






4.00 credits

15.0 h + 5.0 h

Q2

Teacher(s)	Bugli Céline (compensates Govaerts Bernadette) ;Govaerts Bernadette ;
Language :	French
Place of the course	Louvain-la-Neuve
Prerequisites	Concepts and tools equivalent to those taught in teaching units LSTAT2020 Logiciels et programmation statistique de base LSTAT2110 Analyse des données
Learning outcomes	
Evaluation methods	In this course, students are evaluated in two ways: <ul style="list-style-type: none"> • continuous assessment including: <ul style="list-style-type: none"> • mandatory assignments to be delivered during the quarter according to a schedule set at the beginning of the quarter (40% of the final grade) • and a final project to be presented during the last class (40% of the final grade) • an open-book oral exam (20% of the final grade)
Teaching methods	The course consists of a series of activities that lead the student to actively immerse himself in the world of \omicron -omics data. It proposes: <ul style="list-style-type: none"> • 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. The modalities foreseen will evolve according to the health situation.
Content	After reviewing the basics of molecular biology, the course presents a series of \omicron -omics methods and especially related data processing methods: <ul style="list-style-type: none"> • Molecular biology basics. • Revision of multivariate methods useful in \omicron-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	Learning outcomes
Master [120] in Data Science : Statistic	DATS2M	4		
Master [120] in Statistics: Biostatistics	BSTA2M	4		
Master [120] in Statistics: General	STAT2M	4		
Master [120] in Chemistry and Bioindustries	BIRC2M	5		
Certificat d'université : Statistique et science des données (15/30 crédits)	STAT2FC	4		
Master [120] in Agricultural Bioengineering	BIRA2M	4		