



A Bayesian Semiparametric Regression Model for Joint Analysis of Microbiome Data

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The successional dynamics of microbial communities are influenced by the synergistic interactions of physical and biological factors. In our motivating data, ocean microbiome samples were collected from the Santa Cruz Municipal Wharf, Monterey Bay at multiple time points and then 16S ribosomal RNA (rRNA) sequenced. We develop a Bayesian semiparametric regression model to investigate how microbial abundance and succession change with covarying physical and biological factors including algal bloom and domoic acid concentration level using 16S rRNA sequencing data. A generalized linear regression model is built using the Laplace prior, a sparse inducing prior, to improve estimation of covariate effects on mean abundances of microbial species represented by operational taxonomic units (OTUs). A nonparametric prior model is used to facilitate borrowing strength across OTUs, across samples and across time points. It flexibly estimates baseline mean abundances of OTUs and provides the basis for improved quantification of covariate effects. The proposed method does not require prior normalization of OTU counts to adjust differences in sample total counts. Instead, the normalization and estimation of covariate effects on OTU abundance are simultaneously carried out for joint analysis of all OTUs. Using simulation studies and a real data analysis, we demonstrate improved inference compared to an existing method.

Keywords: count data, Laplace prior, metagenomics, microbiome, regularizing prior, process convolution, negative binomial model, 16S ribosomal RNA sequencing

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1. INTRODUCTION

Microbial communities are influenced by several factors whether they live in the host's guts or other occupied niches. Their successional dynamics could further change in response to perturbations of the host or of the surrounding environments (Turnbaugh et al., 2009; Needham and Fuhrman, 2016). Understanding how abiotic and biotic factors influence the dynamics of microbial communities is of great interest in the field of microbiome studies. Recent revolutionary advances in next-generation sequencing (NGS) technologies along with rapidly decreasing costs, have facilitated the accumulation of large datasets of 16S ribosomal RNA (rRNA) amplicon sequences across various disciplines such as medicine, biology, ecology, and environmental sciences (Woo et al., 2008). Sequencing data is usually pre-treated for quality filtering, noise removal and chimera checking through bioinformatics algorithms and the filtered sequences are clustered into Operational Taxonomic Units (OTUs), which represent similar organisms (microbial species) based on sequence homology (called OTU picking). An OTU abundance table is generated,

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