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Community-based semantic subgroup discovery (CBSSD)

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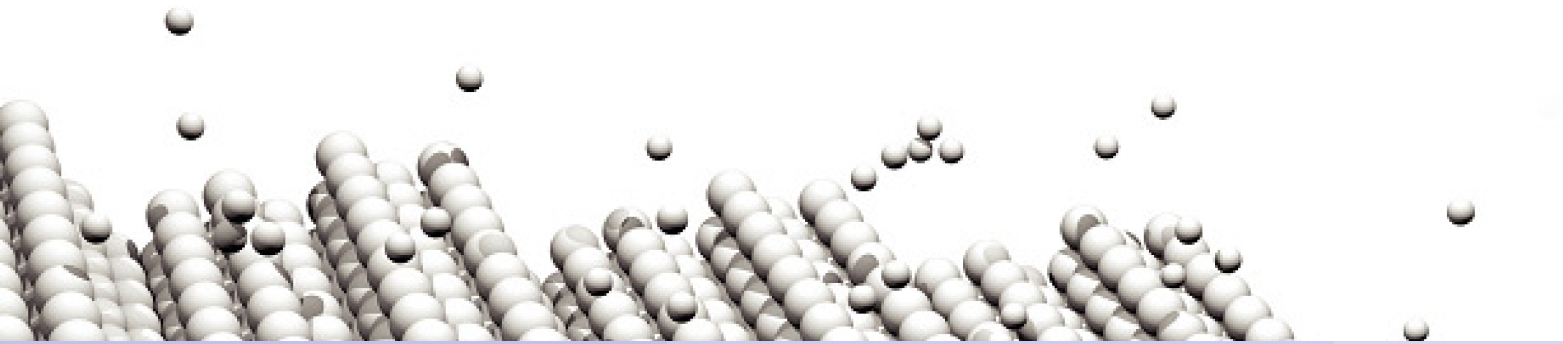

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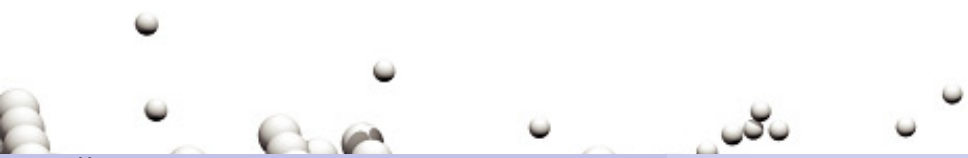


Introduction

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

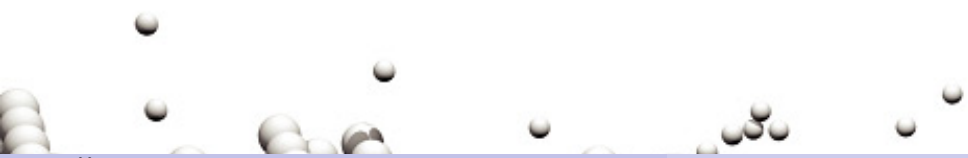
How can an algorithm learn from a complex network?

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

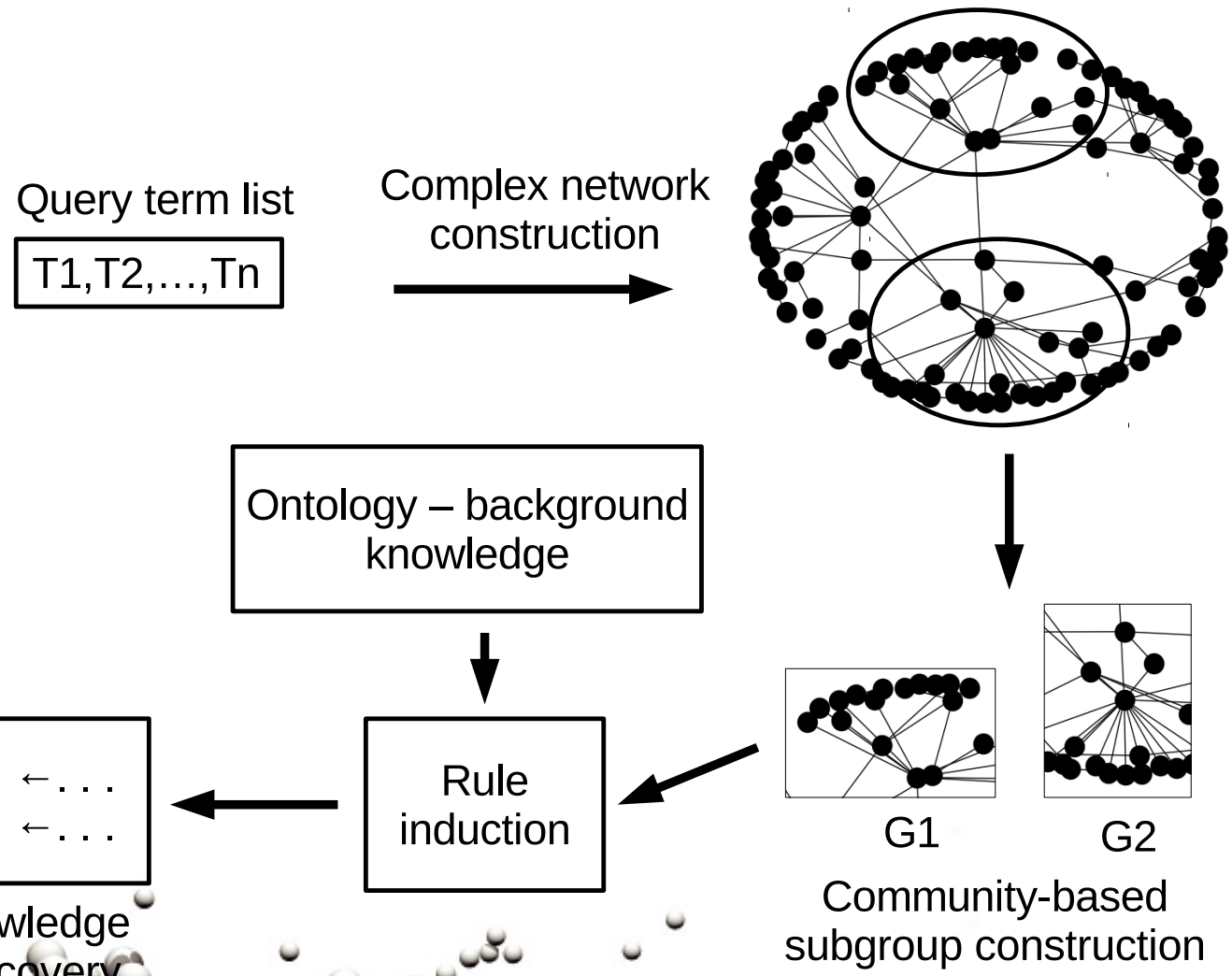
Let $G_1, G_2, .., G_n$ be n distinct genes we are interested in. Although individual genes, or the whole group of genes doesn't return any interesting results, we can further explore the subspace of n genes.

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

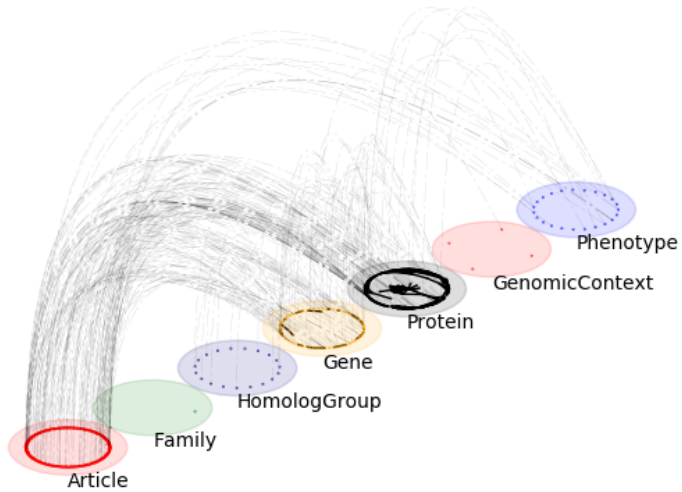
We argue there exists an efficient heuristic-based approach.



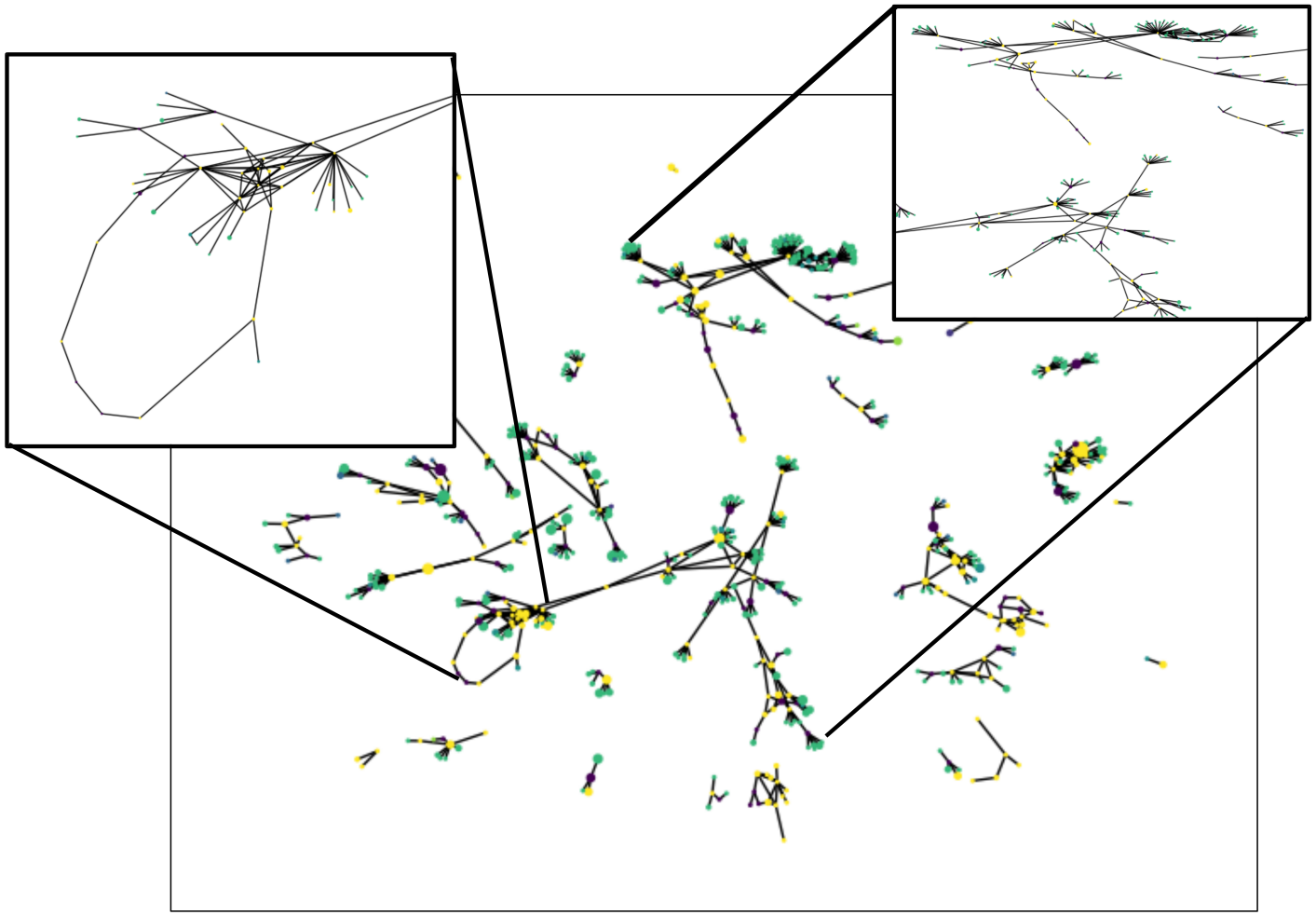
Fighting the combinatorial explosion - network construction

Basic procedure

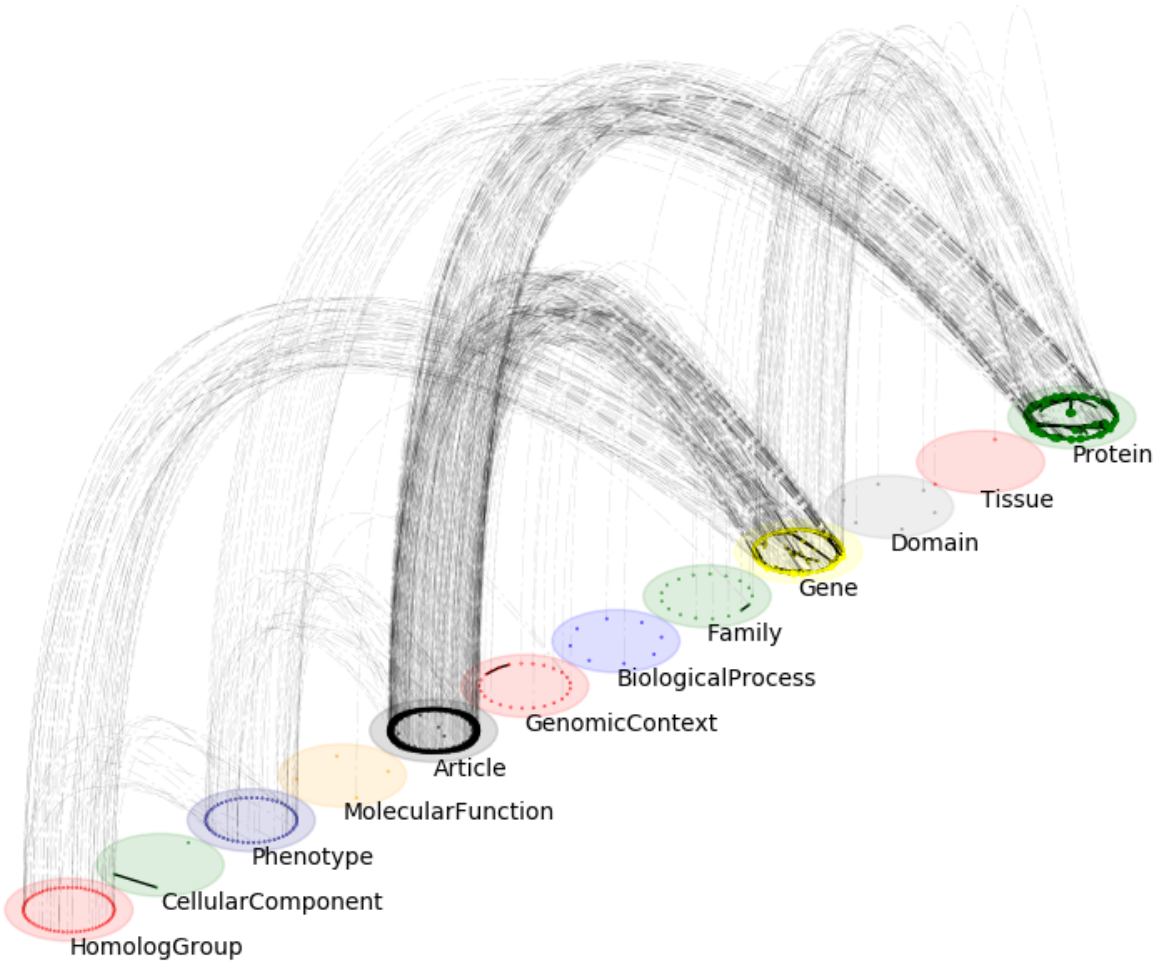
- collect network data on the studied phenomenon
- merge the data into a single heterogeneous network
- simplify the obtained network, or learn directly from it



Example BioMine network



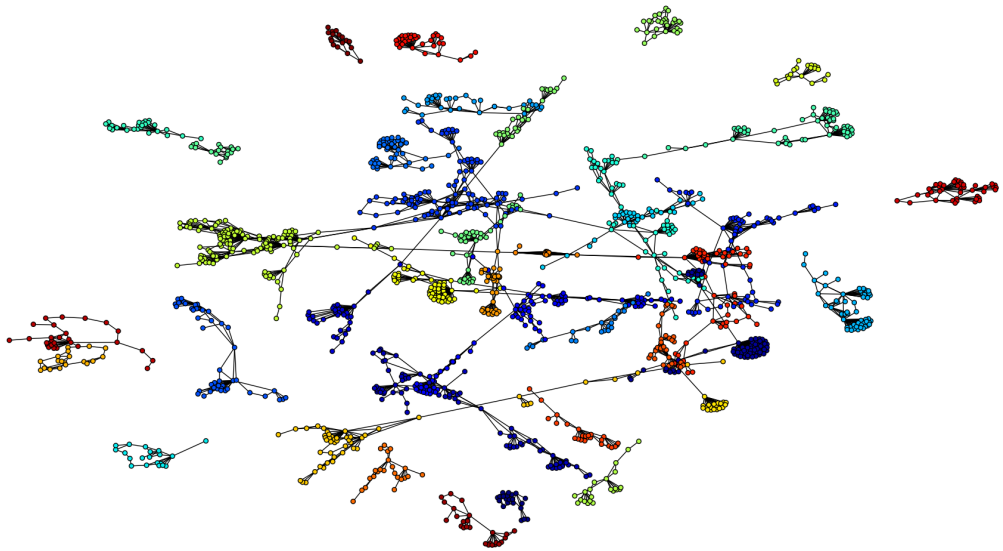
Up to 12 layers of interconnected information



Subset extraction

Extraction algorithm

A multiplex network Λ is decomposed into individual communities via the use of *Louvain* algorithm. Initial term list $\Psi_{1,..,n}$ is then splitted according to community presence, such that each subset of terms $\Psi_{x \in \{1,..,n\}}$ is assigned to a target class ζ_x.



Intermediary result

Constructed $\zeta_{1,..,n}$ are interpreted as target classes for the semantic rule learning step. The objective function thus becomes:

Learning objective

Learn a rule set Δ for individual classes $\zeta_{1,..,n}$ using background knowledge (Ξ) in form of ontologies, such that the likelihood of individual class representation $\zeta_x; x \in \{1, .., n\}$ is maximized.

$$\Delta_{\zeta_1,..,\zeta_n} = \underset{i \in \zeta_1,..,\zeta_n\}}{argmax} \left[P(\Delta_{\zeta_i} | \Xi) \right] \tag{1}$$

Semantic rule learning

Background knowledge representation

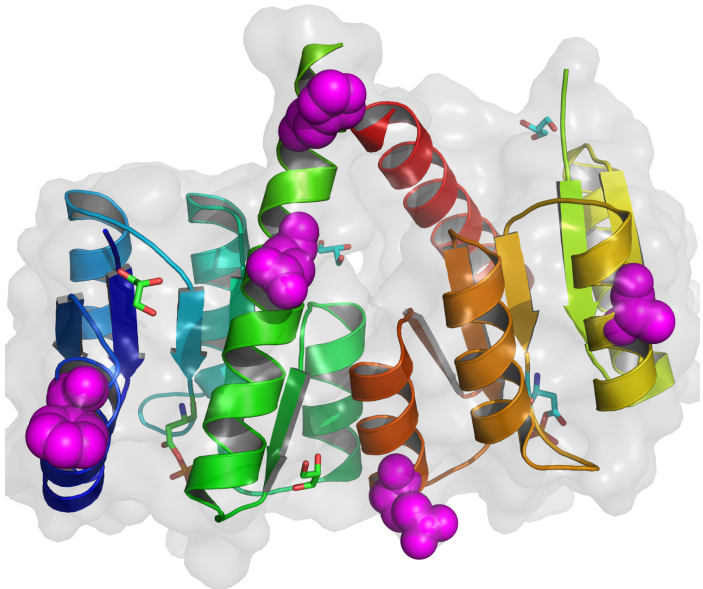
- Individual term sets are fist projected into $\Xi(BK)$ space
- Extensive knowledge from $GO, PFAM, KEGG, ..$ used
- Rules can be generalized
- Supervised descriptive learning task

$$R_1 \rightarrow \bigwedge_i GO_i; i \in \{GO_{R_1}\}$$
$$R_2 \rightarrow \bigwedge_i GO_i; i \in \{GO_{R_2}\}$$
$$\dots$$
$$R_n \rightarrow \bigwedge_i GO_i; i \in \{GO_{R_n}\}$$

Practical example - SNPs

Description

SNPs within protein binding sites previously identified term set ψ indicates association with DNA-related processes, cancer development and membrane mechanisms. We were interested, whether there exist general explanations for latent, community-based patterns.



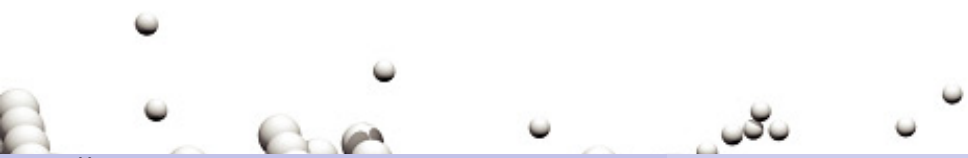
Practical example - SNPs (2)

General result

Largest communities corresponded to the most significant terms, identified in the previous study - proof of structure-based enrichment

Example

Many conjuncts emerged for more marginal communities - this is the new knowledge. For example: *CASR* gene was in previous study not directy associated with arginine-binding process.



Short-term development

Upgraded CD

The InfoMap equation is already used to incorporate the information on multiplex edges.

Ontology processing speedup

Recent work by *Kralj et. al.* present a method capable of significant speedups (10-10x) at no cost with regard learned knowledge representations. This approach makes CBSSD scale better

Representation learning in streaming context

Can the CBSSD learn and update its knowledge in the context of a dynamical process?