The interactions among the constituent members of a microbial community play a major role in determining the overall behavior of the community and the abundance levels of its members. These interactions can be modeled using a network whose nodes represent microbial taxa and edges represent pairwise interactions. A microbial network is a weighted graph that is constructed from a sample-taxa count matrix and can be used to model co-occurrences and/or interactions of the constituent members of a microbial community. The nodes in this graph represent microbial taxa and the edges represent pairwise associations amongst these taxa. A microbial network is typically constructed from a sample-taxa count matrix that is obtained by sequencing multiple biological samples and identifying taxa counts. From large-scale microbiome studies, it is evident that microbial community compositions and interactions are impacted by environmental and/or host factors. Thus, it is not unreasonable to expect that a sample-taxa matrix generated as part of a large study involving multiple environmental or clinical parameters can be associated with more than one microbial network. However, to our knowledge, microbial network inference methods proposed thus far assume that the sample-taxa matrix is associated with a single network. This dissertation addresses the scenario when the sample-taxa matrix is associated with K microbial networks and considers the computational problem of inferring K microbial networks from a given sample-taxa matrix. The contributions of this dissertation include
1) new frameworks to generate synthetic sample-taxa count data.
2) novel methods to combine mixture modeling with probabilistic graphical models to infer multiple interaction/association networks form microbial count data.
3) dealing with the compositionality aspect of microbial count data.
4) extensive experiments on real and synthetic data.

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The public is welcome to attend.