Master Thesis

What is dysbiosys? Evaluation of microbial cross-feeding in health and disease

The Project

Gut microbiota consists of diverse organisms that communicate with each other and the host and manipulate and redistribute energy, thereby providing us with functionalities upon which we depend. It transforms otherwise-indigestible carbohydrates and proteins into short chain fatty acids and organic acids that fuel other bacteria and the host. Advances in metagenome sequencing have revealed a close association of gut microbiota and lifestyle, diet, environment, and diseases such as cancer, obesity, and inflammatory bowel disease. However, mechanistic understanding of how members of the microbial community interact with each other and with the host is limited.

Genome-scale metabolic models are a powerful tool to predict the production of compounds by various species, and computational techniques such as Flux Balance Analysis enable us to determine how production rates are affected by changes in environmental conditions, nutrient availability and interactions with other species.

An important challenge is to characterize differences in gut microbiota between healthy and diseased individuals and model how these variations may impact the disease pathology and progression through a poorly understood process leading to dysbiosis. The aim of this project is get a clearer picture of the of the metabolic and physiological tasks the healthy and dysbiotic microbiomes can achieve.

How can you help us?

- You will start with studying literature on the microbiome of healthy individuals and various diseases.
- Based on the literature and interaction with experts on the microbiome, you will define the healthy microbiome as a list of tasks that the metabolic community can achieve, such as the production of butyrate to fuel the epithelial cells and the ability to fight an infection.
- Finally, you will perform metabolic flux predictions and evaluate the healthy or dysbiotic functions.

What do we expect from you?

- Studies of systems biology, biology, medicine, bioinformatics, biotechnology, or similar
- Interest in the microbiome
- Interest in bioinformatics and metabolic modelling

How can we help you?

We offer you an introduction in the field of microbial metabolic modelling. You'll become part of a great team developing and validating new metabolic methods at JRC computational biomedicine. You'll be supported to finish your thesis in time.

Contact

Zita Soons, PhD.
University Hospital RWTH Aachen
Joint Research Center for Computational Biomedicine
Pauwelsstrasse 19, 3rd floor, D-corridor, room 9
52074 Aachen
Email: zsoons@ukaachen.de
www.ukaachen.de/kuepfer

Metabolic flux predictions

Inputs
Microbial composition patients
Inflammation
Bile flow obstruction
Diet
…

Outputs
Healthy or dysbiotic phenotype