

A U S H A N G

FREIE UNIVERSITÄT BERLIN

Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Dienstag, 15. Februar 2022, 12:00 Uhr

[WebEx](#)

Disputation über die Doktorarbeit von

Herrn Lennard Epping

Thema der Dissertation:

**K-mer-based High-throughput Analysis of the Adaptive Potential of
Campylobacter**

Thema der Disputation:

**Development of Genome-wide Association Studies for microbial
genomic research**

Die Arbeit wurde unter der Betreuung von **Prof. Dr. R. M. Piro** durchgeführt.

Abstract: Genome-wide association studies (GWAS) have been widely applied in human genetic research. At present, more than 50.000 genetic variants correlating with genomic diseases and traits have been identified. The rapid increase and availability of genomes on population-scale level enables microbial research to gain novel insights about the relationships of phenotypic traits and detectable genetic variations in natural bacterial populations.

When applying the concept of GWAS to bacterial populations, several problems with respect to genome plasticity and the population structure of distinct bacterial species need to be addressed [1]. In human genomes, genetic variants are reassorted by meiosis in every generation. As a result, mutations reach a high frequency in multiple genetic backgrounds. Mutations in bacterial genomes, in contrast, can reach high frequencies in a single genetic background. Therefore, it is difficult for association tests to distinguish between a phenotypic effect of a specific mutation and the pool of mutations associated with the particular genetic background within a bacterial population of interest. While human GWAS are usually focused on single nucleotide polymorphisms (SNPs), the high plasticity and variance in the genome content within a single bacterial species limits the use of SNP-based GWAS.

The disputation talk will introduce the concept of GWAS used to study phenotypic-genotypic relationships microbiological research. The main focus of the presentation are adaptations applied to GWAS implemented in the tool SEER [2] in order to overcome problems founded by the considerable plasticity of bacterial genomes and the strong structures of bacterial populations resulting in lineage effects.

Die Disputation besteht aus dem o. g. Vortrag, danach der Vorstellung der Dissertation einschließlich jeweils anschließenden Aussprachen.

Interessierte werden hiermit herzlich eingeladen

Der Vorsitzende der Promotionskommission
Prof. Dr. R.M. Piro