








5.00 credits

30.0 h + 30.0 h

Q1

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| Teacher(s) | Branders Vincent (compensates Dupont Pierre) ;Dupont Pierre ; |
| Language : | English > French-friendly |
| Place of the course | Louvain-la-Neuve |
| Prerequisites | <p>Students are expected to master the following skills :</p> <ul style="list-style-type: none"> • 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, <p>as covered within the courses LEPL1401, LEPL1402, LEPL1109</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"> • 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, <p>as covered within the courses LGBIO1111 and LBIR1250A</p> |
| Main themes | <ul style="list-style-type: none"> • 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 | <p>At the end of this learning unit, the student is able to :</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"> • AA1.1, AA1.2, AA1.3 • AA2.2, AA2.4 • AA4.3 • AA5.3 <p>At the end of this course, students will be able:</p> <ol style="list-style-type: none"> 1 - 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). |

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| Evaluation methods | <p>The final grade consists of</p> <ul style="list-style-type: none"> • 25% for computing projects implemented in groups during the semester • 75% for the final exam <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> |
| Teaching methods | <p>Lectures and computing projects.</p> <ul style="list-style-type: none"> • 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. <p>Practical <i>projects</i> are submitted on line and evaluated on the Inginious platform.</p> |
| Content | <ul style="list-style-type: none"> • Overview of basic concepts in molecular biology • Search in biological databases • 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 | <p>moodle.uclouvain.be/course/view.php?id=1839 https://inginius.info.ucl.ac.be/course/LGBIO2010</p> |
| Bibliography | <p>Recommended textbooks - Ouvrages complémentaires conseillés :</p> <ul style="list-style-type: none"> - <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 | <p>GBIO</p> |

| Programmes containing this learning unit (UE) | | | | |
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| 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 | |  |