Challenges in modeling the human gut microbiome

A paper by Magnúsdóttir et al.1 in a previous issue describes the generation of genome-scale metabolic models (GEMs) for 773 members of the human gut microbiota, referred to as AGORA. It represents a valuable contribution to quantitative analyses of how the many different species of gut microbiota interact and influence host metabolism. At the same time, a detailed analysis of the models described in this work raises several questions.

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