Humans are practically identical in terms of genetic makeup (up to 99.5%) but are more diverse concerning their microbiota (only 10–20% common species). In the **Department of Microbiome Dynamics** (formerly Systems Biology and Bioinformatics) we envision personalized medicines and nutrition focused on the **human gut microbiome**, a key determinant of both human health status and individualized response to diet. With a 150-fold greater gene count than humans, the gut microbiome comprises a rich enzyme repository with massive metabolic productivity and food-metabolizing capacity. We employ experimental meta'omic tools and novel eco-systems biology approaches to study the composition of the host and environmental microbiome and its role in human diseases and infections. Our projects bring together bioinformaticians, microbiologists, data scientists, and clinicians.

Our approach

Our research is highly collaborative and explores the role of the microbiome in globally significant diseases for delivering novel patient-centric therapies. We are studying host-microbiome interactions in metabolic diseases, infection, cancer, and sepsis. To move from correlative to causative evidence between changes in the microbiome and the pathophysiology of diseases, we design cross-sectional and prospective studies as well as randomized controlled intervention studies in disease subjects. We combine our studies with emerging new technologies, including the transplantation of human fecal microbiota to germ-free mice and the evaluation of single species and microbial consortia in cell lines and model gut systems.

We are also working on machine learning methods to combine clinical data, host biological patterns, microbiome, mycobiome, and phageome data to create a comprehensive view of different diseases, identify subtypes, and predict responses to treatment.