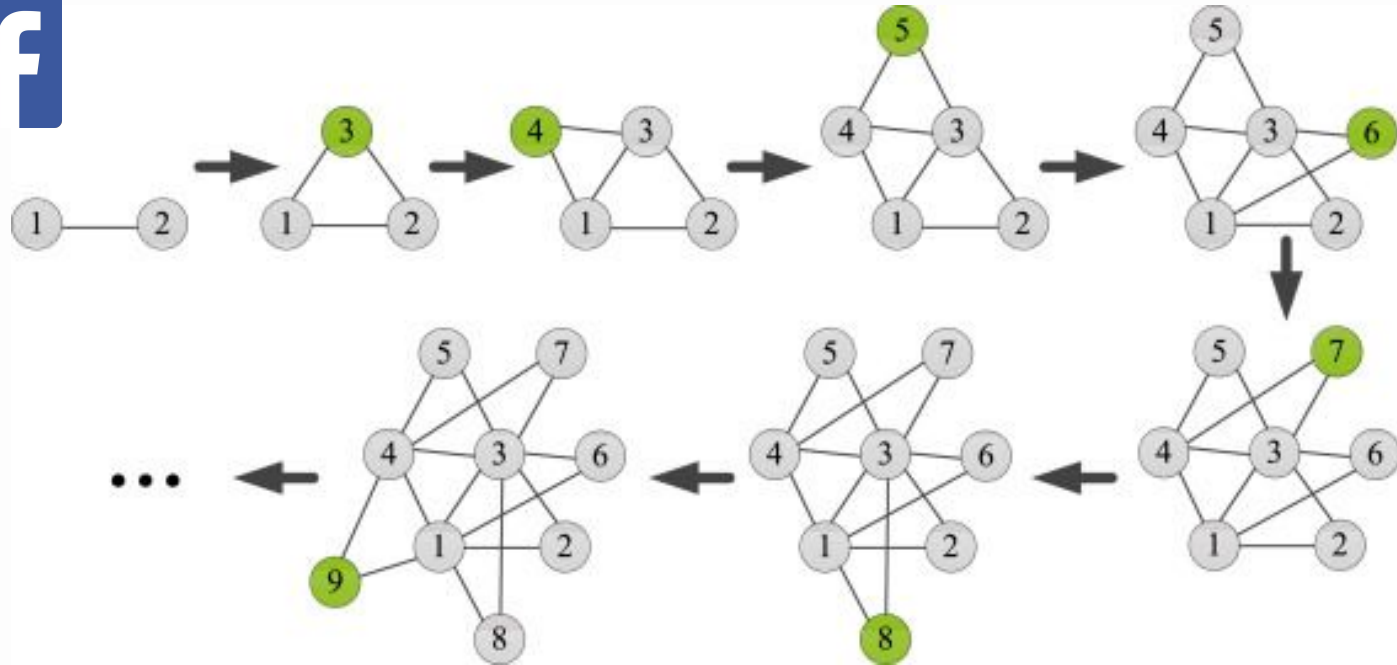# Uncovering Temporal Patterns in *Saccharomyces cerevisiae* Gene Co-expression Networks Through Dynamic Community Detection

CS 198 Proposal: Atienza & Maximo

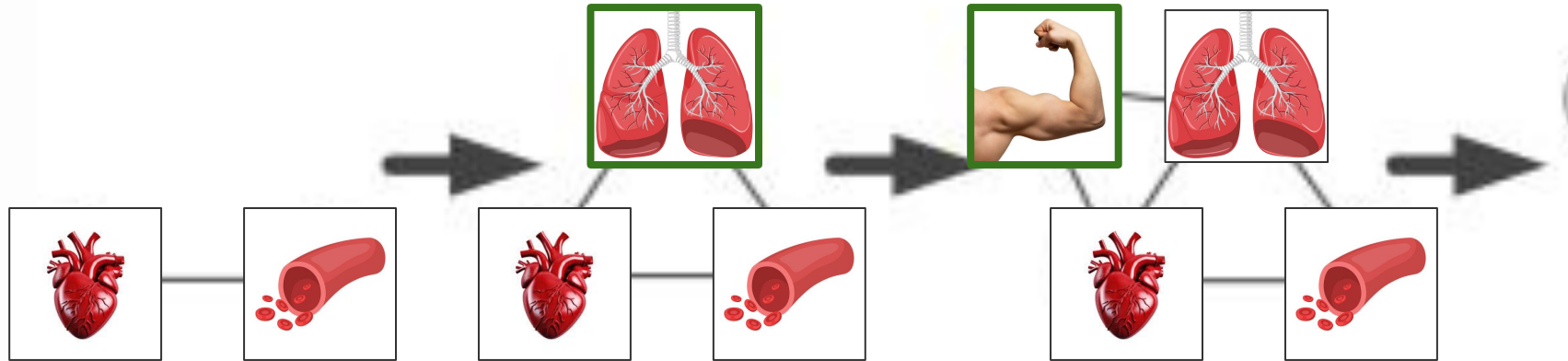**01** **Overview of Biological Networks, Dynamic Community Detection, and Gene Co-Expression Networks**

To put into perspective…

To put into perspective...

...the same goes for genes!

Overview of Biological Networks

Biological systems are inherently complex.

They involve numerous interacting components, such as genes, proteins, and metabolites, all working together to regulate life processes (Barabási and Oltvai, 2004).

They exhibit community structures.

These may pertain to functional modules which work to perform a biological role. It is an interesting area of research for analyzing how certain molecules are grouped within cells (Yu et al., 2013).

They are not static.

The dynamic nature is evident in gene co-expression networks. Studying the structure within these networks can provide insights on the regulation of biological functions and the interactions between genes.

Overview of Dynamic Community Detection

Most of the literature is focused on static relations.

This does not accurately represent the evolutionary world we live in.

Time is an important component in studying these patterns.

The dynamic nature of real-world networks complicates the task of community detection. The need to analyze the knowledge from the temporal dimension has become more urgent, since network events

Over time, the structure of a dynamic network changes.

There are insights to be gained from understanding these changes and their transformations over time.

Overview of Gene Co-expression Networks

They model interactions between genes.

Nodes represent genes, and edges signify co-expression relationships, where the strength of an edge correlates with the similarity in gene expression.

They are dynamic in nature.

There is a need to capture the temporal dynamics of GCNs because gene co-expression patterns fluctuate over time, which also affects the community structure.
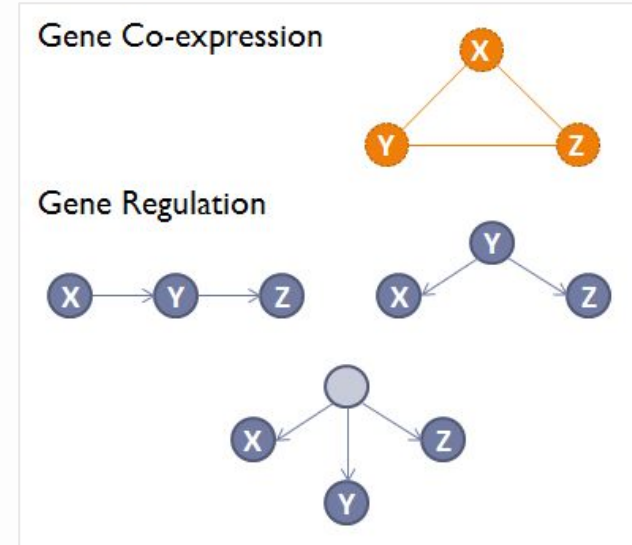
Preliminaries

Gene Co-expression Networks

- Biological Network
- Nodes - Genes; Edges - <u>Coexpression Relationship</u>
  - A measure of similar patterns of activity (i.e. Expression Levels) across different conditions.
  - If a pair of genes have their activity go up or down together, they are said to be <u>coexpressed.</u>
    - They must work together!

https://en.wikipedia.org/wiki/Gene_co-expression_network

Community Detection

- Static Community Detection
  - Assumes the network is fixed throughout different time periods
  - Can reveal hierarchies in networks
- Dynamic Community Detection
  - Detect how communities vary at each time step
  - Can reveal temporal patterns
  - Our method of interest
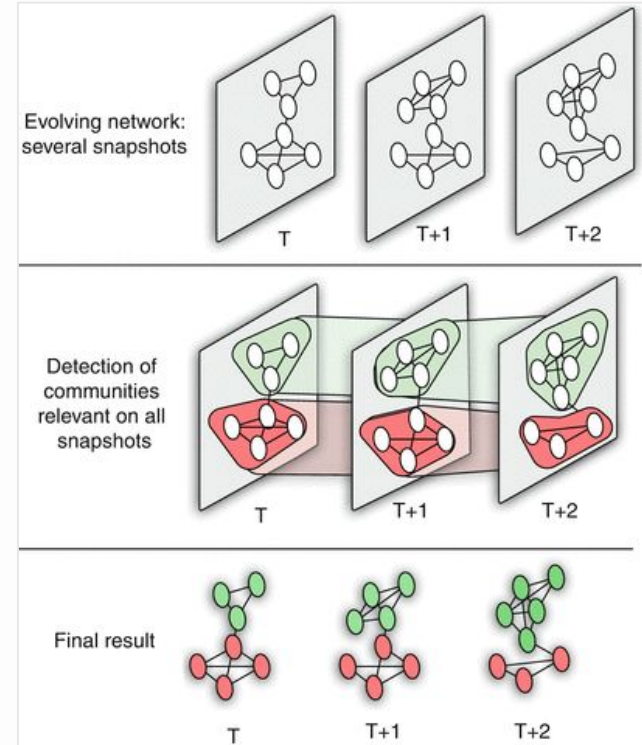
https://link.springer.com/referenceworkentry/10.1007/978-1-4614-6170-8_383

Saccharomyces cerevisiae

- Well documented yeast cells, 6000 genes
- Dataset from Cho et al (1998)
  - Genes across the different phases of the mitotic cell cycle
  - Time-series data
  - How do the gene networks change at different phases of mitosis?

https://byjus.com/biology/mitosis/
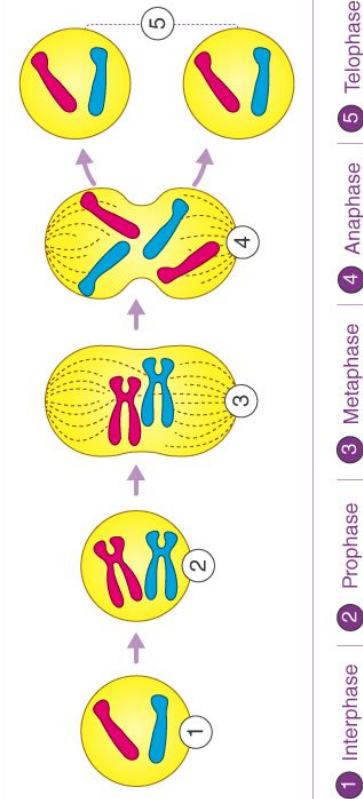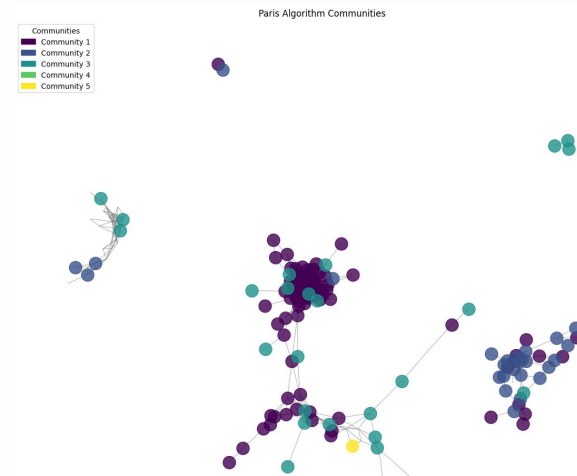
Related Works

Hierarchical CD on GCNs

- Calderon and Ventures (2024)
  - Explored hierarchical CD in *S. cerevisiae* to enhance functional classification of cell-cycle regulated genes
  - Analyzed the performance of three algorithms:
    - Girvan-Newman
    - Paris
    - LFM

Hierarchical CD on GCNs

- Calderon and Ventures (2024)
  - Hierarchical CD is appropriate for GCNs due to their hierarchical nature.
  - Valuable insights into the static structure of GCNs
  - Open problem: dynamic nature of gene interactions

Paris Algorithm Communities
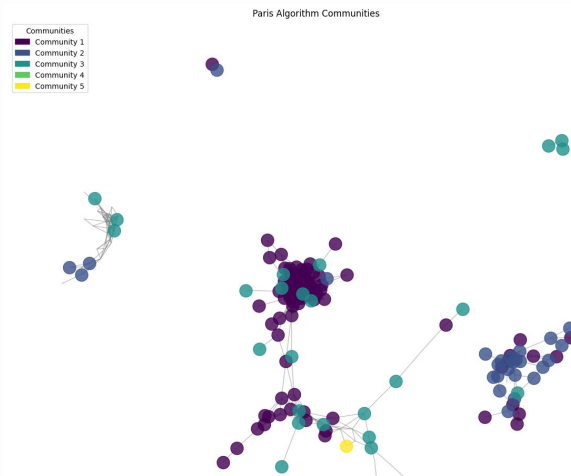
Dynamic Community Detection Algorithms

- C-Blondel Algorithm
  - Proposed by Seifikar et al. (2020)
  - Built upon the Louvain algorithm, and leverages historical information to improve execution time
  - Compresses the network into supernodes and superedges
  - Identifies **destructive nodes** through a degree centrality heuristic
  - Faster than other DCD algorithms (D-Blondel, S-Blondel)
  - Comparable performance in terms of modularity

Dynamic Community Detection Algorithms

- Semi-supervised ENMF (sE-NMF) Algorithm
  - Proposed by Ma and Dong (2017)
  - Combines evolutionary nonnegative matrix factorization (ENMF) and spectral clustering for dynamic community detection, balancing clustering accuracy and temporal consistency
  - Key advantage: Leveraging **a priori information**, avoiding local optima without affecting the run time complexity

Dynamic Community Detection Algorithms

- Semi-supervised ENMF (sE-NMF) Algorithm
  - Evaluated against three well-known DCD algorithms (FacetNet, Kim-Han, DYNMOGA)
  - Particularly interesting network: breast cancer progression based on gene expression data
  - Outperformed the other algorithms in terms of specificity and sensitivity
  - Great potential as a tool for assessing temporal networks of disease progression

04

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Thanks!

Do you have any questions?

Carmelo Ellezandro Atienza | Calvin James Maximo

cratienza1@up.edu.ph | ctmaximo1@up.edu.ph