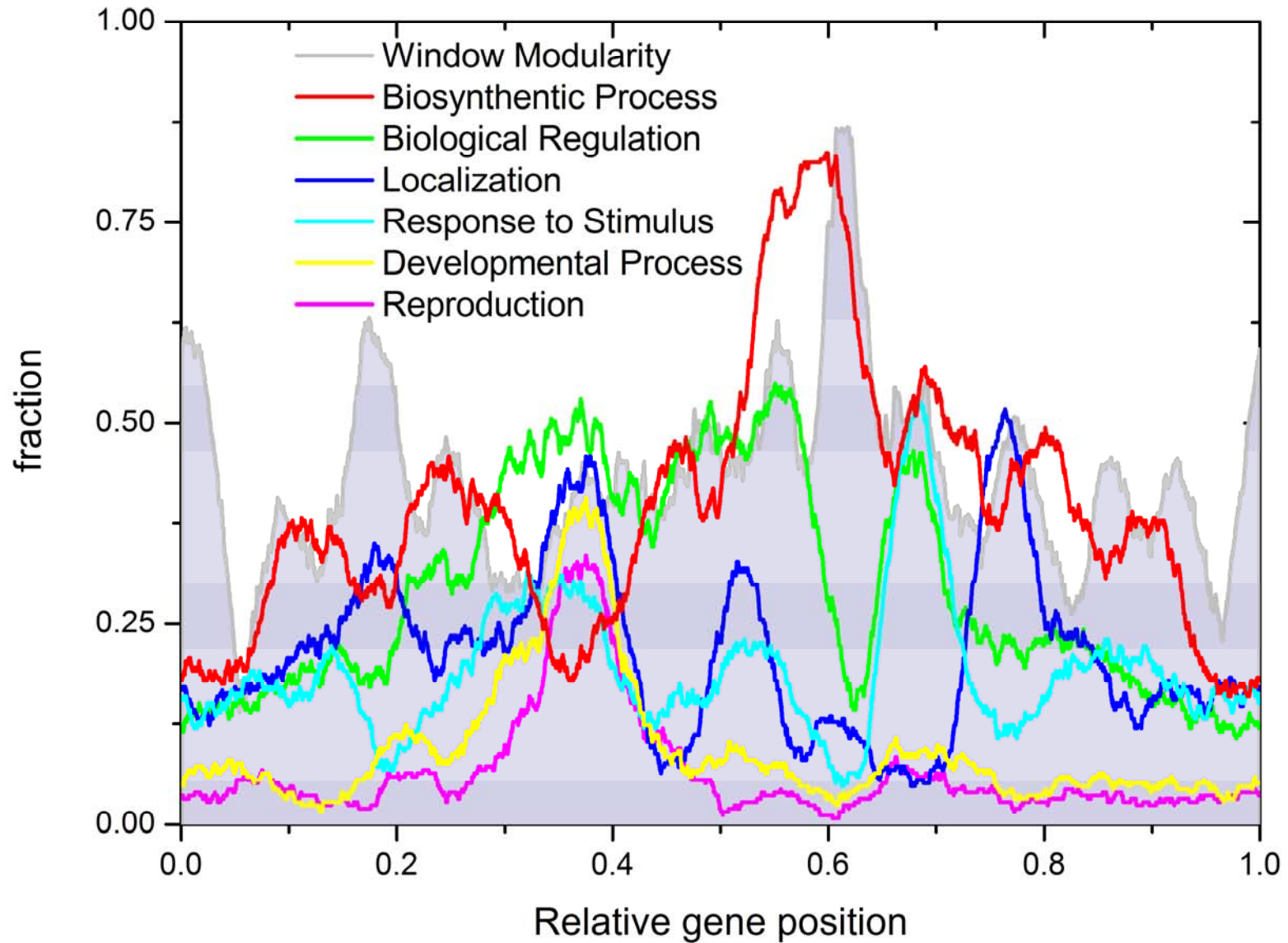
# E agora?

- Dois objetivos:
  - Diagnóstico, análise funcional
  - Evolução

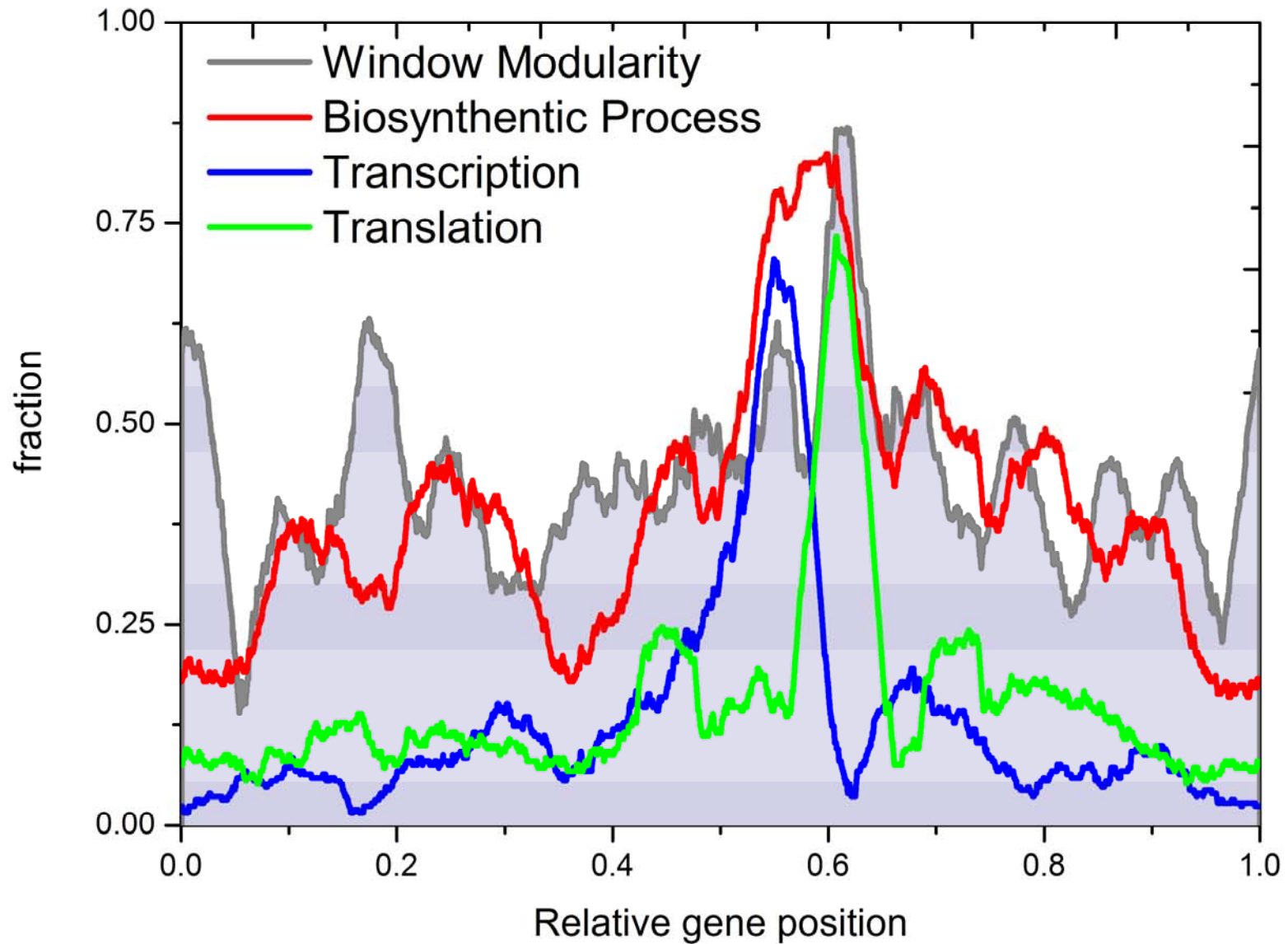
$\alpha=0.50$



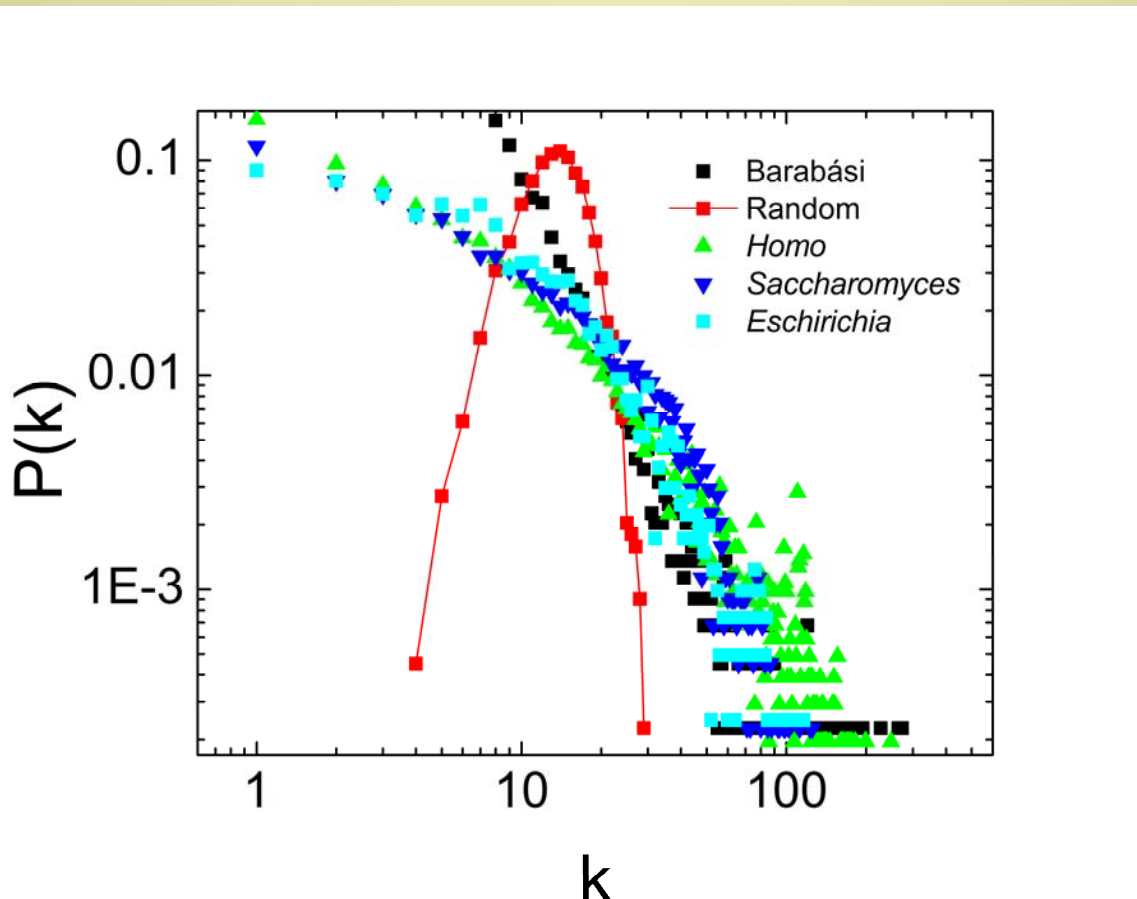
$\alpha=0.5$  window=251



$\alpha=0.5$  window=251



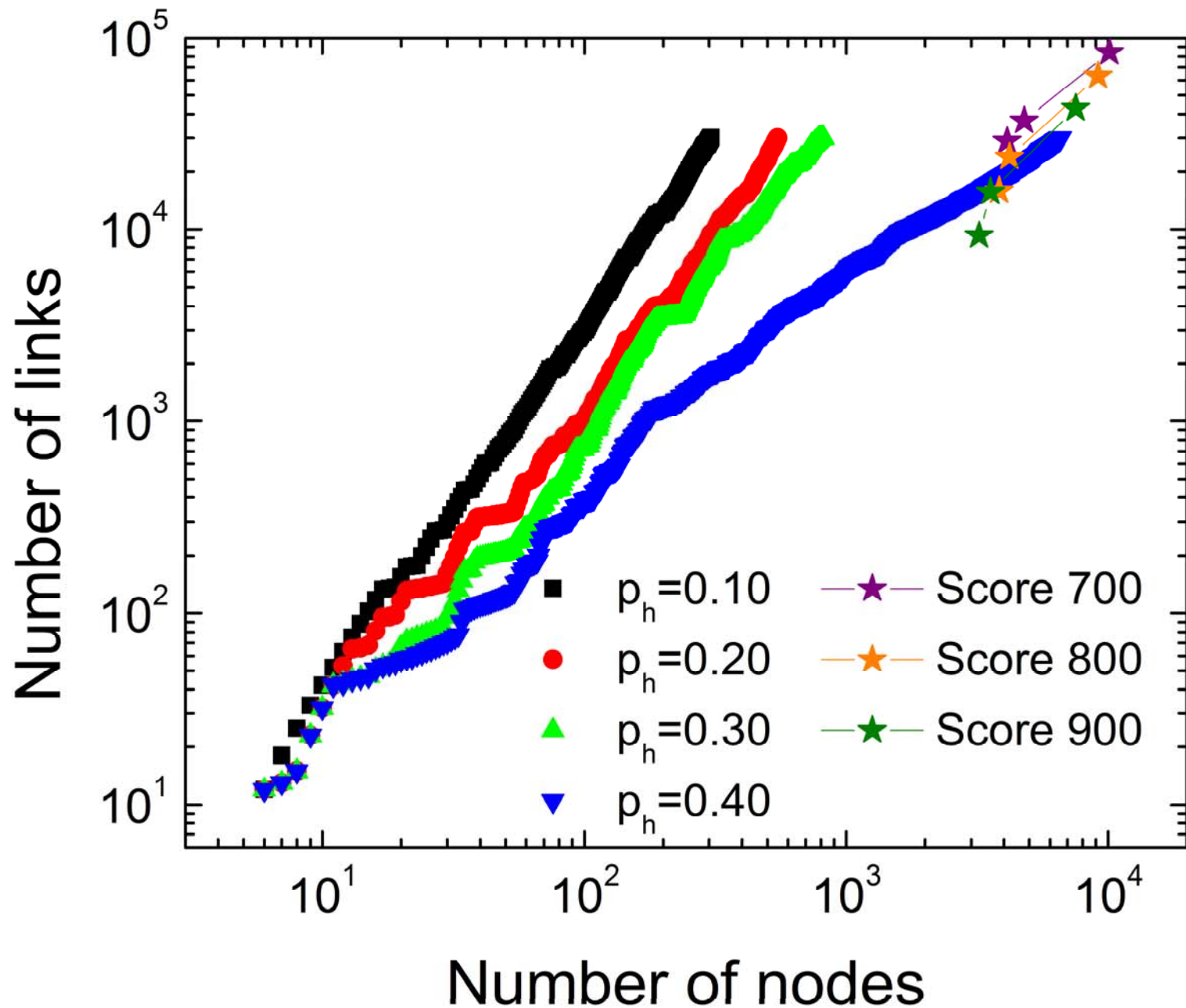
# Distribuição de grau de conectividade

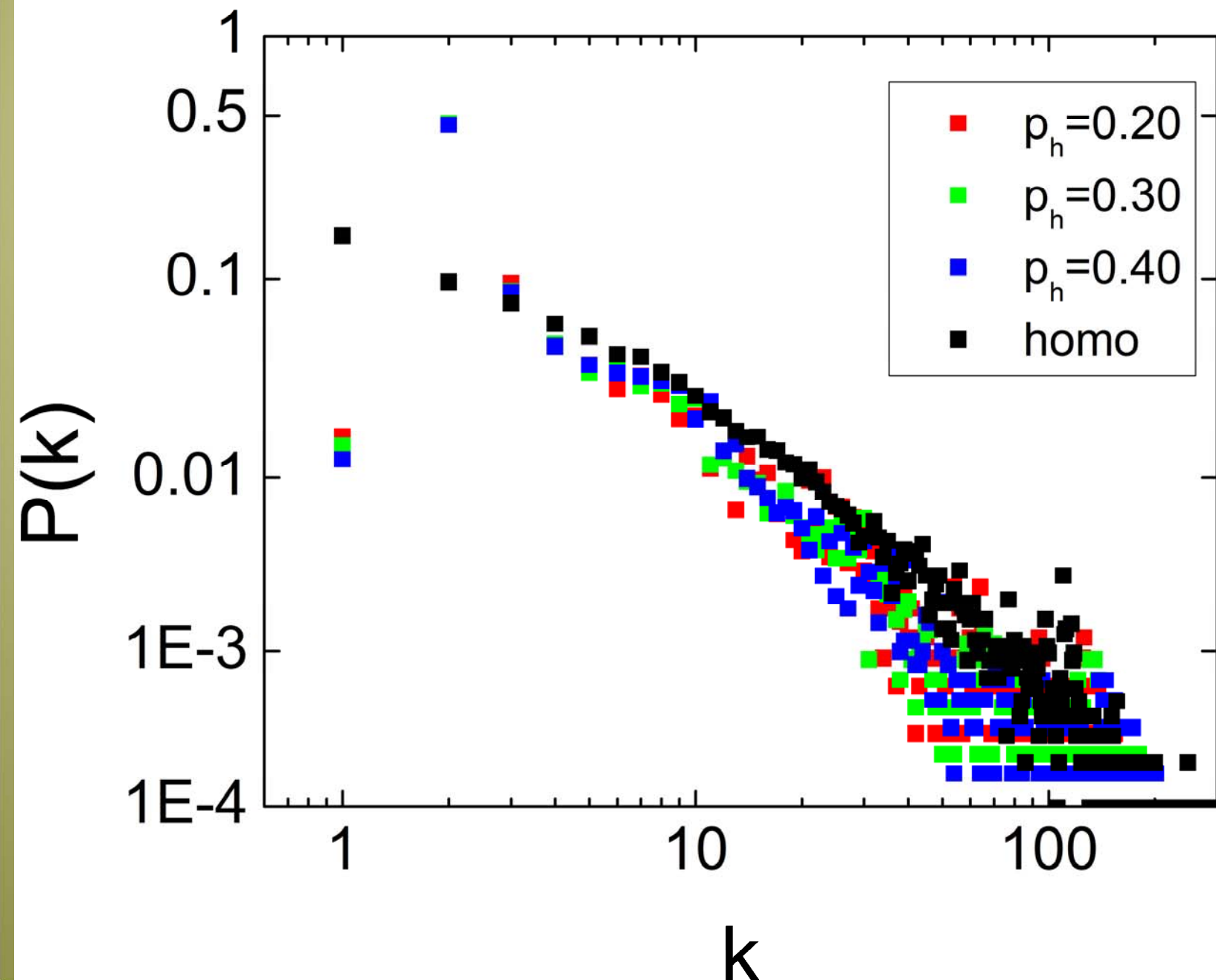


# Como os genes são adquiridos?

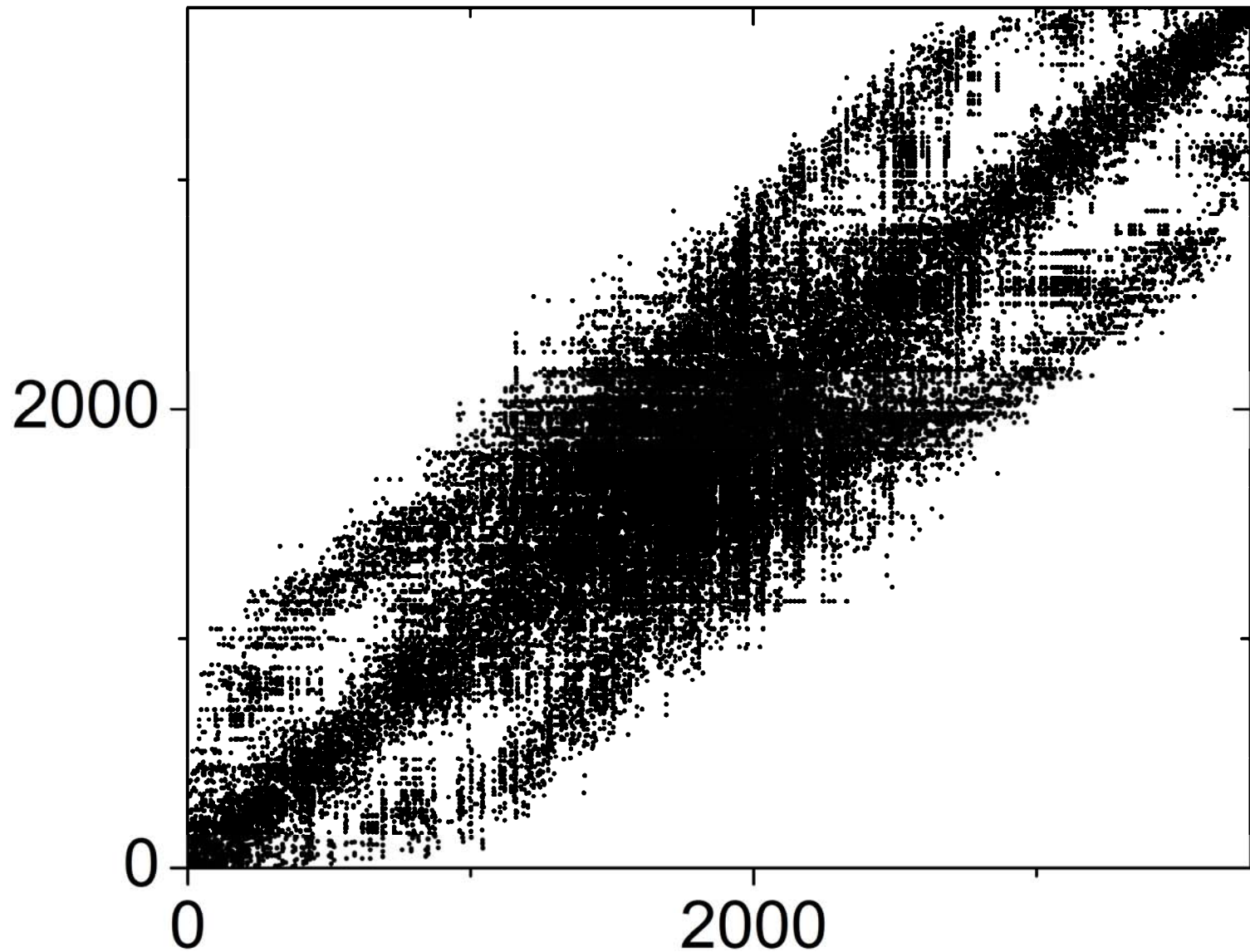
- Aquisição aleatória
- Duplicação (seguida de mutação):
  - $p_h$  : probabilidade de que o novo gene seja aleatório → receita do Barabási
  - $1-p_h$  : probabilidade de mutação → genes menos clusterizados e com menor grau de conectividade têm mais probabilidade de se duplicarem







$p_h = 0.25$     $\alpha = 4.00$



# GNATT: A tool to analyze gene networks

- Considers different databases: NIH/NCBI, KEGG, EMBL, Sanger, etc.
- Deals with different nomenclatures
- Constructs partial gene networks
- Analyzes expression data
- Searches for functional moduli
- Identifies different functions
- Globally organizes gene networks
- Network characterization

# 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<sup>1,3\*</sup>, Rodrigo J. S. Dalmolin<sup>1\*</sup>, José C. F. Moreira<sup>1</sup>, José C. M. Mombach<sup>4</sup> & Rita M. C. de Almeida<sup>2</sup>, *Evolutionary origins of human apoptosis and genome stability gene networks*, to appear.

Obrigada pela atenção!