Network Metamodeling: Effect of Correlation Metric Choice on Phylogenomic and Transcriptomic Network Topology

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Background

Network models involve modelling the similarity between pairs of objects of interest. Meta-modeling involves creating models of models to evaluate the effects of using different input parameters. A parameter of such a network model could be the similarity metric chosen to quantify the similarity between nodes in order to weight the edges. Many similarity metrics exist to quantify different aspects of similarity.

Science

- We explore a variety of similarity metrics for the construction of networks and different approaches for the comparison of networks.
- We constructed network models of phylogenomic and transcriptomic datasets using different similarity metrics and investigated how the choice of similarity metric affects resulting network topology.
- We developed Cross-Network Topological Overlap, a measure for use in the comparison of node neighbourhoods in different networks.

Significance

- The Cross-Network Topological Overlap method allows one to identify the portions of the network affected by the choice of similarity metric.
- The similarity metric chosen can have a large impact on the topology of the resulting network, which carries through to the results of further analyses. The choice of similarity metric could thus greatly impact the resulting biological interpretations
- As each similarity metric describes and quantifies a different aspect of similarity, the use of multiple similarity metrics provides multiple valuable perspectives on the data.
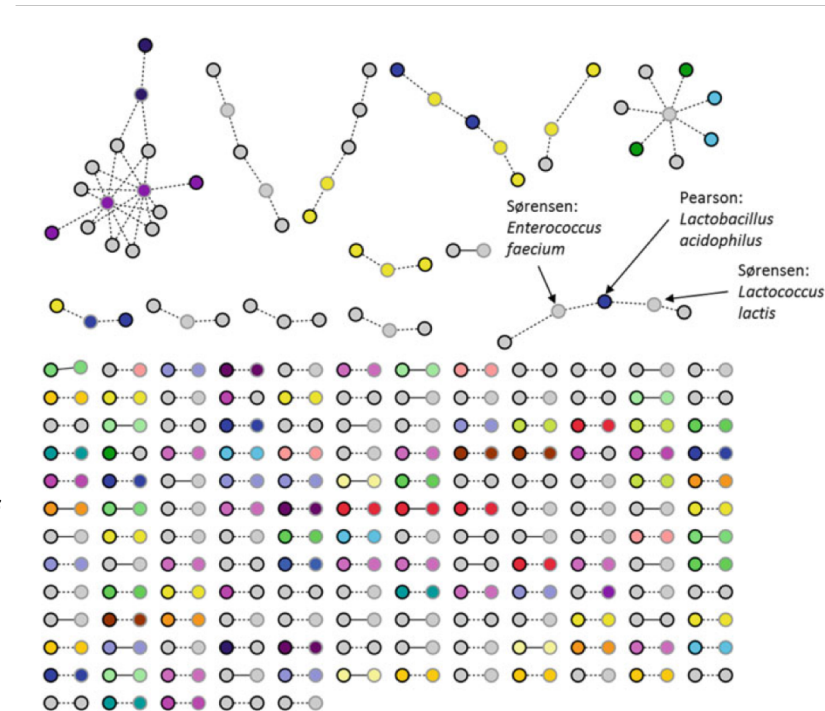
Cross Network topological overlap network for the Pearson and Sørensen Bacterial phylogenomic networks.

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