AUSHANG

FREIE UNIVERSITÄT BERLIN
Fachbereich Mathematik und Informatik

Promotionsbüro, Arnimallee 14, 14195 Berlin

DISPUTATION

Freitag, 23. November 2018, 16:00

Ort: Takustr. 9 (Raum 053), 14195 Berlin

Disputation über die Doktorarbeit von

Herrn Vitor Cedran Piro

Thema der Dissertation:

Reference and taxonomy-based methods for classification and abundance estimation of organisms in metagenomic samples

Disputation
Using whole genome sequences to define taxonomy and delineate prokaryotic species in silico

Die Arbeit wurde unter der Betreuung von **PD Dr. B. Renard** durchgeführt.

Abstract: The definition and delineation of novel prokaryotic species as well as their taxonomy are areas of active discussion in microbial systematics. The clear definition of microbial species and species boundaries are issues of ongoing debate. Besides the theoretical definition, phenotypic characteristics and genotypic data are being jointly used to define species boundaries, an approach called polyphasic taxonomy. Methods like DNA-DNA hybridization, similarity among single marker genes (e.g. 16S rRNA), multilocus sequencing typing are commonly employed. However, defining species based on complementary types of evidence can be costly, time-consuming, difficult to reproduce and prone to bias. Whole genome sequencing is cost-effective, relatively fast and provides a higher resolution than marker genes, posing a promising alternative to the polyphasic method. Full or draft genome sequences are now commonly available and the number of assembled genomes is growing exponentially, enabling a more precise prokaryotic classification in silico. The disputation talk will address changes and insights regarding the delineation of prokaryotic species and their wider taxonomic classification that arise from the availability of whole genome sequences. New developments using the average nucleotide identity measure, such as MiSI (Varghese et al. 2015) and FastANI (Jain et al. 2017), will be presented. Further, recent updates on how whole genome sequence information is being integrated into the existing NCBI Taxonomy database (Ciufo et al. 2018) and the
implications of this for for downstream analysis, particularly for metagenomics, will be discussed.

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
PD Dr. B. Renard