







5.00 credits

30.0 h + 30.0 h

Q1

Teacher(s)	Dupont Pierre ;
Language :	English
Place of the course	Louvain-la-Neuve
Prerequisites	<p>Students are expected to master the following skills :</p> <ul style="list-style-type: none"> <li>• implement and test a solution in the form of a software prototype and/or a numerical model,</li> <li>• demonstrate a good understanding of the basic concepts and the methodology of programming,</li> <li>• make a relevant choice between several data representations and algorithms to process them,</li> <li>• analyse a problem to provide an IT solution and implement it in a high level programming language,</li> <li>• understand and know how to apply in various situations the basic concepts of probability and statistical inference,</li> <li>• use a scientific approach to extract reliable information from a data sample,</li> </ul> <p>as covered within the courses <a href="#">LEPL1401</a>, <a href="#">LEPL1402</a>, <a href="#">LEPL1109</a></p> <p>The following skills are also useful. They are briefly reviewed at the beginning of the LGBIO2010 course :</p> <ul style="list-style-type: none"> <li>• explain the functions that take place in the cells of a living organism,</li> <li>• describe the basic concepts of molecular genetics,</li> <li>• define the different classes of biomolecules and their links within the cell processes and structures,</li> </ul> <p>as covered within the courses <a href="#">LGBIO1111</a> and <a href="#">LBIR1250A</a></p>
Main themes	<ul style="list-style-type: none"> <li>• Introduction to molecular biology</li> <li>• Searching methods in biological databases</li> <li>• Sequence comparisons, sequence alignment algorithms</li> <li>• Motif search</li> <li>• Hidden Markov models</li> <li>• Gene expression measurement technology</li> <li>• Transcriptome analysis methods</li> <li>• Inference of interaction networks</li> <li>• Phylogeny</li> </ul>
Learning outcomes	<p><b>At the end of this learning unit, the student is able to :</b></p> <p>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 :</p> <ul style="list-style-type: none"> <li>• AA1.1, AA1.2, AA1.3</li> <li>• AA2.2, AA2.4</li> <li>• AA4.3</li> <li>• AA5.3</li> </ul> <p>At the end of this course, students will be able:</p> <ol style="list-style-type: none"> <li>1 - to master the basic concepts of molecular biology for appropriate use of bioinformatics tools,</li> <li>- to design and develop tools or methods for database management, information extraction and data mining,</li> <li>- to formulate informed decisions between the many computational methods that are available for solving biological questions,</li> <li>- to carry out a collaborative project aiming at the resolution of a bioinformatics problem and taking benefit from complementary student's education and expertise,</li> <li>- to use the information available in major sequence databases (Genbank, Uniprot) with a critical mind and with discernment,</li> <li>- to master a software environment such as R (Bioconductor).</li> </ol>

<p>Evaluation methods</p>	<p>The final grade consists of</p> <ul style="list-style-type: none"> <li>• 25% for computing projects implemented in groups during the semester</li> <li>• 75% for the final exam</li> </ul> <p>The projects cannot be re-implemented for the second session. Hence, the project grade is fixed at the end of the semester.</p> <p>The final exam is, by default, a written exam (on paper or, when appropriate, on a computer).</p>
<p>Teaching methods</p>	<p>Lectures and computing projects.</p> <ul style="list-style-type: none"> <li>• The projects are made in groups of (max) 2 students to implement, possibly to adapt, concrete algorithms covered in the course lectures.</li> <li>• The projects are implemented in R. An R tutorial is included at the beginning of the first project.</li> </ul> <p>Practical <i>projects</i> are submitted <b>on line</b> and evaluated on the Inginious platform.</p>
<p>Content</p>	<ul style="list-style-type: none"> <li>• Overview of basic concepts in molecular biology</li> <li>• Search in biological databases</li> <li>• Sequence comparison, pairwise and multiple sequence alignments</li> <li>• Hidden Markov models</li> <li>• Phylogenetic tree inference algorithms</li> <li>• Gene expression analysis methods (transcriptomics)</li> <li>• Biomarker selection</li> <li>• Predictive modeling</li> </ul>
<p>Inline resources</p>	<p><a href="https://moodle.uclouvain.be/course/view.php?id=1839">moodle.uclouvain.be/course/view.php?id=1839</a></p>
<p>Bibliography</p>	<p>Recommended textbooks - Ouvrages complémentaires conseillés :</p> <ul style="list-style-type: none"> <li>- <i>Biological Sequence Analysis : Probabilistic Models of Proteins and Nucleic Acids</i>, R. Durbin et al., Cambridge University Press, 1998.</li> <li>- <i>Inferring Phylogenies</i>, J. Felsenstein, Sinauer Associates; 2nd ed., 2003.</li> <li>- <i>Bioinformatics, Sequence and Genome Analysis</i>, D. Mount, Cold Spring Harbord Laboratory Press, 2nd ed., 2004.</li> <li>- <i>Introduction to Computational Genomics : a case-study approach</i>, N. Cristianini M. Hand, Cambridge University Press, 2007.</li> </ul>
<p>Faculty or entity in charge</p>	<p>GBIO</p>

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