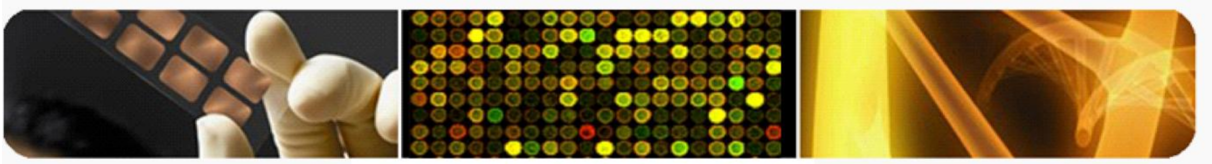

Genomics, application to transcriptomics: Next generation sequencing (NGS), Microarrays and Data Analysis

AIM

Overview of the different technologies available to perform genomics studies, focus on transcriptomics (microarrays, RNA-Seq).

Learn how to choose the right tools depending on the application and the biological questions.

Learn how to analyze and interpret a transcriptomics data set.

PROGRAM *(provisional)*

Day 1

9h00-9h30: Welcome

9h30-10h30: Introduction to Genomics – Global overview of the different types of analysis and tools – Introduction to databases (Karine Robbe-Sermesant).

10h30-11h15: Microarrays and High Throughput Sequencing: presentation of the technologies, application to transcriptomics (Laure-Emmanuelle Zaragosi).

11h15-11h30: Break

11h30-12h30: Practical course (I) (Karine Robbe-Sermesant and Laure-Emmanuelle Zaragosi):

- Exploration of GEO et Array Express databases
- Expression Atlas

12h30-14h: Lunch

14h00-14h30: Basics of statistics for differential expression analysis: data normalization, statistical analyses and clustering (Agnes Paquet)

14h30-17h00: Practical course (II) (Agnes Paquet, Karine Robbe-Sermesant, Nicolas Nottet,)

- Differential analysis (DE) with GEO2R
- Clustering with GenePattern
- Initiation to the use of Genome browsers (UCSC, Ensembl)

Day 2

9h30-10h15: NGS experiments data analysis. Genome mapping, transcripts quantification (Kevin Lebrigand).

10h15-10h35: Application example: MicroRNA Data Analysis from a Small RNA-Seq experiment (Laure-Emmanuelle Zaragosi).

10h35-11h00: Break

11h00-12h30: Practical course (III) (Kevin Lebrigand, Laure-Emmanuelle Zaragosi, Karine Robbe-Sermesant)

- Transcriptomics data visualization on genome browsers

12h30-14h00: Break

14h00-14h15: The future of next generation sequencing (Kevin Lebrigand)

14h15-14h45: Biological interpretation of transcriptomics studies: main goals of system biology approaches, comparison of tools (Bernard Mari).

14h45-17h00: Practical course (IV) (Bernard Mari, Laure-Emmanuelle Zaragosi, Nicolas Nottet , Agnes Paquet) Integration of transcriptomics data with protein interaction and regulation networks: IPA (Ingenuity Pathway Analysis) training course.