Multiplex Biological Networks

Communities

I2M

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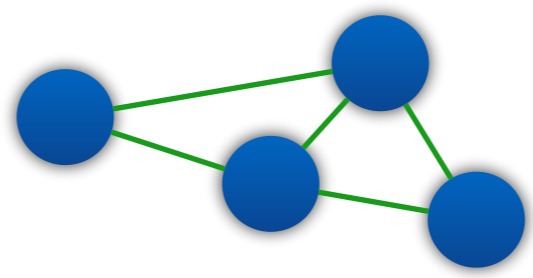**BioNetVisa WS
25/11/2015
Singapore**
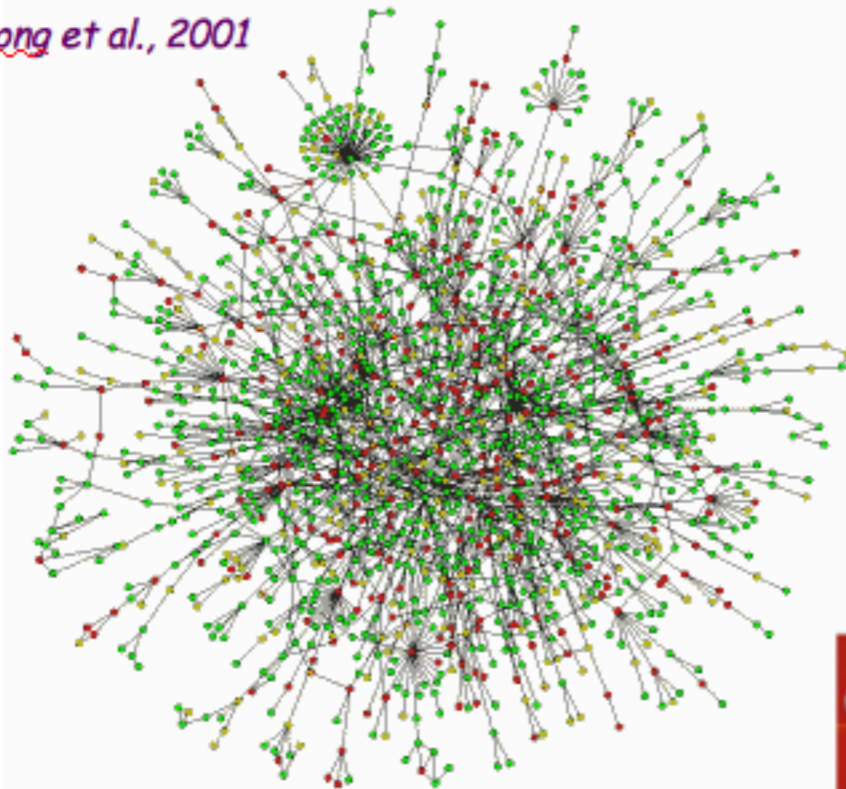
Systems Biology

Genotypes
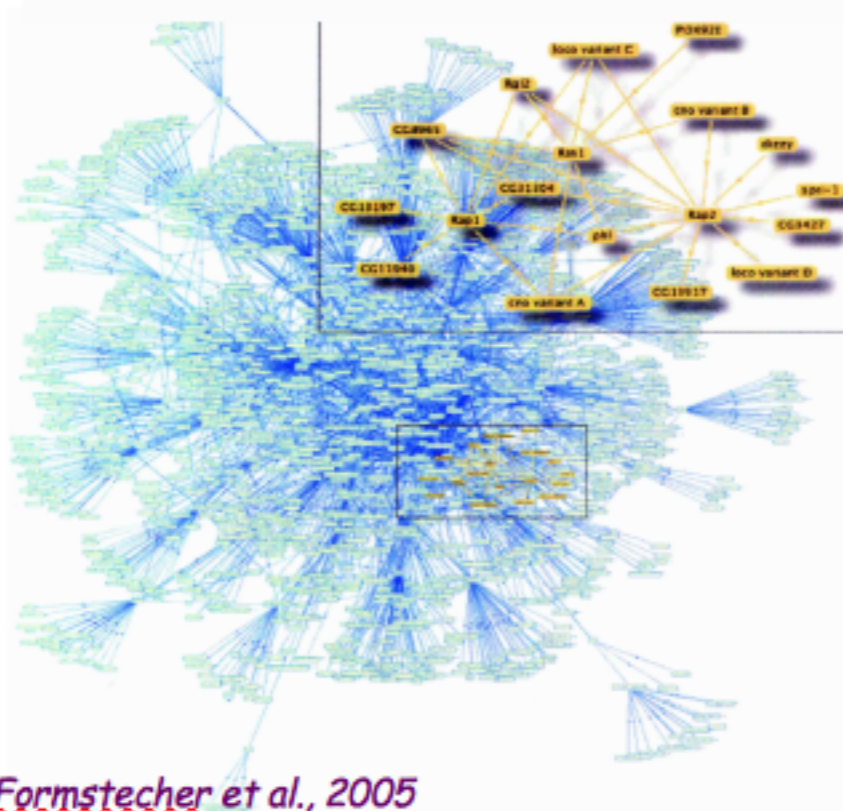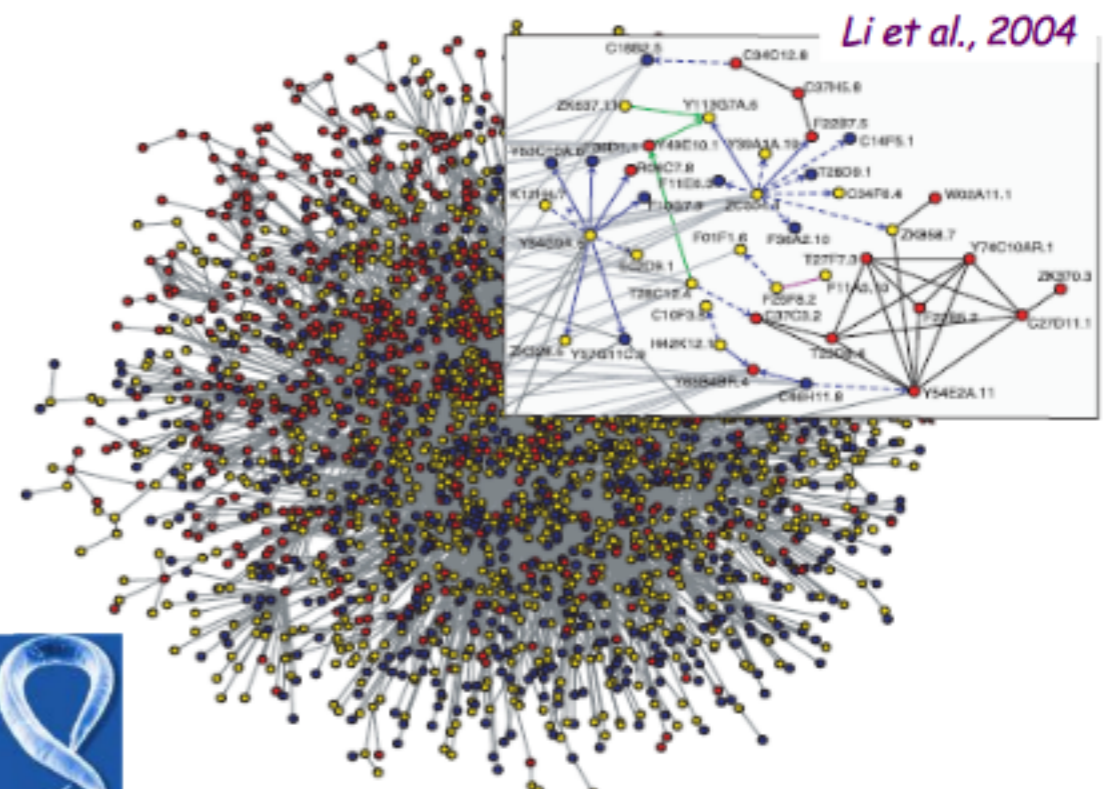
-Omics Networks

Phenotypes

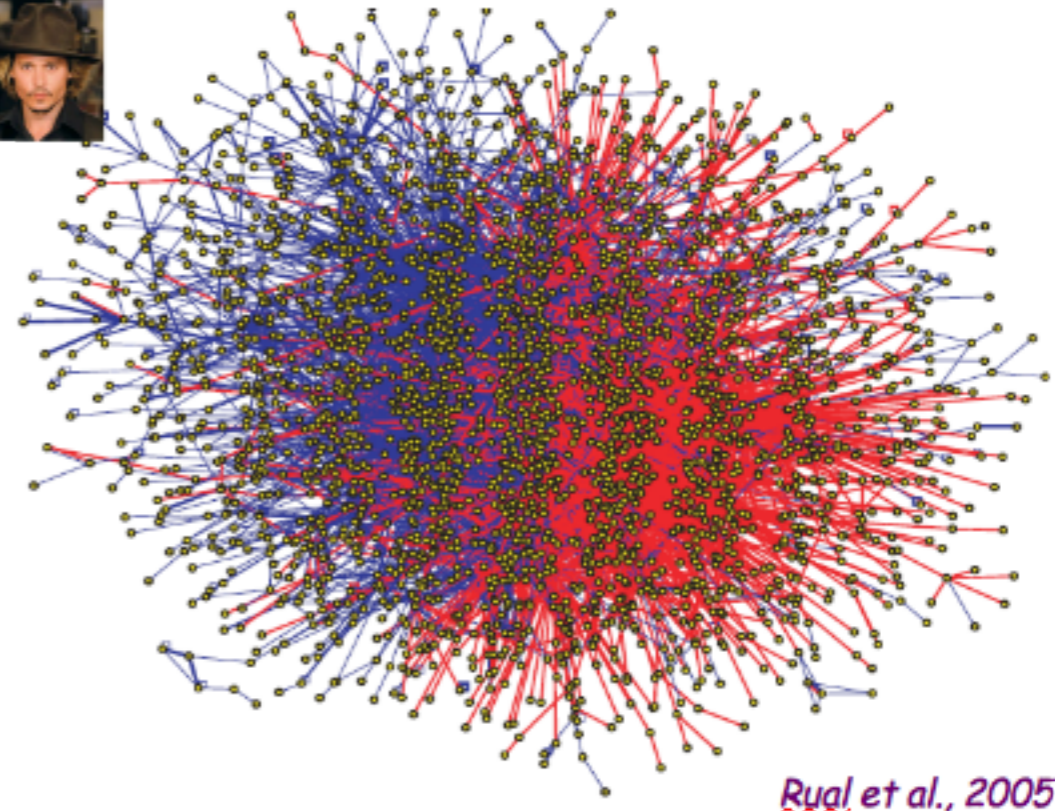# Large-scale Protein-protein Interaction Networks
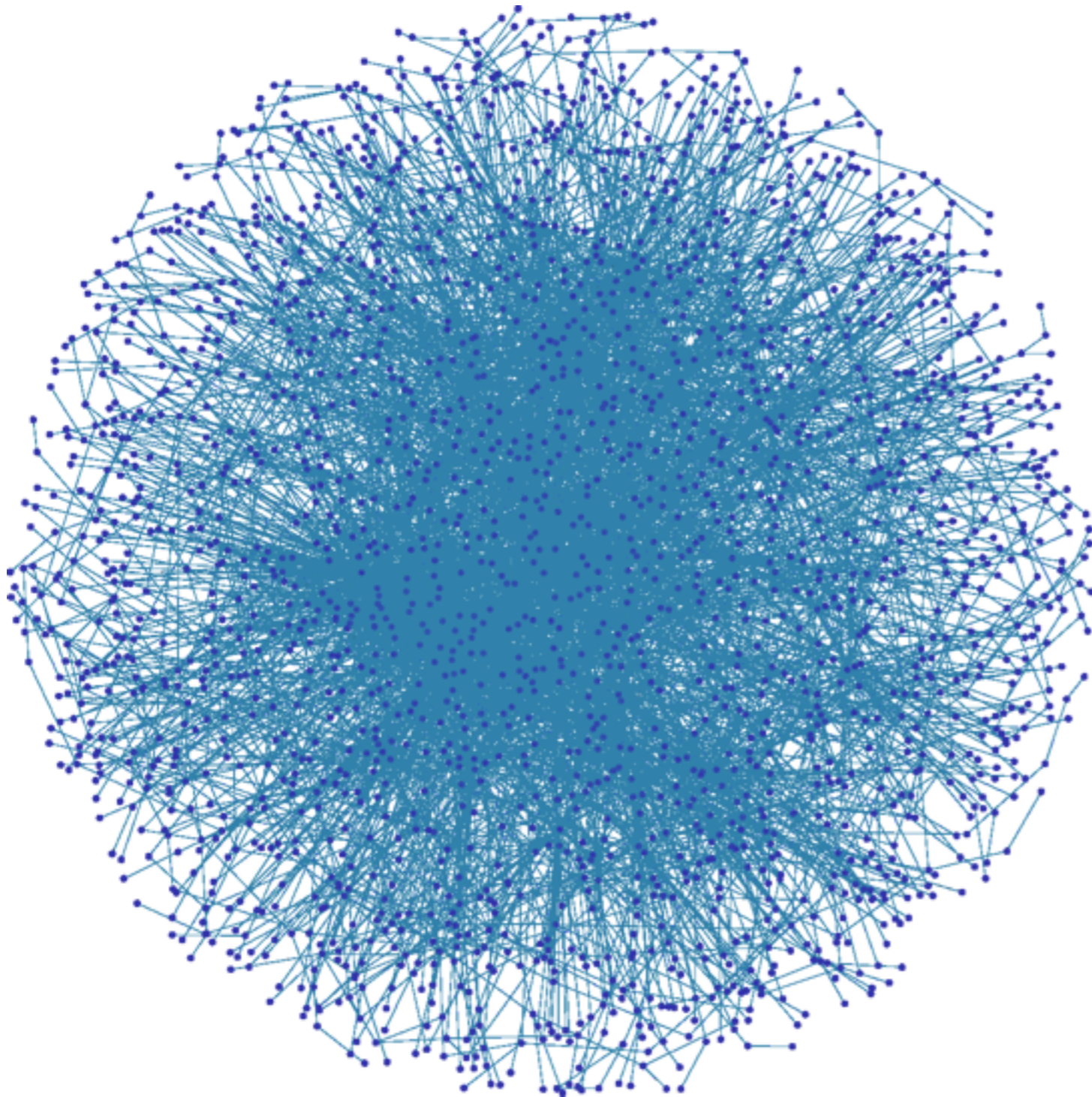

Jeong et al., 2001

Li et al., 2004

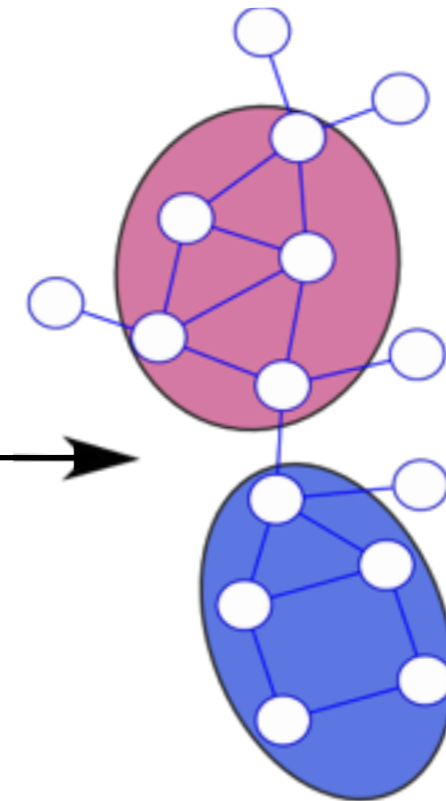Formstecher et al., 2005
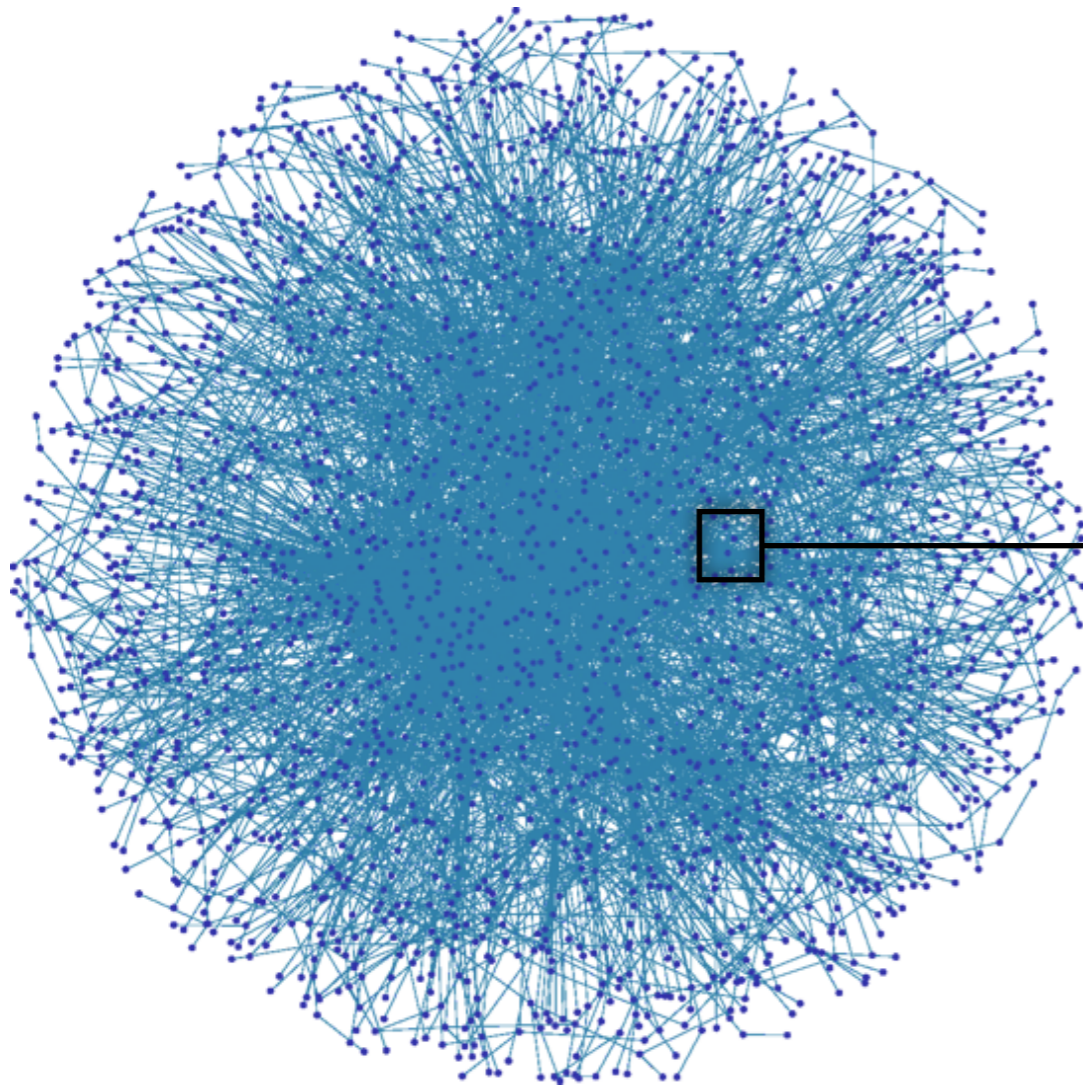
Rual et al., 2005

Interactomes

How to extract relevant biological information ?

Identification of communities
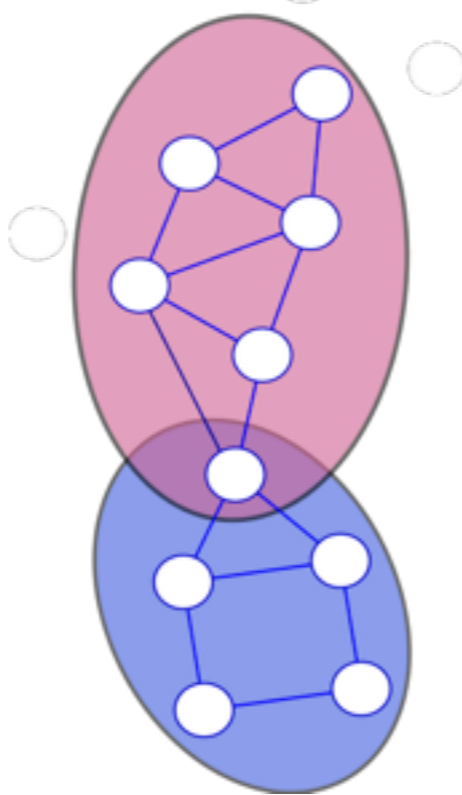
Classes / Clusters / Modules
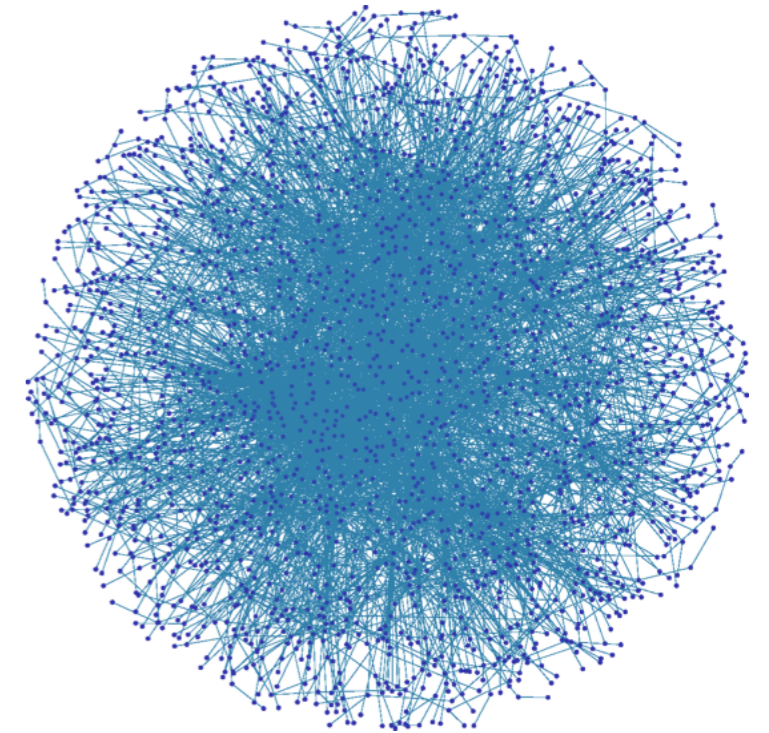

Group of tightly linked genes/proteins ➡️ **Protein cellular functions**

Protein - Structures

Functional modules

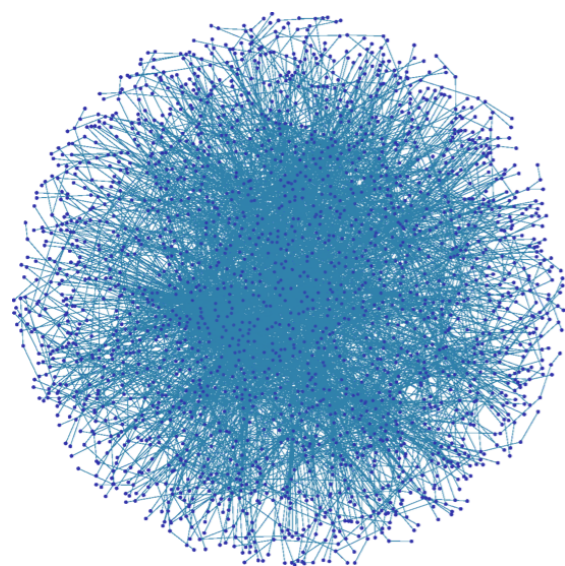**Interaction Networks**

Comprehensiveness

Precision

Inspired from P. Aloy, ECCB 2014

- Topology : Density, **Modularity**
- Integration of external data
- Overlapping / Disjoint

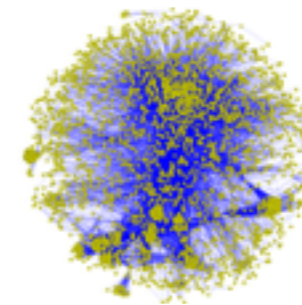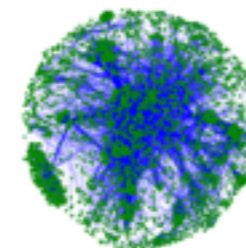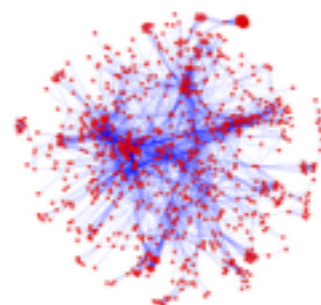# Multiple networks to depict protein cellular functions
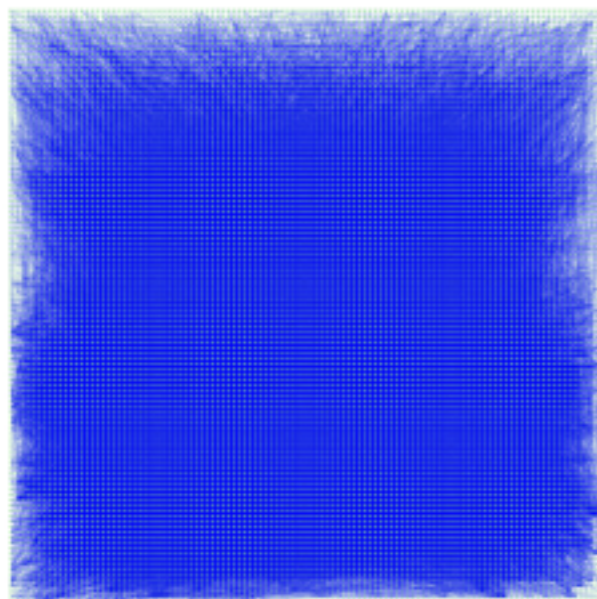
PPI (12110 / 60669)

Pathway-related (8839 / 166761)

Spike   Biocarta   Kegg   Nci
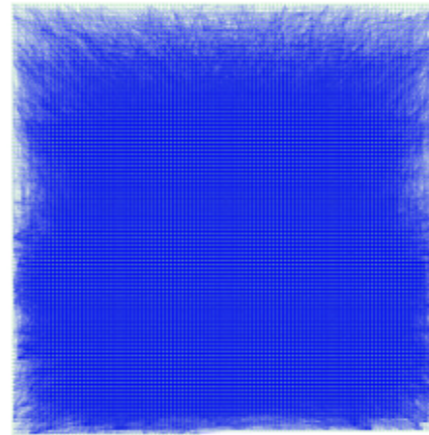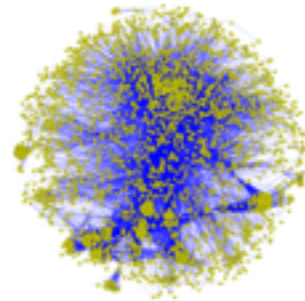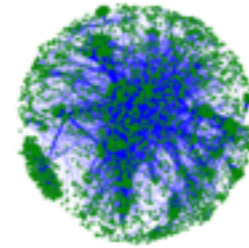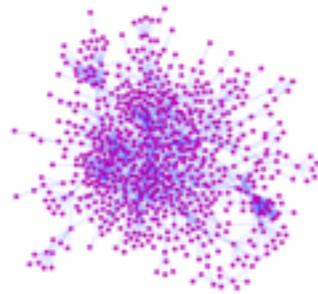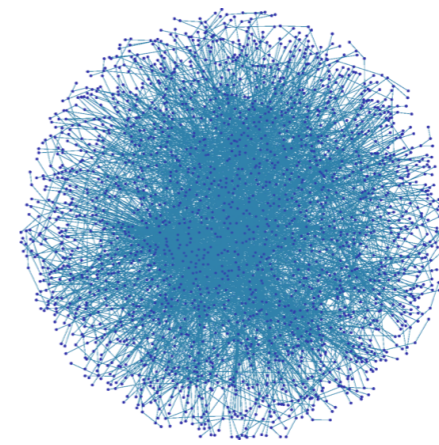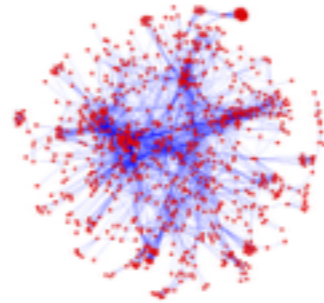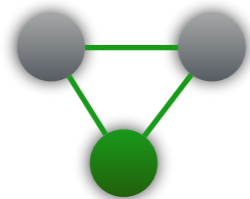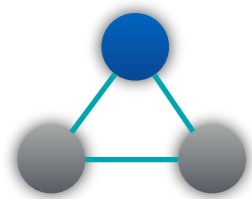
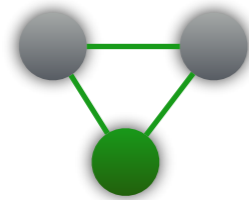**Co-Expression** (9912 / 1107547)
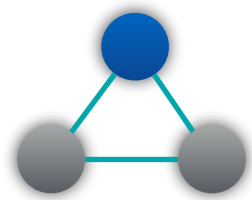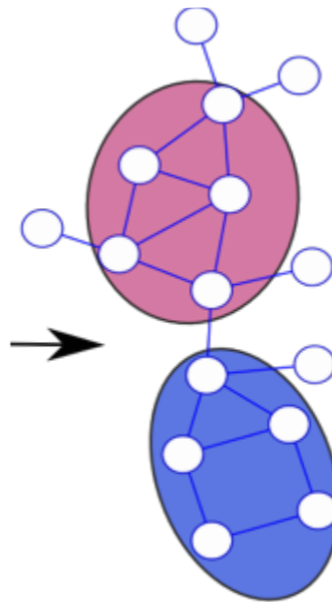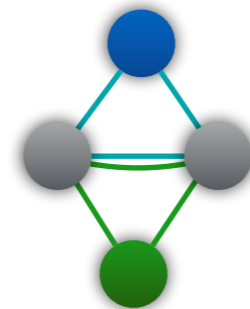
CORUM complexes (2528 / 36762)

- **Does the combination of networks improves the detection of communities?**

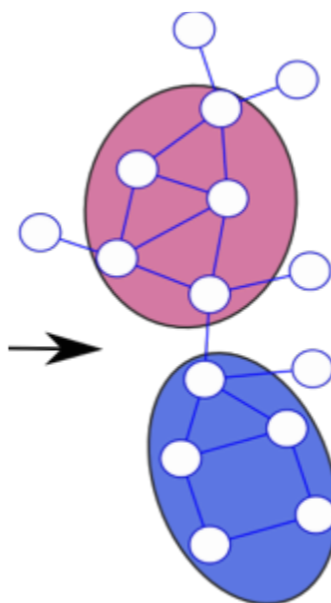- **How to combine multiple networks to identify communities?**
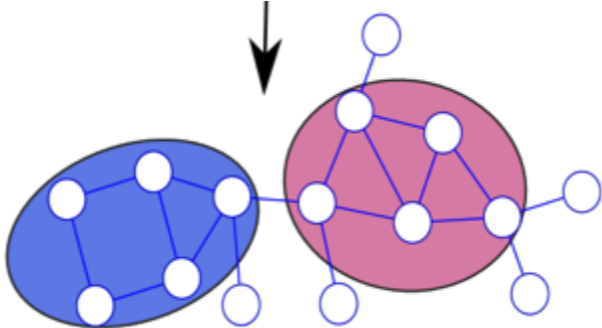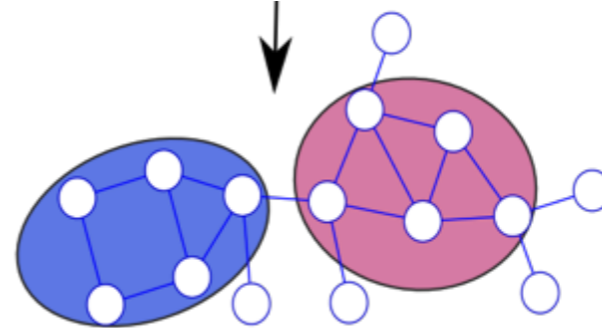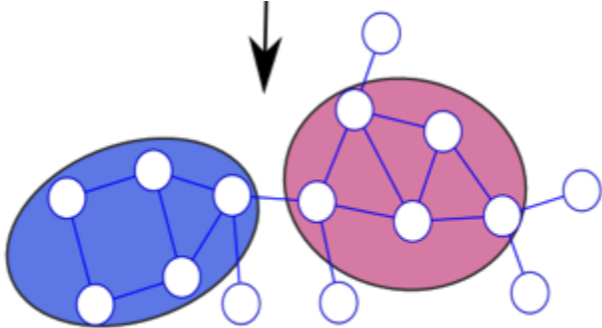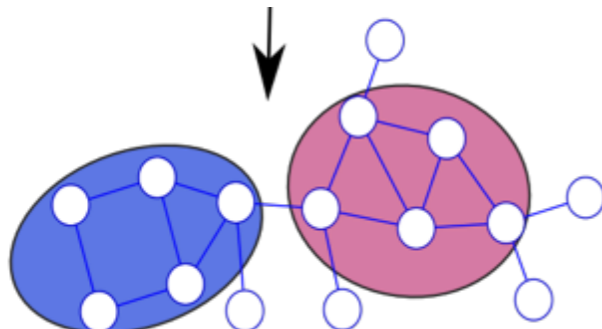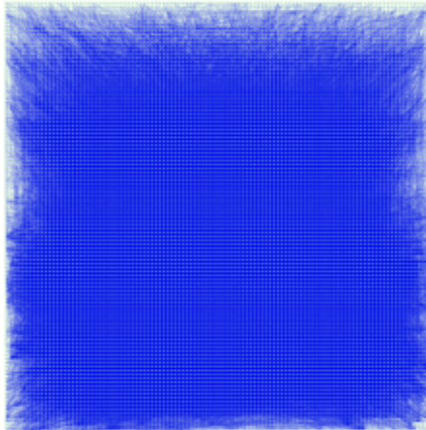
Network aggregation
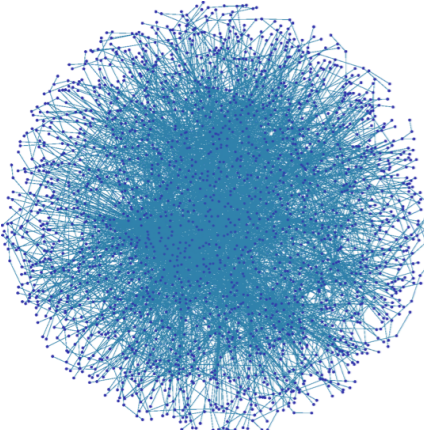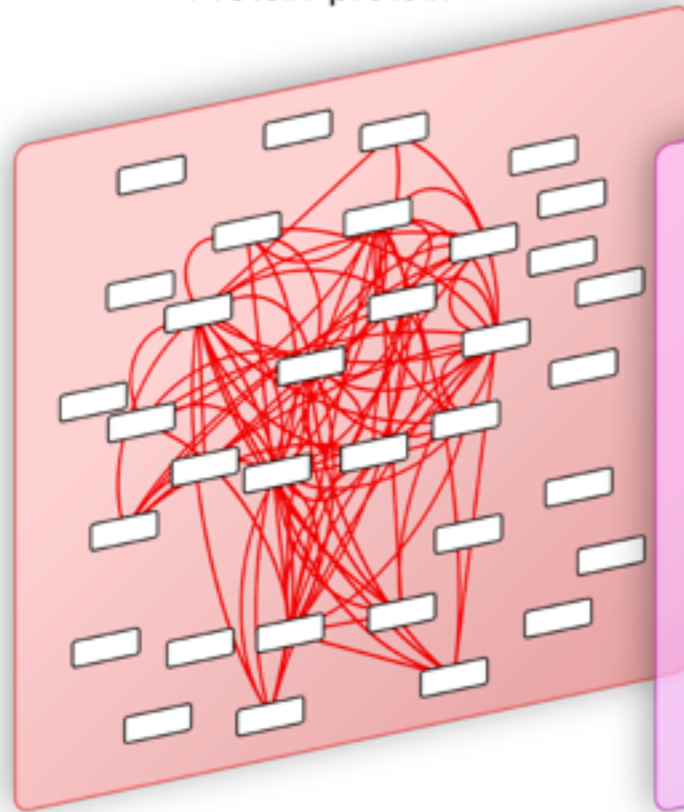
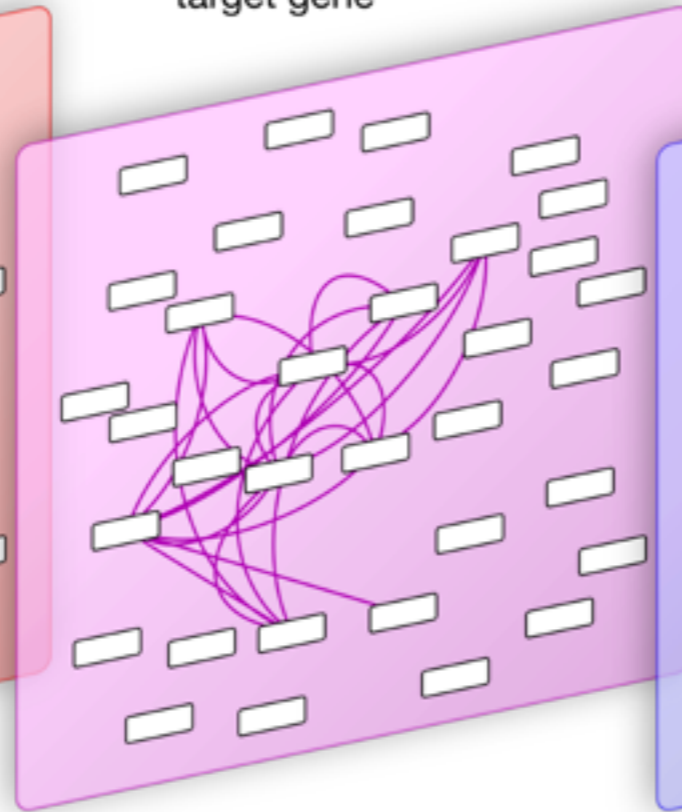Union, Sum

Intersection

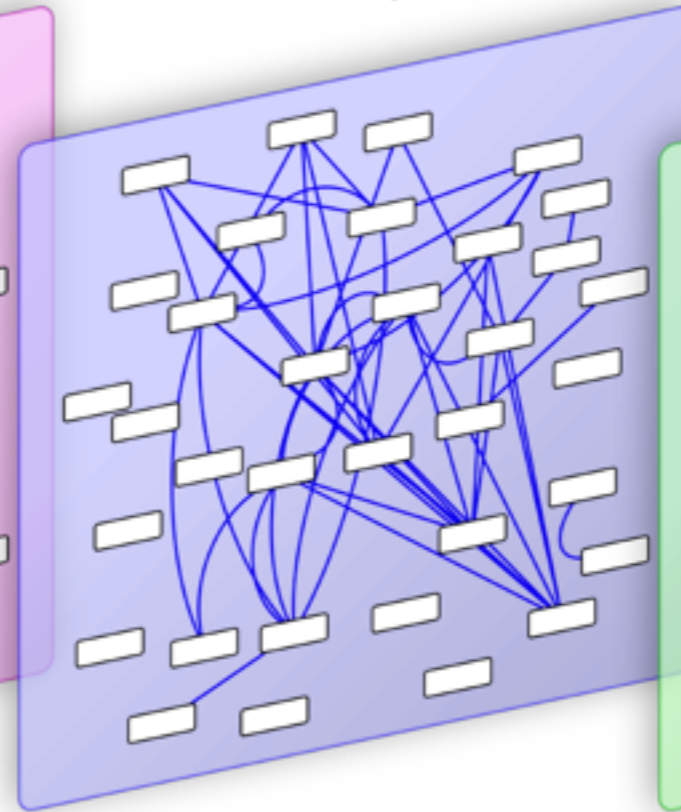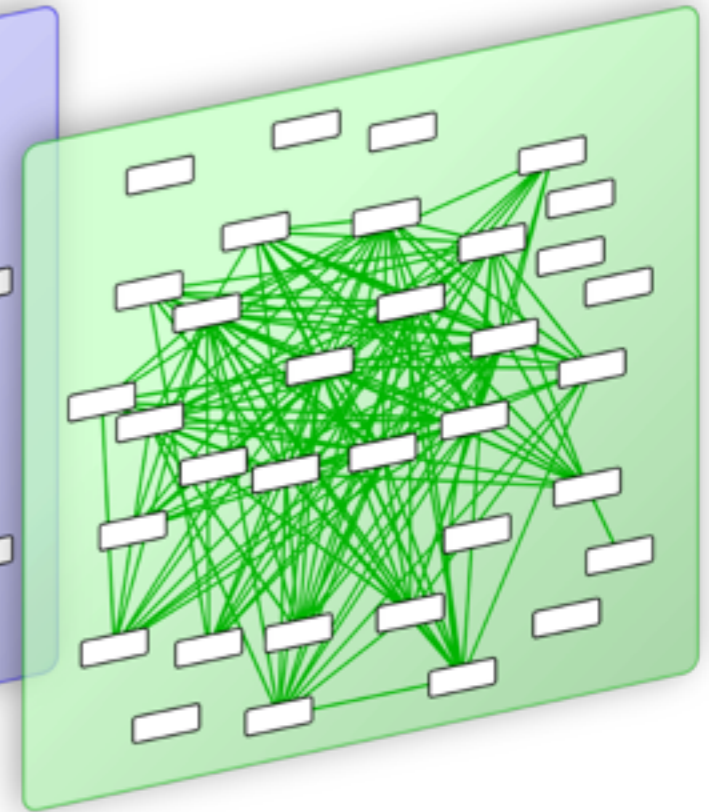# Consensus partitioning

Multiplex framework

Protein-protein
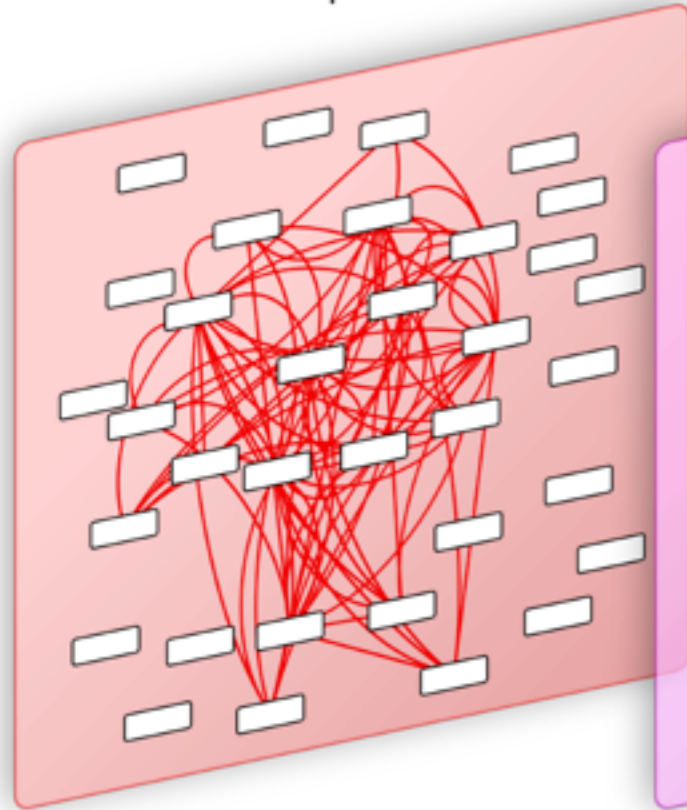
Transcription Factor - target gene

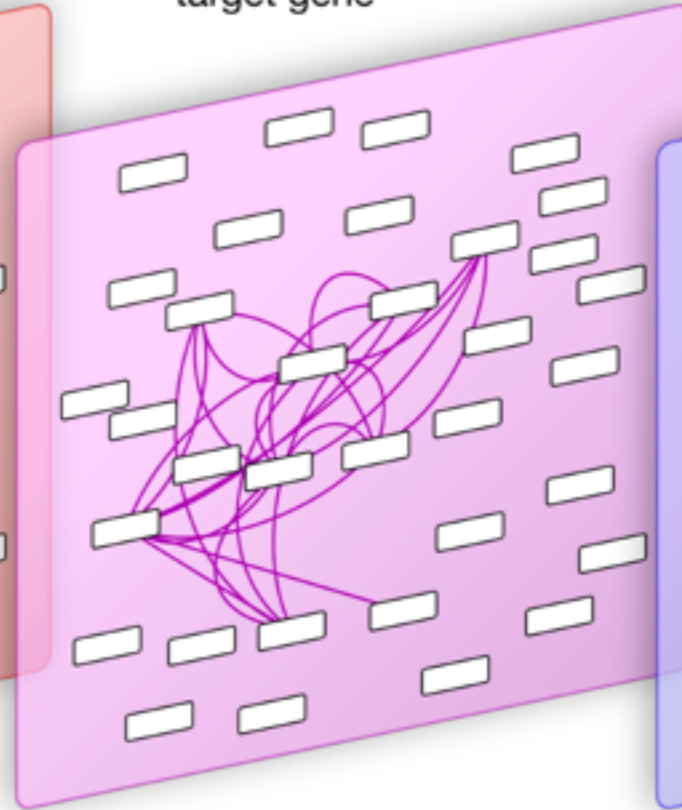Pathways

Complexes

Multiplex, Multi-layer, Multislice
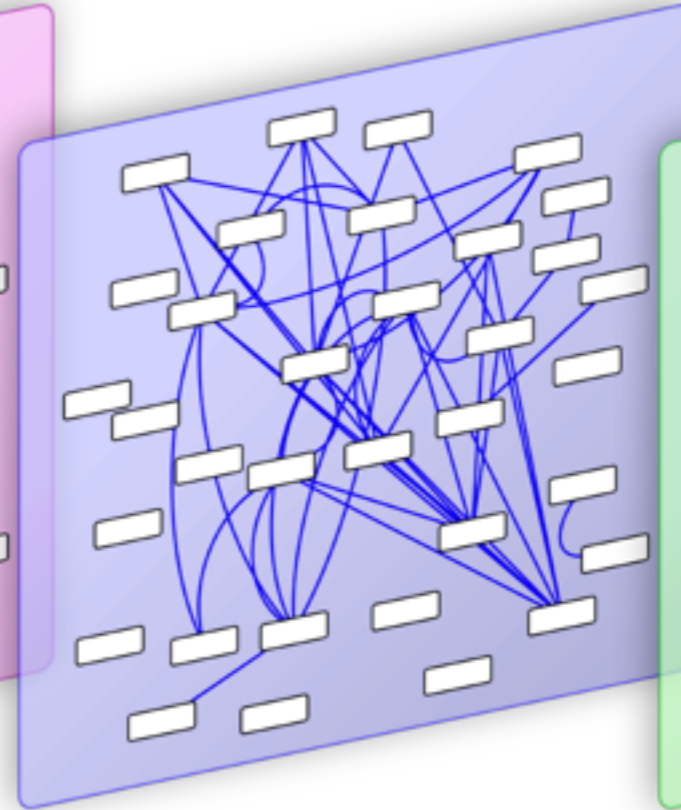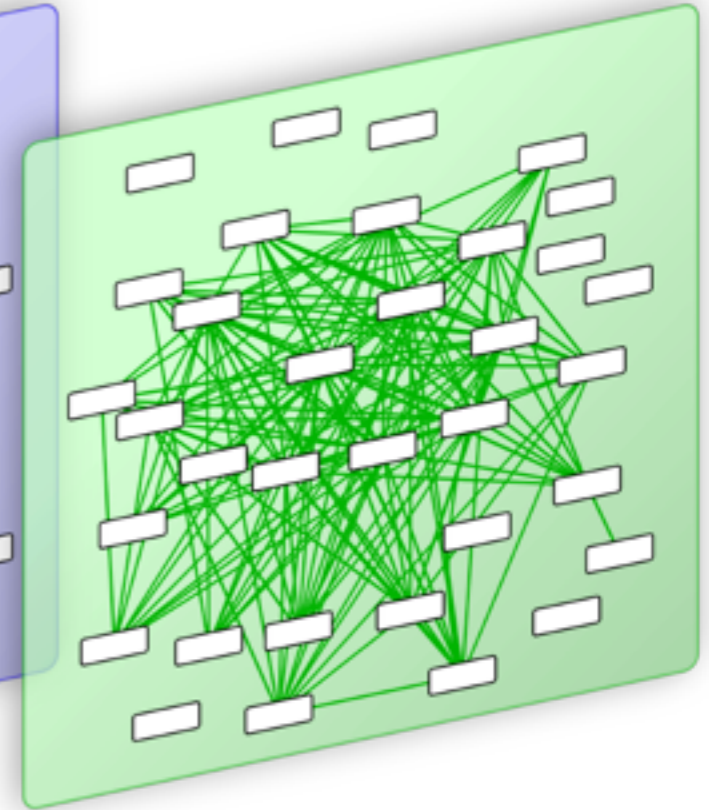
Multiplex framework

Protein-protein

Transcription Factor - target gene
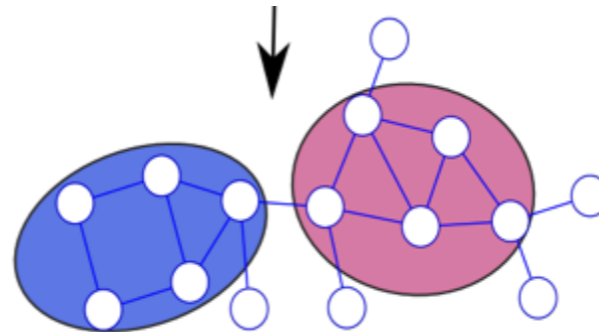
Pathways

Complexes

- **Multiplex-modularity**

Protocole

- **Multiplex framework**
  - Multiplex-modularity
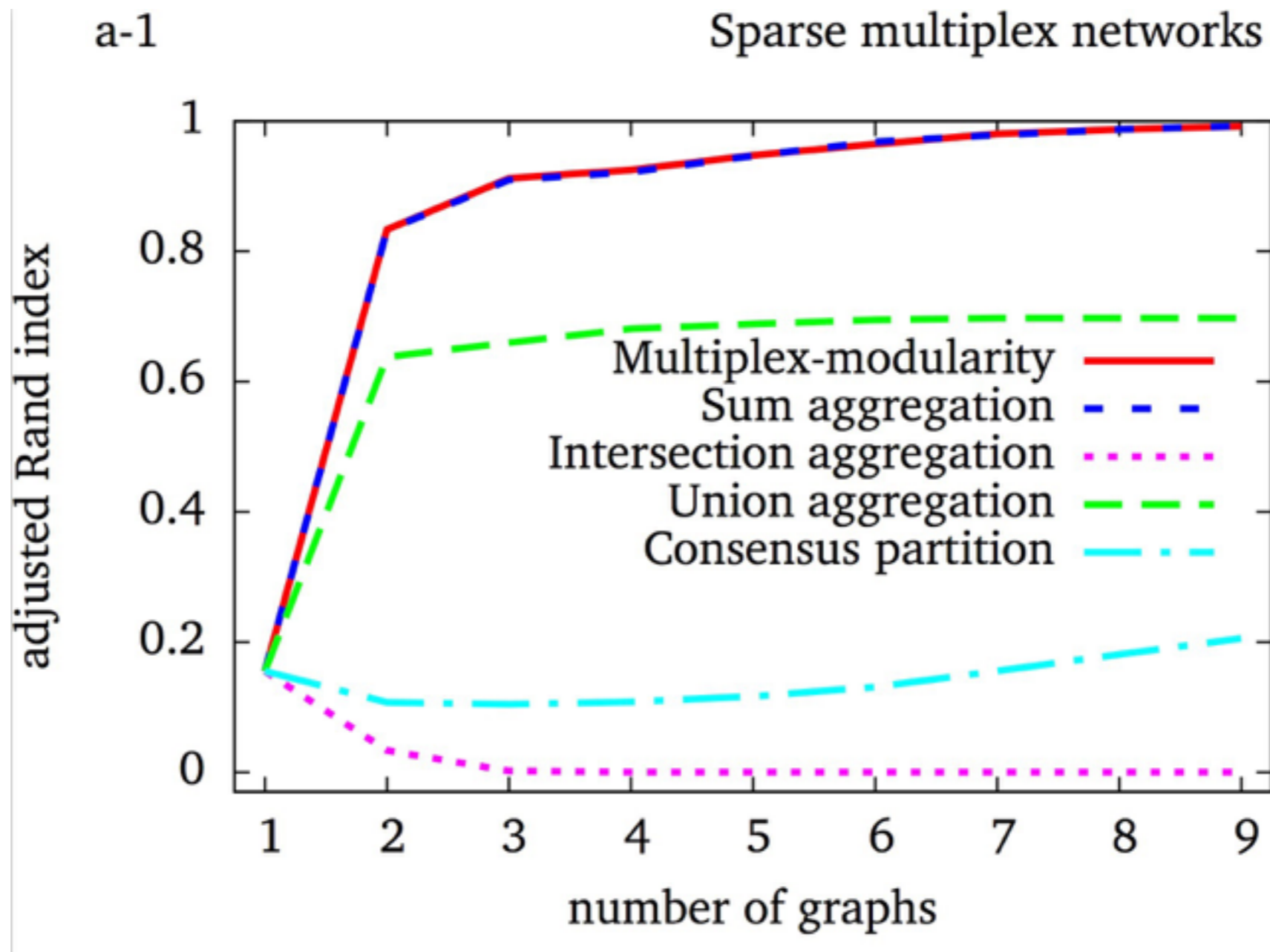 - Mx-modularity Optimization (adapted Louvain algo)

- **Networks aggregation**
  - Modularity

- **Consensus partition**
  - Modularity Optimization (Louvain algo)

Simulations (SBMs)

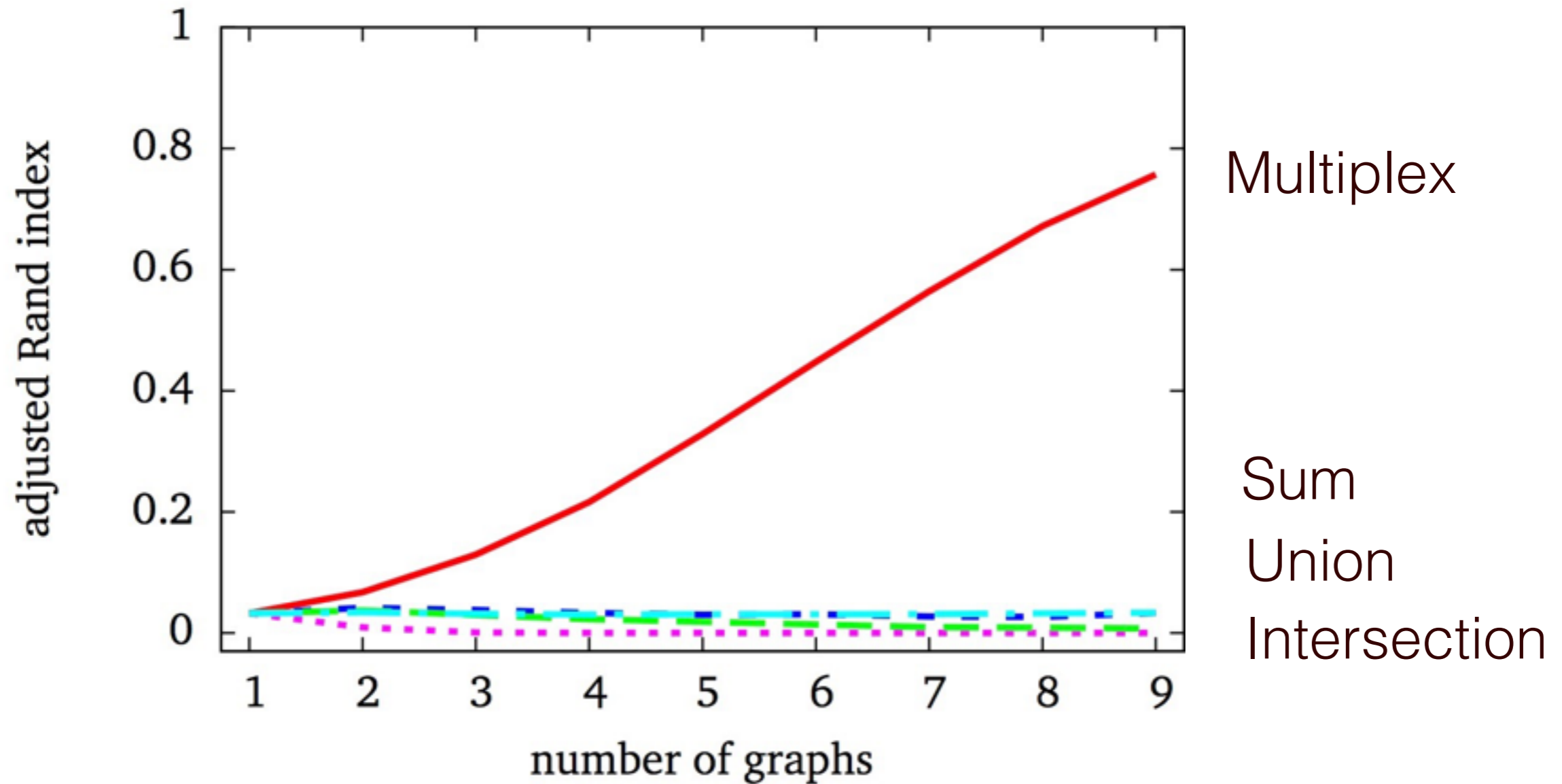**Considering many networks improves the detection of communities**

Simulations (SBMs)

b-2

Mixed multiplex networks with missing data

Multiplex

Sum

Union

Intersection

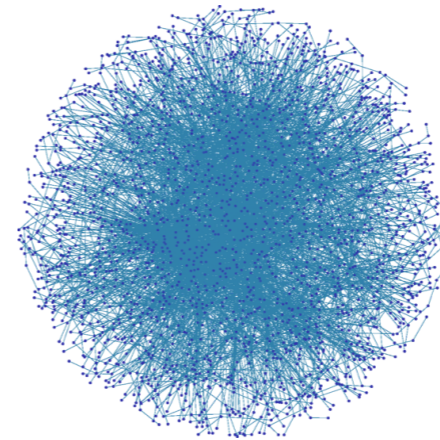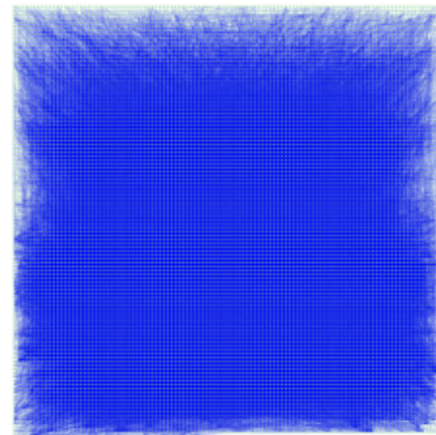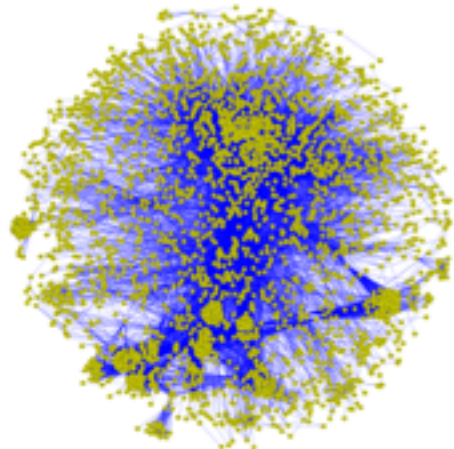**Mx framework more efficient with heterogeneous and incomplete networks**

Application to real biological networks
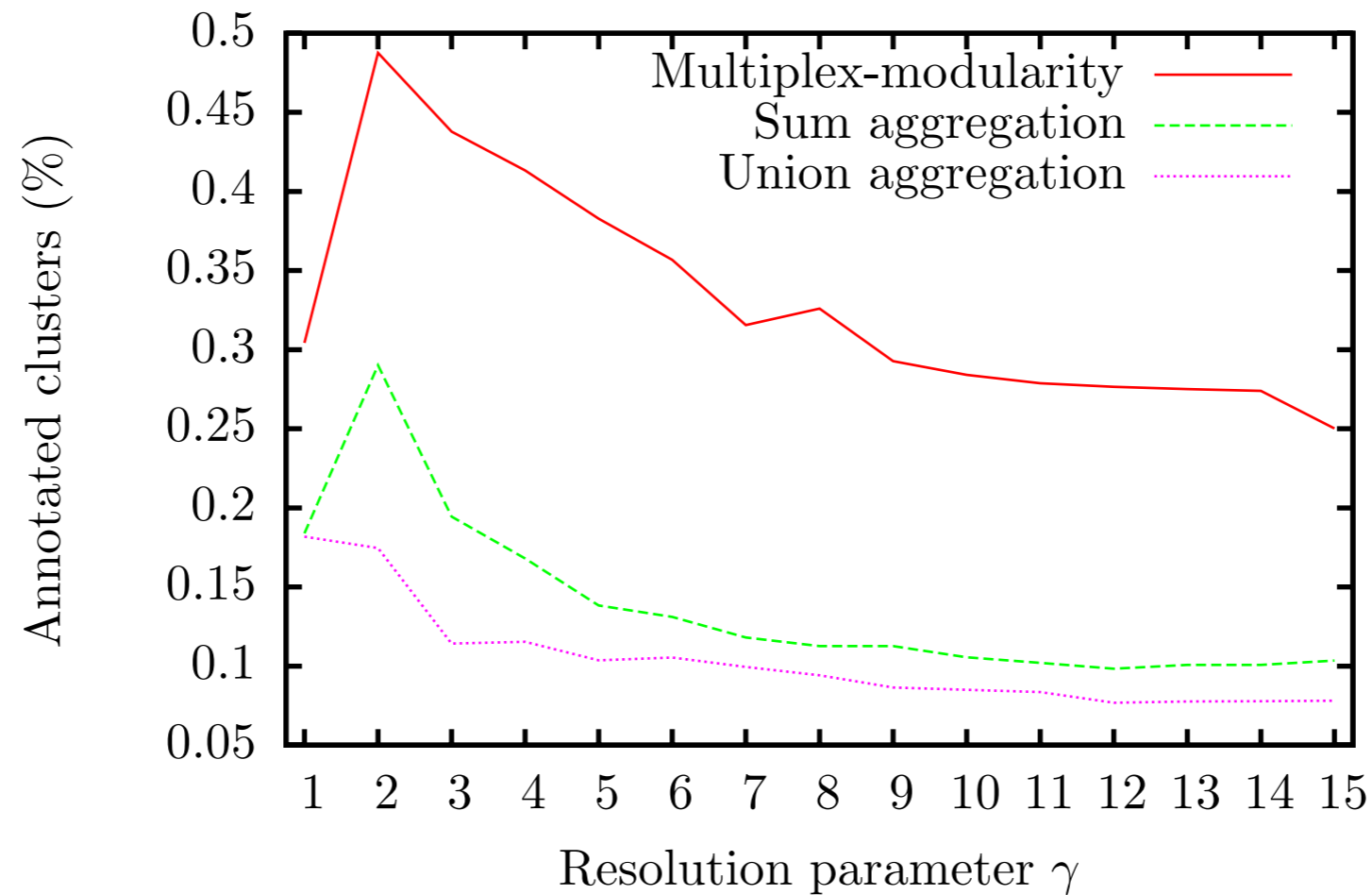

Pathways   Co-expr   PPI   Complexes

- Granularity parameter from 1 to 15
- Community number, sizes, similarities

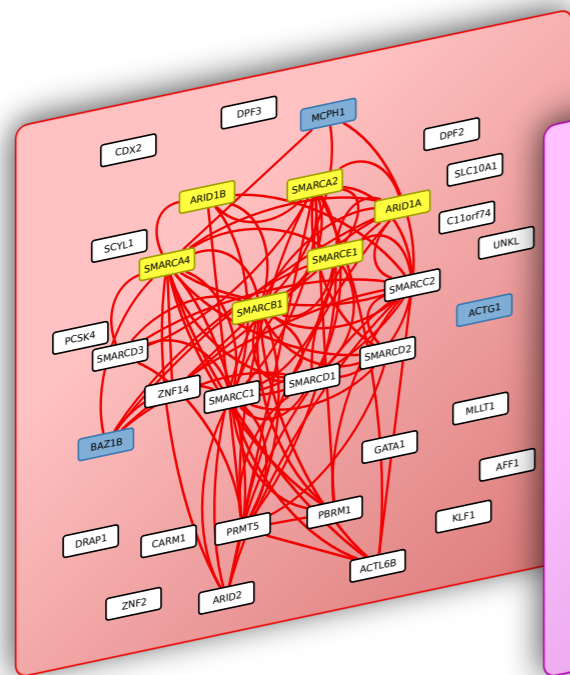**=> More balanced**

Community GOBP annotations

=> More annotated

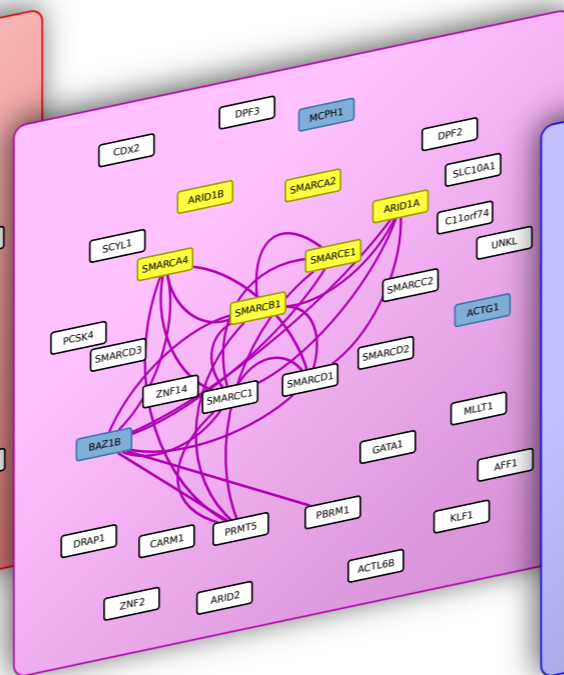**=> Multiplex framework is well suited to identify communities from multiple biological networks**
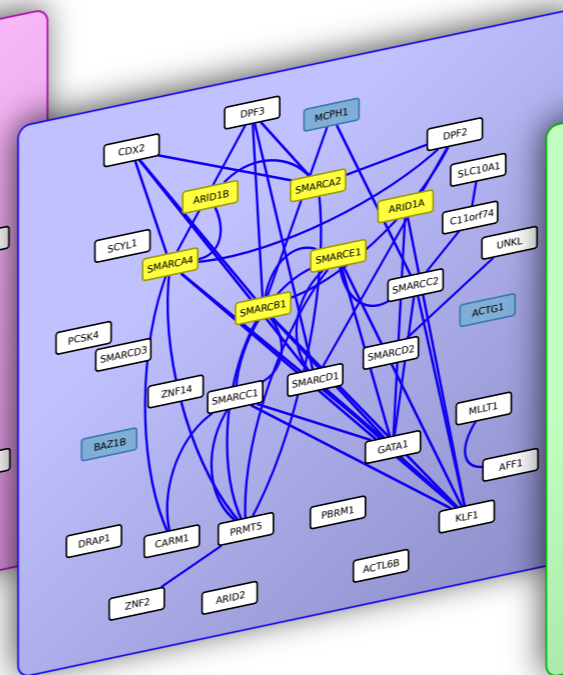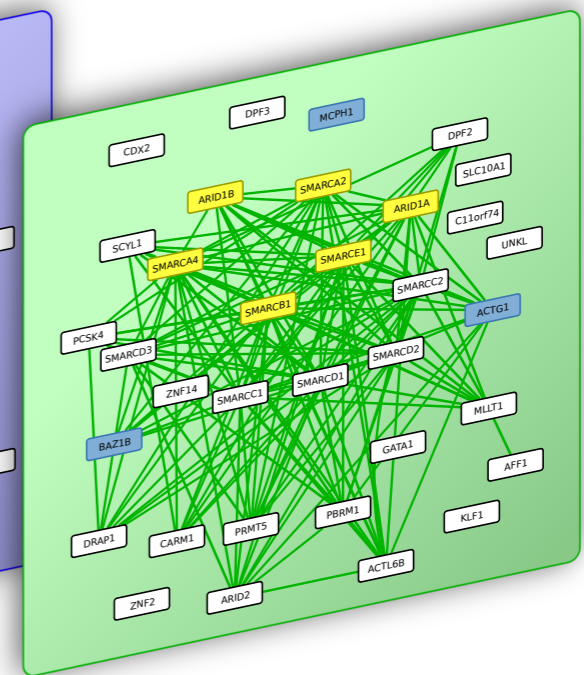
Module enriched in Coffin-Siris syndrome genes

https://github.com/gilles-didier/MolTi

Acknowledgments

PEPS