

GENOPOLE SUMMER SCHOOL

**BIOINFORMATICS AND
BIostatistical TOOLS
IN MEDICAL GENOMICS**

SUMMER SCHOOL 2019
Day to day programme

DAY 1 D 1 Monday, June 25

13:30 – 14:00 Welcome and Registration

14:00 – 14:45 Talk: qcGenomics: From the qualification of public CHIP-Seq and Related Deep Sequencing-Generated Datasets, towards their comparative analysis in a Web-based empowered environment

Marco-Antonio MENDOZA-PARA, team leader CNRS, Genoscope-UMR 8030, Centre national de séquençage, Institut Jacob, CEA, Evry

Objectives and outcomes: assessing quality descriptors with the NGS-QC Generator; to interpret the generated reports and to explore the database of QC indicators

14:00 – 14:45 Intitiation to LINUX
Nicolas WIART, Lilia MESROB, Florian SANDRON, CNRGH, CEA

19:00 – 21:00 DINNER

DAY 2 D 2 Tuesday June 25 PRACTICAL SESSION - BIOINFORMATICS

8:00 – 8:45 BREAKFAST

9:00 – 12:00 Transcriptomics (including coffee break)
Fariza TAHI, Université d'Evry-Val d'Essonne

- RNA secondary structure prediction and identification and prediction of ncRNAs in large-scale genomic sequences

12:00 – 13:30 LUNCH

13:30 – 17:00 Generation and analysis of data (including coffee break)
Valentin LOUX, INRA,

- Workflow for quality Control, alignment and variant calling - GALAXY

17:00 – 18:00 FREE TIME: time for self-training or for sport activities proposed on the campus site

18:00 – 19:00 Flash talk session I (by the participants)

- Presentation by the trainees of their research work

19:00 – 21:00 DINNER

DAY 3 D 3 Wednesday, June 27 PRACTICAL SESSION – BIOSTATISTICS

8:00 – 8:45 BREAKFAST

9:00 – 12:30 Variation in the human genome – 1 (SNPs, CNV...) (including coffee break)
Vincent MEYER, Lilia MESROB, Florian SANDRON, CNRGH, CEA

- Whole Exome/Genome Sequencing as a strategy to identify the genetic bases of common Mendelian disorders and rare diseases.

12:00 – 13:30 LUNCH

13:30 – 17:30 Variation in the human genome - 2 (SNPs, CNV...) (including coffee break)
Continuation

18:30 – 19:30 Talk: Using computers to understand microbial communities
Prof. Mihai POP, Department of Computer Science – Director, Institute for Advanced Computer Studies (UMIACS), University of Maryland

Abstract: Microbes are everywhere. They inhabit virtually all ecosystems of our planet as well as the bodies of all living organisms. In humans, microbial communities are critical for health, and disruption of the normal microbiota have been associated with a number of diseases. Understanding our world's microbial communities is, however, impossible without the help of advanced genomic technologies and sophisticated computational algorithms. In my talk I will describe how computers are used to analyze microbial communities, and will highlight some recent results from my lab.

19:00 – 21:00 DINNER

DAY 4 D 4 Thursday, June 28 PRACTICAL SESSION – BIOSTATISTICS

8:00 – 8:45 BREAKFAST

9:00 – 12:30 Network-based visualization of genomics data (including coffee break)
Andrei ZINOVYEV and Inna KUPERSTEIN, Institut Curie - Inserm U900 - Systems Biology of Cancer Institut Curie

Objective and outcomes: to provide to the students practical experience of using biological networks for omics data visualization. After this session, students will master using several popular platforms for network-based visualization of genomics data: Cytoscape, NaviCell, MINERVA. The students will be able to visualize a transcriptomic, proteomic, mutational, copy-number profile on an existing biological network (for example, from Atlas of Cancer Signaling Network), or to construct an ad hoc biological network from a pathway database, and use it for data visualization.

12:30 – 14:00 LUNCH

14:00 – 18:00 Metagenomics : Bioinformatics tools for the study of microbial communities in human health (including coffee break)
Katarzyna HOOKS, Université de Bordeaux and CNRS

Outcomes: After this workshop you will be able to: find a suitable tool to analyse the metagenomic sequencing, extract publicly available data from repositories (e.g. EBI Metagenomic), analyse and visualise it using web-based resources.

18:30 – 19:30 Free time for self-training or for activities in the campus

19:30 – 21:00 DINNER

DAY 5

D 5 Friday June 29

PRACTICAL SESSION – Genome and transcriptome analysis

8:00 – 8:45 BREAKFAST

9:00 – 12:30

Statistical methods (1) *(including coffee break)*

Christophe AMBROISE, Université d'Evry-Val d'Essonne

Guillem RIGAILL, Inra Université d'Evry Val d'Essonne

- Transcriptome / RNA-Seq analysis (Whole Transcriptome Sequencing): quantification and differential expression ;
- How to choose the appropriate statistical methodologies: detecting bias and troubleshoots and interpreting statistical results.

12:30 – 13:30 LUNCH

13:30 – 17:30

Statistical methods (2)

Christophe AMBROISE, Université d'Evry-Val d'Essonne

Guillem RIGAILL, Inra and Université d'Evry Val d'Essonne

- Statistical inference /hypothesis testing
- Quantitative genetics

18:00 End of the summer school - departure