

Outline of the Seminar Paper

Community Detection in Bacterial and Viral Networks

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Proposed Structure of the Paper (15–20 pages)

1. Introduction (2–3 pages)

(a) Motivation

- Why networks are important?
- Biological networks (protein interactions, gene regulation)
- Why community detection?

(b) Definition of a Network

- Graph as a mathematical object
- Nodes and edges
- Adjacency list
- Adjacency matrix
- Directed vs. undirected networks
- Weighted vs. unweighted networks
- Weighted undirected network: $G = (V, E, W)$

(c) What can we do with Networks?

- Descriptive statistics
- Structural analysis
- Clustering and communities
- Prediction of Future Community Behavior

2. Network Summary Statistics (2–3 pages)

(a) Basic Metrics

- Number of nodes
- Number of edges
- Density
- Average degree

(b) Degree Distribution

- Scale-free networks
- Power-law behavior (if relevant)

(c) Centrality Measures

- Degree centrality
- Betweenness centrality
 - Node betweenness
 - Edge betweenness
- Closeness and betweenness (brief)

3. Similarity Measures for Community Comparison (2 pages)

- (a) Adjusted Rand Index (ARI)
- (b) Adjusted Mutual Information (AMI)
- (c) Comparison of ARI and AMI
 - When to use which measure

4. Community Detection Methods (4–5 pages)

- (a) Modularity
 - Basic idea
 - Modularity formula:

$$Q = \frac{1}{2m} \sum_{ij} (A_{ij} - P_{ij})\delta(c_i, c_j)$$

- (b) Edge Betweenness (Girvan–Newman)

- Main focus of the paper
 - Idea: edges with high betweenness separate communities
 - Algorithm:
 - i. Compute edge betweenness
 - ii. Remove the strongest edge
 - iii. Repeat
 - Advantages and disadvantages

- (c) Louvain Method

- Greedy optimization of modularity
 - Very fast
 - Hierarchical structure
 - Limitations of Louvain
 - Motivation for improvement -> Leiden

- (d) Leiden Method

- Improvement over Louvain
 - Guarantees well-connected communities
 - State-of-the-art method

5. Data Description (2 pages)

(a) Data Source

- Bacterial protein similarity networks
- Viral protein similarity networks

(b) Descriptive Comparison of Bac and Vir

- Size
- Density
- Degree distributions

(c) Network Construction

- Nodes represent proteins
- Edges represent sequence similarity
- Weights: bit score
- bit score formula:

$$S' = \frac{\lambda S - \ln K}{\ln 2}$$

(d) Preprocessing

- Filtering
- Removal of self-loops
- Largest connected component

6. Experimental Setup (2 pages)

(a) Implementation

- Python (NetworkX)
- https://github.com/j0nascz/Paper_SMNCA.git

(b) Parameters

- Louvain: resolution parameter
- Leiden: resolution parameter
- Edge betweenness: number of cuts

(c) Evaluation Criteria

- Pairwise comparison between methods and parameter settings
 - Changing parameters(e.g resolution parameter) in Leiden and Lovain and comparing results with ARI and AMI

7. Results (3–4 pages)

(a) Method Comparison

- Tables: number of communities
- Modularity values
- Runtime

- (b) Hyperparameter Sensitivity Analysis
 - Plots: resolution vs. number of communities
 - ARI and AMI vs. resolution

- (c) Interpretation
 - Stability of communities

8. Discussion (2 pages)

- Why do Bac and Vir differ?
 - Structural differences between the networks
 - Effect on detected communities
- Which method is more stable?
 - Interpretation of stability based on ARI and AMI
 - Intra-method vs. inter-method differences
- Interpretation of ARI/AMI results
- Resolution limit problem

9. Conclusion (1 page)

- Summary of findings
- Main insights
- Methodological implications
- Outlook and future work