



### Programme of Course "Bioinformatica"

<ul style="list-style-type: none"> <li>• Code: DS9001</li> <li>• Type of course unit: Elective (Bachelor Degree in Computer Science curriculum General), Elective (Master Degree in Computer Science curriculum General)</li> <li>• Level of course unit: Undergraduate Degrees, Postgraduate Degrees</li> <li>• Semester: 2</li> </ul>		
Number of ects credits: (Master Degree in Computer Science) 6 (workload 150 hours)		
Teachers: Antiniscia Di Marco (antiniscia.dimarco@univaq.it)		
1	<b>Course objectives</b>	The course introduces the bioinformatics by identifying the principal problems and solutions the algorithms can deal with and provide, respectively. Moreover, it provides an overview of the main on-line Data bases on biology data and presents their structures and the services they provide to end users. Finally, an introduction to system biology is given, focusing on computer science formal tools (such as, petri nets) that can be used to model biology phenomena or systems.
2	<b>Course content and learning outcomes (dublin descriptors)</b>	<p>Topics of the module include:</p> <ul style="list-style-type: none"> <li>• 1. Biological databases of genes, polimorfisms e mutations.</li> <li>• 2. Biological databases of metabolic pathways.</li> <li>• 3. Alignment algorithms and substitution matrices.</li> <li>• 4. Pattern search, phylogenetic trees. Genome wide character association.</li> <li>• 5. Computational models for System Biology.</li> <li>• 6. BioPhyton</li> </ul> <p>On successful completion of this module, the student should :</p> <ul style="list-style-type: none"> <li>• Demonstrate detailed knowledge of: i) alignment algorithms and of the phylogenetic analysis; ii) the functioning and regulation of prokaryotic and eukaryotic cells; iii) Phyton language and BioPhyton libraries; iv) computational modeling for simple biological systems represented as pathways.</li> <li>• Use and organize databases of genomics, proteomics and metabolomics data; Be able to apply phylogenetic analysis to simple genomics data. Use BioPhyton libraries for bioinformatics aims. Use of Petri Nets to model biological pathways.</li> <li>• Be able to: i) evaluate and interpret current literature in areas of bioinformatic practice for analysis of DNA sequence. ii) obtain quantitative results from computational methods. iii) to interpret quantitative results from computational methods.</li> <li>• Be able to report on the bioinformatics experiments and studies conducted on DNA sequences and pathways. Have the capacity to discuss the theoretical basics of DNA sequence analysis.</li> <li>• Demonstrate capacity to select programs for problem solving and write programs</li> </ul>
3	<b>Course prerequisites</b>	Basic knowledge of imperative and object-oriented programming techniques.
4	<b>Teaching methods and language</b>	<p>The course will be composed by around 40 hours of theory and 20 hours of (computer science!) laboratory during which the theoretical concepts are showed on concrete examples.</p> <p><b>Language:</b> Italian</p> <p><b>Reference textbooks</b></p> <ul style="list-style-type: none"> <li>• Volker Sperschneider, <i>Bioinformatics.Problem Solving Paradigms</i> . Springer.</li> <li>• <i>selected scientific publications</i>.</li> <li>• <i>Teacher Notes</i>.</li> <li>• <i>Tutorial of on-line data base</i>.</li> </ul>
5	<b>Assessment</b>	Project and oral exam. Mid-term exam

<b>methods</b>
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