UCLouvain

lstat2340

2019

Statistical Analyses of ¿omics Data

In view of the health context linked to the spread of the coronavirus, the methods of organisation and evaluation of the learning units could be adapted in different situations; these possible new methods have been - or will be - communicated by the teachers to the students.

3 credits	15.0 h	Q2

Teacher(s)	Bugli Céline ;Govaerts Bernadette ;
Language :	French
Place of the course	Louvain-la-Neuve
Aims	*The contribution of this Teaching Unit to the development and command of the skills and learning outcomes of the programme(s) can be accessed at the end of this sheet, in the section entitled "Programmes/courses offering this Teaching Unit".*
Evaluation methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** The evaluation is based on: • Small projects proposed after each course, • a final project and a linked oral presentation, • an oral exam (with open documentation).
Teaching methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** The course consists of a series of activities that lead the student to actively immerse himself in the world of -omics data. It proposes: • presentations by specialists active in the field, • mini-projects of data processing to be carried out each week, • interactive computer work during the course, • a laboratory visit, • a final project on data proposed by the various participants in the course or data repositories.
Content	After reviewing the basics of molecular biology, the course presents a series of -omics methods and especially related data processing methods: • Molecular biology basics. • Revision of multivariate methods useful in -omics methods (PCA, Clustering...) and application in R + RMarkdown. • Transcriptomic data acquisition method (micro-arrays, q-PCR...). • Pretreatment and analysis of transcriptomic data (background correction, normalization,.... + hypothesis tests with multiplicity correction). • Use of prediction and classification models from chemometry and machine learning for the analysis of omic data (PLS, O-PLS, trees...). • Acquisition and processing of proteomic data. • Acquisition and processing of metabolomic data (including detailed pre-processing of 1H-NMR data). • Processing of metagenomic data.
Inline resources	Moodle Site: https://moodleucl.uclouvain.be/course/view.php?id=10846
Faculty or entity in charge	LSBA

Programmes containing this learning unit (UE)

Program title	Acronym	Credits	Prerequisite	Aims
Master [120] in Statistic: Biostatistics	BSTA2M	3		🔍
Certificat d'université : Statistique et sciences des données (15/30 crédits)	STAT2FC	3		🔍
Master [120] in Statistic: General	STAT2M	3		🔍
Master [120] in Data Science : Statistic	DATS2M	3		🔍