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Deconvolving taxonomic contributions to observed differences in the microbiome of COPD patient groups

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Abstract

While recent years have seen the development of tools for the analysis of microbiomic datasets generated using pyrosequencing of the small 16S ribosomal subunit of bacteria, there do not exist rigorous statistical methods for determining the relative contribution of various levels of taxonomic classification to observed differences in the microbiome of patients. Using existing tools (e.g. the edgeR package in R) one can test for differences between the quantity of a given species between patient groups, but there are no tools that allow a researcher to test for differences between species, genera, families, orders, classes and phyla simultaneously in a rigorous manner. The simple approach of testing for a difference between 2 phyla by grouping all species within those phyla into 2 groups and testing for a difference between the 2 groups is incorrect unless one accounts for measurements coming from the same subject in some fashion. We have developed a method that allows one to conduct such an analysis by using a negative binomial random effects model for the species level counts with random effects hierarchically grouped into the various taxonomical levels. The method also allows for variance regularization. A Bayesian approach to inference is adopted and Markov chain Monte Carlo is used to obtain parameter estimates and identify differences among the patient groups at all taxonomic levels. We applied the method to a data set arising from pyrosequencing of bronchio-alveolar lavage fluid from 22 COPD patients and 10 controls. The analysis identified differences at multiple taxonomic levels.

Biography

Cavan Reilly received his Ph.D from Columbia University in 2000 and became an Assistant Professor at the University of Minnesota the same year. In 2007 he was promoted to Associate Professor at the same institution. He has published over 50 peer reviewed articles covering many topics at the intersection of statistics, molecular biology and clinical medicine and has authored a textbook on this topic.