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*Exploring Microbiome Dynamics by Sparse Vector Autoregressive Modeling*

Microbial interactions play important roles on the structure and function of complex microbial communities. With the rapid accumulation of high-throughput metagenomic or 16S rRNA sequencing data, it is possible to infer complex microbial interactions. Co-occurrence patterns of microbial species among multiple samples are often utilized to infer interactions. There are few methods to consider the temporally interacting patterns among microbial species. In this work, we present a Graph-regularized Vector AutoRegressive (GVAR) model to infer causal relationships among microbial entities. The new model has advantage comparing to the original vector autoregressive (VAR) model. Specifically, GVAR can incorporate similarity information for microbial interaction inference—i.e. GVAR assumed that if two species are similar in the previous stage, they tend to have similar influence on the other species in the next stage. We apply the model on a time series dataset of human gut microbiome which was treated with repeated antibiotics. The experimental results indicate that the new approach has better performance than several other VAR-based models and demonstrate its capability of extracting relevant microbial interactions.