Modeling the dynamics of a small community of interacting human colon bacteria

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The human gut microbiota is a complex ecosystem wherein many microbial species interact. How such interactions contribute to the collective behavior of this ecosystem remains less understood despite its importance for human health. Here, we focus on a small, yet complex, community of three bacterial species inhabiting the gut microbiota. By combining an in silico and in vitro approach, we aim at predicting the dynamics of this interacting community.

Batch fermentations of mono- and co-cultures with 3 selected strains of species occurring in the human colon were performed, during which microbial growth and metabolite concentration were measured. In bi- and tri-culture, microbial interactions such as competition and cross-feeding affected the growth of a strain of a certain species.

To better understand the effect of the interactions on the observed dynamics, we developed a mathematical model consisting of ordinary differential equations. Bacterial growth was modeled with Monod-like growth kinetics. Competition and cross-feeding are taken into account through explicit modeling of the nutrient production and consumption. We used mono-culture time series to fit growth rates and yield coefficients of bacteria. Incorporating these parameters to simulate co-cultures, and comparing the prediction to the measurements, we underpredicted the growth rate of one species in co-culture, suggesting a metabolic adaptation of the bacteria when interacting with other species. We then used the data of bi-culture experiments to fit the model parameters, which led to a good description of the tri-culture dynamics. Furthermore, we observed that the time that species needed to adapt to their environment influenced which species eventually were dominant. In conclusion, the model provides a quantitative description of the measurements and highlights emergent behavior in co-cultures. Thus we are paving the way towards predictive multi-species modeling.