

Mapping Host-Pathogen Interactions via Gene Co-expression Networks

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Figure: Plant Pathology

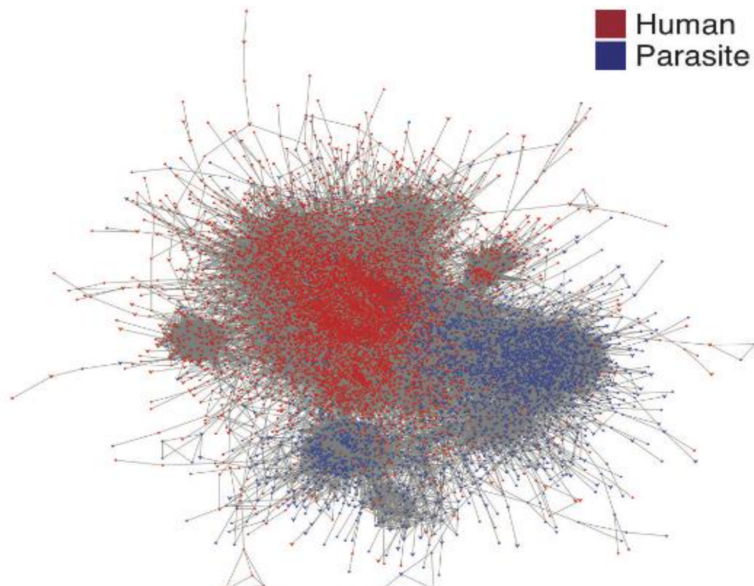
- Data
- Gene Expression
- **Method**: Weighted correlation network analysis

Method:

- 1 Gene co-expression similarity measure s_{ij}
- 2 Construct an adjacency matrix $A = (a_{ij}) = \begin{cases} 1 & \text{if } s_{ij} > \tau \\ 0 & \text{otherwise} \end{cases}$
- 3 Topological overlapping matrix (TOM)

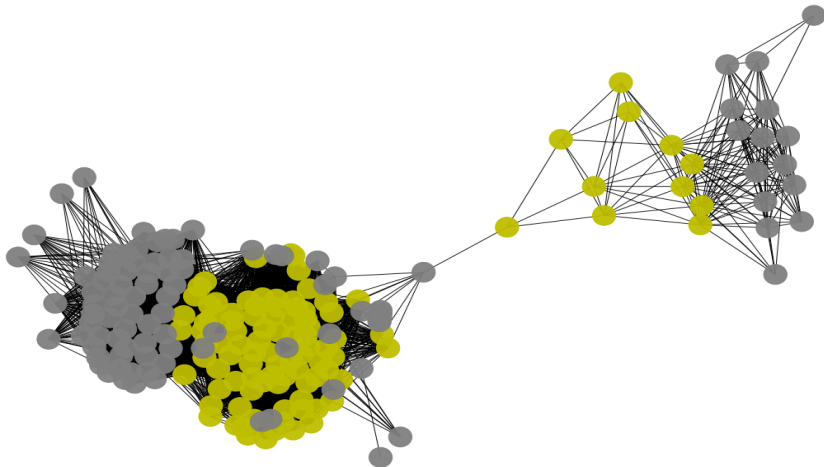
Weighted correlation network analysis

Human
Parasite

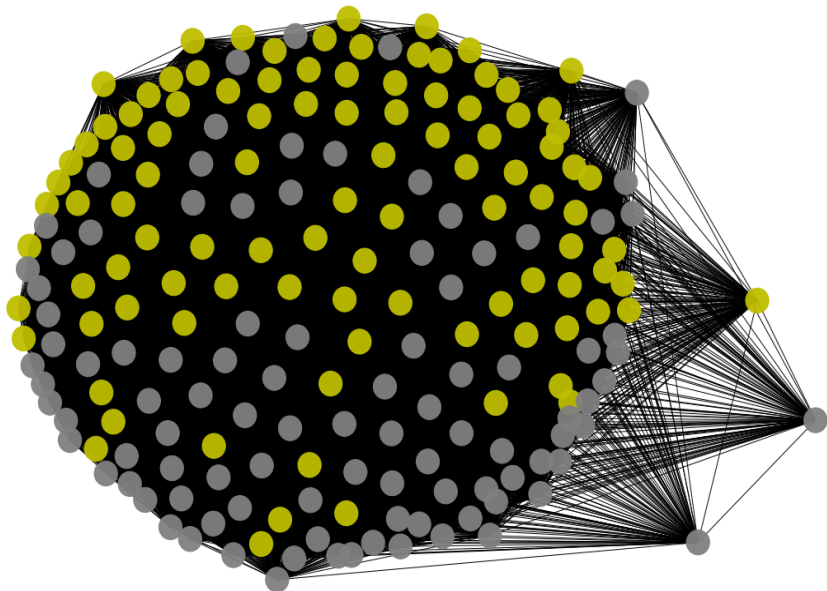


Weighted correlation network analysis - Result

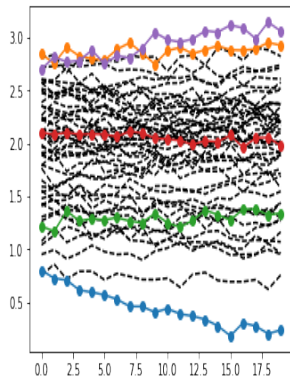
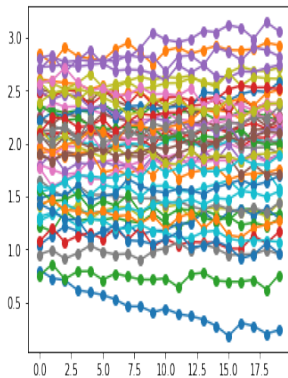
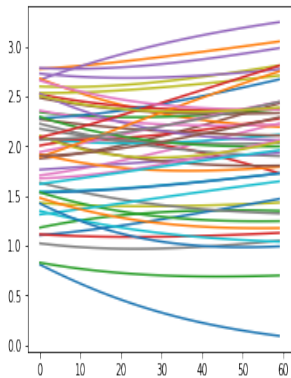
100 genes from pathogen and 100 from host



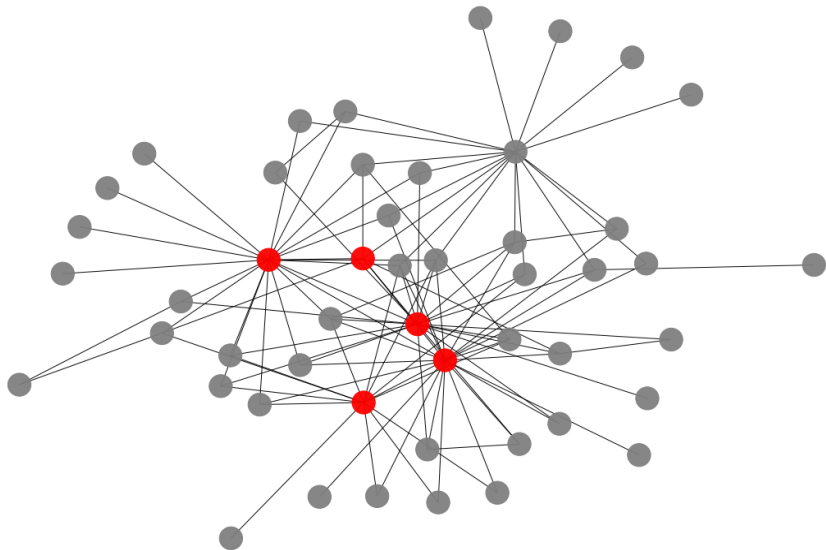
Weighted correlation network analysis - Result



Simulation

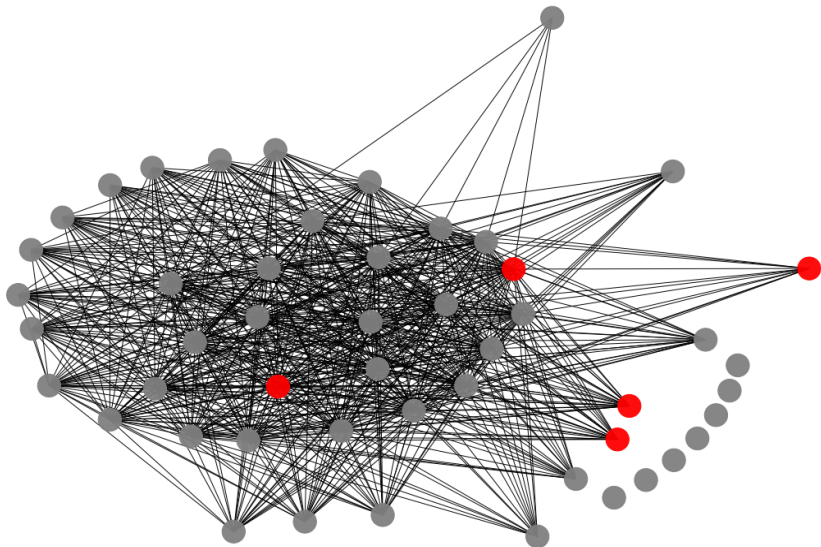


Simulation



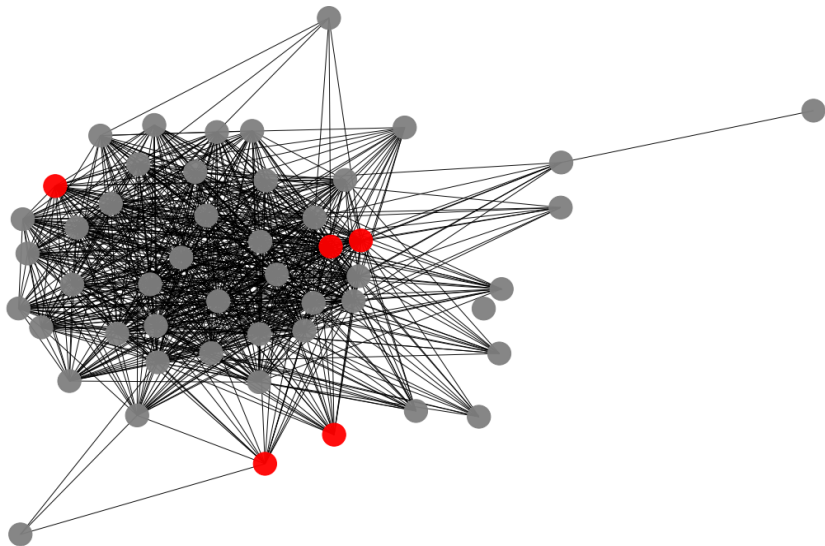
Simulation

Based on observation on 5 time points



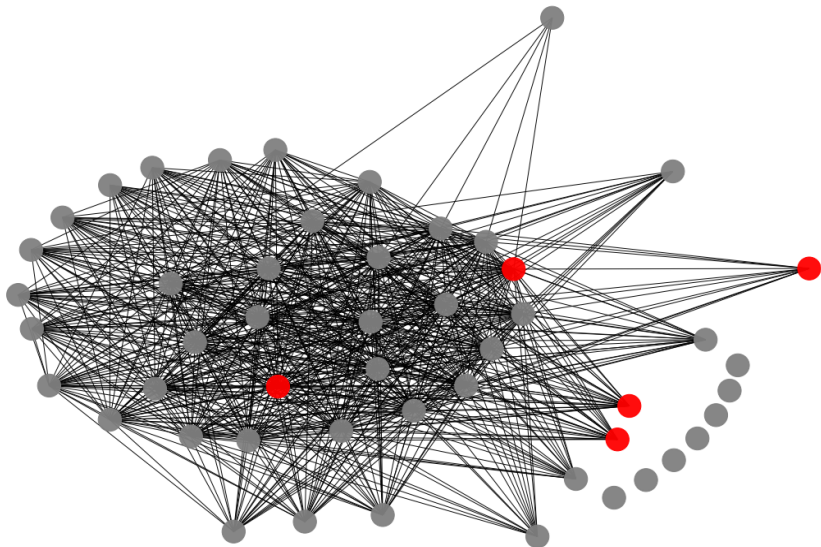
Simulation

Based on observation on 10 time points



Simulation

Based on observation on 20 time points



Future work:

- Continue numerical experiment
 - Can we construct correlation network using time series data?
 - If yes, how much data we need?

- Other approaches

- Dynamic Bayesian networks

Penfold, Christopher A., and David L. Wild. "How to infer gene networks from expression profiles, revisited." Interface focus 1.6 (2011): 857-870