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A Bayesian framework for identifying consistent patterns of microbial abundance between body sites. (English) [Zbl 1445.92165](#)

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Summary: Recent studies have found that the microbiome in both gut and mouth are associated with diseases of the gut, including cancer. If resident microbes could be found to exhibit consistent patterns between the mouth and gut, disease status could potentially be assessed non-invasively through profiling of oral samples. Currently, there exists no generally applicable method to test for such associations. Here we present a Bayesian framework to identify microbes that exhibit consistent patterns between body sites, with respect to a phenotypic variable. For a given operational taxonomic unit (OTU), a Bayesian regression model is used to obtain Markov-Chain Monte Carlo estimates of abundance among strata, calculate a correlation statistic, and conduct a formal test based on its posterior distribution. Extensive simulation studies demonstrate overall viability of the approach, and provide information on what factors affect its performance. Applying our method to a dataset containing oral and gut microbiome samples from 77 pancreatic cancer patients revealed several OTUs exhibiting consistent patterns between gut and mouth with respect to disease subtype. Our method is well powered for modest sample sizes and moderate strength of association and can be flexibly extended to other research settings using any currently established Bayesian analysis programs.

MSC:

[92C70](#) Microbiology

[62P10](#) Applications of statistics to biology and medical sciences; meta analysis

[62F15](#) Bayesian inference

Keywords:

[association](#); [Bayesian](#); [consistent pattern](#); [microbial abundance](#); [microbiome](#); [zero-inflated beta regression](#)

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