

Computer reconstruction of the ecological structure of the synthetic microbial community, which models core human gut microbiota

Kropochev A.^{1,2*}, Klimenko A.I.¹, Lashin S.A.^{1,2}

¹ *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

² *Novosibirsk State University, Novosibirsk, Russia*

* e-mail: kropochev@bionet.nsc.ru

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Motivation and Aim: At present, environmental modeling experiences a shift from taxonomy-based analysis to functioning, since the trait-based approaches allow for a deeper mechanistic understanding of environmental processes. However, it should be noted that such approaches require careful study of the methodology and taking into account a large amount of heterogeneous information. Human gut microbiota is a complex microbial community that plays a significant role in preserving human's health. Despite human gut microbiota's being extensively studied, there is no structured source of information on ecological interactions of its key players. Therefore, at the first stage, our goal is the reconstruction of the ecological structure of the microbial community, which models core human gut microbiota. This will be the basis for the further construction of qualitative and quantitative ecological models using trait-based approaches.

Methods and Algorithms: For our study, we chose a synthetic microbial community from the large intestine comprised of the species that collectively possess its core metabolic capacities [1].

Primary reconstruction of the ecological structure includes:

- 1) Using @MInter text mining system [2] to identify microbial interactions in the community;
- 2) Expert analysis of the literature obtained by using text-mining algorithms and author search;
- 3) Using bioinformatics analysis to fill the gaps in knowledge obtained from the literature.

Results: We have qualitatively reconstructed the network of metabolic interactions between members of the microbial community, described the metabolism of glycans, short-chain fatty acids, amino acids, sulfates and other metabolites.

Conclusion: The reconstruction we obtained summarizes the accumulated knowledge on the metabolism of bacteria in our community and can be used as a basis for further model building.

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References

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