



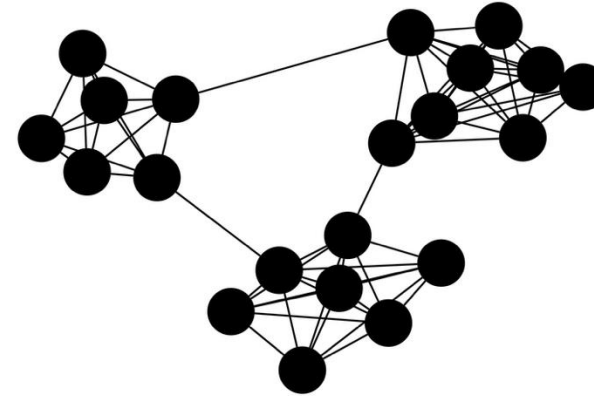
EURO^{4SEE}

Residue Networks: Understanding the Time Evolution and Mutations of
Proteins from a Graph Theoretical Perspective

Tandac Furkan Guclu
Sabancı University

BC revisited

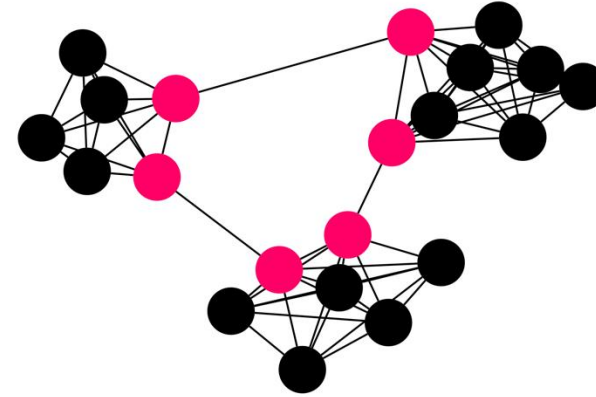
- A central node/edge has an impact on information flow in a network
- A common centrality measure is BC
- The ratio for the number of the shortest paths travelled through an arbitrary element and the number of all shortest path between those nodes, calculated for all node pairs.



$$BC(X) = \sum \left(\frac{P(a, b|X)}{P(a, b)} \right)$$

BC revisited

- A central node/edge has an impact on information flow in a network
- A common centrality measure is BC
- The ratio for the number of the shortest paths travelled through an arbitrary element and the number of all shortest path between those nodes, calculated for all node pairs
- High BC residues are important for protein function



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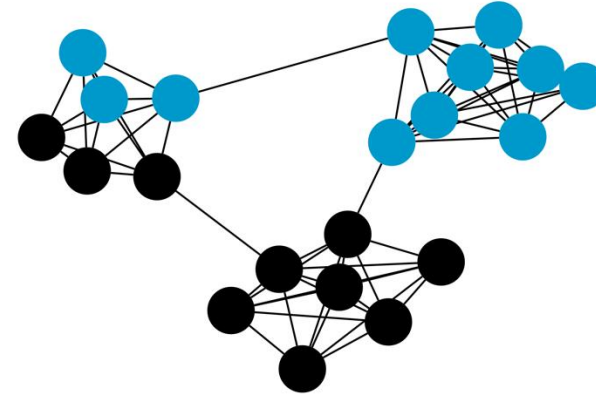
Sheik Amamuddy *et al.*, J Chem Inf Model 2020.

Penkler *et al.*, J Chem Inf Model 2018.

Ozbaykal *et al.*, Proteins 2015.

Community detection

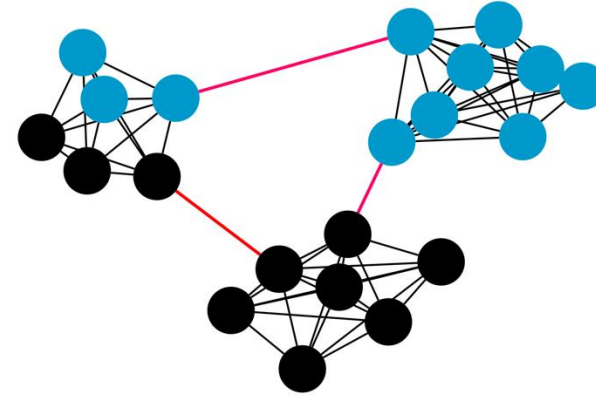
- Community analysis shows close-knit groups in a network
- A community is a group of nodes that connected to each other, without an edge to outer nodes
- Girvan-Newman algorithm removes the most central (highest BC) edge one-by-one and searches for communities



1. Calculate edge BC
2. Remove the edge with highest BC
3. Check for emergence of new communities
4. Return to step 1 and iterate

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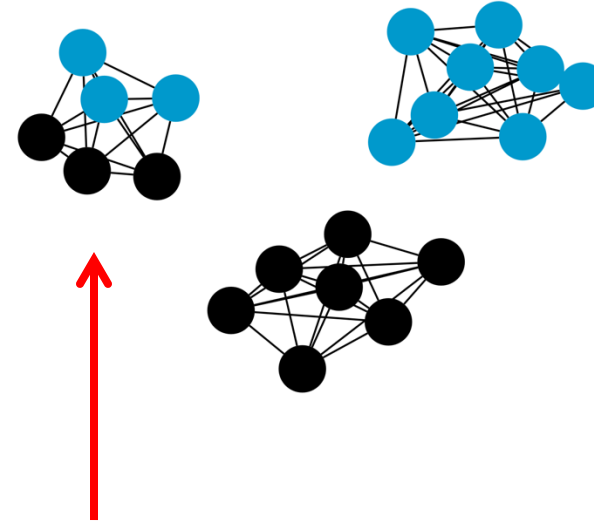


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Community composition

- Assessing the composition of communities and scoring the structural origins of members shed light on communication between the segments

$$\Omega = 3$$



Blue and Black together in a community in this instance so the score is 1.

Thanks!



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