**From hairballs to hypotheses: microbial network analysis**

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The construction of microbial networks has become a popular method to analyse microbial sequencing data, with dozens of network inference tools available. However, these tools usually return "hairballs", i.e. densely connected networks, which require further analysis in order to derive biological hypotheses from them. Here, I will present a set of tools designed to address this challenge, including microbetag for annotating, manta for clustering, anuran for comparing and mako for querying microbial networks.