GenoScreen

Innovative Genomics

Our 2025 training courses

SUMMARY

ABOUT OUR TRAININGS

Our trainings will enable you to gain autonomy regarding bioinformatic analysis, assimilate the theoretical concepts and acquire the skills you need to use and to configure the tools needed to generate robust results from your NGS data.

All trainings are taught by our experts. Sessions are combining theoretical presentations and practical work to help you assimilate the concepts and to understand how the tools work.

Each tool used will be presented individually, so you can better understand how it works, its conditions and its limits. The results obtained at each stage will be explained and commented, making them easier to interpret.

OUR TRAININGS IN BIOINFORMATICS

To meet all your needs, our bioinformatics trainings are available in two formats: regular sessions with training modules, or customized sessions with modules tailored to your needs.

REGULAR SESSIONS

All our training courses are carried out using the user interface: Galaxy

USER INTERFACE:

- Use of the open-source Galaxy platform.
- Easy-to-use tools.
- No need for computing infrastructure.
- No need to write a single line of code!

PREFERRED OPTION

- economical
- easy access

Work with GenoScreen-supplied datasets on our trainings, designed by our bioinformatics experts.

Contact us to get the dates of upcoming training sessions.

CUSTOMIZED SESSIONS

Choose between using a user interface or a command-line tool.

COMMAND LINE :

- Gain greater control over your analysis and understand how tools work in depth.
- Get the ability to use any tool available on the market.

FLEXIBLE OPTION

- customizable
- expertise

Schedule a training session at any time, address specific topics, use your own NGS data.

One-day introductory command line training is also available to provide you with all the rudiments required to use it.

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BIOINFORMATICS TRAINING SESSION

NGS DATA QUALITY CONTROL (REFERENCE: GFBQCN)

LOCATION
GENOSCREEN (Lille – 59)

DURATION
½ day

PRICE
Regular session: 500 € excl. taxes

DATES
Sessions: from May 21 to 23, 2025
from October 15 to 17, 2025

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.

Please contact us for more information: click here

TYPE
60% theoretical and 40% practical.

REQUIREMENTS
Basic knowledge of molecular biology, theory of NGS technologies.

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

PARTICIPANTS
PhD, engineers and others willing to discover and to gain autonomy in genomic data assembly and analysis techniques.

AIMS
By the end of the course, the candidate will have mastered quality analysis techniques, the choice of filtering parameters and will be able to detect the presence of a contaminant in a data set.The aim of this training is to obtain a data set of sufficient quality for further bioinformatic downstream analysis. This course will cover the processing of data from Illumina® and Oxford Nanopore Technologies® sequencing technologies.

PROGRAM
- FASTQ format reminder and raw data quality control.
- Metrics description such as basecalling, GC content distributions (basecalling), GC content distributions, biological contamination biological contamination detection methods.
- Filter parameter selection for different data sets.
- Obtain and interpret descriptive statistics for a raw data set and a filtered data set.

GENOSCREEN IS A REGISTERED TRAINING ORGANIZATION UNDER NUMBER 31 59 06657 59 (DRTEFP LILLE, FRANCE).

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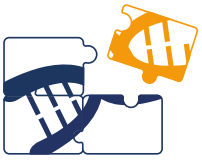

BIOINFORMATICS TRAINING SESSION

DE NOVO ASSEMBLY (REFERENCE: GFBASN)

LOCATION
GENOSCREEN (Lille – 59)

DURATION
½ day

PRICE
Regular session: 500 € excl. taxes

DATES
Sessions: from May 21 to 23, 2025
from October 15 to 17, 2025

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.

Please contact us for more 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.

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BIOINFORMATICS TRAINING SESSION

BLAST MASTERY (REFERENCE : GFBMBB)

LOCATION
GENOSCREEN (Lille – 59)

DURATION
½ day

PRICE
Regular session: 500 € excl. taxes

DATES
Sessions: from May 21 to 23, 2025
from October 15 to 17, 2025

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.

Please contact us for more information: click here

TYPE
70% theoretical and 30% practical.

REQUIREMENTS
Basic knowledge of molecular biology, theory of NGS technologies.

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 this training course, the candidate will have the theoretical and practical skills to carry out sequence annotation for prokaryotic and eukaryotic genomes. The various structural and functional annotation strategies will also be covered, and practical examples will be used to identify the genes present in a genome and describe their function(s). During this course, the focus will be on the optimized use of BLAST («Basic Local Alignment Search Tool») for querying databases for nucleic or protein sequence comparison/annotation/identification.The understanding and ability to establish optimal parameters will be paired with knowledge regarding metrics in order to optimally interpret results.

PROGRAM
- Introduction to sequence annotation, reminders of gene structure.
- Description of the different structural and functional for prokaryotic and eukaryotic genomes. and eukaryotic genomes.
- Explanation of the various BLAST variants: BLASTn, megaBLAST, BLASTp, BLASTx, tBLASTx, etc.
- Using BLAST on public and private databases or private databases.

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BIOINFORMATICS TRAINING SESSION

SEARCH FOR GENETIC VARIANTS
(SUBSTITUTION, INSERTION, DELETION) (REFERENCE: GFBMUT)

LOCATION
GENOSCREEN (Lille – 59)

DURATION
1 day

PRICE
Regular session: €950excl.tax/person

DATES
Sessions: from May 21 to 23, 2025
from October 15 to 17, 2025

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.

Please contact us for more information: click here

TYPE
60% theoretical and 40% practical.

REQUIREMENTS
Basic knowledge of molecular biology, theory of NGS technologies.

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

PARTICIPANTS
PhD, engineers and others wishing to acquire the fundamentals of genetic variant research for ad hoc mutations (substitution, insertion, deletion).

AIMS
The main objective of this training session is to provide the theoretical knowledge for calling variants, in particular ad hoc mutations including substitutions, as well as small insertions and deletions (indels) from high-throughput sequencing data.

PROGRAM
- Theoretical overview of the various classes of genetic variants and how they can be detected using high-throughput sequencing data.
- Data mapping on a reference genome.
- Presentation of a variant calling workflow.

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