



BIOINFORMATICS TRAINING SESSION

DE NOVO ASSEMBLY (REFERENCE: GFBASN)

LOCATION

GENOSCREEN (Lille - 59)

DURATION

½ day

PRICE

Regular session: 500 € excl. taxes

DATES

Sessions: April 2nd to 5th October 14th to 18th

Conditions

- Trainings combine theoretical presentations and practical work.
 Tangible examples are presented
- Individual assessment of knowledge acquisition
- Training materials provided

CUSTOMIZED SESSION

On-site trainings with content and duration tailored to your objectives.

information: click here

TYPE

60% theoretical and 40% practical.

REQUIREMENTS

Basic knowledge of molecular biology, theory of NGS technologies and NGS data quality control knowledge.

EQUIPMENT

You will need a Linux, Mac OS or Windows computer able to connect to the Internet.

PARTICIPANTS

PhD, engineers and others willing to acquire the fundamentals of sequence annotation.

AIMS

By the end of the course, the candidate will have the theoretical and practical skills needed to perform *de novo* genome assembly using data from «short reads» (Illumina®) and «long reads» (Oxford Nanopore Technologies Technologies® and Pacific Biosciences®). The focus will be on understanding the advantages and limitations of different approaches to *de novo* genome assembly. The emphasis will also be on the quality control of the assemblies carried out, with particular focus on the parameters to be observed and the evaluation of the overall quality of an assembly.

PROGRAM

- Introduction to the general concept of *de novo* assembly.
- Theoretical presentation of assembly algorithms.
- De novo assembly from «short read» data.
- Hybrid de novo assembly with «short read» and «long read» data.
- Quality control of assemblies.

