2013

Freie Universität Berlin

DFG Deutsche Forschungsgemeinschaft

Freie Universität Berlin

Dematheis, Flavia

Charité Berlin

Sur, Saubashya

DFG-GRK 1673 „Functional Molecular Infection Epidemiology“

16 -18 July, 2013

Freie University, Department of Veterinary Medicine, Veterinarium Progressum, (Haus 9), Oertzenweg 19b, Berlin

[WORKSHOP IN BIOINFORMATICS]

The course provides training on the fundamental concepts underpinning the topics of NGS, genome annotation, study of the population structure, SNP analysis, bioinformatics approach for studying human-pathogen interactions and protein homology modeling.

Venue:	Freie University, Department of Veterinary Medicine, Veterinarium Progressum, (Haus 9), Oertzenweg 19b, Berlin
Date:	16 -18 July, 2013
Organizers:	F. Dematheis, T. Semmler, L.H. Wieler, FU, Berlin S. Saubashya, R. Schumann, Charité, Berlin
Participation:	Open application
Registration:	Write an e-mail to flavia.dematheis@fu-berlin.de
Requirements:	Personal PC and previous software installation

Overview

This workshop is aimed at early-stage graduate students and researchers who are involved in bioinformatics-based projects with little or no experience in computational biology. The course will provide practical training in bioinformatics in the context of biological research and its theory. In particular, the training program will include fundamental concepts underpinning the topics of NGS, genome annotation, study of population structure, SNP analysis, bioinformatics approach for studying human-pathogen interactions and protein homology modeling. This workshop will involve hands-on training in using widely-available software packages. Therefore, students willing to take part in the course are encouraged to bring their own laptop, and take care of the previous installation of some of the software which will be used during the workshop (see the requirements listed below). Please note that the course will not cover aspects of computer programming.

What will it cover?

The course covers data analysis of *Escherichia coli* experiments. Topics will include: genome annotation using RAST, PAGIT; data handling and visualization using Artemis; manual curation using Prodigal and Artemis; tools to investigate mobile genetic elements (MGE); evolution and recombination events using nextGenBRAT; web resources for human pathogen genomes; *Insilico* SNP analysis in human genome; bioinformatics approach to study human-pathogen interactions and protein homology modeling.

What will I learn?

After this course you should be able to…

- Get an idea about web resources on human pathogen genomes.
- Grasp the reasons why NGS pushed bioinformatics needs up.
- Know how to explore a draft genome using free available software.
- Annotate sequences manually using widely available tools and resources.
- Investigate the evolution and genetic population structure using free available software.
- Technical know -how about SNP analysis in the human genome.
- To model a protein using freely available tools.
- Utilize bioinformatics tools to study pathogen human interactions

Programme

Time	Topic	Trainer
Day 1		
9:00	• Web resources for human pathogen genomes. • Overview of NGS, advantages and drawbacks. • NGS dataset assembly and visualization using Geneious (Practical session)	S. Sur, F. Dematheis and T. Semmler
12:00	Lunch	
13:00	• How to access the information contained in a genome through the annotation. ○ Web tool : RAST (Practical session) ○ PAGIT for complete genomes ○ Pipeline ABACAS and RATT for draft genomes ○ Manual curation of the annotation using Prodigal, Artemis and Geneious (Practical session)	F. Dematheis and T. Semmler
17:00	Close	
Day 2		
9:00	• Evolution and mobile genetic elements (MGE) ○ Software available • Evolution and recombination events ○ BAPS and nextGenBRAT (Practical session)	F. Dematheis and T. Semmler
12:00	Lunch	
13:00	• *Insilico* SNP analysis in human genome (Practical) ○ Software available	S. Sur
17:00	Close	
Day 3		
9:00	• Introduction to Protein homology modeling-Overview • Protein homology modeling (Practical session): ○ MODELLER, CLUSTAL W, SWISS-PDB VIEWER, CHIMERA (Practical session)	S. Sur
12:00	Lunch	
13:00	• Bioinformatics approach to study human-pathogen interactions ○ Software available	S. Sur
17:00	Close	

Requirements:

- Laptop
- Installation of the software: Prodigal, Artemis, GENEIOUS, BAPS, nextGenBRAT, CLUSTAL W; MODELLER; SWISS-PDB Viewer, CHIMERA, SUMOsp, iGPS and Cytoscape. Software are free downloadable at the websites specified in the following table.

Software	Website
Prodigal	http://code.google.com/p/prodigal/downloads/list
Artemis	http://www.sanger.ac.uk/resources/software/artemis/
GENEIOUS	http://www.geneious.com/web/geneious/download-geneious
BAPS	http://www.helsinki.fi/bsg/software/BAPS
nextGenBRAT	http://www.helsinki.fi/bsg/software/BRAT-NextGen/
CLUSTAL W	http://www.clustal.org/download/1.X/ftp-igbmc.u-strasbg.fr/pub/ClustalW/
MODELLER	http://salilab.org/modeller/download_installation.html
SWISS-PDB Viewer	http://spdbv.vital-it.ch/disclaim.html
CHIMERA	http://www.cgl.ucsf.edu/chimera/download.html
SUMOsp	http://sumosp.biocuckoo.org/down.php
iGPS	http://igps.biocuckoo.org/down.php
Cytoscape	http://www.cytoscape.org/download.html