



**Universidad Nacional de Colombia (UNAL) Sede  
Manizales  
Undergraduate Program in  
Information Systems  
SILABO**

**CB309. Bioinformatics (Mandatory)**

2022-II

<b>1. General information</b>	
1.1 School	: Sistemas de Información
1.2 Course	: CB309. Bioinformatics
1.3 Semester	: 9 <sup>no</sup> Semestre.
1.4 Prerequisites	: <ul style="list-style-type: none"><li>• CS212. Algorithm Analysis and Design. (5<sup>th</sup> Sem)</li><li>• MA307. Mathematics applied to computing . (6<sup>th</sup> Sem)</li></ul>
1.5 Type of course	: Mandatory
1.6 Learning modality	: Face to face
1.7 Horas	: 1 HT; 2 HL;
1.8 Credits	: 2

<b>2. Professors</b>

<b>3. Course foundation</b>
<p>The use of computational methods in the biological sciences has become one of the key tools for the field of molecular biology, being a fundamental part of research in this area.</p> <p>In Molecular Biology, there are several applications that involve both DNA, protein analysis or sequencing of the human genome, which depend on computational methods. Many of these problems are really complex and deal with large data sets.</p> <p>This course can be used to see concrete use cases of several areas of knowledge of Computer Science such as Programming Languages (PL), Algorithms and Complexity (AL), Probabilities and Statistics, Information Management (IM), Intelligent Systems (IS).</p>

<b>4. Summary</b>
1. Introduction to Molecular Biology 2. Sequence Comparison 3. Phylogenetic Trees 4. DNA Sequence Assembling 5. Secondary and tertiary structures 6. Probabilistic Models in Molecular Biology

<b>5. Generales Goals</b>
<ul style="list-style-type: none"><li>• That the student has a solid knowledge of molecular biological problems that challenge computing.</li><li>• That the student is able to abstract the essence of the various biological problems to pose solutions using their knowledge of Computer Science</li></ul>

## 6. Contribution to Outcomes

This discipline contributes to the achievement of the following outcomes:

- 1) Analyze a complex computing problem and to apply principles of computing and other relevant disciplines to identify solutions. (**Assessment**)
- 2) Design, implement and evaluate a computing-based solution to meet a given set of computing requirements in the context of the program's discipline. (**Usage**)
- 6) Apply computer science theory and software development fundamentals to produce computing-based solutions. (**Usage**)
- 7) Develop computational technology for the well-being of all, contributing with human formation, scientific, technological and professional skills to solve social problems of our community. (**Usage**)

## 7. Content

### UNIT 1: Introduction to Molecular Biology (4)

#### Competences:

#### Content

- Review of organic chemistry: molecules and macromolecules, sugars, nucleic acids, nucleotides, RNA, DNA, proteins, amino acids and levels of structure in proteins.
- The Dogma of Life: From DNA to Proteins, Transcription, Translation, Protein Synthesis.
- Genome study: Maps and sequences, specific techniques

#### Generales Goals

- Achieve a general knowledge of the most important topics in Molecular Biology. [Familiarity]
- Understand that biological problems are a challenge to the computational world. [Assessment]

**Readings:** Clote and Backofen (2000), Setubal and Meidanis (1997)

### UNIT 2: Sequence Comparison (4)

#### Competences:

#### Content

- Sequences of nucleotides and amino acid sequences.
- Sequence alignment, paired alignment problem, exhaustive search, Dynamic programming, global alignment, local alignment, gaps penalty
- Comparison of multiple sequences: sum of pairs, complexity analysis by dynamic programming, alignment heuristics, star algorithm, progressive alignment algorithms.

#### Generales Goals

- Understand and solve the problem of aligning a pair of sequences. [Usage]
- Understand and solve the problem of multiple sequence alignment. [Usage]
- Know the various algorithms for aligning existing sequences in the literature . [Familiarity]

**Readings:** Clote and Backofen (2000), Setubal and Meidanis (1997), Pevzner (2000)

<b>UNIT 3: Phylogenetic Trees (4)</b>	
<b>Competences:</b>	
<b>Content</b>	<b>Generales Goals</b>
<ul style="list-style-type: none"> <li>• Phylogeny: Introduction and phylogenetic relations</li> <li>• Phylogenetic trees: definition, type of trees, problem of search and reconstruction of trees</li> <li>• Reconstruction methods: parsimony methods, distance methods, maximum likelihood methods, confidence of reconstructed trees</li> </ul>	<ul style="list-style-type: none"> <li>• Understand the concept of phylogeny, phylogenetic trees and the methodological difference between biology and molecular biology. [Familiarity]</li> <li>• Understand the problem of the reconstruction of phylogenetic trees, to know and apply the main algorithms for the reconstruction of phylogenetic trees. [Assessment]</li> </ul>
<b>Readings:</b> Clote and Backofen (2000), Setubal and Meidanis (1997), Pevzner (2000)	

<b>UNIT 4: DNA Sequence Assembling (4)</b>	
<b>Competences:</b>	
<b>Content</b>	<b>Generales Goals</b>
<ul style="list-style-type: none"> <li>• Biological basis: ideal case, difficulties, alternative methods for DNA sequencing</li> <li>• Formal Assembly Models: Shortest Common Superstring, Reconstruction, Multicontig</li> <li>• Algorithms for sequence assembly: representation of overlaps, paths to create superstrings, voracious algorithm, acyclic graphs.</li> <li>• Assembly heuristics: search for overlays, ordering fragments, alignments and consensus.</li> </ul>	<ul style="list-style-type: none"> <li>• Understand the computational challenge of the Sequence Assembly problem. [Familiarity]</li> <li>• Understand the principle of formal model for assembly. [Assessment]</li> <li>• Know the main heuristics for the problem of assembly of DNA sequences [Usage]</li> </ul>
<b>Readings:</b> Setubal and Meidanis (1997), Aluru (2006)	

<b>UNIT 5: Secondary and tertiary structures (4)</b>	
<b>Competences:</b>	
<b>Content</b>	<b>Generales Goals</b>
<ul style="list-style-type: none"> <li>• Molecular structures: primary, secondary, tertiary, quaternary.</li> <li>• Prediction of secondary structures of RNA: formal model, pair energy, structures with independent bases, solution with Dynamic Programming, structures with loops.</li> <li>• <i>Protein folding</i>: Estructuras en proteínas, problema de protein folding.</li> <li>• <i>Protein Threading</i>: Definitions, Branch Bound Algorithm, Branch Bound for protein threading.</li> <li>• <i>Structural Alignment</i>: Definitions, DALI algorithm</li> </ul>	<ul style="list-style-type: none"> <li>• Know the protein structures and the necessity of computational methods for the prediction of the geometry. [Familiarity]</li> <li>• Know the algorithms for solving prediction problems of secondary structures RNA, and structures in proteins. [Assessment]</li> </ul>
<b>Readings:</b> Setubal and Meidanis (1997), Clote and Backofen (2000), Aluru (2006)	

UNIT 6: Probabilistic Models in Molecular Biology (4)	
Competences:	
Content	Generales Goals
<ul style="list-style-type: none"> <li>• Probability: Random Variables, Markov Chains, Metropoli-Hasting Algorithm, Markov Random Fields, and Gibbs Sampler, Maximum Likelihood.</li> <li>• Hidden Markov Models (HMM), parameter estimation, Viterbi algorithm and Baul-Welch method, Application in paired and multiple alignments, Motifs detection in proteins, in eukaryotic DNA, in sequences families.</li> <li>• Probabilistic phylogeny: probabilistic models of evolution, likelihood of alignments, likelihood for inference, comparison of probailistic and non-probabilistic methods</li> </ul>	<ul style="list-style-type: none"> <li>• Review concepts of Probabilistic Models and understand their importance in Computational Molecular Biology. [Assessment]</li> <li>• Know and apply Hidden Markov Models for various analyzes in Molecular Biology.. [Usage]</li> <li>• Know the application of probabilistic models in Phylogeny and to compare them with non-probabilistic models[Assessment]</li> </ul>
<b>Readings:</b> Durbin et al. (1998), Clote and Backofen (2000), Aluru (2006), Krogh et al. (1994)	

## 8. Methodology

El profesor del curso presentará clases teóricas de los temas señalados en el programa propiciando la intervención de los alumnos.

El profesor del curso presentará demostraciones para fundamentar clases teóricas.

El profesor y los alumnos realizarán prácticas

Los alumnos deberán asistir a clase habiendo leído lo que el profesor va a presentar. De esta manera se facilitará la comprensión y los estudiantes estarán en mejores condiciones de hacer consultas en clase.

## 9. Assessment

**Continuous Assessment 1** : 20 %

**Partial Exam** : 30 %

**Continuous Assessment 2** : 20 %

**Final exam** : 30 %

## References

- Aluru, Srinivas, ed. (2006). *Handbook of Computational Molecular Biology*. Computer and Information Science Series. Chapman & Hall, CRC: Boca Raton, FL.
- Clote, P. and R. Backofen (2000). *Computational Molecular Biology: An Introduction*. 279 pages. John Wiley & Sons Ltd.
- Durbin, R. et al. (1998). *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids*. Cambridge University Press, p. 357. ISBN: 9780521629713.
- Krogh, Anders et al. (1994). "Hidden Markov Models in Computational Biology, Applications to Protein Modeling". In: *J Molecular Biology* 235, pp. 1501–1531.
- Pevzner, Pavel A. (2000). *Computational Molecular Biology: an Algorithmic Approach*. The MIT Press: Cambridge, Massachusetts.
- Setubal, João Carlos and João Meidanis (1997). *Introduction to computational molecular biology*. Boston: PWS Publishing Company, pp. I–XIII, 1–296. ISBN: 978-0-534-95262-4.