Joint de.NBI & DZIF Metagenomics Training Course 2016

Date: August 29th to September 2nd, 2016
Location: Bielefeld University
Website: https://www.cebitec.uni-bielefeld.de/brf/index.php/training/upcoming-workshops

The aim of this five day workshop will be to give students an overview of the tools and bioinformatics techniques available for the analysis of next generation sequence data from microbial communities. The format will comprise a mixture of lectures and hands-on tutorials where students will process example data sets in real-time. Students will also be encouraged to bring their own data for analysis.

Organizers: Andreas Bremges (DZIF; Andreas.Bremges@helmholtz-hzi.de), Sebastian Jünemann (de.NBI; jueneman@CeBiTec.uni-bielefeld.de)

Lecturers: Dr. Alex Sczyrba (Bielefeld University, DE), Dr. Christopher Quince (Glasgow University, UK), Dr. A. Murat Eren (University of Chicago, USA)

Module I will focus on the analysis of NGS amplicon sequences (e.g. 16S rRNA). The entire process from initial sequence data through paired-end read assembly, quality filtering, OTU clustering, and taxonomic classification will be addressed in the first and second part using state-of-the-art bioinformatics tools (e.g. USEARCH, QIIME, MOTHUR). The third part will put emphasis on community analysis and ecological interpretation including diversity estimations, multivariate statistics, indicator species analysis, and probabilistic models.

Module II will focus on the analysis of shotgun metagenome sequence data from microbial communities. This will cover lectures and tools for *de novo* sequence assembly, similarity- and composition-based tools for the taxonomic assignment (binning) of unassembled and assembled samples, draft genome recovery for abundant community members, gene prediction and an overview of functional annotation methods.

	Monday	Tuesday	Wednesday	Thursday	Friday
Morning	Arrival & Registration	WGS Metagenomics I - Intro	WGS Metagenomics III - Binning	16S Amplicon Analysis II - Methods	WGS Metagenomics IV - Profiling
Afternoon	Welcome, Cloud & Linux Introduction, data pre-processing	WGS Metagenomics II - Assembly	16S Amplicon Analysis I - Intro	16S Amplicon Analysis III - Statistics	Analysis of own data & Departure

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

DZIF

Joint de.NBI & DZIF Metagenomics Training Course 2016

Learning Goals and Prerequisites

Basic knowledge in microbiology, NGS-based analysis, microbiomics, metagenomics, and experience with a Linux operating system are recommended but not required for attendance. This course covers lectures as well as hands-on training on selected tools and is aimed at students from any career level, from under-graduate to professorial, with aforementioned background. An opportunity to analyze own data sets will be given on the final day if possible. The main learning goals of this course are:

- Sequence data pre-processing: From raw data to high quality sequencing reads
- Introduction into 16S SOPs: From amplicons to classified OTUs
- Problems and pitfalls in 16S based research: A short outline and possible solutions
- Assembly of metagenomes: From environmental reads to genomic bins
- Analysis of metagenome assemblies: From bins to the description of known and unknown microbes
- Metagenomic profiling: From sequencing data to identified and quantified organisms

Application and Registration

Participation in the training course is free of charge. Travel and accommodation expenses are to be paid by the participants. A list of hotels and further advice on travel organization will be given on the course website. This course is limited to 24 participants who will be selected based on registration time and application letter. For your application, please provide some short information about your scientific background, whether you are a de.NBI or a DZIF member, your level of experience on the command line (linux/unix), and your experience within the field of metagenomic analysis and related bioinformatic tools. If you intend to bring your own data sets, please describe them briefly in addition.

Registration: Email to jueneman@cebitec.uni-bielefeld.de or
andreas.bremges@helmholtz-hzi.de (subject MG-course2016)
Deadline: **August the 10th, 2016**