

Spiru Haret University
Faculty of Engineering and Computer Science
Department of Engineering and Computer Science

1. Opening description

Department: Engineering and Computer Science
Opening title: **ASSOCIATE PROFESSOR PhD**
Opening position: **4**
Subjects:

*Introduction to bioinformatics,
Bioinformatics.*

2. Opening-related activities

Teaching and seminar:

Introduction to bioinformatics (1st year, 1st semester),

2 course hours = 2 agreed hours.

2groups x 2hours = 2 agreed hours.

Bioinformatics (3rd year, 2nd semester)

2 course hours = 2 agreed hours

2groups x 2hours = 2 agreed hours.

Total number of hours = 8 agreed hours.

3. Competitive examination topics

Introduction to bioinformatics

1. Biological databases. Introduction.
2. Queuing search algorithms
3. Sequence distance
4. Dynamic programming – Needleman-Wunsch global alignment algorithm
5. Dynamic programming – Smith-Waterman local alignment algorithm
6. Complex models – repetitive sequences, overlapping sequences, hybrid sequences
7. Substitution matrix

Bioinformatics

1. Types of biological data and their employment using computational tools; Major bioinformatics resources – NAR, NCBI, EMBL-EBI and Expasy databases; Research databases: PubMed, PubMed Central and Public Library of Sciences
2. Nucleic acid sequence databases – NCBI, EMBL and DDBJ. Protein sequence databases – NCBI Protein, TrEMBL and Uniprot. Similarity search engines – BLAST and FASTA
3. Protein structure databases – RCSB PDB, SCOP and CATH. Databases of metabolic pathways – KEGG, BioCyc and Reactome. Protein – protein interaction databases – STRING, Consensus PathDB and BioGRID.
4. Genomic databases, Gene expression databases – 4DXpress, ArrayExpress and GEO; Genome databases – GeneCards and OMIM. Immunological databases.
5. Multiple sequence alignment, Algorithms. Examples.
6. Sequence modelling
7. Markov chain models
8. Phylogenetic analysis.

9. Parsimony method.

4. Course topics

Introduction to bioinformatics

Dynamic programming. Local alignment algorithms. Global alignment algorithms
Substitution matrix

Bioinformatics

Multiple sequence alignment algorithms
Sequential analysis using a Markov chain model

5. References

1. Charras C., Lecroq T., Handbook of Exact String Matching Algorithms, <https://www-igm.univ-mlv.fr/~lecroq/string/string.pdf>.
2. Cristianini N., Hand M., Introduction to Computational Genomics : a case-study approach, Cambridge University Press, 2007.
3. Durbin R. et al., Biological Sequence Analysis : Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 1998.
4. Felsenstein J., Inferring Phylogenies, Sinauer Associates; 2nd ed., 2003.
5. Gusfield Dan. Algorithms on strings, trees, and sequences: computer science and computational biology. Cambridge, UK: Cambridge University Press, 1997 (<http://www.inf.ufes.br/~berilhes/Cursos/TBO2008-1/gusfield.pdf>)
6. Lesk Arthur M., Introduction to Bioinformatics (4 th edition), Oxford Univ. Press, Oxford UK, 2014.
7. Măndoiu Ion I., Zelikovsky A., Bioinformatics Algorithms, Wiley, 2008.
8. Mihalaş G.I., Neagu M., Neagu A., Textbook of Biophysics, Ed. Eurobit, Timișoara, 2001. 2nd ed., 2004.
9. Needleman Saul B., Wunsch, Christian D., A general method applicable to the search for similarities in the amino acid sequence of two proteins. Journal of Molecular Biology. 48 (3): 443–53, 1970.
10. Smith, Temple F., Waterman, Michael S., Identification of Common Molecular Subsequences, Journal of Molecular Biology. 147 (1): 195–197, 1981.
11. Thompson JD., Linard B., Lecompte O., Poch O., A comprehensive benchmark study of multiple sequence alignment methods: current challenges and future perspectives. PLOS ONE. 6 (3): e18093, 2011.
12. Yoon, Byung-Jun, Hidden Markov Models and their Applications in Biological Sequence Analysis, <http://dx.doi.org/10.2174/138920209789177575> .

Head of Department

Associate Professor **Nicoleta Magdalena Iacob**, PhD