Microbial communities are essential for all ecosystems on earth, including our own body. However, due to the uncultivability of most members, the majority of these communities are poorly studied. The sequencing of genomes of uncultivable microbes now results in a extremely quickly growing number of partial genome sequences of medium and even high quality. The rapid, automatic annotation and comparative analysis of high numbers of metagenomic bins, as well as the reconstruction of microbial interaction networks, requires novel bioinformatics tools that are specifically adapted to these problems.

In my talk, I will discuss the current approaches and standards for prokaryotic genome sequencing and annotation. I will particularly discuss the recent improvements in genome-centric metagenomics and critically assess the quality of draft genome data. I will present recent work on large-scale comparative genomics and the automatic prediction of phenotypic traits. I will discuss our PhenDB tool, a freely available resource to analyse entire collections of metagenomic bins for microbial traits. PhenDB provides a first taxonomic and functional overview of a bin collection and thereby simplifies the identification of interesting metagenomic bins for follow-up analysis. Finally I will give an outlook towards genome-scale models of metabolism in microbial communities.

Date: Monday, February 17th, 2020
Time: 20:00 h
Room: Hörsaal 2, Pharmazentrum (ground floor)
(Klingelbergstrasse 50)
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