

5.00 credits

30.0 h + 30.0 h

Q1

Teacher(s)	Branders Vincent (compensates Dupont Pierre) ;Dupont Pierre ;
Language :	English > French-friendly
Place of the course	Louvain-la-Neuve
Prerequisites	Students are expected to master the following skills : • implement and test a solution in the form of a software prototype and/or a numerical model; • demonstrate a good understanding of the basic concepts and the methodology of programming; • make a relevant choice between several data representations and algorithms to process them; • analyse a problem to provide an IT solution and implement it in a high level programming language; • understand and know how to apply in various situations the basic concepts of probability and statistical inference; • use a scientific approach to extract reliable information from a data sample. as covered within the courses LEPL1401 , LEPL1402 , LEPL1109 The following skills are also useful. They are briefly reviewed at the beginning of the LGBIO2010 course : • explain the functions that take place in the cells of a living organism; • describe the basic concepts of molecular genetics; • define the different classes of biomolecules and their links within the cell processes and structures. as covered within the courses LGBIO1111 and LBIR1250A
Main themes	• Introduction to molecular biology • Searching methods in biological databases • Sequence comparisons, sequence alignment algorithms • Motif search • Hidden Markov models • Gene expression measurement technology • Transcriptome analysis methods • Inference of interaction networks • Phylogeny
Learning outcomes	At the end of this learning unit, the student is able to : With respect to the AA referring system defined for the Master in biomedical engineering, the course contributes to the development, mastery and assessment of the following skills : • AA1.1, AA1.2, AA1.3 • AA2.2, AA2.4 • AA4.3 • AA5.3 At the end of this course, students will be able: • to master the basic concepts of molecular biology for appropriate use of bioinformatics tools; • to design and develop tools or methods for database management, information extraction and data mining; • to formulate informed decisions between the many computational methods that are available for solving biological questions; • to carry out a collaborative project aiming at the resolution of a bioinformatics problem and taking benefit from complementary students education and expertise; • to use the information available in major sequence databases (Genbank, Uniprot) with a critical mind and with discernment; • to master a software environment such as R (Bioconductor).

Evaluation methods	Computation of the global grade for the course The final grade consists of • 25% for computing projects implemented in groups of (max.) 2 students during the semester • 75% for the final exam The projects cannot be re-implemented for the second session. Hence, the project grade is fixed at the end of the semester. The final exam is, by default, a written exam (on paper or, when appropriate, on a computer). Rules for student collaboration and use of external resources, including generative AIs Collaborative studying between students is encouraged during project follow-up sessions and via an exchange forum on Moodle. Each group of (max.) 2 students is expected to submit their own solution to each project. The use of public resources (e.g. stackoverflow.com), including generative AIs (e.g. chatGPT) is permitted, as long as each (fragment of) code submitted by the student group mentions specifically all the resources used. The distribution or exchange between groups of students of (fragments of) code is not authorized by any means (GitHub, Facebook, Discord, etc.), even after the project deadlines. Failure to comply with these rules for any project will result in an overall grade of 0 for all projects. These rules are explained in detail during the first class (see course Moodle site).
Teaching methods	Lectures and computing projects. • The projects are made in groups of (max) 2 students to implement, possibly to adapt, concrete algorithms covered in the course lectures. • The projects are implemented in R. An R tutorial is included at the beginning of the first project. Practical <i>projects</i> are submitted on line and evaluated on the Inginious platform.
Content	• Overview of basic concepts in molecular biology • Search in biological databases • Read alignment and genome assembly • Sequence comparison, pairwise and multiple sequence alignments • Hidden Markov models • Phylogenetic tree inference algorithms • Gene expression analysis methods (transcriptomics) • Biomarker selection • Predictive modeling
Inline resources	moodle.uclouvain.be/course/view.php?id=1839 https://inginius.info.ucl.ac.be/course/LGBIO2010
Bibliography	Recommended textbooks - Ouvrages complémentaires conseillés : - <i>Biological Sequence Analysis : Probabilistic Models of Proteins and Nucleic Acids</i>, R. Durbin et al., Cambridge University Press, 1998. - <i>Inferring Phylogenies</i> , J. Felsenstein, Sinauer Associates; 2nd ed., 2003. - <i>Bioinformatics, Sequence and Genome Analysis</i> , D. Mount, Cold Spring Harbord Laboratory Press, 2nd ed., 2004. - <i>Introduction to Computational Genomics : a case-study approach</i> , N. Cristianini M. Hand, Cambridge University Press, 2007.
Faculty or entity in charge	GBIO

Programmes containing this learning unit (UE)				
Program title	Acronym	Credits	Prerequisite	Learning outcomes
Master [120] in Biomedical Engineering	GBIO2M	5		
Master [120] in Statistics: Biostatistics	BSTA2M	5		
Master [120] in Computer Science and Engineering	INFO2M	5		
Master [120] in Computer Science	SINF2M	5		
Master [120] in Mathematical Engineering	MAP2M	5		
Master [120] in Data Science Engineering	DATE2M	5		
Master [120] in Data Science: Information Technology	DATI2M	5		