



**NATIONAL UNIVERSITY OF ENGINEERING
COLLEGE OF SCIENCES
COMPUTER SCIENCE PROGRAM**

CC471 – COMPUTATIONAL BIOLOGY

I. GENERAL INFORMATION

CODE	: CC471 – Computational biology
SEMESTER	: 7
CREDITS	: 04
HOURS PER WEEK	: 6 (Theory – Laboratory)
PREREQUISITES	: CC302 Distributed parallel language oriented to objects CH061 Biology
CONDITION	: Mandatory

II. COURSE DESCRIPTION

Interpret biological problems using computer techniques. Analyze and implement algorithms and structures applicable to the biology field.

III. LEARNING UNITS

1. Introductory concepts

- I: Introduction to history of genetics.
- II: Basic concepts of molecular biology.
- III: Classic problems in bioinformatics.
- IV: Collection and storage tools of sequences in laboratory.
- V: Software resources, introduction to BLAST, CLUSTALW.
- VI: Chains, graphs and algorithms.

2. Sequence Alignment

- I: Introduction to sequence alignment.
- II: Comparison of sequence pairs
- III: Alignment of global sequences.
- IV: Alignment of multiple sequences.
- V: Hidden Markov chains.
- VI: Exact, approximate and heuristic methods of sequence alignment.
- VII: Problems derived from the alignment of sequences.

3. Clustering

- I: The problem of clustering.
- II: Hierarchical clustering.
- III: Neighbor joining algorithm / Average linkage algorithm.
- IV: Non-hierarchical clustering or K-means.
- V: EST clustering.

4. Phylogenetic trees

- I: Introduction to phylogeny.
- II: Common algorithms.
- III: Biological applications.
- IV: Exact algorithms.
- V: Probabilistic algorithms.

5. Sequence Mapping

- I: Problem of the double digest and partial digest.
- II: Techniques used in the mapping of sequences.
- III: Mapping with Non-unique probes M.
- IV: Mapping with unique probes.
- V: Intervals graphs.
- VI: Mapping with frequency signals of restriction.

6. Introduction to Proteins Structure

- I: Biological foundations of proteins.
- II: Motivation for the prediction of protein structures.
- III: Rigid alignment of proteins.
- IV: Alignment technique by Hashing Geometric.
- V: Prediction of protein structures.

IV. BIBLIOGRAPHY

- A Clote, P. and Backofen, R. Computational Molecular Biology, An Introduction. Wiley, 2000.
- Jones, N. A. and Pevzner, P. A. An Introduction to Bioinformatics Algorithms. The MIT Press. 2004.
- Mount, D. W. Bioinformatics: Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, 2001.