MEDNARODNA PODIPLOMSKA ŠOLA JOŽEFA STEFANA

JOŽEF STEFAN INTERNATIONAL POSTGRADUATE SCHOOL

Community-based semantic subgroup discovery (CBSSD)

Blaž Škrlj, Anže Vavpetič, Jan Kralj, Nada Lavrač

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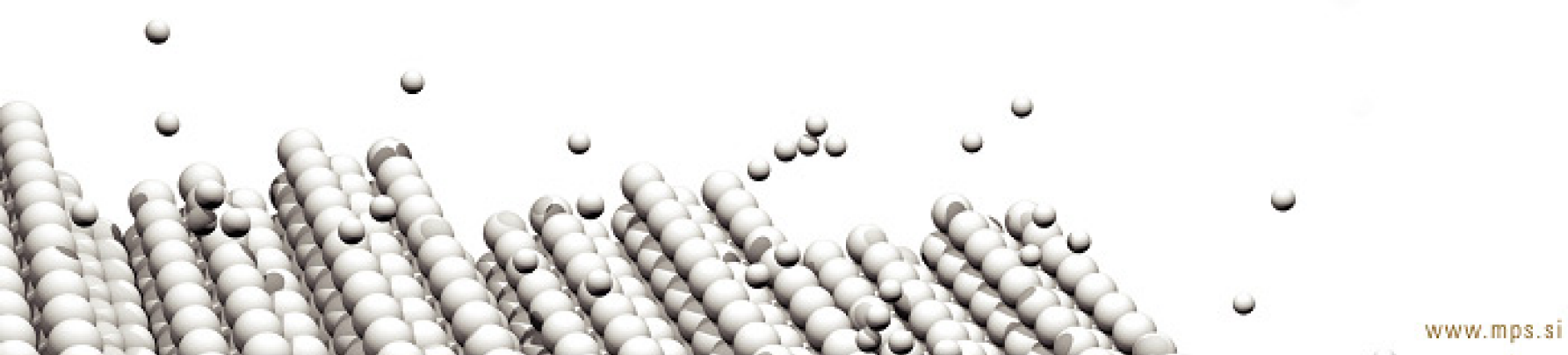

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Introduction

Properties of biological networks

- Multiple types of nodes and edges $\rightarrow$ heterogenous networks
- Possible connections between distinct entities
- Large in some sub-domains
- Not trivial to interpret

How can an algorithm learn from a complex network?

Network representation

Important network features can be encaptured via community detection, graphlets, semantic clustering and other methods..

Example use

Such methodology is used to infer protein-RNA interactions, identify expression patterns, compare protein structures, fuse systems-level data etc.

Problem definition

Term-subset enrichment

Let $t_1, t_2, .., t_n$ represent individual terms of interest from the whole term set ψ. Identify subsets $\Lambda_1, \Lambda_2, .., \Lambda_n \subseteq \psi$, which represent interpretable patterns, previously unknown to a human observer.

Example situation

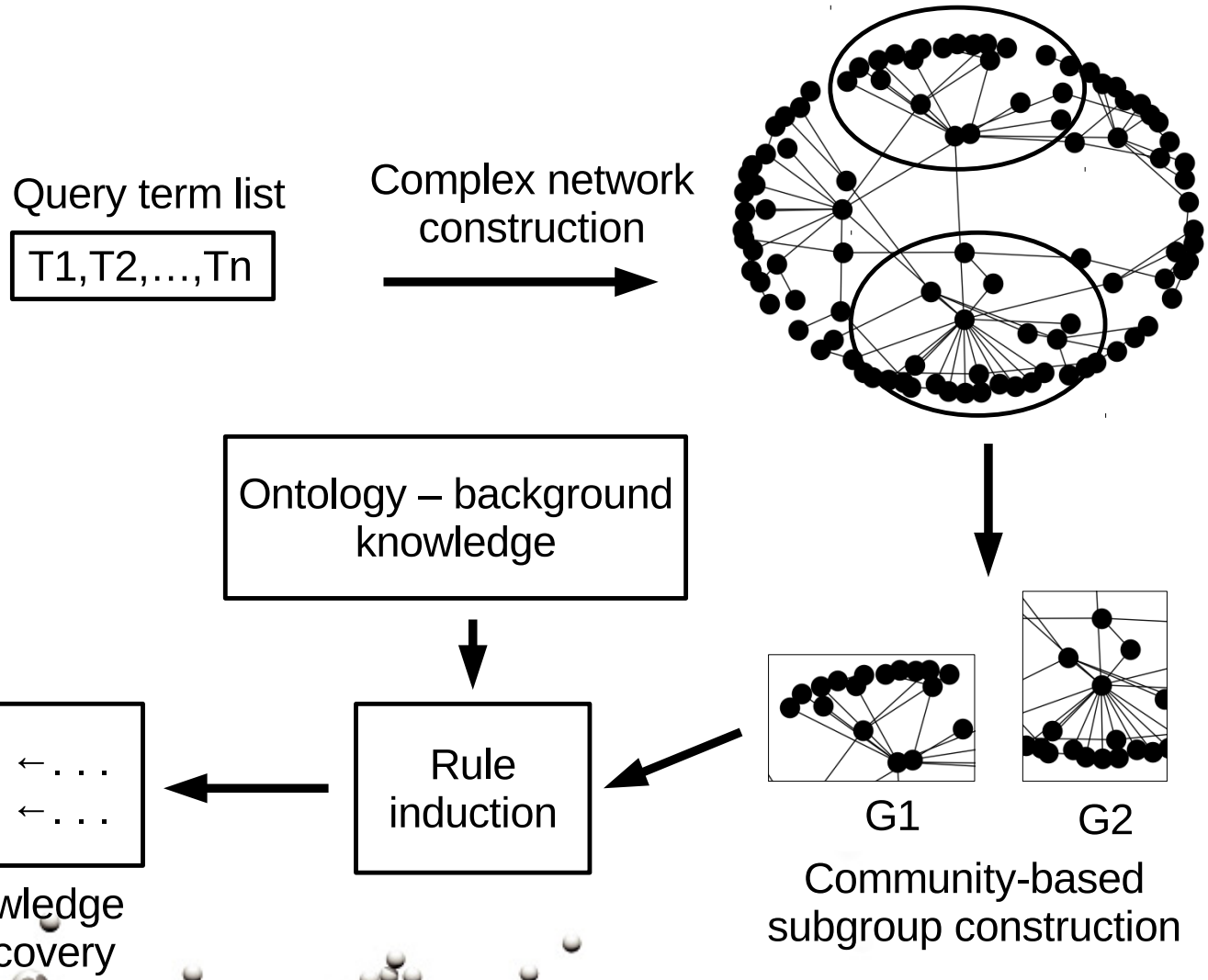
Let $G_1, G_2, .., G_n$ be n distinct genes we are interested in. Although individual genes, or the whole group of genes doesn't return any interesting results, we can further explore the subspace of n genes.

Problem

Exploring all possible combinations can be computationally expensive procedure, as there are $\sum_{i=2}^{n} \frac{n!}{(n-i)!i!}$ possible options.

Fighting the combinatorial explosion

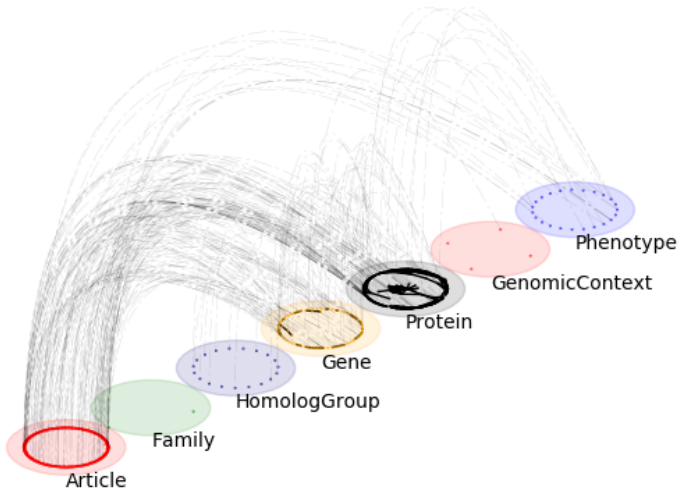
We argue there exists an efficient heuristic-based approach.



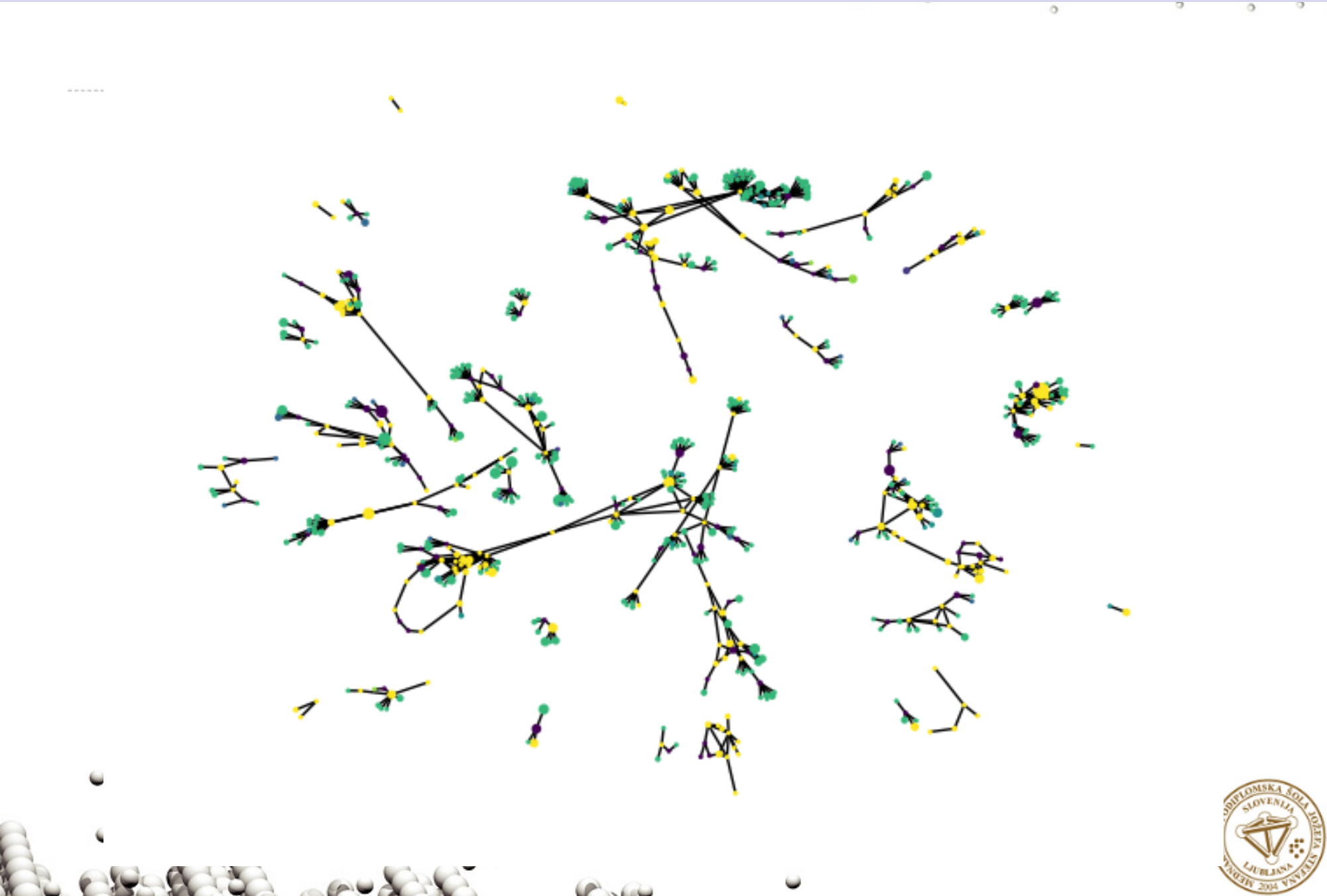
Fighting the combinatorial explosion - network construction

Basic procedure

- collect network data on the studied phenomenon
- merge the data into a single heterogeneous network
- simplify the obtained network, or learn directly from it



Example BioMine network



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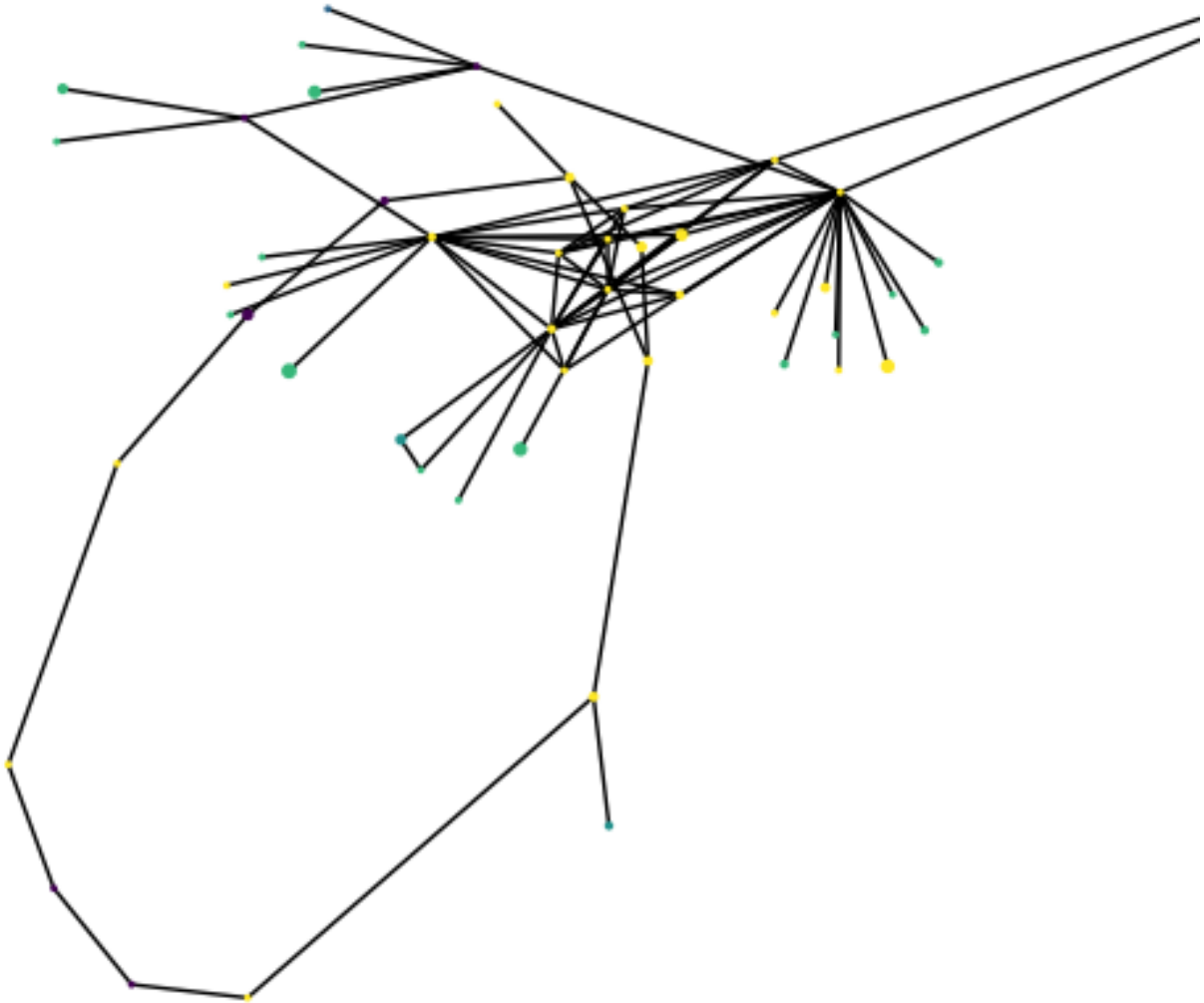

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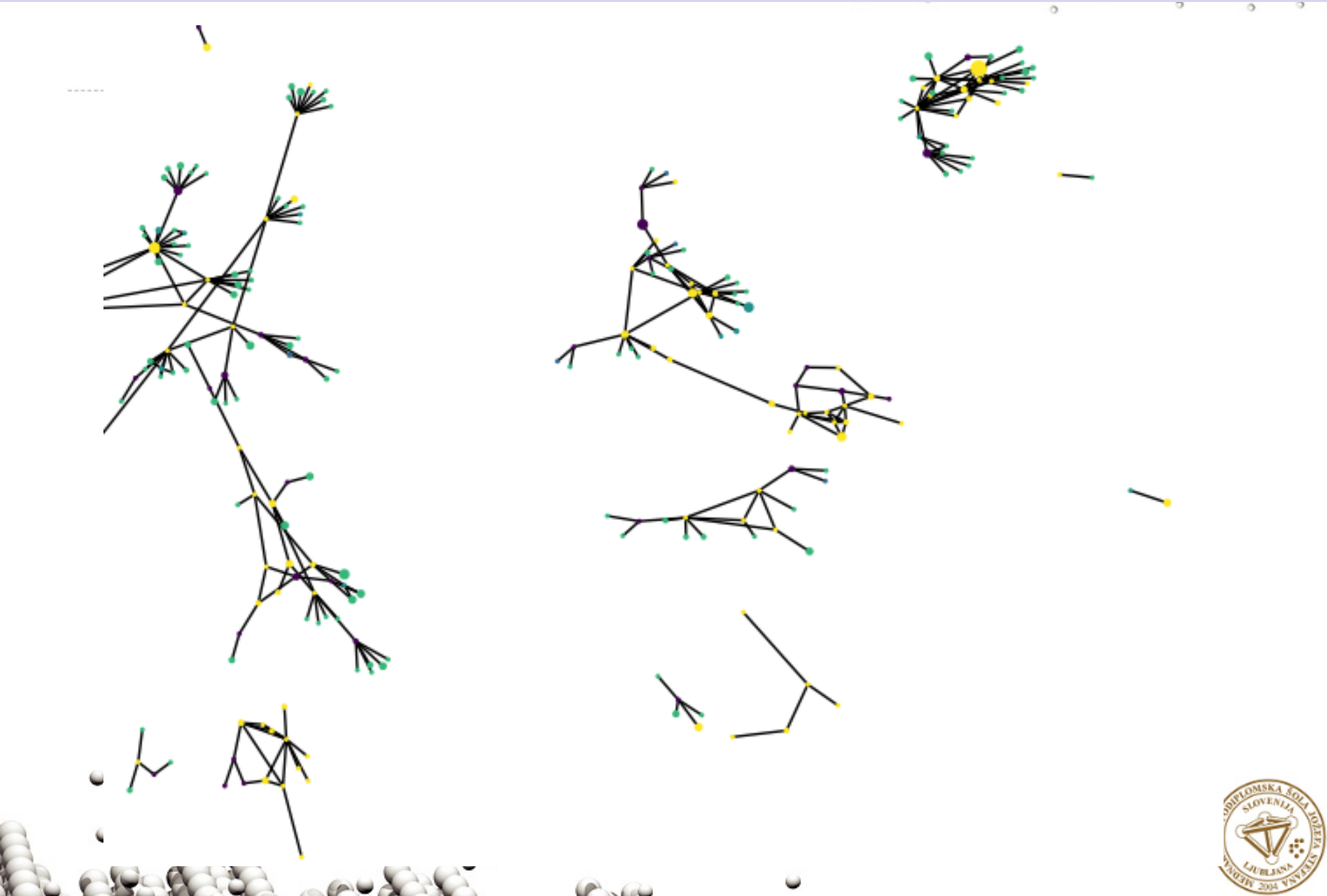
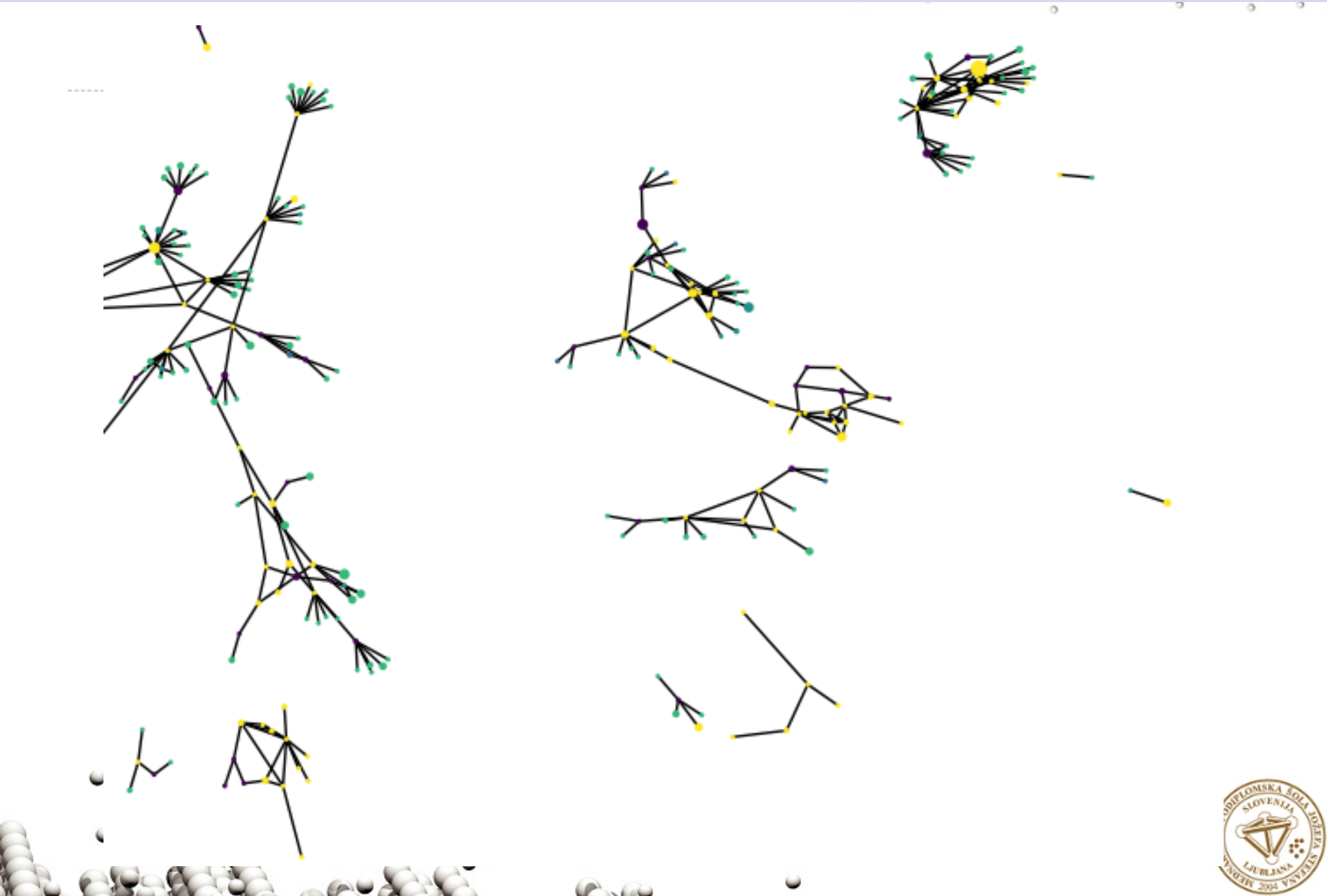
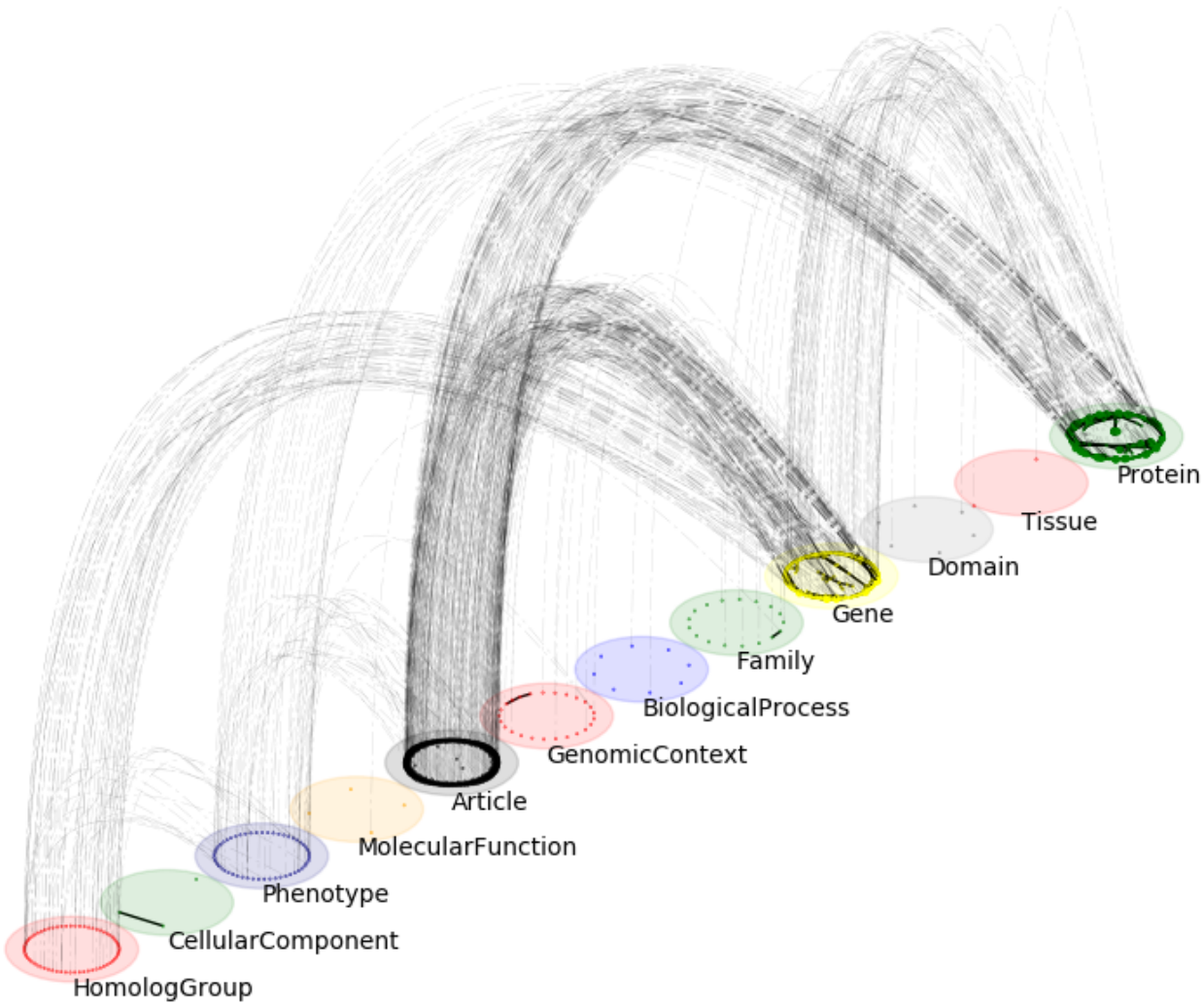


Example BioMine network



Up to 8 layers of interconnected information



Subset extraction

Extraction algorithm

A multiplex network Ψ is decomposed into individual communities via the use of *Louvain* algorithm. Initial term list ψ is then splitted according to community presence, such that initial terms $t_1, t_2, .., t_n$ are assigned to a subset $\phi \in \psi$ *iff* $t_{x..y} \in \Psi_{x..y}$.