lgbio2010
2018

Bioinformatics

5 credits	30.0 h + 30.0 h	Q2

Teacher(s)	Dupont Pierre ;
Language :	English
Place of the course	Louvain-la-Neuve
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
Aims	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 student's 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). - - - - *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	The final grade consists of • 25% for computing projects implemented in groups 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.
Teaching methods	Lectures and computing projects. The projects are made in groups of 2 students to implement, possibly to adapt, concrete algorythms covered in the course lectures. Students are free to choose the software environment or language (R, Python, ...) to implement these projects but the R language is recommended. An R tutorial is included at the beginning of the first project.
Content	• Overview of basic concepts in biochemistry and molecular biology • Major Sequence and structure repositories and associated search tools • Sequence comparison • Sequence statistics • Pairwise sequence alignment • Database search for homology • Hidden Markov models • Multiple sequence alignment and profiles

	• Transcriptome profiling • Gene expression analysis • Gene regulatory networks • Molecular Phylogeny
Inline resources	Moodle http://moodleucl.uclouvain.be/course/view.php?id=8915
Bibliography	• Required teaching material include all documents (lecture slides, project assignments, complements, ...) available on the Moodle website for this course. • Les supports obligatoires sont constitués de l'ensemble des documents (transparents des cours magistraux, énoncés des travaux pratiques, compléments, ...) disponibles sur le site Moodle du cours. - Bioinformatics, Sequence and Genome Analysis, D. Mount, Cold Spring Harbord Laboratory Press, 2nd ed., 2004. - Introduction to Computational Genomics : a case-study approach, N. Cristianini M. Hand, Cambridge University Press, 2007. - Biological Sequence Analysis : Probabilistic Models of Proteins and Nucleic Acids, R. Durbin et al., Cambridge University Press, 1998. - Inferring Phylogenies, J. Felsenstein, Sinauer Associates; 2nd ed., 2003.
Faculty or entity in charge	GBIO

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