





4.00 credits

15.0 h

Q2

Teacher(s)	Bugli Céline ;Govaerts Bernadette ;
Language :	French
Place of the course	Louvain-la-Neuve
Learning outcomes	
Evaluation methods	<p>In this course, students are evaluated in two ways:</p> <ul style="list-style-type: none"> <li>• continuous assessment including:                             <ul style="list-style-type: none"> <li>• mandatory assignments to be delivered during the quarter according to a schedule set at the beginning of the quarter (40% of the final grade)</li> <li>• and a final project to be presented during the last class (40% of the final grade)</li> </ul> </li> <li>• an open-book oral exam (20% of the final grade)</li> </ul>
Teaching methods	<p>The course consists of a series of activities that lead the student to actively immerse himself in the world of <math>\omicron</math>-omics data. It proposes:</p> <ul style="list-style-type: none"> <li>• presentations by specialists active in the field,</li> <li>• mini-projects of data processing to be carried out each week,</li> <li>• interactive computer work during the course,</li> <li>• a laboratory visit,</li> <li>• a final project on data proposed by the various participants in the course or data repositories.</li> </ul> <p>The modalities foreseen will evolve according to the health situation.</p>
Content	<p>After reviewing the basics of molecular biology, the course presents a series of <math>\omicron</math>-omics methods and especially related data processing methods:</p> <ul style="list-style-type: none"> <li>• Molecular biology basics.</li> <li>• Revision of multivariate methods useful in <math>\omicron</math>-omics methods (PCA, Clustering...) and application in R + RMarkdown.</li> <li>• Transcriptomic data acquisition method (micro-arrays, q-PCR...).</li> <li>• Pretreatment and analysis of transcriptomic data (background correction, normalization,.... + hypothesis tests with multiplicity correction).</li> <li>• Use of prediction and classification models from chemometry and machine learning for the analysis of omic data (PLS, O-PLS, trees...).</li> <li>• Acquisition and processing of proteomic data.</li> <li>• Acquisition and processing of metabolomic data (including detailed pre-processing of 1H-NMR data).</li> <li>• Processing of metagenomic data.</li> </ul>
Inline resources	Moodle Site: <a href="https://moodleucl.uclouvain.be/course/view.php?id=10846">https://moodleucl.uclouvain.be/course/view.php?id=10846</a>
Faculty or entity in charge	LSBA

Programmes containing this learning unit (UE)				
Program title	Acronym	Credits	Prerequisite	Learning outcomes
Master [120] in Statistics: General	<a href="#">STAT2M</a>	4		
Master [120] in Agricultural Bioengineering	<a href="#">BIRA2M</a>	4		
Master [120] in Statistics: Biostatistics	<a href="#">BSTA2M</a>	4		
Certificat d'université : Statistique et sciences des données (15/30 crédits)	<a href="#">STAT2FC</a>	4		
Master [120] in Data Science : Statistic	<a href="#">DATS2M</a>	4		