Network analysis
from Babelomics 5

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José Carbonell Caballero

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- Some exercises
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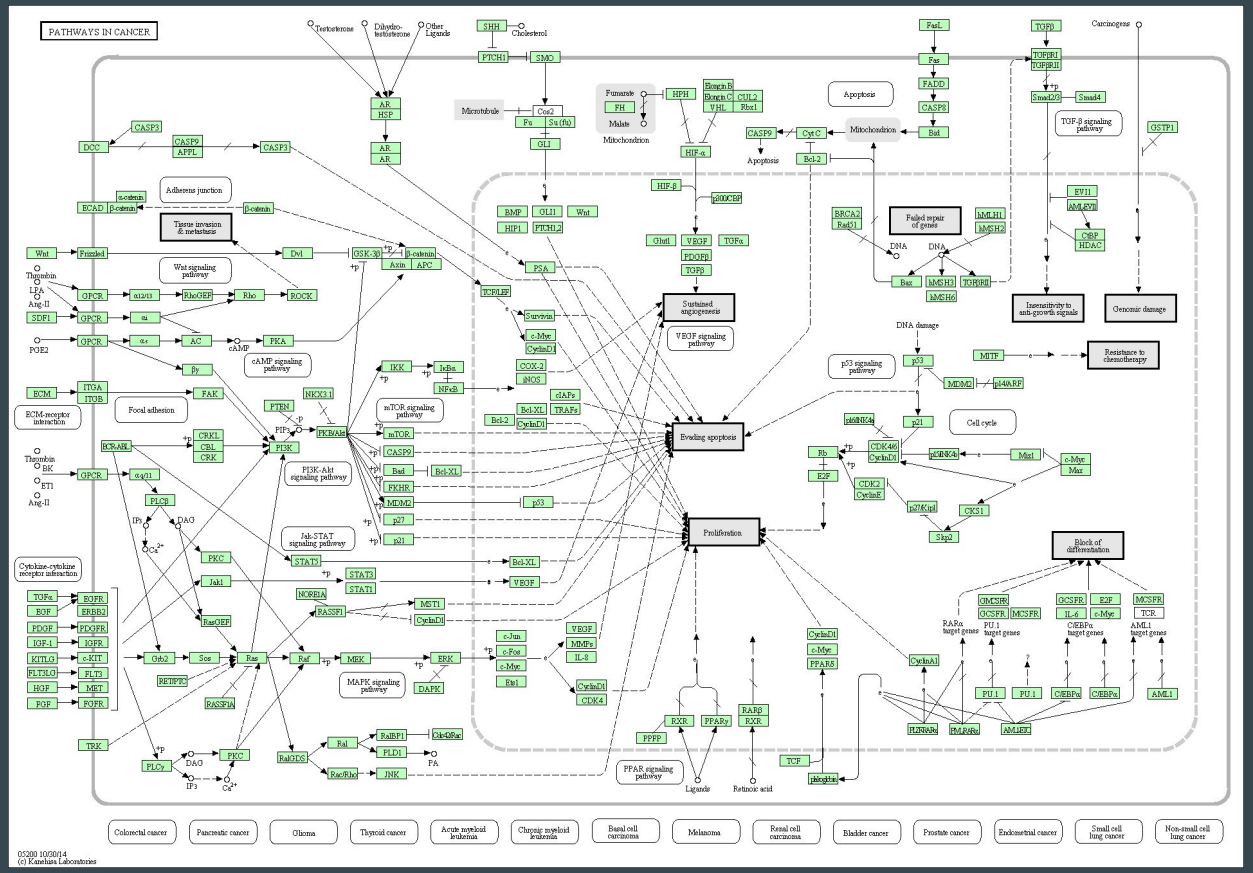
- Some exercises
- Exercises

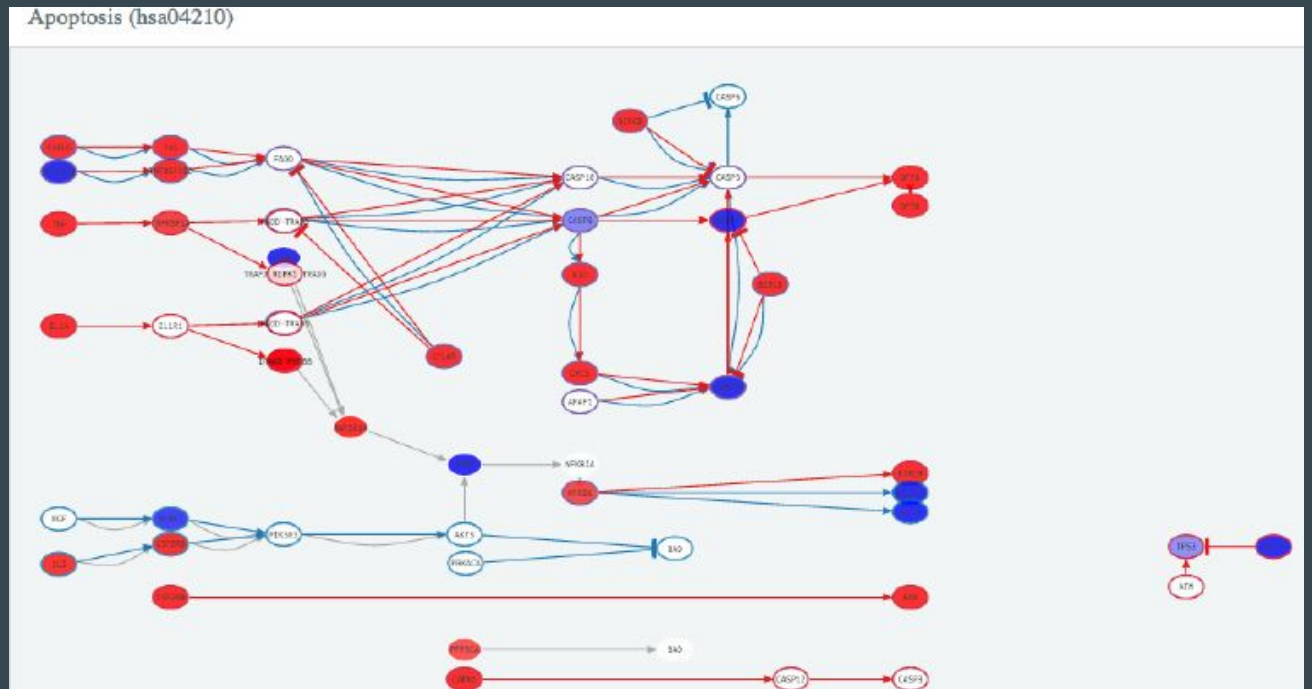
Networks in molecular biology

- Systems biology is the clue
  - Complex biological systems are mathematically modelled as a whole



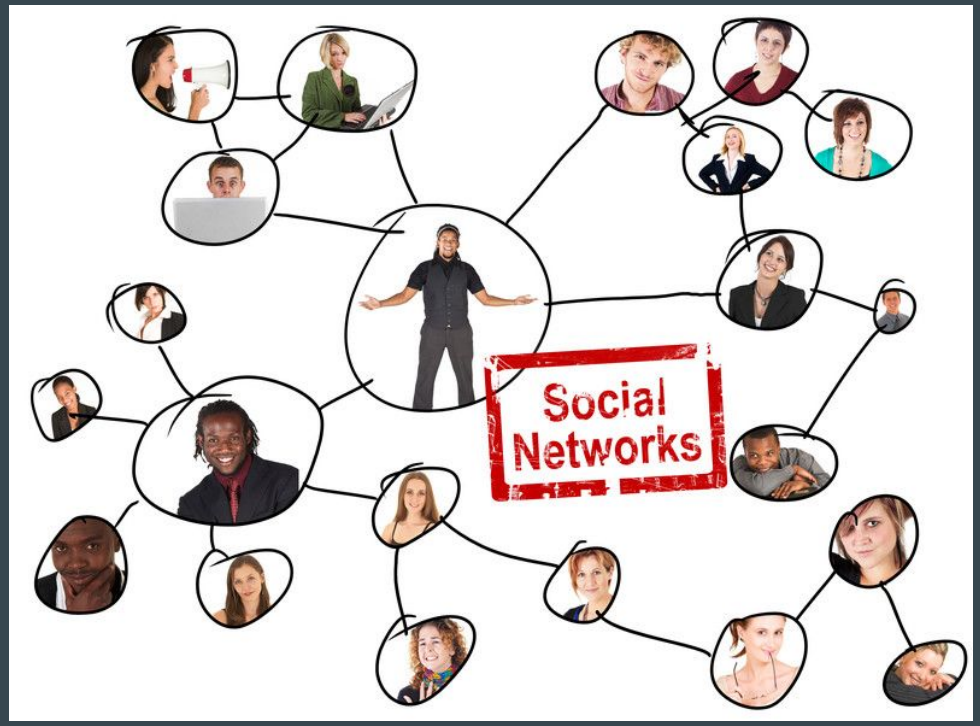
Networks in molecular biology

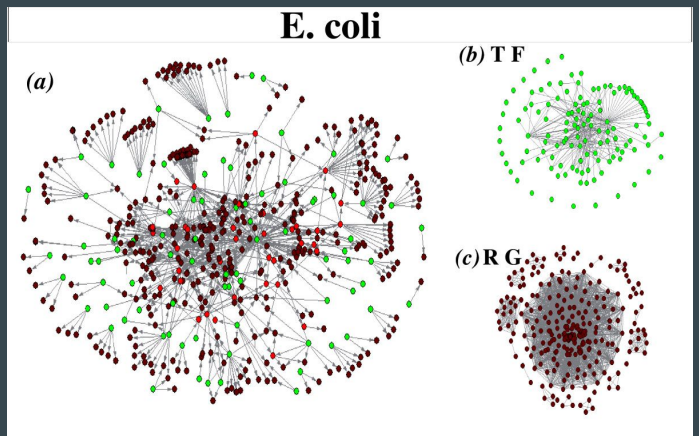
- ...some derived concepts
  - How the system is impaired rather than its elements
  - Explain origin of diseases
  - Face gene heterogeneity



Networks in molecular biology

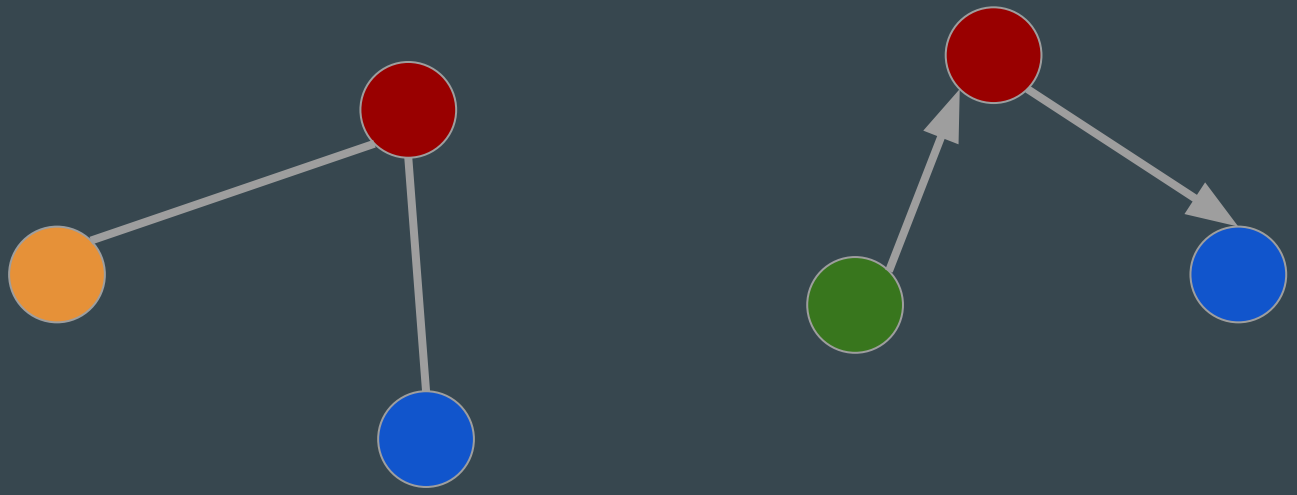
- Networks are extremely useful to represent different systems and their inner interactions elements





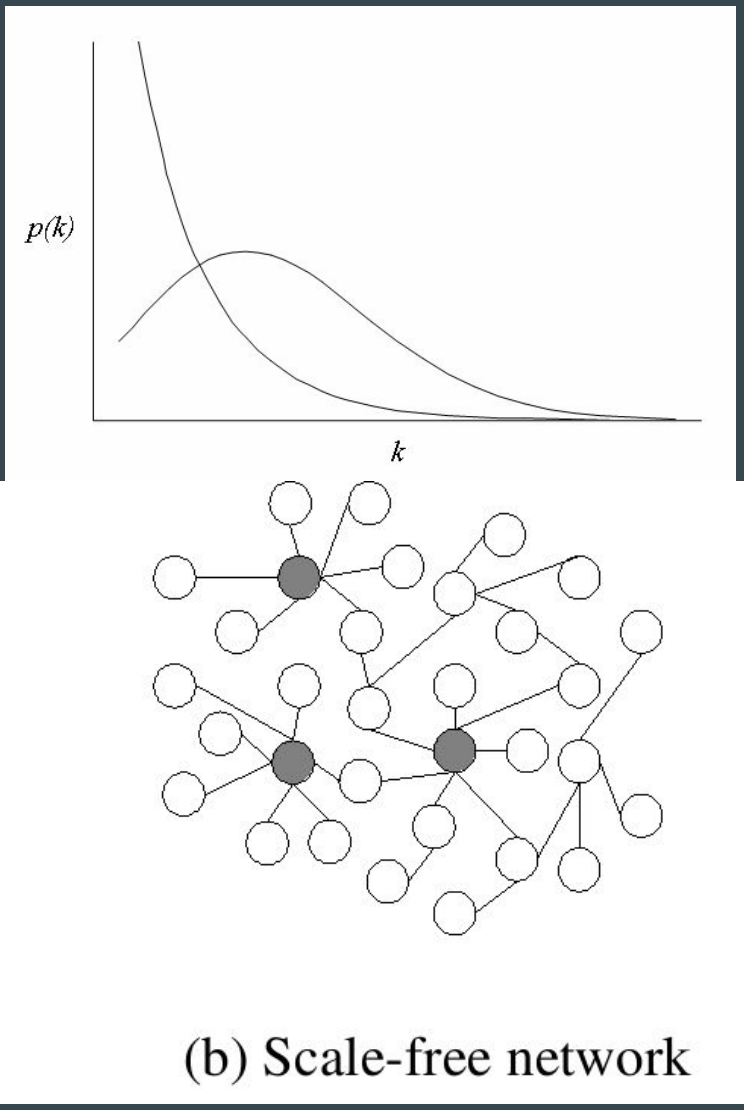
Networks in molecular biology

- Knowledge is represented as a graph
  - Proteins are the vertices
  - Interactions are the edges



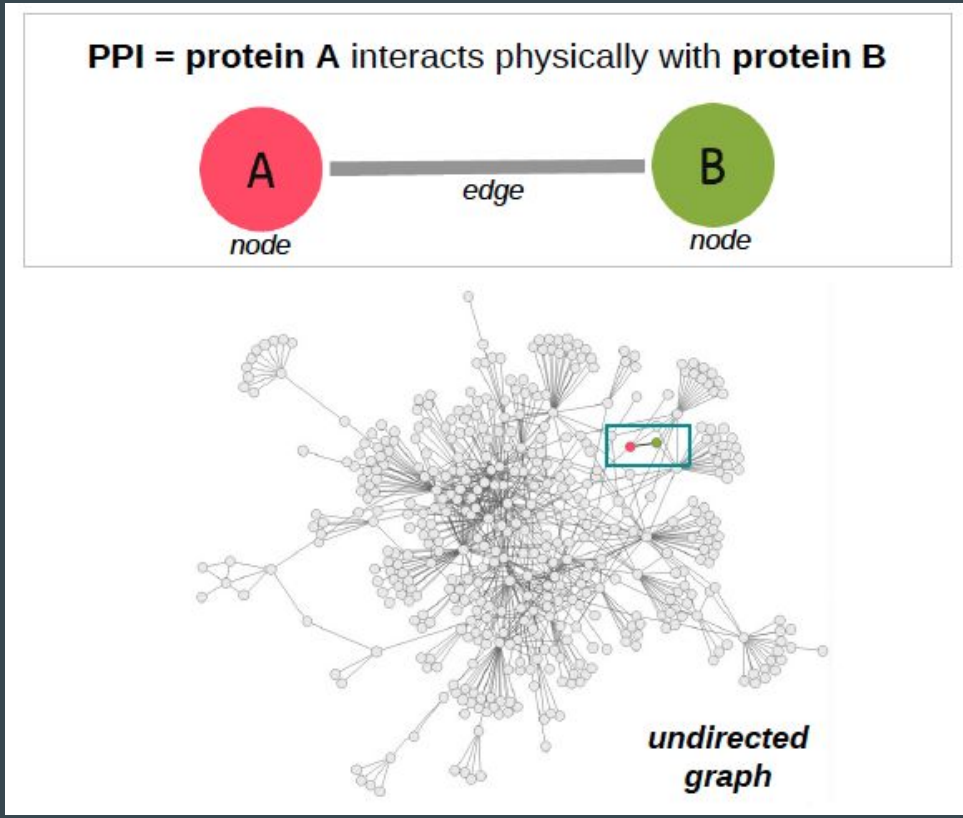
Networks in molecular biology

- Biological networks
  - Scale-free (power law)



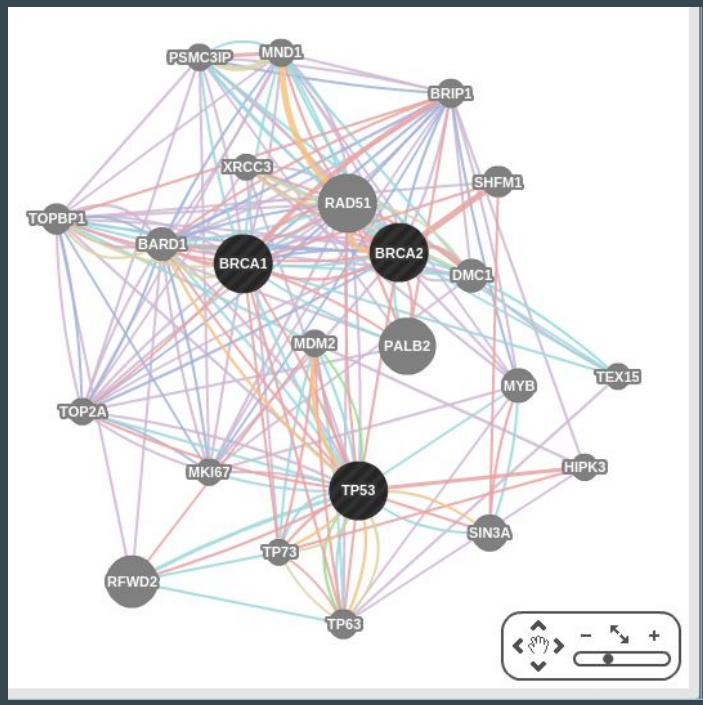
Networks in molecular biology

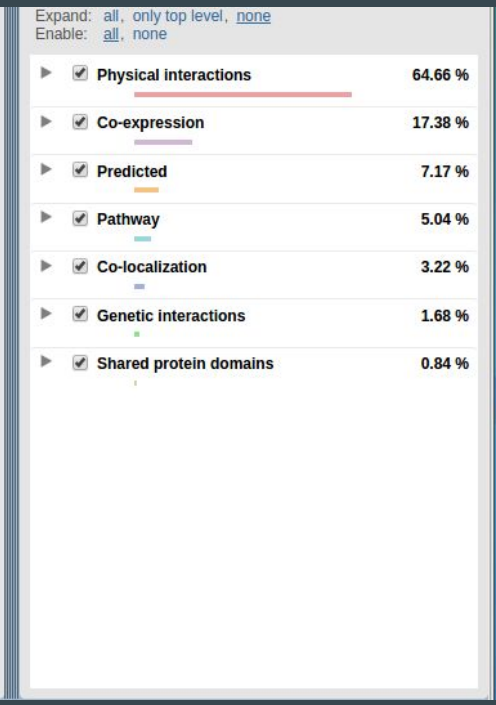
- Types of networks (aka interactomes)
  - Protein-protein interactions



Networks in molecular biology

- Types of networks (aka interactomes)
  - Post-translational modifications
  - Coexpression
  - Functional terms
  - ...

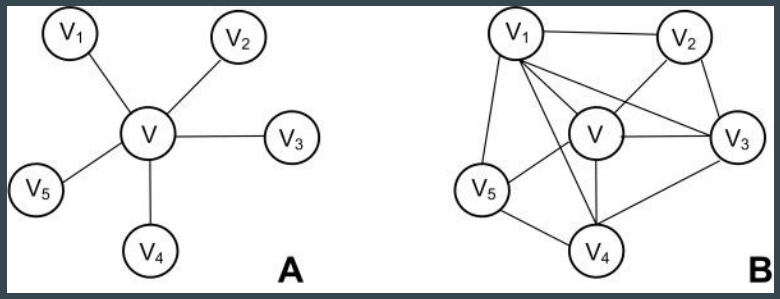




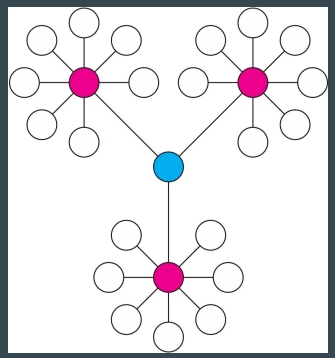
Networks in molecular biology

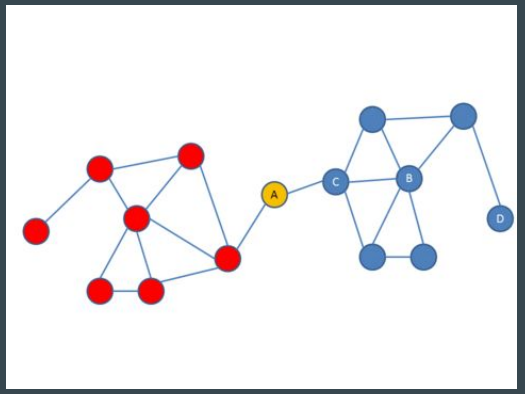
Network are evaluated through some parameters:

- At a network level:
  - Number of components
  - Clustering coefficient



- At a gene level:
  - Closeness centrality
  - Betwenness centrality
  - Degree





Networks in molecular biology

Disease-gene prioritization approaches

ARTICLE

Walking the Interactome for Prioritization of Candidate Disease Genes

Sebastian Köhler,[1,2] Sebastian Bauer,[1,2] Denise Horn,[1] and Peter N. Robinson[1,*]

The identification of genes associated with hereditary disorders has contributed to improving medical care and to a better understanding of gene functions, interactions, and pathways. However, there are well over 1500 Mendelian disorders whose molecular basis remains unknown. At present, methods such as linkage analysis can identify the chromosomal region in which unknown disease genes are located, but the regions could contain up to hundreds of candidate genes. In this work, we present a method for prioritization of candidate genes by use of a global network distance measure, random walk analysis, for definition of similarities in protein-protein interaction networks. We tested our method on 110 disease-gene families with a total of 783 genes and achieved an area under the ROC curve of up to 98% on simulated linkage intervals of 100 genes surrounding the disease gene, significantly outperforming previous methods based on local distance measures. Our results not only provide an improved tool for positional-cloning projects but also add weight to the assumption that phenotypically similar diseases are associated with disturbances of subnetworks within the larger protein interactome that extend beyond the disease proteins themselves.

Bioinformatics Advance Access published July 30, 2014

Walking the interactome for candidate prioritization in exome sequencing studies of Mendelian diseases

Damian Smedley [1,†], Sebastian Köhler [2,†], Johanna Christina Czeschik [3], Joanna Amberger [4], Carol Bocchini [4], Ada Hamosh [4], Julian Veldboer [2,5], Tomasz Zemojtel [2,6], and Peter N Robinson [2,5,7,8*]

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BRIEFINGS IN FUNCTIONAL GENOMICS. VOL 10. NO 5. 280–293 doi:10.1093/bfgp/elr024

Network-based methods for human disease gene prediction

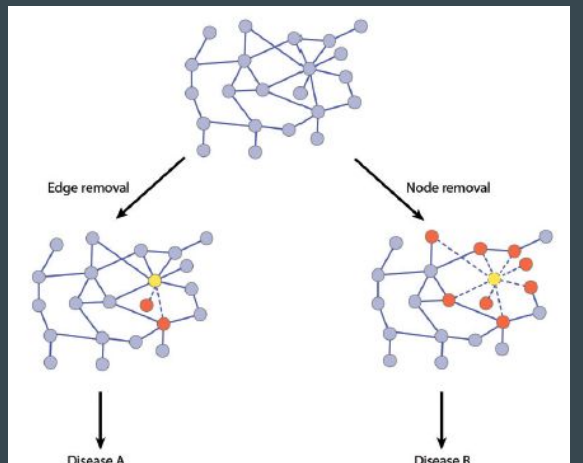
Xiujuan Wang, Natali Gulbahce and Haiyuan Yu

Advance Access publication date 15 July 2011

Abstract

Despite the considerable progress in disease gene discovery, we are far from uncovering the underlying cellular mechanisms of diseases since complex traits, even many Mendelian diseases, cannot be explained by simple genotype–phenotype relationships. More recently, an increasingly accepted view is that human diseases result from perturbations of cellular systems, especially molecular networks. Genes associated with the same or similar diseases commonly reside in the same neighborhood of molecular networks. Such observations have built the basis for a large collection of computational approaches to find previously unknown genes associated with certain diseases. The majority of the methods are based on protein interactome networks, with integration of other large-scale genomic data or disease phenotype information, to infer how likely it is that a gene is associated with a disease. Here, we review recent, state of the art, network-based methods used for prioritizing disease genes as well as unraveling the molecular basis of human diseases.

Keywords: *human diseases; disease network; disease gene prediction; protein–protein interaction; molecular network*

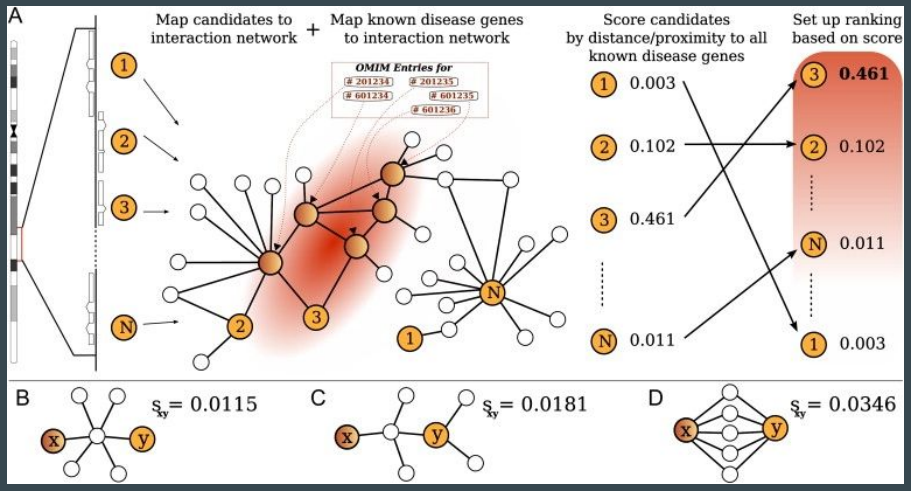


Networks in molecular biology

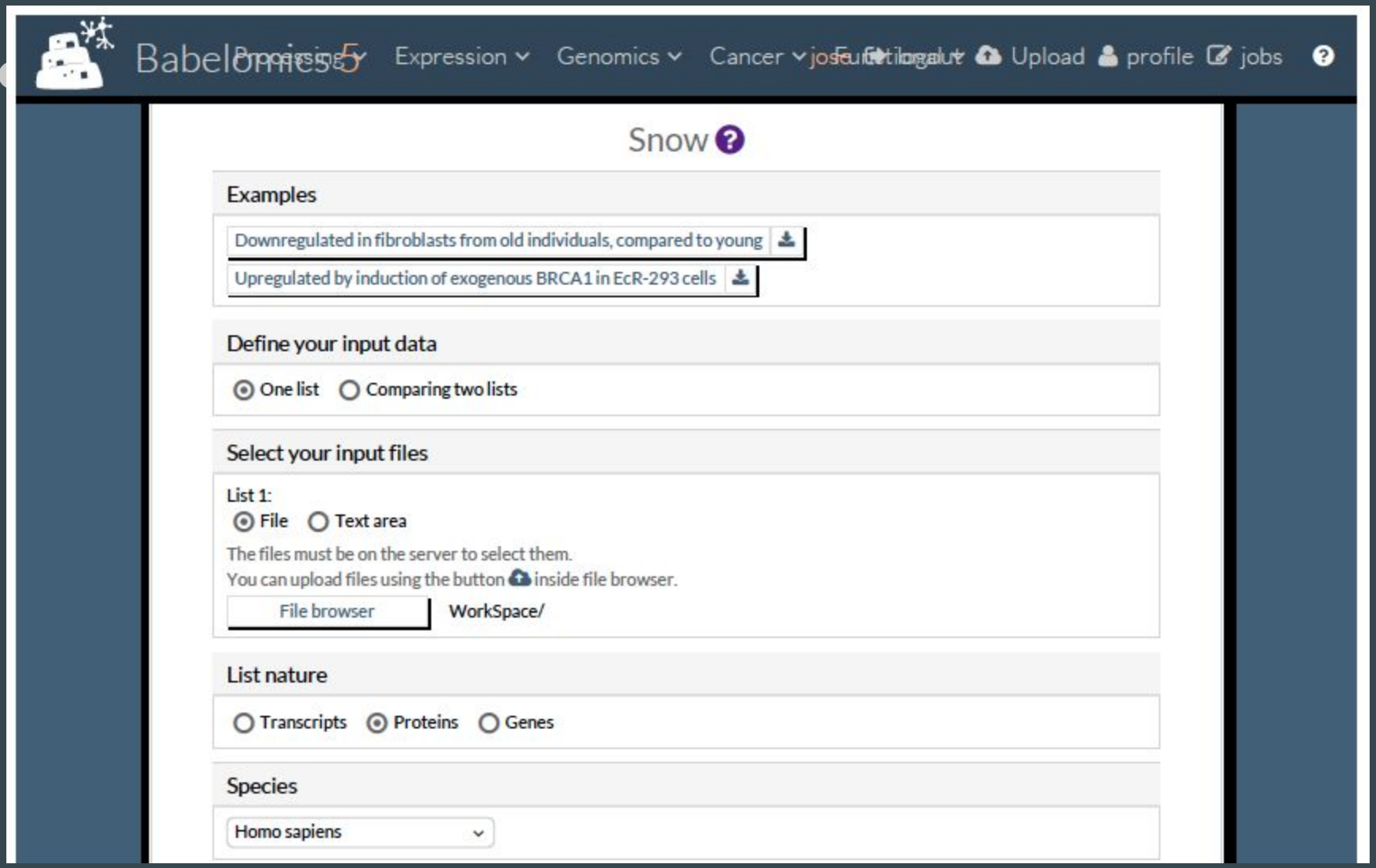
Gene prioritization approaches

Endeavour

exomewalker

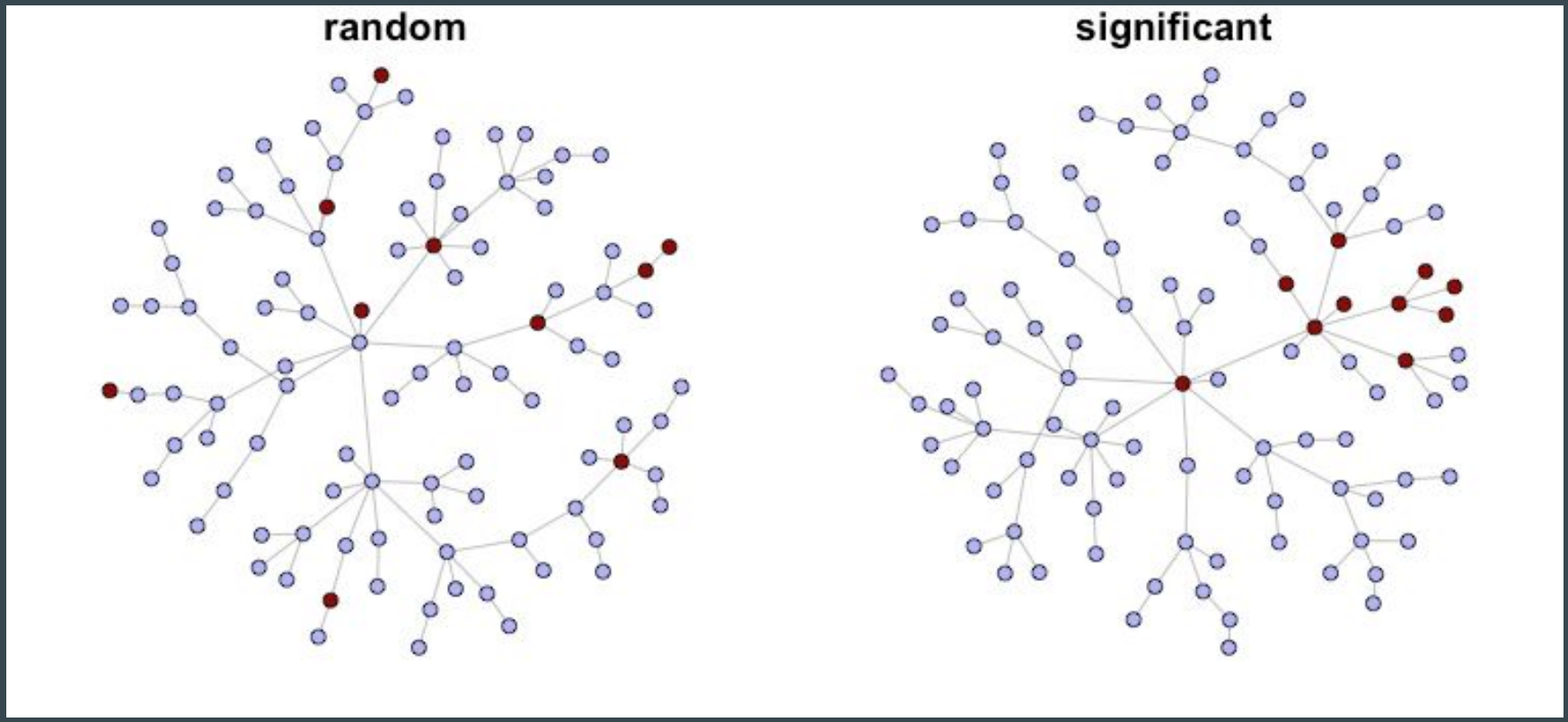


Network enrichment (SNOW)

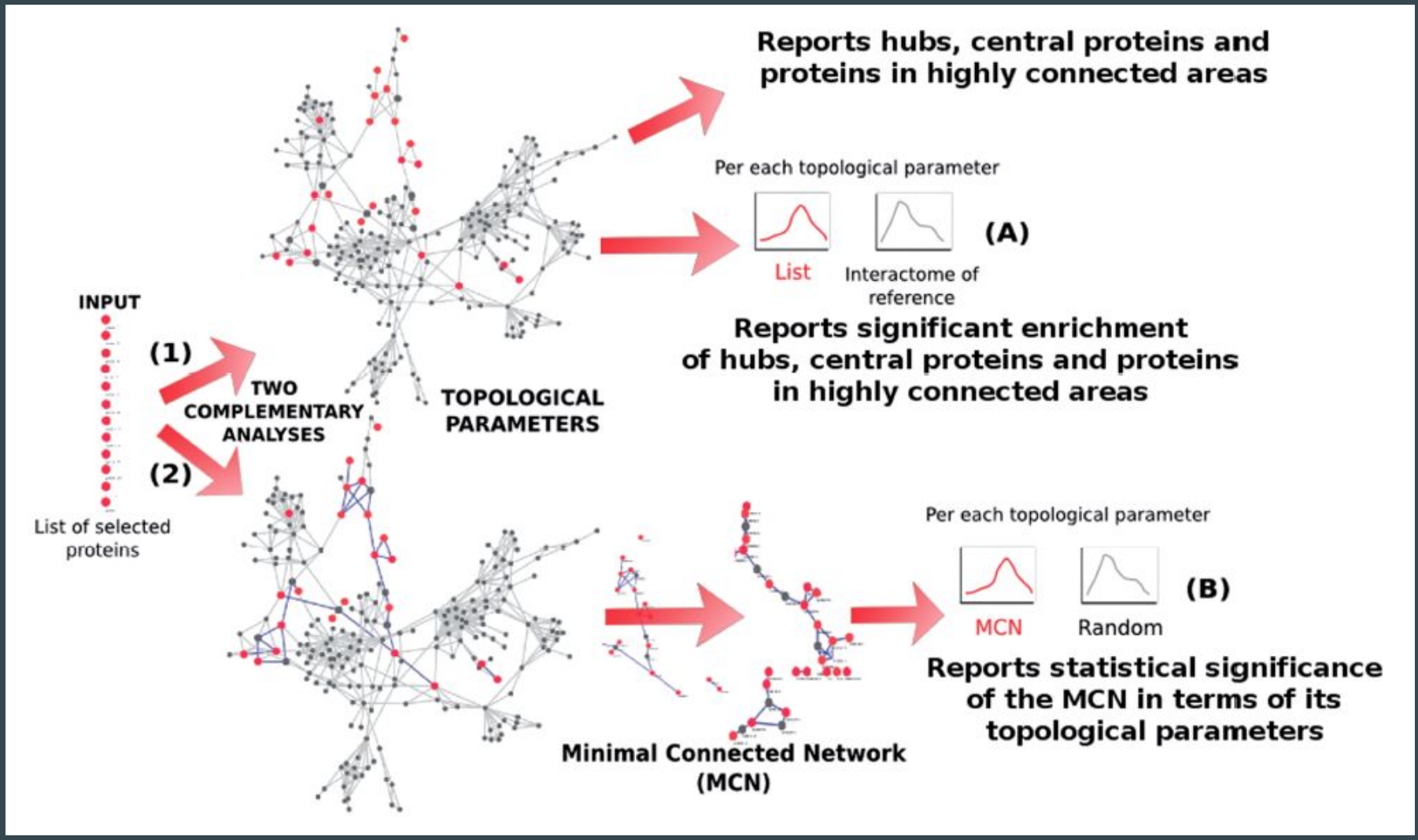


Network enrichment (SNOW)

- GOAL: it determines whether a set of input genes represents a biologically meaningful network

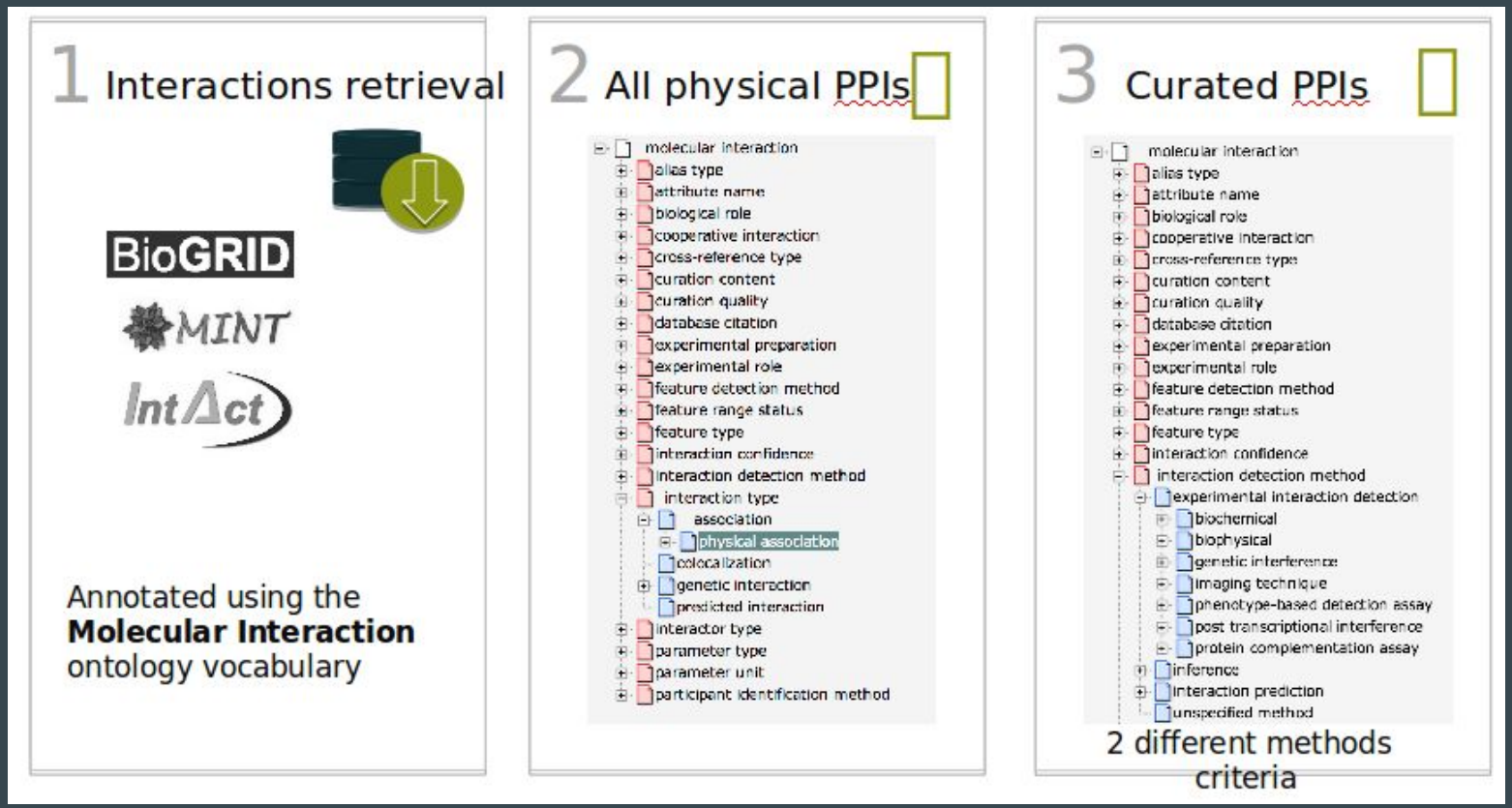


Network enrichment (SNOW)

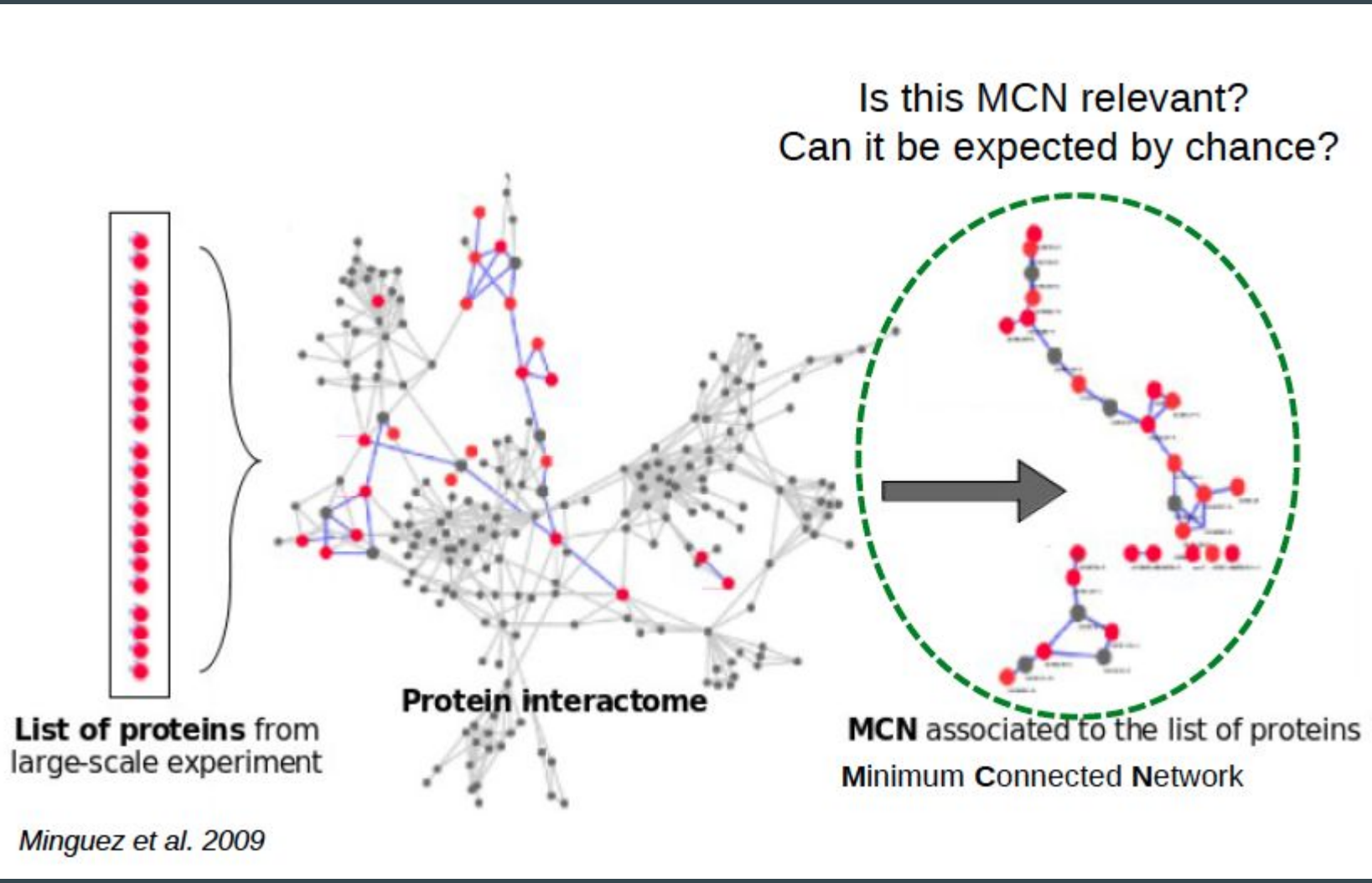


Network enrichment (SNOW)

Interactome construction



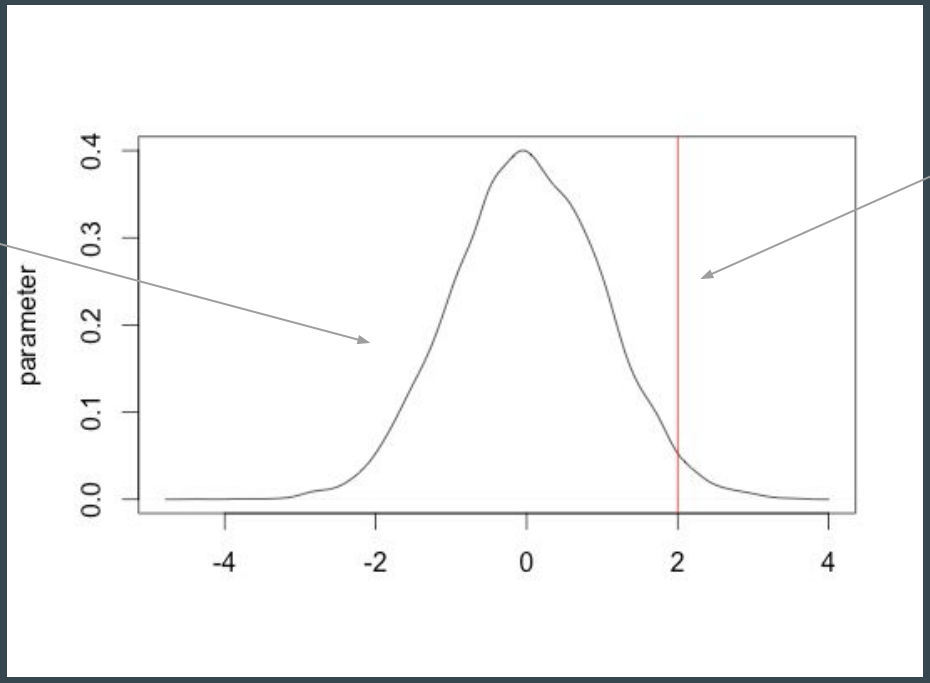
Network enrichment (SNOW)



Network enrichment (SNOW)

Comparison against N random networks (of similar size)

distribution of random networks



value of input network

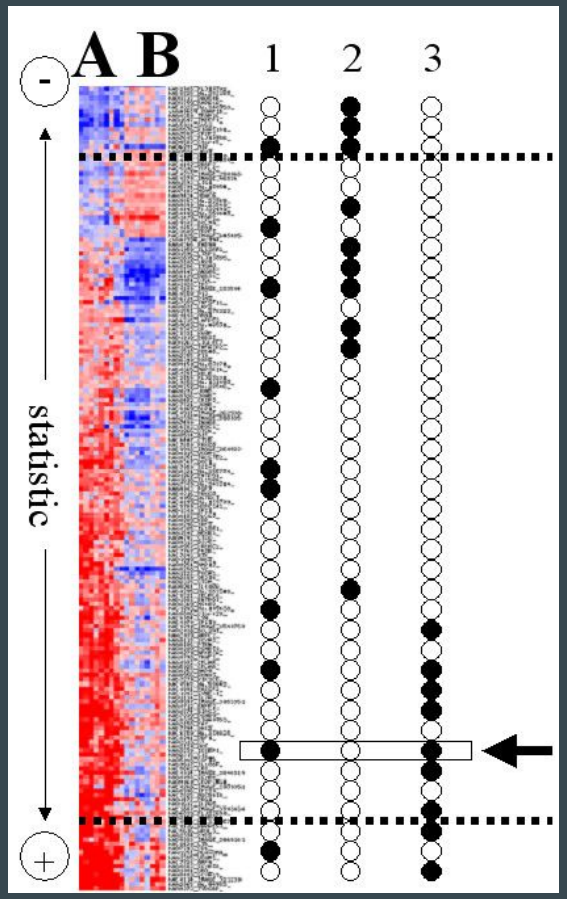
Some exercices

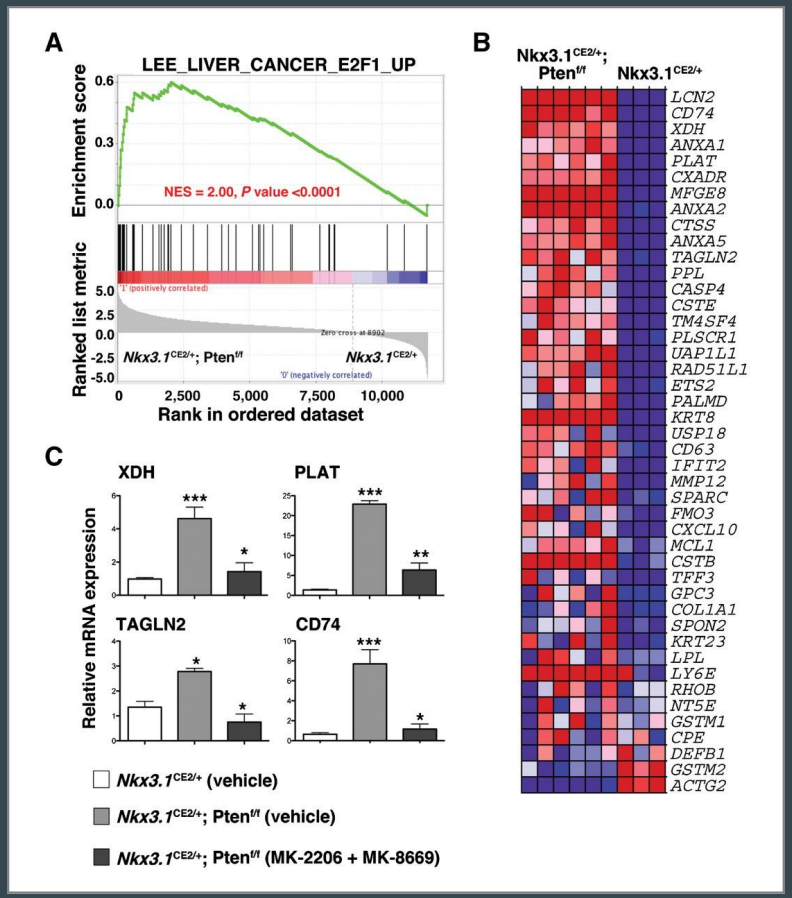
Worked examples of SNOW in Babelomics 5 wiki

https://github.com/babelomics/babelomics/wiki/network-enrichment-(snow)

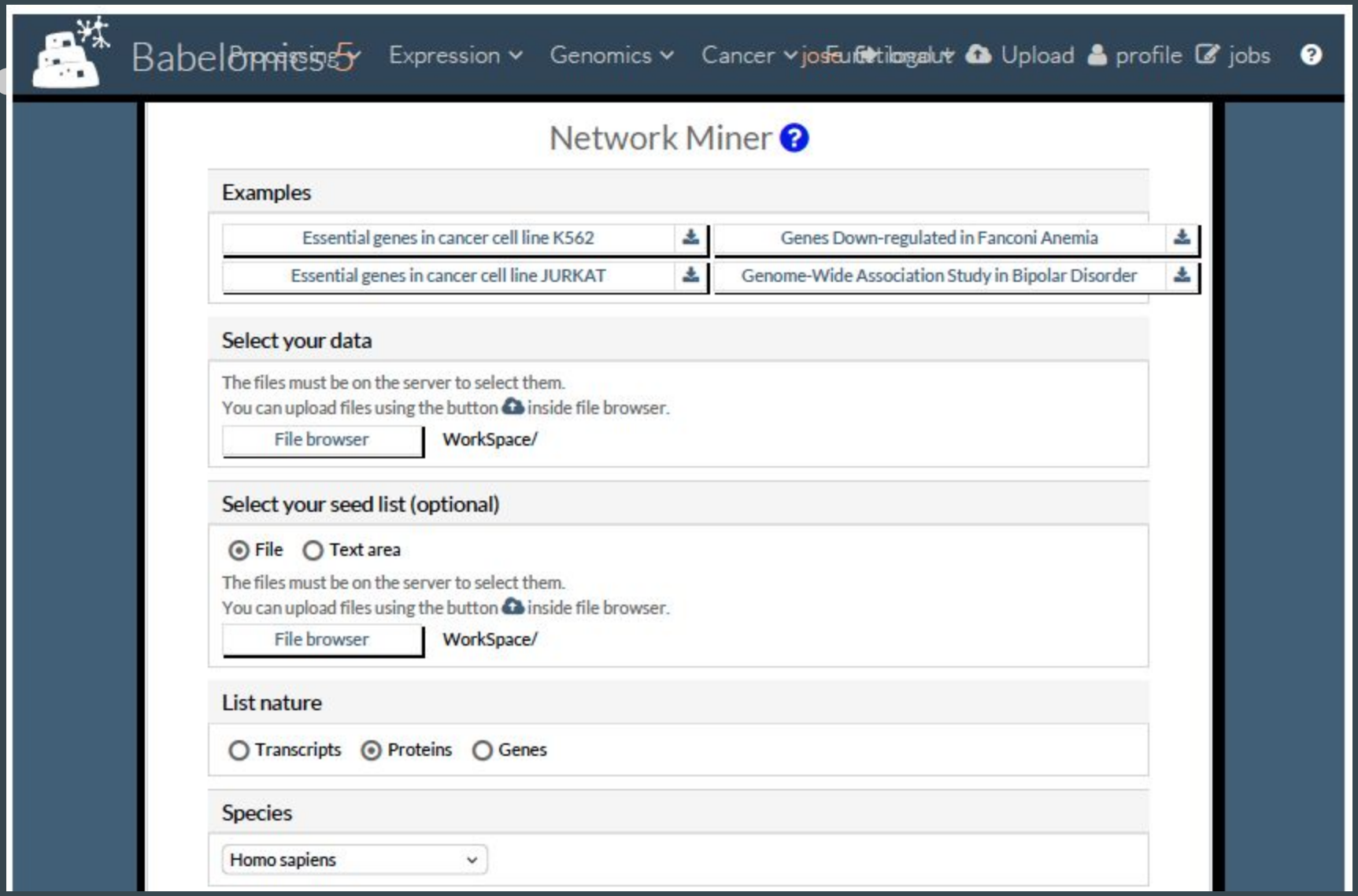
Gene set network enrichment (Network miner)

- Gene set enrichment



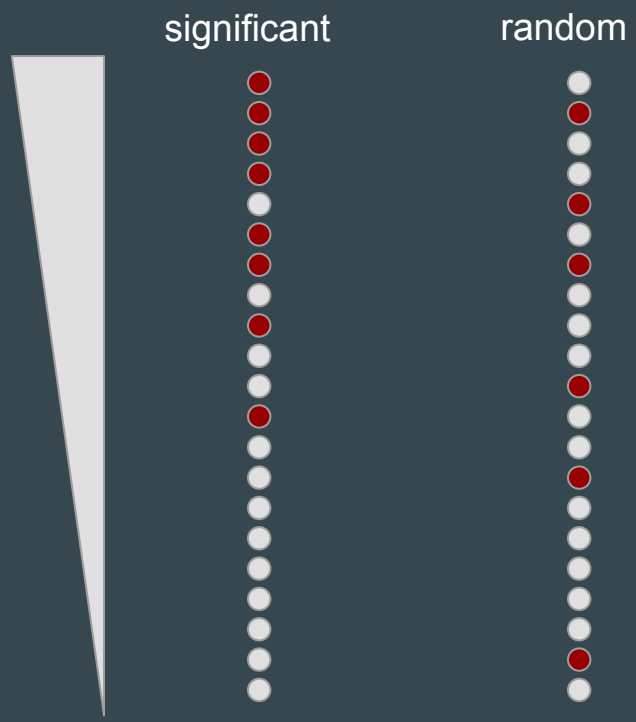


Gene set network enrichment (Network miner)

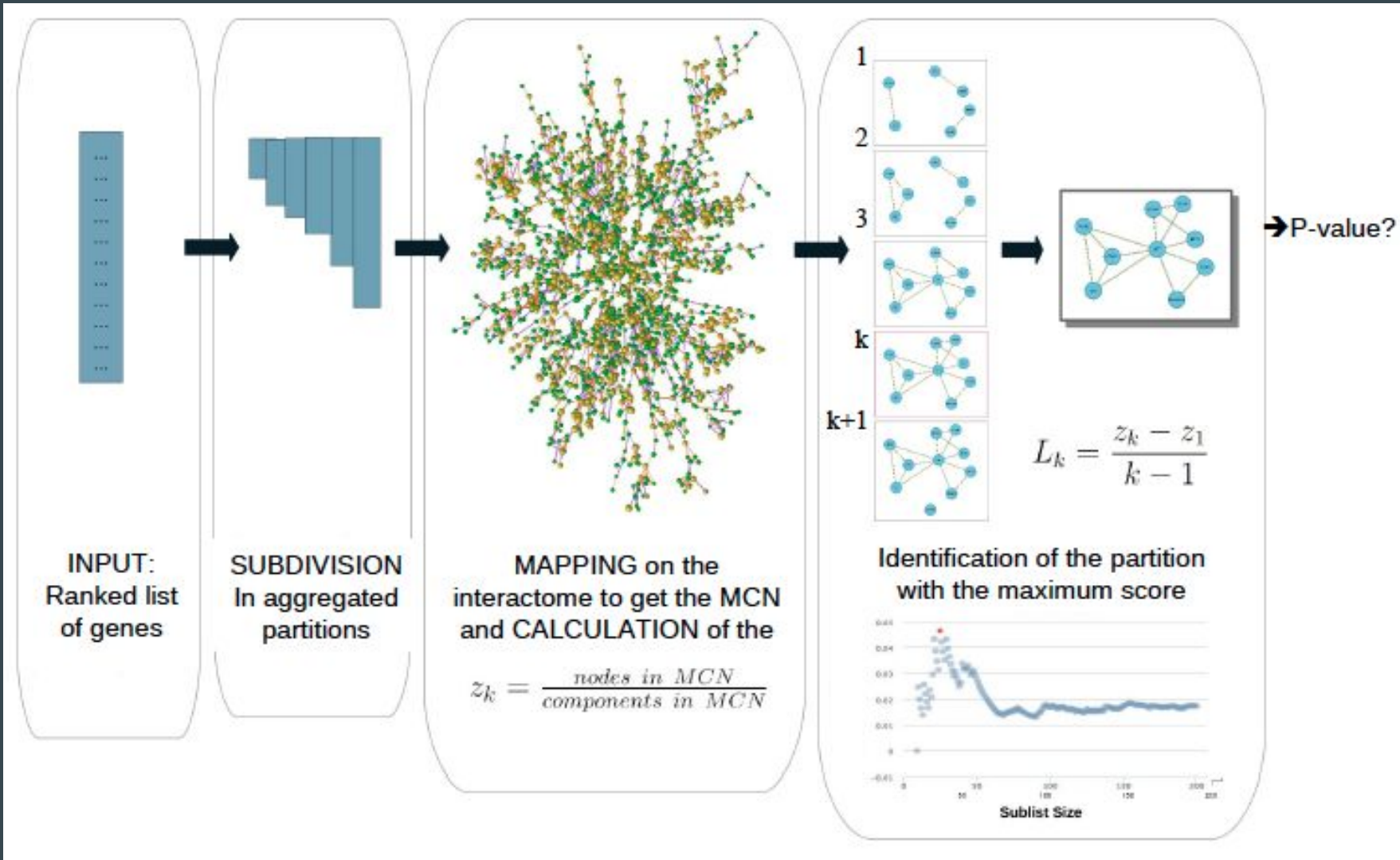


Gene set network enrichment (Network miner)

- GOAL: Is there a latent sub-network related to ranking criteria?
- input is a ranked list (diff. expression, GWAS, …)



Gene set network enrichment (Network miner)



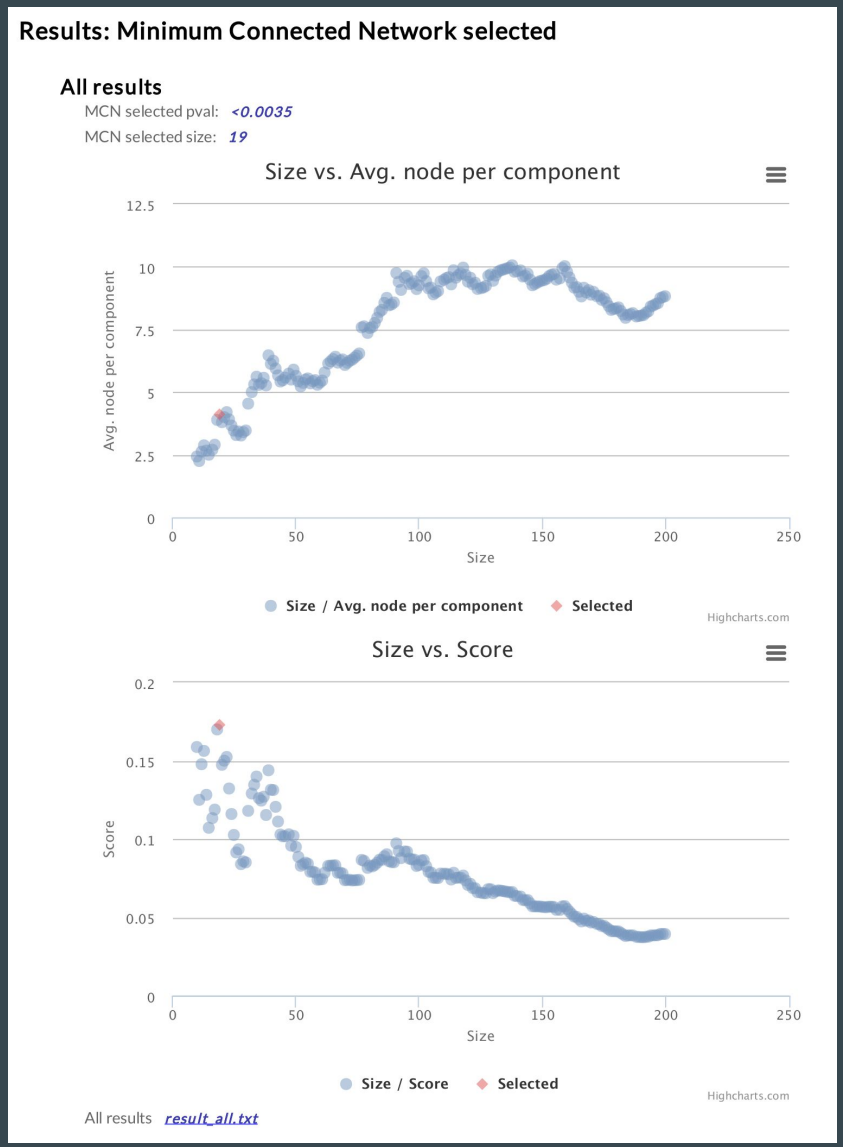
Gene set network enrichment (Network miner)

Enrichment score

(a) First, ordering the parameter of interest z_k according to the ranked list, all relative maxima are identified. The partitions so selected (S_k^{max}) represent situations where a new protein capable of connecting to the previous ones is added to the previous partitions.

(b) Second, the score L_k *is* computed as $L_k = (z_k - 1)/(k-1)$ for all the selected partitions S_k^{max}. The score can be seen as a balance between the increase in connected nodes and the distance to the top of the ranked list ($k = 1$).

(c) Third, we choose the partition S_{best} and index k_{best} corresponding to the highest L_k computed in b) form the S_k^{max} chosen in (a).



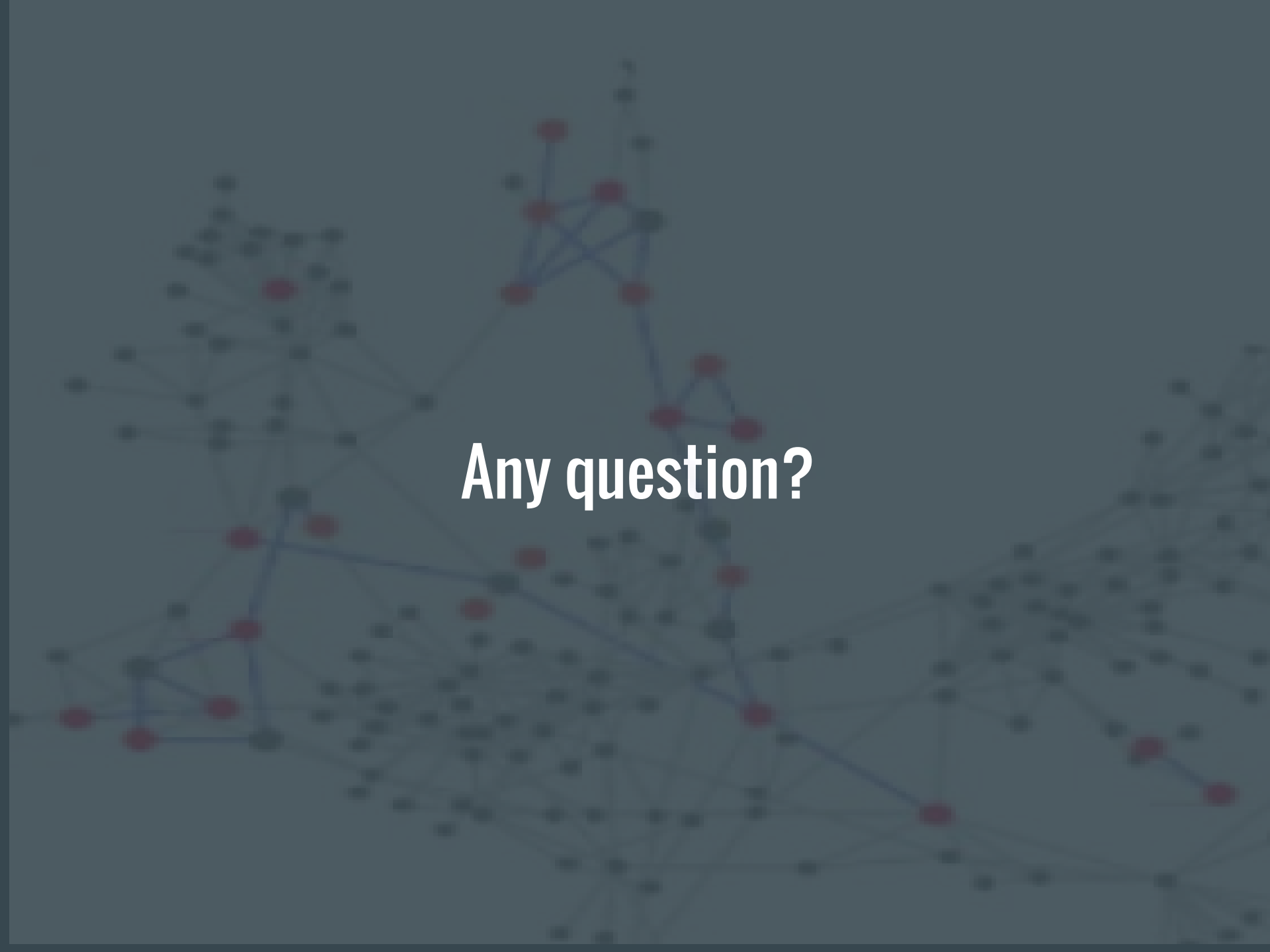
Some exercises...

Worked examples of NM on Babelomics 5 wiki

https://github.com/babelomics/babelomics/wiki/Gene%20Set%20Network%20Enrichment%20(Network%20Miner)

Some conclusions

- Systems biology provides us a global view of our living system
- Networks are extremely useful to represent inner interactions
- Networks can be measured by different topological parameters


Any question?