

Genomics, Transcriptomics and Epigenomics

Lecturers

Jean-François FLOT (Coordinator) and Matthieu DEFRANCE

Course mnemonic

BINF-F402

ECTS credits

5 credits

Language(s) of instruction

English

Course period

First term

Campus

Solbosch

http://webext.pasteur.fr/tekaia/BCGA2012/TALKS/FT_Unix.pdf
<https://www.cs.usfca.edu/~parrr/course/601/lectures/unix.util.html>

Regarding R:

<https://www.guru99.com/r-tutorial.html>

<https://www.statmethods.net/r-tutorial/index.html>

<https://www.tutorialspoint.com/r/index.htm>

It will also be very useful for participants in the course to have a command-line environment ready on their personal computer prior to the beginning of the course. Users of Linux and OSX operating systems will have such environment available without additional effort, but Windows users should install the Windows Subsystem for Linux (<https://docs.microsoft.com/en-us/windows/wsl/install>) [<https://www.slothparadise.com/setup-bash-windows-10-developers-ultimate-setup/>] or Cygwin (<https://www.cygwin.com/>) if they are running an older version of Windows.

Course content

The course will comprise this year twelve four-hour sessions. The teaching language will be English.

The course will take place each Wednesday from 14:00 to 18:00

Sessions 1 to 6 : Introduction to Omics and NGS data analysis

Sessions 7 to 12 : gGenome assembly, theory and practice

Objectives (and/or specific learning outcomes)

At the end of this course students will be able to:

- > explain the different methods used to sequence DNA and RNA as well as to process bioinformatically the resulting data (processing different file formats using the command line, converting data from one format into another, checking the quality of the sequences);
- > explain the different methods used to assemble de novo, map and annotate genomic data, as well as to perform genome assemblies and estimate the quality of the result obtained;
- > explain the different approaches used in epigenomic studies as well as to analyse the resulting datasets.

Pre-requisites and co-requisites

Required knowledge and skills

To make the best out of the course it is recommended that students do some self study on how to use the command line and R.

Regarding the *nix (unix, linux, osx and the like) command line:

<https://datacarpentry.org/shell-genomics/>

http://linuxcommand.org/lc3_learning_the_shell.php

Teaching method and learning activities

The sessions combine theoretical lectures and applications.

Contribution to the teaching profile

Acquiring the basic concepts and knowledge of informatics and biology required for devising projects in bioinformatics and modelling.

Mastering the mathematical, statistical and informatic knowledge on which bioinformatic and modelling studies are resting.

Analyzing critically original research articles in bioinformatics and modelling.

Understanding the evolution of knowledge on a given subject as well as collecting and managing scientific articles pertaining to it.

Being able to use existing bioinformatic resources and to develop new programs (algorithms, databases, analytic tools, etc.).

Writing a research report with clarity and rigor.

Presenting orally in a clear and concise way the results of a work and facing the questions and criticisms of the public.

References, bibliography and recommended reading

Haddock & Dunn, 2010. Practical Computing for Biologists. Sinauer Associates. 538 pp. ISBN 9780878933914

Wang, 2016. Next-Generation Sequencing Data Analysis. CRC Press. 246 pp. ISBN 9781482217889

Other information

Place(s) of teaching

Solbosch

Contact(s)

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Evaluation method(s)

Project

Determination of the mark (including the weighting of partial marks)

50% project 1

50% project 2

Main language(s) of evaluation

English

Programmes

Programmes proposing this course at the faculty of Sciences

MA-BINF | **Master in Bio-informatics and Modelling** | finalité Research/unit 1 and MA-BIOR | **Master in Biology of Organisms and Ecology** | finalité Research/unit 2 and finalité Erasmus Mundus Joint Master Degree in Tropical Biodiversity and Ecosystems - TROPIMUNDO/unit 1

