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German Network for Bioinformatics Infrastructure

BiGi Metagenomics Training Course 2015

Date: 23.11.2015 - 25.11.2015
Location: Bielefeld University
Website: http://www.cebitec.uni-bielefeld.de/polyomics/index.php/training

Contents:

This course will broach the issues of targeted and untargeted metagenome analysis based on high-throughput next generation sequencing (NGS) data. In the first part of this course, different aspects of general NGS data handling and present different techniques and tools for quality measurement, filtering, and sequence correction will be covered. A compact introduction into the Linux operating system and the usage of the command line interface will be given if required. The second part of this course focuses on analyzing 16S amplicon data. The main aspects here are the common pipeline steps beginning with data pre-processing, OTU clustering, taxonomic classification, normalization, and different statistical measurements like rarefaction analysis. In the third part, advantages and disadvantages of whole metagenome sequencing will be illustrated with main focus on taxonomic and functional analysis with the aid of different bioinformatic tools. Two different techniques to analyze WGS metagenome data are part of this section: (1) for read based approaches the software solution MGX, an integrated platform for metagenome analysis and data visualization, will be introduced; (2) in the assembly based approach reconstructs genomes by assembling reads into contigs which are subject to binning methods to group individual contigs into genome bins. For analyzing metagenome assemblies the EMGB platform will be presented.

	Monday	Tuesday	Wednesday
Morning	Arrival & Registration	16S Amplicon Analysis II & WGS Metagenomics I	WGS Metagenomics II & Introduction into MGX
Afternoon	Introduction & 16S Amplicon Analysis I	WGS Metagenomics II	Analysis of own data & Departure

Bundesministerium für Bildung und Forschung

PtJ Projektträger Jülich Forschungszentrum Jülich

Universität Bielefeld

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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 given by experts of Bielefeld and Giessen University and is aimed at PhD students and postdoctoral fellows 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
▸ Read-based analysis of WGS metagenomic reads: Introduction into the client/server application MGX
▸ Assembly of metagenomes: From environmental reads to genomic bins
▸ Assembly-based analysis of metagenomes: Introduction into the Elastic MetaGenome Browser EMGB

Application and Registration:

Participation in the training course is free of charge. Travel and accommodation expenses is 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 16 participants who will be selected based on registration time and application letter. For your application, please provide some short information about your scientific background 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 **bigi@denbi.de** (subject MG-course2015)
Deadline: 09.11.2015

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