doi 10.18699/bgrs2024-8.4-13

Quantifying ecological functional groups in the human gut microbiome: metagenomics meets trait-based ecology

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Key words: trait-based ecology; ecological functional groups; metagenomics; human gut microbiome

Motivation and Aim: The human gut microbiota plays a crucial role in digestive function, metabolism of short-chain fatty acids, vitamins and other compounds, immune function and maintenance of body health. Yet most software tools for functional analysis of metagenomic and metatranscriptomic data from the gut microbiota assess a wide range of potentially active functions and do not target specific processes that are key to a given ecosystem. Moreover, since generally functional traits of microorganisms have a limited phylogenetic conservatism trait-based ecology appears to be a well-suited approach to describe such complex ecosystems operating in terms of interactions between the ecological functional groups (EFGs) identified on the basis of ecologically relevant traits rather than taxonomic units. In this study we use specific trait-determining genetic features (TDGFs) to distinguish EFGs.

Methods and Algorithms: The program for the analysis of the ecological structure of the symbiotic human gut microbiota (EcoStructSHGM) is implemented in Python as a bioinformatics pipeline. We use Kallisto for TDGF quantification, jellyfish for k-mer quantification, bowtie2 and fastp for quality and contamination control as well as the algorithms that we have developed specifically for quantifying EFGs. The UniProtKB database has been used to create amino-acid catalogue of human gut microbiota TDGFs.

Results: We have developed a method for bioinformatic quantification of ecological functional groups in the human gut microbiota covering such processes as acetogenesis, butyrate production, sulfate reduction and mucin degradation, which employs available metagenomic or metatranscriptomic data to quantify the abundance or activity of relevant EFGs. The developed method was verified using publicly available data from the study of the effect of diet on mucin layer stability and compared with HumanN 3 software for the functional metagenomics analysis showing high consistency and recall of our method. We have also created amino-acid catalogue of human gut microbiota TDGFs, which allows to use EcoStructSHGM for analysing taxonomically diverse microbial communities.

Conclusion: The developed method for quantifying ecological functional groups in the human gut microbiome based on metagenomics data takes advantage of trait-based ecology approach to identify ecological functional groups in samples by their specific trait-determining genetic features, which allows to focus a functional metagenomics analysis on the processes, which are highly relevant for an ecosystem under investigation.

Funding: The study is supported by the Budget Project FWNR-2022-0006.