

Protein interaction networks: centrality, modularity, dynamics, and applications

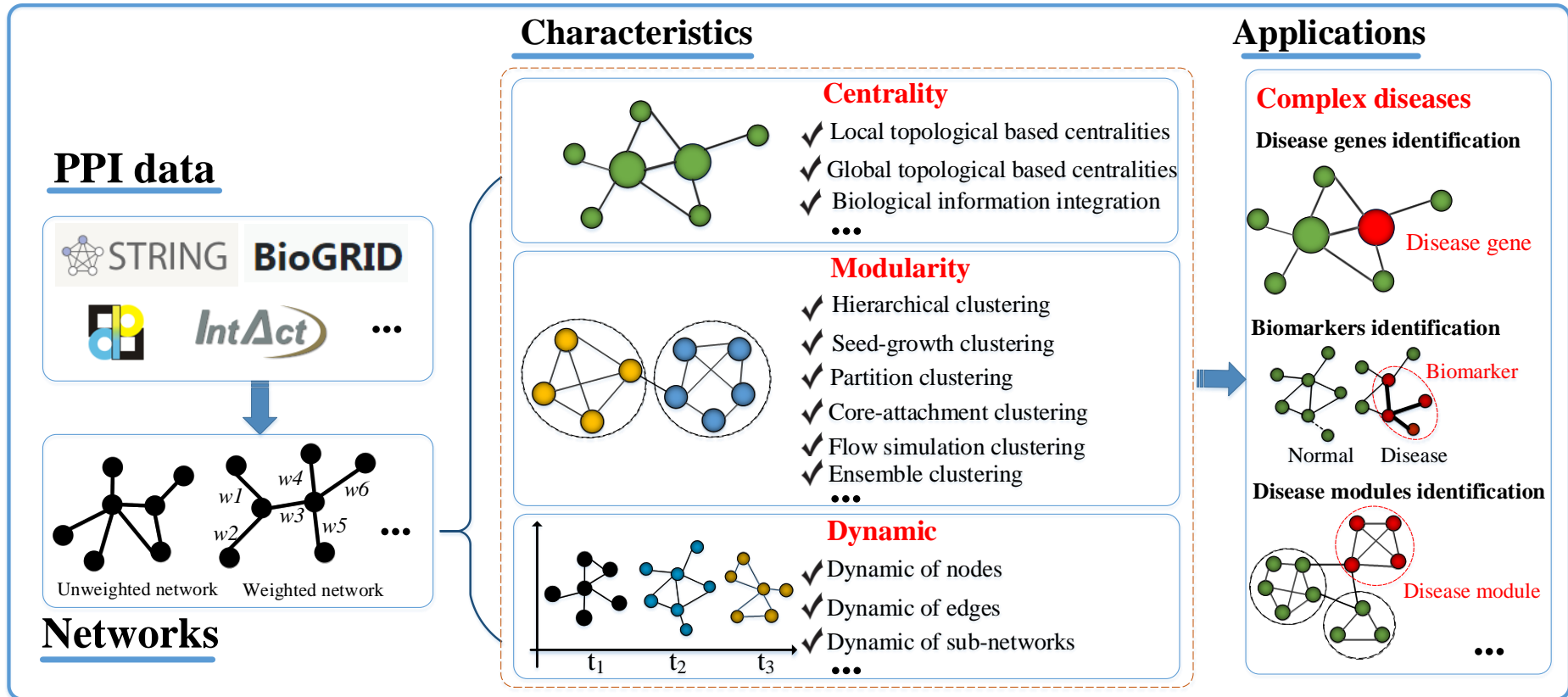
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Main Work

- In this review , we focus on a range of computational approaches for analyzing protein interaction networks(PINs). We show recent advancements in three main characteristics of PINs, including centrality, modularity, and dynamics. And we also introduce applications of PINs analysis to the complex diseases-related studies and discuss the challenges in this areas.

The flow chart of analysis procedure



- Collecting PPI data and constructing protein interaction networks (PINs)
- Analyzing three main characteristics of PINs: centrality, modularity, and dynamics
- Applications of PINs in the identification of disease genes, biomarkers, disease modules, and so on