

Computer reconstruction of the ecological structure of intestinal microbiota communities based on high-throughput sequencing data

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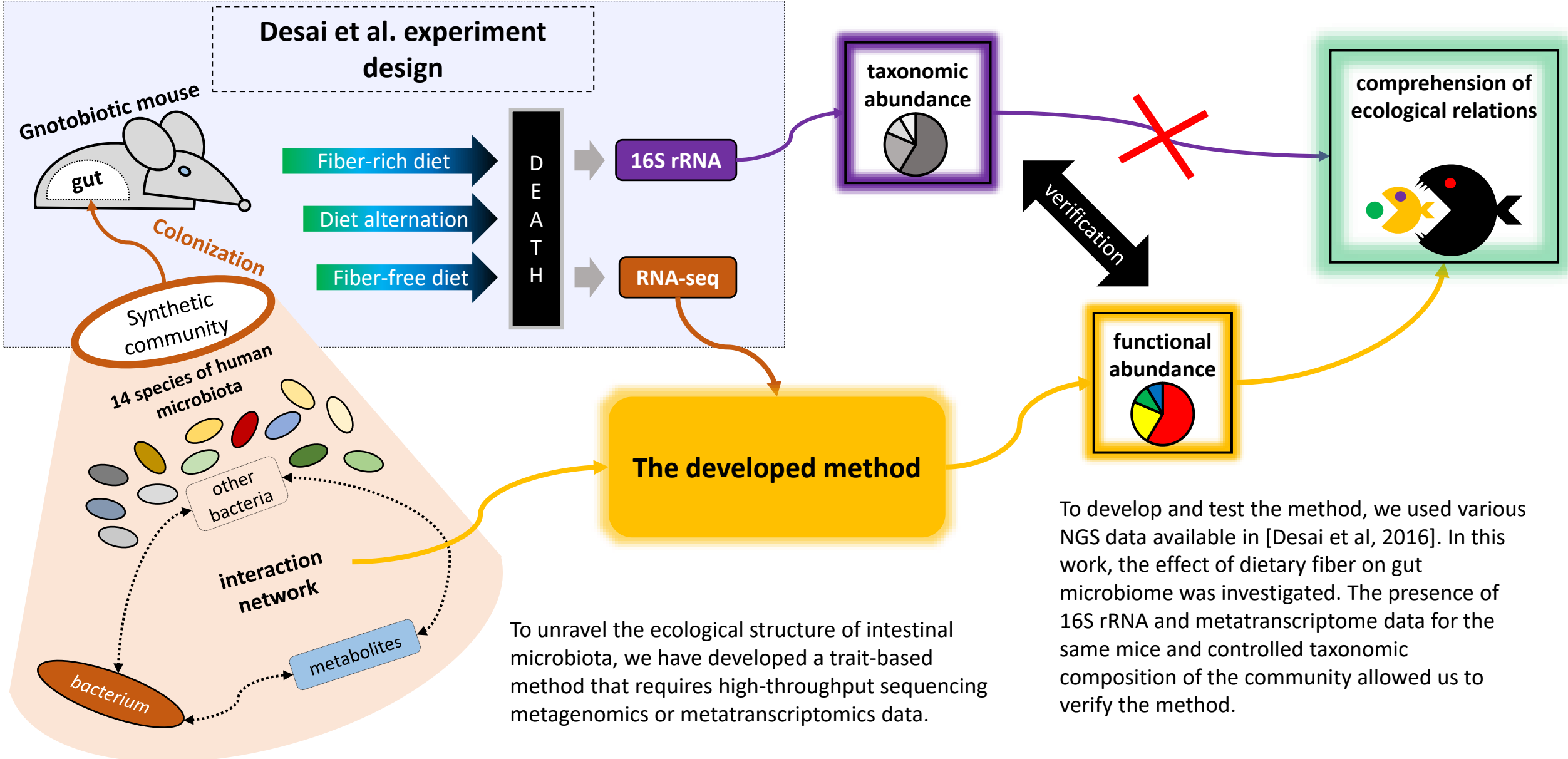
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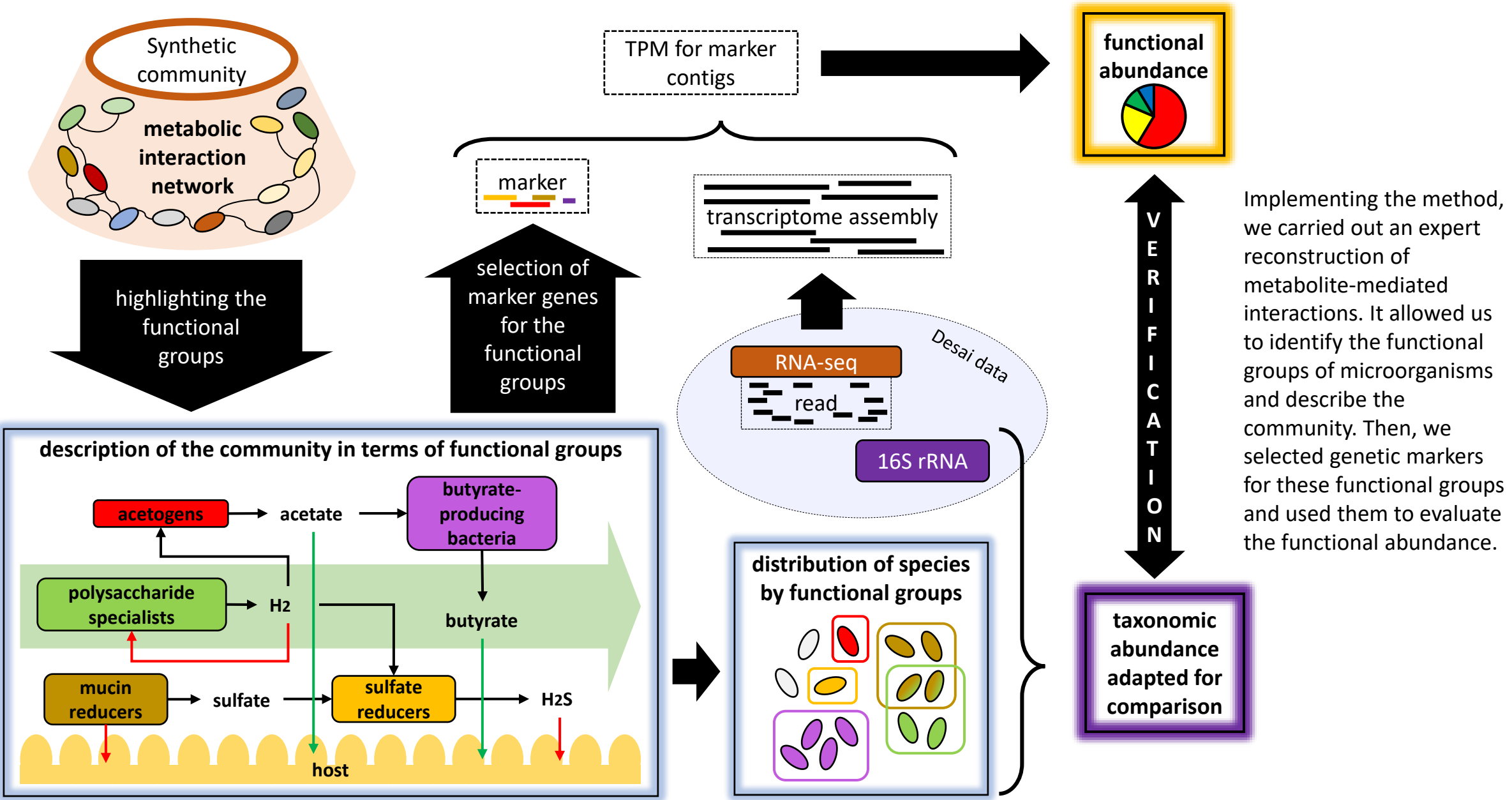
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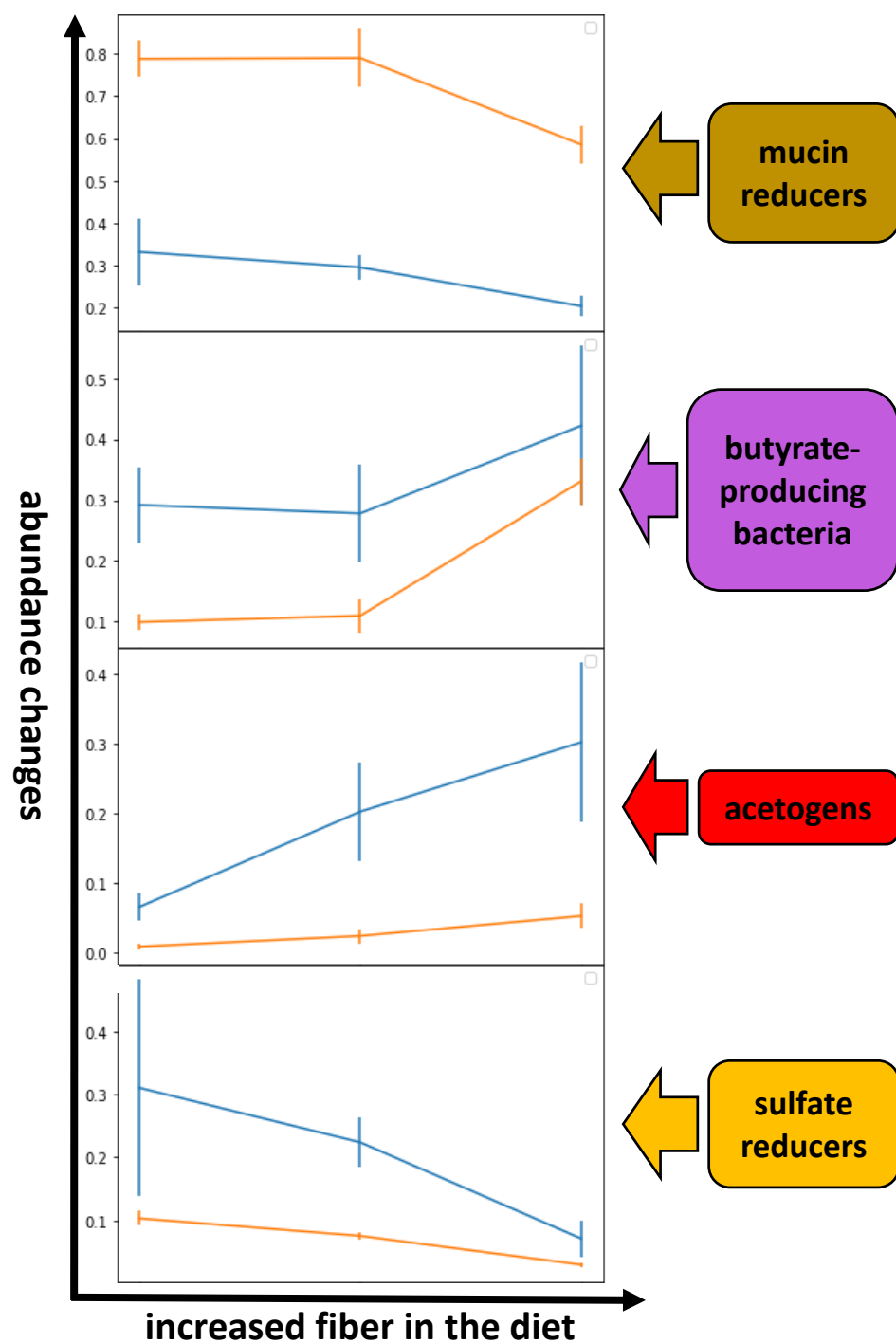
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From high-throughput sequencing data to quantitative comprehension of ecological relations



The developed method: from metatranscriptomics data to the functional abundance







Successful verification

The abundance of mucin-degrading bacteria decreases on a fiber-rich diet while bacteria additionally switch to the decomposition of mucin in the absence of fibers. These facts completely reproduce the results obtained in the article reflected in the terms of functional groups.

The abundance of butyrate-producing bacteria increases when changing to a fiber-rich diet, which can be seen both from the results of metagenomic analysis based on 16S rRNA data and from the results obtained by our method.

Abundance of acetogens and sulfate-reducing bacteria demonstrate an inverse relationship to each other when changing diets. They are competitors for the hydrogen. Under sulfate-rich conditions implicated by mucin decomposition, sulfate reducers dominate, and the reverse situation shows the domination of acetogens.

Thus, the dynamics of change in abundance is the same for these two methods, which allows us to report the successful verification of our method.

 functional abundance
 taxonomic abundance

References:

- Desai M.S. et al. A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility // Cell. 2016. Vol. 167, № 5. P. 1339-1353.e21.