CoNet – a Co-occurrence Network inference tool
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Microorganisms interact in various ways, e.g. as parasites or predators, as competitors for scarce resources, in cross-feeding chains etc. Such ecological interactions as well as niche preferences and random factors shape the abundances of microorganisms. In recent times, more and more metagenomic experiments measure the abundance of microbial DNA across multiple samples, spanning diverse environments from the ocean to the human body. These abundances are the starting point for co-occurrence analysis, which aims at predicting ecological relationships (who interacts with whom) by constructing association networks (who is frequently found together with whom). Here we present CoNet, which offers a variety of association network construction routines. CoNet is available at:
http://systemsbiology.vub.ac.be/conet

Typical similarity-based association network construction workflow

For each pair of taxa, the similarity of the two abundance profiles is assessed. Popular scoring functions include measures of correlation (e.g. Spearman, Pearson), dissimilarity (e.g. Bray-Curtis, Kullback-Leibler) and similarity (e.g. mutual information).

As a Cytoscape plugin, CoNet makes use of the network visualization and analysis power of Cytoscape [1]. A special feature of CoNet is its capacity to combine several measures into an ensemble approach. The idea of ensemble is that different prediction methods have different weaknesses, so that faulty predictions are only supported by a minority of the methods.

As a general-purpose association network inference tool that supports a variety of popular similarity-based network inference approaches and offers unique features such as the combination of methods into an ensemble approach. Though CoNet was designed to analyze data from metagenomic experiments, it can infer relationships between any set of repeatedly observed objects (genes, compounds etc.) and could thus prove useful in a variety of settings.

References