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Spatiotemporal microbiota dynamics from quantitative in vitro and in silico models of the gut[1]

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The human gut harbors a dynamic microbial community whose composition bears great importance for the health of the host. Here, we investigate how colonic physiology impacts bacterial growth behaviors, which ultimately dictate the gut microbiota composition. Combining measurements of bacterial growth physiology with analysis of published data on human physiology into a quantitative modeling framework, we show how hydrodynamic forces in the colon, in concert with other physiological factors, determine the abundances of the major bacterial phyla in the gut. Our model quantitatively explains the observed variation of microbiota composition among healthy adults, and predicts colonic water absorption (manifested as stool consistency) and nutrient intake to be two key factors determining this composition. The model further reveals that both factors, which have been identified in recent correlative studies, exert their effects through the same mechanism: changes in colonic pH that differentially affect the growth of different bacteria. Our findings show that a predictive and mechanistic understanding of microbial ecology in the human gut is possible, and offer the hope for the rational design of intervention strategies to actively control the microbiota.

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[2] work done in collaboration with Jonas Cremer and Markus Arnoldini