# Computational Methods for Functional Genomics

**Titulaire**
Vincent DETOURS (Coordonnateur)

**Mnémonique du cours**
BINF-F401

**Crédits ECTS**
5 crédits

**Langue(s) d'enseignement**
Inconnu

**Période du cours**
Deuxième quadrimestre

**Campus**
Plaine

## Contenu du cours

The course starts by presenting microarray technologies and the preprocessing steps required before any biological investigation can be carried out. Next, I introduce methods basically extending the pre-genomics, low-throughput gene expression experiments to genome-wide screens. Then the course unfolds with the presentation of recent tools that operate, not at the level of individual gene, but at the level of functionally related gene sets and global molecular phenotypes. More specifically we will learn about:

> normalization of genome-wide assays
> basics of NGS sequence alignment-selection of differentially expressed genes
> dimensionality reduction-gene set analysis methods-supervised and unsupervised classification of genome-wide expression profiles-typical statistical illusions that may arise from the above,-survival analysis
> insight about the global correlation structure presernt in biological systems

Computational methods will be introduced together with examples of groundbreaking applications to biomedical research. For examples, the student will learn for example:

-to what extent the glogal gene expression varies among different human populations,

-how to predict cancer outcome from gene expression profile,

-how to establish connection between drugs and biological conditons from gene expression databases,

-etc.

## Objectifs (et/ou acquis d'apprentissages spécifiques)

Understand how and why functional genomics contributes to transform our understanding of biological systems. Provide critical assessment of the functional genomics literature. Acquire practical know how of basic concept of tools.

## Méthodes d'enseignement et activités d'apprentissages

The course does not present a nicely polished texbook view of science, but science in the making with its ectics, turn arounds and controversies. Lectures are interupted by hands-on exercises in which the student actually use the methods on real life data and reproduce published research results.

### Contribution au profil d'enseignement

Functional genomics is the study of the genome and the deployement of its products in living systems. The key feature of functional genomics assays is their exhaustiveness. Instead of focusing on particular genes or biological function, functional genomics investigation addresses all genes and all functions at once. This results in massive data generation and requires specific computational approaches.

Functiuonal genomics is a major subfield of bioinformatics in terms of scientific attention, investments and jobs.

The course focuses on genome-wide mRNA gene expression, i.e. the first and most tractable level of genomic information deployement. It will present the strenghts and limits of computational methods deployed in current functional genomics research. The objective is to promote critical reading of the literature in the field, to introduce tools and promote their creative but biologically relevant use to tackle real life research problems. Thus, the course is biologically oriented: I focus on research applications. Details on the mathematical underpinning of the methods I present are addressed in other courses of the master, for example the statistics and machine learning modules.

The course most specifically addresses the teaching goals 1.1, 1.2,1.5, 2.1-3, 3.1-4, 4.1, 4.2, 5.1 and 5.3 of the Master.

### Références, bibliographie et lectures recommandées

NA

## Autres renseignements

### Lieu(x) d'enseignement

Plaine

### Contact(s)

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## Méthode(s) d'évaluation

Examen écrit et Projet

### Examen écrit

Question fermée à Réponses Multiples (QRM)

Examen à livre ouvert

### Méthode(s) d'évaluation (complément)

The student will be evaluated from a personal project.

### Construction de la note (en ce compris, la pondération des notes partielles)

NA

## Langue(s) d'évaluation principale(s)

Français et Anglais

## Programmes

### Programmes proposant ce cours à la faculté des Sciences

MA-BINF | Master en bioinformatique et modélisation | finalité Approfondie/bloc 1 et MA-IRBC | Master : bioingénieur en chimie et bioindustries | finalité Spécialisée/bloc 2

### Programmes proposant ce cours à l'école polytechnique de Bruxelles

MA-IRBC | Master : bioingénieur en chimie et bioindustries | finalité Spécialisée/bloc 2 et MA-IRCB | Master : ingénieur civil biomédical | finalité Spécialisée/bloc 2