MetaPrism: A Toolkit for Joint Taxa/Gene Analysis of Metagenomic Sequencing Data

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Abstract

Background In microbiome research, metagenomic sequencing generates enormous amounts of data. These data are typically classified into taxa for taxonomy analysis, or into genes for functional analysis. However, a joint analysis where the reads are classified into taxa-specific genes is often overlooked.

Result To enable the analysis of this biologically meaningful feature, we developed a novel bioinformatic toolkit, MetaPrism, which can analyze sequence reads for a set of joint taxa/gene analyses: 1) classify sequence reads and estimate the abundances for taxa-specific genes; 2) tabularize and visualize taxa-specific gene abundances; 3) compare the abundances between groups, and 4) build prediction models for clinical outcome. We illustrated these functions using a published microbiome metagenomics dataset from patients treated with immune checkpoint inhibitor therapy and showed the joint features can serve as potential biomarkers to predict therapeutic responses.

Conclusions MetaPrism is a toolkit for joint taxa and gene analysis. It offers biological insights on the taxa-specific genes on top of the taxa-alone or gene-alone analysis. MetaPrism is open source software and freely available at <https://github.com/jiwoongbio/MetaPrism>. The example script to reproduce the manuscript is also provided in the above code repository.

Full-text

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