



Deep sequencing technology
for transcriptome analysis:
bioinformatics tools and illustrations

Deep sequencing technology for transcriptome analysis: bioinformatics tools and illustrations

- **Practical course for analysing RNAseq data**
- **From the experimental design to the analysis of selected genes**
- **Hands-on with free and available web tools**

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Program

Complete week: 3/12/2018 – 7/12/2018

- Monday: Introduction to Next-Generation sequencing, focus on RNAseq
Presentation of the study and experimental design
Presentation of databases and files, quality check
- Tuesday: Introduction to Galaxy website and tools
Mapping, Visualisation
- Wednesday : Normalisation & Quantification of expression
Differential analysis and Gene Ontology
- Thursday: Statistical analysis
Functionnal annotation, clustering,
Gene set enrichment analysis
- Friday: On-line and written examination

Practical details

- Complete week in english
- Everyday: 9h30 - 17h30
- Detailed program will be posted on:

[Dashboard](#) > [Sciences](#) > [UFR Sciences du vivant \(SDV\)](#) > [M2](#) > [M2 MEG – RNAseq](#)

- Progressive Learning Path during the week to assess essential notions
- Final examination the same week : short MCQ and 2 written questions on Friday
- Limited to **17 students**
NO prior knowledge of bioinformatics required : use of Galaxy, extensive tutorials, and R programming only upon request or out of curiosity
- Medical students are welcome ! (data from a project with medical application)