In the name of God

Ph.D. Program in Bioinformatics

Course Characteristics and Items

Course title: Advanced Bioinformatics
Number of units: 3
The number of hours: 64
Unit type: 2 Theoretical and 1 Practical
Course type: Mandatory
Prerequisite: -
Practical training: has it ☑ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☑ Seminar☑
Degree: MSc ☐ Ph.D. ☑ MSc & Ph.D. ☐

Course Objectives:

The aim of this course is to make the students familiar with new hot topics in the field of bioinformatics. After completing the course, students have an overview of the most important bioinformatics techniques. Students will be familiarized with the cutting edge subjects, after surveying scientific papers weekly.

Headlines:

- Introduction and bioinformatics history
  - Review on gathering and storing bioinformatics sequences, biological databases, sequence alignment, multiple sequence alignment, searching and finding similar sequences (homology and BLAST), phylogenetic prediction
- Secondary biological databases
- Knowledge bases
- Protein-Protein interaction networks data
- Signaling networks data
- Cancer networks data
- Regulatory networks data
- Genome structure determination and next generation sequencing
- RNA-Seq data analysis
- Microarray and related data analysis
- Introduction to biological networks
- Introduction to systems biology
- Introduction to synthetic biology
- Introduction to Brain Networks
- Weekly review and survey of new bioinformatics papers and project

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: 0	

References:

1. Bioinformatics and Functional Genomics, 3nd Edition, Jonathan Pevsner, 2015, Wiley-Blackwell, USA
2. Bioinformatics for Biologists, Pavel Pevzner, Ron Shamir, 2014, Cambridge University Press, UK
3. Bioinformatics: An Introduction, Jeremy Ramsden,2015, Springer, USA
4. Essential Bioinformatics, Jin Xiong, 2006, Cambridge University Press, UK

Course title: Algorithms in Bioinformatics
Number of units: 3
The number of hours: 48
Unit type: Theoretical
Course type: Mandatory
Prerequisite: -
Practical training: has it ☑ doesn’t have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☑ Seminar☑
Degree: MSc ☐ Ph.D. ☑ MSc & Ph.D. ☐

Course Objectives:

In this course, students will be familiarized with various methods of natural sequence generation and processing. State of the art algorithms for high-throughput sequencing data analysis will be introduced. Learning Graph-based algorithms for better biological networks understanding and preparation of students for effective and novel algorithm design are the other important aims of this course. After completing the course, students will be ready to solve a variety of problems, using existing algorithms or design a new one.

Headlines:

- Course introduction and introductory concepts
- Processing and analyzing biological sequences including applications of dynamic programming, alignment, and multiple alignments, Markov chains, hidden Markov models and its applications in biological sequences, different methods of searching in sequence databases, motif finding, …
- Introduction to next-generation sequencing methods in genome, transcriptome, metagenome, metatranscriptome
- De novo assembly algorithms, mapping assembly for different sequencing data
- Applications of Graph and tree based algorithms in bioinformatics, creating and interpreting trees and phylogenetic relationships.
- Different biological networks algorithms e.g. link prediction, motif finding, finding modules, node clustering, …

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: 0	

References:

1. Algorithms in Computational Molecular Biology, M. Elloumi, A. Y. Zomaya, Wiley, 2011.

2. An Introduction to Bioinformatics Algorithms (Computational Molecular Biology), N. C. Jones and P. A. Pevzner, MIT Press, 2004.
3. Algorithmic Aspects of Bioinformatics, Hans-Joachim Bockenhauer and D. Bongartz, Springer, 2007.
4. http://bioinformatics.msu.edu/ngs-summer-course-2014
5. Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology, D. Gusfield, Cambridge University Press, 1997.
6. Biological sequence analysisProbabilistic models of proteins and nucleic acids, R. Durbin, S. R. Eddy, A. Krogh, G. Mitchison, Cambridge University Press, 1998.

Course title: Biological Databases
Number of units: 3
The number of hours: 64
Unit type: 2 Theoretical and 1 Practical
Course type: Mandatory
Prerequisite: -
Practical training: has it ☑ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☑ Seminar☑
Degree: MSc ☐ Ph.D. ☑ MSc & Ph.D. ☐

Course Objectives:

One of the aims is to make the students familiar with different biological databases, methods for accessing stored data and biological data integration. So, students should learn ways of creating databases for efficient biological data storage. The ability to design and implementation of proper graphical user interfaces for storing and retrieving data from different databases are other objectives of this course.

Headlines:

- Course introduction and basic concepts of databases
- Database architecture, introduction to database models e.g. flat, hierarchical, network, relational, object-oriented, semi-structured.
- Database management systems, relational databases design, and ER model, normalization, and optimization
- Heterogeneous database integration
- Introduction to genome databases and genetic sequence e.g. GenBank, Ensemble, …. Explorers, standard file formats, protein databases
- Introduction to transcriptome databases, biological pathways, gene regulation, protein interaction databases
- Introduction to metagenome and metatranscriptome databases
- Introduction to particular phenotype and disease databases for human and other species
- Introduction to creating and programming biological databases
- Introduction to biological databases API and their usage
- Introductory and Advanced SQL (MySQL, SQLite)
- Connecting to database using programming languages
- NoSQL Databases
- Big Data storage and management, introduction to big data processing approaches e.g. MapReduce
- Introduction to cloud computing, data storage, and management in cloud space.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: 0	

References:

1. Marketa Zvelebil, Jeremy O. Baum, “Understanding Bioinformatics”, Garland Science, 2008.
2. Peter Revesz, “Introduction to Databases: From Biological to Spatio-Temporal”, Springer London, 2012.
3. Abraham Silberschatz, Henry F. Korth, S. Sudarsham, “Database System Concepts”, 6th h ed., McGraw-Hill, 2011.
4. Baoying Wang, Ruowang Li, William Perrizo, “Big Data Analytics in Bioinformatics and Healthcare”, Medical information science, 2015.
5. Jake Chen and Amandeep S. Sidhu, “Biological Database Modeling”, Artech House, 2007.
6. Remez Elmasri and Shamkant B. Navathe, “Fundamentals of Database Systems”, Addison Wesley, 5th ed., 2003.
7. John V. Carlis, Joseph Maguire, “Mastering Data Modeling: A User-Driven Approach”, Addison Wesley, 2000.
8. C.J. Date, “Relational Database”, Writings 1994-1997, Addison Wesley, 1998.

Course title: Seminar in Bioinformatics
Number of units: 1
The number of hours: 16
Unit type: Theoretical
Course type: Mandatory
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar☑
Degree: MSc ☐ Ph.D. ☑ MSc & Ph.D. ☐

Course Objectives:

Familiarizing students with research work presentation as lecture, poster, and paper

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
0%	0%	Written Test: 0%	0%
		Practical: 100%	

Course title: Biochemistry of Cellular Signaling
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is a description of cellular signaling structural and biochemical properties and their regulation. Also, the tool used to signal transduction. As well as principles of signaling organization and interplay of signaling pathways.

Headlines:

- Review on cellular signaling mechanisms
- Cell signaling receptors e.g. Intracellular receptors (structure/function, coactivator/corepressor, direct path to nucleus, JAK/STAT), cell surface receptors, G-Protein coupled receptor, Receptors with Tyrosine-specific protein kinase activity, ligand-gated ion channel receptor
- Second messengers
  - cAMP
  - Calcium
  - Lipophilic
  - Reactive oxygen species, reactive nitrogen species
  - Signal transduction by Ser/Thr-specific protein kinases and protein phosphatase
  - Signal transduction by ras proteins
- Cellular signaling in health and disease; cell proliferation (MAPs), signaling pathways of growth factors, apoptosis (regulated proteolysis in apoptosis and signal transduction by TNF and $NF-k\beta$ and apoptosis regulation), and cancer

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 60%	0%
		Practical: -	

References:

1. Cell signaling Edited by B.D. Gomperts, I. M. Kramer and P.E.R. Tatham, 2009
2. Biochemistry of Signal Transduction and Regulation 4th Edition, Edited by G. Krauss 2008

Course title: Computational Genomics
Number of units: 2
The number of hours: 48
Unit type: 1 Theoretical and 1 Practical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

This course is a practical aspect of topics in mandatory courses and along that practical projects will be accomplished in various bioinformatics subjects. The aim is to prepare students for doing research about their thesis.

Headlines:

- Principles, definitions, and ideas in Genome-wide projects
- Principles of appropriate data collecting and handling in genome-wide projects
- Principles of genomic data refinement
- Genomic data analysis and classification and creating appropriate data for computations
- Principles of genome-wide computations
- Principles of genome-wide data analysis and interpretation
- Weekly seminars (every student gives two presentations per term)
- Project

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
0%	0%	Written Test: 0%	80%
		Practical: 20%	

References:

1. Cristianini N., Hahn M.W. Introduction to Computational Genomics: A Case Studies Approach, Cambridge University Press, London 2007.
2. Introduction to Genomics, Arthur M. Lesk, 2012, Oxford University Press; UK
3. Computational Genomics, Srinivas Aluru, 2016, 2nd edition, Chapman & Hall, USA

Course title: Structural Bioinformatics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

To make the students familiar with analysis and prediction of biomolecular structures and primary structural databases.

Headlines:

- Historical introduction to development of methods and problems in structural bioinformatics
- Potential energy surface, energy minimization methods or molecular structure optimization
- Elements of proteins and nucleic acids structure
- Introduction to experimental methods for biomolecular structure determination.
- Review on protein folding problem and models for describing this phenomenon.
- Main file formats for representation, record, and storage of biomolecular structures e.g. PDB, mmCIF, XML
- Important databases for record and storage of protein and nucleic acid structure information.
- Methods and algorithms in biomolecular structure analysis e.g. structure comparison, structural similarity, superposition of structures, and classification of structures.
- Methods in Proteins and nucleic acids secondary structure determination and prediction.
- Methods of protein structural domain identification and prediction.
- Protein-protein and protein-ligand interaction analysis and prediction and their networks.
- Methods of Protein structure prediction e.g. homology modeling, fold recognition and Ab initio methods
- Knowledge-based and physics-based approaches in scoring function and force fields design.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
40%	30%	Written Test: 30%	0%
		Practical: -	

References:

1. Structural Bioinformatics, Jenny Gu, Philip E. Bourne, John Wiley & Sons, 2011.

2. Computational Methods for Protein Structure Prediction and Modeling, Ying Xu, Dong Xu, Jie Liang, John Wooley, Springer, 2007.
3. Protein Structure Prediction, Daisuke Kihara, Springer (Humana Press), 2014.

Course title: Computational Drug Design
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

An introduction to drug design by computational methods.

Headlines:

- Definition of drug and its receptor
- History and discovery of novel drugs
- Drug development process
- Main issues in drug discovery process
- Drug design process
- Ligand-based drug design
- Structure-based drug design
- Tools and computational techniques (homology modeling, molecular mechanics, protein folding, docking, pharmacophore models, QSAR, 3D-QSAR, Chemoinformatics)
- ADMET
- Virtual Screening
- Fragment-based drug design

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Young D.C. Computational Drug Design: A Guide for Computational and Medicinal Chemists. Wiley-Interscience. 2009
2. Bultinck P., Tollenaere J.P., Langenaeker W., Winter H.D. Computational Medicinal Chemistry for Drug Discovery. CRC. 2003.
3. Zheng, Y., Rational Drug Design Methods and Protocols, Springer. 2012.
4. Tari, L. W. Structure-Based Drug Discovery, Springer. 2012.

Course title: Chemoinformatics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

To make the students familiar with elements of chemoinformatics and modeling the activity of chemical and biological molecules.

Headlines:

- Molecular concepts and molecular representation
- Chemical compounds and drug databases
- Searching chemical and drug structures
- Chemical and biological compounds structure optimization and conformational search
- Calculation of Physical and chemical descriptors of biological and chemical compounds
- Calculation of structure descriptors
- Calculation of Quantitative structure and activity relationships
- Methods for chemical and biological data analysis
- Classification of chemical and biological data
- Statistical evaluation of chemoinformatics results
- Applications of chemoinformatics study in bioinformatics

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Gastiger, J. Cheminformatics, WILEY-VCH Verlag GmbH & Co.,Germany, 2003.
2. Leach, A.R., An introduction to cheminformatics, Springer, Netherlands, 2007.
3. Bunin, B. A., Siesel, B., Morales, G. A, Bajorath, J., Chemoinformatics: Theory, practice, & Products, Springer, Netherlands, 2007.
4. Bajorath, J., Chemoinformatics and Computational Chemical Biology, Springer, London, 2011.

Course title: Chemometrics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is to make the students familiar with various methods of chemometrics that are used for processing and extracting information from experimental data.

Headlines:

- Introduction to chemometrics, its relation to other fields, introducing different branches of chemometrics
- Definitions and concepts e.g. normal distribution, F-Test, t-Test, χ^2-test, one and two way analysis of variance
- Linear algebra, vectors, and matrices, different mathematical operations on vectors and matrices
- Newton method, Levenberg-Maquardt method
- Multivariate calibration methods(MVC), classical least squares (CLS), inverse least squares (ILS), multivariate linear regression(MLR), Principal component regression(PCR), and model Cross-validation.
- Working with Excel, including data analysis, regression, correlation
- Working with Matlab, including concepts and elementary commands, using various Matlab toolboxes and performing Chemometrics methods using them, and Matlab programming.
- Methods of modeling chemical data, including hard-modeling methods, soft-modeling methods, multivariate curve resolution methods(MCR)
- Factor analysis (FA), FA steps, target factor analysis(TFA), evolutionary factor analysis(EFA)
- Experimental design methods
- Full factor design (Full FD), parameters interaction
- Fractional factor design (Fractional FD), resolution of the design
- Central composite design(CCD), and response surface methodology (RSM)

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
0%	20%	Written Test: 40%	30%
		Practical: 10%	

References:

1. Richard G. Brereton. Chemometrics.John Wiley2003
2. Howard Mark, Jerry Workman Jr. Chemometrics in Spectroscopy. Elsevier, 2007
3. James N. Miller, Jane C. Miller. Statistics and Chemometricsfor AnalyticalChemistry, 2010

Course title: Machine Learning
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

In this course, the student will be familiarized with various approaches to machine learning and after completing the course has skills for design an efficient strategy to solve problems using existing tools or implement a new one.

Headlines:

- Course introduction and elementary concepts
- Learning theory, supervised learning, unsupervised learning, and semi-supervised learning
- Supervised learning methods and regression
- Various parameter estimation methods
- Artificial neural networks and deep learning
- Evaluating machine learning models
- Various methods of feature generation and selection
- Various methods of unsupervised learning and their evaluation
- Semi-supervised learning methods
- Graphical models and Bayesian networks
- Ensemble methods

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Sergios Theodoridis, Konstantinos Koutroumbas, "Pattern Recognition", 3rd Edition, Elsevier Academic Press, 2006.
2. Cristopher M. Bishop, "Pattern Recognition and Machine Learning", Springer, 2006.
3. Richard O. Duda, Peter E. Hart, David G. Stork, "Pattern Classification", 2nd Edition, John Wiley & Sons, 2001.
4. Ethem Alpaydin, "Introduction to Machine Learning", the MIT Press, 2004.

Course title: Complex Networks
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

This course surveys mathematical theories of emergence and evolution of networks, especially biological systems. Applying network analysis to deepen the understanding of the natural phenomenon is one of the primary objectives. Studies on existing real-world networks (biological, social, and computer), node interaction surveys, static and dynamic models of network emergence will be covered. In this course, the student shall further learn to model complex systems and design algorithms for network data analysis.

Headlines:

- Course Introduction and basic concepts
- Complex systems, hierarchical structures, percolation theory, and random walk on networks
- Introducing biological intracellular networks and their properties
- Various models of dynamic complex networks, introducing phase transition concept
- Random networks, watts-Strogatz model, small-world networks
- Local-world evolving networks
- Network controllability and visibility

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Networks: An Introduction, M. E. J. Newman, Oxford University Press, Oxford (2010)
2. Reuven Cohen and Shlomo Havlin, Complex Networks: Structure, Robustness and Function, Cambridge University Press, Cambridge (2010). Quite a short book, but it covers most of the topics of the course, at least to some extent, and some others that are not in the book by Newman.
3. S.N. Dorogovtsev, Lectures on Complex Networks, Oxford University Press, Oxford (2010).

4. R. K. Ahuja, T. L. Magnanti, and J. B. Orlin, Network Flows: Theory, Algorithms, and Applications, Prentice Hall, Upper Saddle River, NJ (1993)
5. A. Barrat, M. Barthelemy, and A. Vespignani, Dynamical Processes on Complex Networks, Cambridge University Press, Cambridge (2008)
6. G. Caldarelli, Scale-Free Networks: Complex Webs in Nature and Technology, Oxford University Press, Oxford (2007)
7. C. D. Meyer, Matrix Analysis and Applied Linear Algebra, SIAM, Philadelphia, PA (2000)
8. M. E. J. Newman, A.-L. Barabasi, and D. J. Watts, The Structure and Dynamics of Networks, Princeton University Press (2006)

Course title: Modeling Metabolic Networks
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

Introducing various methods of modeling metabolic networks and their practical applications in biology and biotechnology

Headlines:

- Review on network biology
- Review on linear algebra and convex analysis
- Review on basic concepts in metabolism (metabolite, interaction, metabolic flux, reversibility of reactions, …)
- Metabolic network reconstruction
- Constraint-based modeling of metabolic networks
- Flux balance analysis
- Flux coupling analysis and flux correlation analysis
- Flux variability analysis and alternative optima analysis
- Mutation effects studies (MOMA and ROOM)
- Strain Design
- Pathway analysis in metabolic networks
- Modeling of regulation in metabolic networks
- Metabolic control analysis
- Metabolic flux analysis
- Principles of metabolic engineering

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
40%	30%	Written Test: 30%	0%
		Practical: -	

References:

1. Palsson, B. O. (2006) Systems Biology: Properties of Reconstructed Networks. Cambridge University Press.

Course title: Molecular Evolution and Phylogenetics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is to make the student familiar with the relevant molecular evolution processes, concepts and methods of phylogenetics and using them in data analysis related to molecular evolution processes.

Headlines:

- Introduction to relation between population genetics, molecular evolution, and bioinformatics
- Natural selection
- Molecular basis of evolution
- Evolutionary changes of DNA sequences and proteins
- Molecular clock
- Phylogenetic trees
- Phylogenetic inference
- Applications of molecular phylogenetics
- Molecular evolution and population genetics
- Genome evolution
- Weekly seminars

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
40%	30%	Written Test: 30%	0%
		Practical: -	

References:

1. Molecular Evolution and phylogenetics by Masatoshi Nei and Sudhir Kumar, 2000.
2. Evolution by Carl T. Bergstrom and Lee Alan Dugatkin, 2012.
3. The Logic of Chance: The Nature and Origin of Biological Evolution by Eugene V. Koonin, 2011.

Course title: Molecular Modeling
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

To make the students familiar with basic topics in molecular modeling with emphasis on biological systems.

Headlines:

- Historical introduction to the development of methods and issues in molecular modeling.
- The mathematical expression of molecular structures, coordinate systems for describing molecular movements, coordinate and internal variables.
- Introduction to quantum approaches in molecular modeling e.g. Hartree-Fock, density function, and semi-empirical methods.
- Concepts related to potential energy surface of simple and complex molecules, minimum and saddle points.
- Energy minimization methods and algorithms, and structure optimization e.g. steepest descent, and conjugate gradient methods.
- Molecular mechanic approaches and force fields.
- Force fields for biological systems e.g. CHARMM, and AMBER.
- Methods and algorithms of analysis and searching conformations e.g. simulated annealing, and evolutionary algorithms.
- Elements of molecular dynamics simulation
- Concepts and methods of molecular structure analysis, structural similarity measurement, structural superposition, coarse-grained coordinate calculation e.g. radius of gyration, RMSD, number of atom contacts, accessible surface area, …
- Methods for the description of the solvent and its effects on molecular modeling, including implicit and explicit solvent models, generalized Born model and multicenter models
- Methods of analysis and prediction of protein-ligand binding e.g. molecular docking.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
40%	30%	Written Test: 30%	0%
		Practical: -	

References:

1. Molecular Modeling Principles and Applications, Andrew R. Leach, Pearson Education, 2001.
2. Molecular Modeling of Proteins, Andreas Kukol, Springer (Humana Press), 2008.
3. New Algorithms for Macromolecular Simulation, T. J. Barth, M. Griebel, D. E. Keyes, R. M. Nieminen, D. Roose, T. Schlick, Springer, 2006.

Course title: Stochastic Processes
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn’t have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is familiarity with discrete time stochastic processes. Nowadays, researchers are using Markov and hidden Markov models frequently. In this course, this topic will be covered.

Headlines:

- Introduction: short review on concepts, properties of random variables, distribution functions, and definition of stochastic process.
- Markov chains: transition function, calculations using transition function, collision times, transition matrices, transient and recurrent states, absorption probabilities, martingales, birth-death chains, branching chains.
- Stationary distributions for a Markov chain: elementary properties of a stationary distribution, examples of stationary distributions, positive recurrent and null states, irreducible chains, queuing chain.
- Jump Markov Processes: birth-death processes, Poisson processes, pure jump Markov Processes properties, second order processes, Gaussian processes, Bayesian processes

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Stochastic Processes: Theory for Applications, Robert G. Gallager, 2014, Cambridge University Press.
2. Pierr Bremoud, (1999) Markov Chains, Monte Carlo Simulations and Queues.
3. Karlin, S. and Taylor, M.H. (1975) A first course in Stochastic Process.

Course title: Introduction to Dynamical Systems
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn’t have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is to make familiar the students with principles of dynamical systems.

Headlines:

- lagrangians and Euler's equations, vector fields, bifurcation concepts with examples from physics and biomathematics, Lorenz system, logistic system, stationary points , stable manifolds , limit cycles , α-limit and β-limit sets and some fundamental theorems e.g. stable manifolds theorem, Poincare-Bendixon theorem, hatman-grobman theorem and Lyapunov's theorems, bifurcation theory and codim 1 and 2, normal forms theorem, structural stability and hyperbolicity, bifurcation diagrams and bifurcation without parameters, Lyapunov methods and laSalle’s principle, some analytical problems of numerical methods in dynamical systems.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Applications of Dynamical Systems in Biology and Medicine, Trachette Jackson and Ami Radunskaya, 2015, Springer, USA
2. Differential Equations, Dynamical Systems, and an Introduction to Chaos, Third Edition, 2012, Morris W. Hirsch and Stephen Smale, Academic Press, USA
3. y.a. kuzenetsav, elements of applied bifurration theory, spiringer, 1998.
4. h, khalili, nonlinear systems and control-hall, 1996
5. v.i. arnold, ordinary differential equations, the mit press, 1998.

Course title: DNA Computing
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is learning algorithms that have been designed based on DNA computing.

Headlines:

- Molecular computing
- Introduction to molecular computing
- Biomolecular basis
- Adleman's experiment
- Molecular algorithms for solving NP problems
- Molecular algorithms for solving Hamiltonian circuit and traveling salesman problems.
- Molecular algorithms for solving shortest path problem
- Memory modeling
- Molecular computing algorithms for logical and computational operators
- Automata modeling
- Turing machine modeling
- Applying dynamic programming on DNA computers.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Paun, G., Rosenberg, G. and Saloma, A., DNA computing, Springer Verlag, 1998
2. DNA Computing and Molecular Programming, Satoshi Murata and Satoshi Kobayashi, 2014,Springer, USA
3. Theoretical and Experimental DNA Computation, Martyn Amos, 2010, Springer, USA

Course title: Evolutionary Algorithms
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is algorithm design based on an evolutionary method that applies to solving problems which cannot be solved in polynomial time.

Headlines:

- A survey on combinatorial optimization algorithms
- Introduction to genetic algorithms
- Genetic algorithms in natural evolution
- Tabu search annealing simulation
- Artificial neural networks
- Neural networks evolution, genetic algorithms implementation

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Evolutionary Optimization Algorithms, Dan Simon, 2013, Wiley, USA
2. A Field Guide to Genetic Programming, Riccardo Poli and William B. Langdon, 2008, Wiley, USA
3. Multimodal Optimization by Means of Evolutionary Algorithms, Mike Preuß, 2016, Springer, USA
4. Goldberg, "Genetic Algorithms", in Search, Optimization and Machine Learning. Addison Wisley 1989.
5. Mitchell, "An introduction to genetic algorithms", MIT Press 1998.

Course title: Bayesian Statistics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is familiarity with Bayesian philosophy vs frequentist methods. Computational methods, such as MCMC will be introduced to take advantage of Bayesian methods.

Headlines:

- Elements
- Probability and Bayes's theorem: examples, random variables, expectation and variance
- Bayesian inference for normal distribution and likelihood function, HDR, normal distribution variance, conjugate distributions, a normal distribution with unknown expectation and variance, the conjugate prior for normal distribution.
- Other statistical distributions: binomial, reference prior for binomial likelihood function, Jeffrey's rule, uniform distribution
- Hypothesis tests: one-way tests, Lindley's method, point null hypotheses with prior information, point null hypotheses for normal distribution

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 60%	0%
		Practical: -	

References:

1. Kendall's Advance theory of Statistics. (1994) Bayesian Inference, Vol.2B.
2. Bayesian Data Analysis, Andrew Gelman and John B. Carlin, 2013, Third Edition, Chapman & Hall/CRC, USA
3. Introduction to Bayesian Statistics, William M. Bolstad, 2007, 2nd Edition Aug 15, Wiley-Interscience, USA
4. Doing Bayesian Data Analysis, John Kruschke, 2014, 2nd Edition, Academic Press, USA

Course title: Pattern Recognition
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is familiarity with pattern recognition in systems.

Headlines:

- Introduction to pattern recognition, classification problems, clustering, statistical and fuzzy approach to classification and clustering, neural networks as a tool for nonlinear pattern recognition
- Statistical pattern recognition
    - Bayesian decision theory, optimized Bayesian classifiers with minimum probability of error, minimum risk
    - Optimized Gaussian classifiers, classifier evaluation, and confusion matrix
    - Density function estimation using parametric and nonparametric methods
    - Linear classifiers and minimum sum of square errors
    - Introduction to classification using support vector machines and kernel-based methods
- Pattern recognition using artificial neural networks
    - Nonlinear classification and k-nearest neighbor method
    - MLP and RBF neural nets as tools for classification and clustering
    - Neural nets issues: training, number of neurons in hidden layers, convergence, normalization, data partitioning, weight initialization, weight drifting, stopping rules, excitatory functions
- Clustering
    - Introduction to clustering
    - Cluster types and cluster separation measures
    - Sequential, Hierarchical and C-means clustering
    - Fuzzy clustering: fuzzy C-means, Gustafson-Kessel, gath-geva methods
    - Cluster validity
    - Introduction to feature extraction and feature selection
    - PCA using SVD of covariance or separability matrix

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 60%	0%
		Practical: -	

References:

1. Pattern Recognition, Sergios Theodoridis (Author), Konstantinos Koutroumbas, 2008, 4th Edition, Academic Press, USA
2. Introduction to Pattern Recognition, Sergios Theodoridis, Aggelos Pikrakis, Konstantinos Koutroumbas, Dionisis Cavouras, 2010, Academic Press, USA
3. Statistical Pattern Recognition, Andrew R. Webb, Keith D. Copsey, 2011, 3rd Edition, Wiley, USA

Course title: Design and Analysis of Algorithms
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is learning different methods of algorithm design for solving problems in polynomial and nonpolynomial time.

Headlines:

- Algorithm design
- Methods of computational complexity calculation
- Different problem-solving techniques
  - Divide and conquer
  - Dynamic programming
  - Greedy
  - Backtrack
  - Branch and bound
- P, NP, NP-hard, and NP-complete problems
- Recognizing NP problems e.g. Hamiltonian circuit, and SAT
- Problem-solving using approximation and heuristic algorithms and some examples
- Problem-solving using parallel algorithms and some examples

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Corman. Liserson and Reivest, Introduction to algorithms, Academic Press.Brassard, G. and Bratley, G., Algorithms: Theory and Practice, Prentice Hall, 1988.
2. Introduction to the Design and Analysis of Algorithms, Anany Levitin, 2011, 3rd Edition), Pearson publisher, USA

3. Algorithms, Robert Sedgewick and Kevin Wayne, 2011, 4th Edition, Addison-Wesley Professional, USA

Course title: Multivariate Analysis
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

Headlines:

- Multivariate and marginal distributions, famous multivariate families (exponential, hyperbolic, …), multivariate normal distribution and its properties, univariate or multivariate distributions derived from multivariate normal distribution (…), Principles of multivariate hypotheses test, principles of multivariate parameter estimation, confidence intervals, designs with multivariate regression…, multivariate normal hypotheses test, and other distributions.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Anderson, T.W. (1984), An Introduction to Multivariate Analysis, John Wiley, New York
2. Bilodeau, M. and Brener, D. (1999), Theory of Multivariate Statistics, Springer.
3. Mardia, K., Kent, J.T. and Bibby, J. (1979), Multivariate Analysis, Academic Press

Course title: Enzyme Kinetics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

- To make the students familiar with the simple and complex kinetics of enzymatic reactions.
- Applications of theories of enzyme kinetics in the study of ion or small molecule binding to enzymes and survey on its effects in biocatalytic activity of enzyme
- Enzyme inhibitor and activator design

Headlines:

- Chapter One: Kinetics of enzymatic reactions
    - Kinetics of enzymes with one active site
    - Rapid equilibrium and uniform state method
    - Initial velocity and Michaelis-Menten equation
    - Enzyme assays
    - Enzyme kinetics constant determination: Hanes–Woolf, Lineweaver–Burk, and Eadie–Hofstee methods
    - limitations of Michaelis-Menten equation
    - Dixon method for determination of enzyme kinetic constant
    - Michaelis constant for substrate and product and velocity of enzymatic reaction
    - Two form enzymes and action of two enzymes on a substrate
- Chapter Two: enzyme inhibition kinetics
    - Reversible and irreversible inhibitors
    - Partial and complete inhibitors
    - Competitive, non-competitive, uncompetitive, and mixed inhibitors
    - General theory of inhibition
    - Degree of inhibition
- Chapter Three: kinetics of multisite enzyme reactions
    - Multi-site non-cooperative enzyme
    - Multi-site cooperative and allosteric enzymes: Hill equation
    - Random and ordered bisubstrate enzymes
    - Bisubstrate enzymes with Ping-Pong mechanism
- Chapter Four: The kinetics of enzyme activation

  - Nonessential activators of enzyme
  - Essential activators of enzyme
  - Substrate activators
  - The competition between inhibitor and activator
  - Anti-activator and anti-inhibitor of the enzyme
- Chapter Five: The effects of environmental factors on enzyme kinetics
  - The impact of temperature on enzyme activity
  - Activation energy and Arrhenius equation
  - The impact of pH on enzyme activity
  - kinetics of enzyme inhibition due to pH change
  - Dixon-webb logarithmic plot
  - The impact of pH on ionized groups effective on enzyme activity
  - The impact of buffer type and ionic potency on enzyme activity
  - The impact of metal ions on enzyme activity and structure

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Enzyme Kinetics, I. H. Segel, John Wiley & Sons, New York, 1993
2. Biochemical Calculations, I. H. Segel, John Wiley & Sons, New York, 1976
3. Enzyme Kinetics: Principles and Methods, H. Bisswanger (Translated by L. Bubenheim), Wiley, Weinheim: Germany, 2002
4. Enzyme Kinetics, V. Leskovac, Plenum Pub., New York, 2003
5. Enzymes & Their Inhibitory: Drug Development, H. J. Smith and C. Simons, CRC Press, Boca Raton, 2005

Course title: Genomics and Gene Regulation
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this Optional course is to make the students familiar with basic topics in organism's genome and the role of various pieces of the genome in gene expression.

Headlines:

- Structural genomics: genome size in organisms, mechanism of genome size variation, genome organization, genome rearrangement
- Epigenomics: principles and concepts of epigenetics in gene expression
- Functional genomics: cis and trans elements in gene expression regulation, biological variations in gene expression, genomic disorders
- Students seminar presentation (two weeks) in selected topics: personal genomics and medicinal genetics, pharmacogenomics, genome evolution, …
- Lab: basic techniques of DNA and RNA extraction, polymerase chain reactions, ...

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Human molecular genetics (2003), Read & Astrachan, Bios.
2. The evolution of the genome (2005), T. Ryan Gregory (editor), Elsevier.
3. Genoms (2007), Brown.
4. Gene ExpressionAug, G. S. Miglani, 2013, Alpha Science, USA
5. Gene Expression and its Regulation: Laying the Foundation for Molecular Biology, Werner Maas, 2013, XLIBRIS, USA

Course title: Biomolecular Recognition
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☑ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☐
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

To make the students familiar with the rules of interaction and targeted binding of biological macromolecules with other related molecules.

Headlines:

- Importance of biomolecular recognition in biological processes
- Physical basis of molecular interaction and related molecular properties
- Different types of molecular forces e.g. van der Waals, electrostatic, hydrogen, halogen, hydrophobic, …
- Solvent effects on molecular recognition and its calculation methods
- Molecular recognition in protein-protein, protein-nucleic acid, and nucleic acid-nucleic acid interactions.
- Molecular recognition in receptor-ligand systems.
- Peptide design and drug design based on principles of molecular recognition
- The role of molecular recognition in the immune system and antigen-antibody interactions.
- Molecular recognitions mechanisms in biological networks
- Databases related to biomolecular recognition

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
40%	30%	Written Test: 30%	0%
		Practical: -	

References:

1. Principles of Molecular Recognition, A.D. Buckingham, A.C. Legon, S.M. Roberts, Springer, 2012.
2. Molecular recognition mechanisms, Michel Delaage, VCH Publishers, 1991.
3. Protein-Ligand Interactions: From Molecular Recognition to Drug Design, Hans-Joachim Böhm, Gisbert Schneider, Wiley, 2003.
4. Cellular and Biomolecular Recognition, Raz Jelinek, John Wiley & Sons, 2009.

5. Pharmacological Aspects of Molecular Recognition, F. S. Dukhovich, Nova Publishers, 2005.

Course title: Special Topics in Bioinformatics
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn’t have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is presenting new topics in bioinformatics that have not proposed as standard courses yet. New subjects will be introduced in the format of seminars based on scientific papers, and the students will be familiar with nature of these investigations.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
30%	-	Written Test: -	40%
		Practical: 30%	

Course title: Advanced Data Mining
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

Data analysis of text, graphs (biological, social, web networks, and …), spatial, temporal, and time series has more complexities than common methods in data mining. In this course methods for mining complex data will be explored. Also, we will review clustering methods completely. Dealing with big data is another topic.

Headlines:

- Introduction
- Review on probability, decision, and information theories.
- Unsupervised learning (clustering)
- K-means clustering
- Distribution based clustering (EM)
- Link-based clustering (hierarchical)
- Density-based clustering
- Graph-based clustering (Chameleon, …)
- High dimensional clustering (subspace clustering, …)
- Clustering validation techniques
- Dimensionality reduction and review on some techniques e.g.
  - Filter-type methods, F-test, mutual information
  - Max-relevance min-redundancy algorithm, feature stability algorithms
  - Wrapper methods, search methods, floating search methods
- Sequence and time series mining (models for time series and sequence data)
- Mining methods in biological networks
- Mining methods in graphs and trees
- Applications in the web (e.g. web advertising, viral marketing, recommender systems, …)
- Working with RapidMiner, Matlab, R, …

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	20%	Written Test: 30%	30%
		Practical: -	

References:

1. Anand Rajaraman, Jure Leskovek, Jeffery D. Ullman, Mining of massive Datasets, Cambridge University Press, 2012.
2. Jiawei Han, Micheline Kamber, Jian Pei, Data Mining: Concepts and Techniques, Third Edition, the Morgan Kaufmann Series in Data Management Systems, 2011.
3. Lei Tang, Huan Liu, Community Detection and Mining in Social Media, Morgan and Claypool Publishers, 2012.
4. Mehryar Mohri, Afshin Rostamizadeh, and Ameet Talwalker. Foundations of Machine Learning. MIT Press, 2012.
5. Kevin Murphy, Machine Learning: a Probabilistic Perspective, 2012.
6. Christopher M. Bishop, Pattern Recognition and Machine Learning, Springer

Course title: Cell and Molecular Mechanism of Cancer
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

To make the students familiar with cell and molecular mechanisms of cancer

Headlines:

- Introduction: including cell transformation steps and molecular properties of colorectal tissue
- Molecular mechanisms of cell Epithelial- mesenchymal transition
- Intercellular connections and their relations to cancer
- Deregulation of $G1 \rightarrow S$ phase of cell cycle
- Deregulation of $G2 \rightarrow M$ phase of cell cycle
- Senescence cancer cells
- Cell apoptosis and cancer
- Oncogenes and their activation mechanism in human cancers
- Super Surgen tumors and their mechanisms of inactivity in human cancers
- Introducing the most important methods of signal transduction and mechanisms of their deregulation in human cancers
- Genetic instability in cancer
- Angiogenesis mechanisms
- Cell and molecular mechanisms of metastasis
- Novel approaches in human cancer therapy
- Seminar presentation

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
10%	-	Written Test: 70%	20%
		Practical: -	

References:

1. Volgelstein B and kinzler, KW the Genetic Basis of Human cancer. Mc Graw Hill, 2nd edition.
2. Research and Review articles. (Nature Review cancer)

Course title: Data Mining in Medical Systems
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn’t have ☐ Scientific journey ☐ Workshop ☐
Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

The aim of this course is to make the student familiar with novel topics in data mining in medicine and healthcare

Headlines:

- Introduction to classification rule and association rule
- Making decision tree using OneR algorithm
- Entropy
- Regression
- Logistic function
- Naïve Bayes method
- Likelihood calculation
- Precision and recall measures in classification
- A priori algorithm for finding frequent itemset
- A_close algorithm
- GSP algorithm
- K_means, DBSCAN, and hierarchical methods for clustering
- CLIQUE algorithm
- Calculation of Closeness and Interconnectivity between clusters

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
30%	30%	Written Test: 30%	10%
		Practical: -	

References:

1. Data Mining: Practical Machine Learning Tools and Techniques Third Edition. Ian H. Witten, Eibe Frank Mark A. Hall .2011. Elsevier. USA
2. Data Mining and Medical Knowledge Management: Cases and Applications. Petr Berka, Jan Rauch, Djamel Abdelkader Zighed. 2009. IGI Global. USA

Course title: Modeling of Biological Systems
Number of units: 2
The number of hours: 32
Unit type: Theoretical
Course type: Optional
Prerequisite: -
Practical training: has it ☐ doesn't have ☐ Scientific journey ☐ Workshop ☐ Laboratory ☐ Seminar ☑
Degree: MSc ☐ Ph.D. ☐ MSc & Ph.D. ☑

Course Objectives:

In this course at first various standard methods and tools for modeling physiological systems will be introduced, and then novel approaches of modeling complex biological systems will be proposed.

Headlines:

- Introduction: needs, concepts, importance and applications, and various modeling approaches
- Modeling biological systems process
- Modeling biological systems, methods, and applications
- Methods of model identification: parametric and nonparametric models
- Model validation
- Case studies: cell, neurological system, blood flow, respiration, muscle
- Methods and novel concepts in modeling biological systems: computational intelligence-based methods, cellular automata, expert systems, and modular structures.

Evaluation Method

Continuous evaluation (To be specified in percentage)	midterm (To be specified in percentage)	Final Test (To be specified in percentage)	Project (To be specified in percentage)
20%	-	Written Test: 50%	30%
		Practical: -	

References:

1. C. Cobelli, E. Carson, Introduction to Modeling in Physiology and Medicine, Academic Press (Elsevier), 2008.
2. J. Keener, J. Sneyd, Mathematical Physiology, Springer, 2009.
3. J. Haefner, Modeling of Biological System: Principles and Application, Springer, 2005.
4. U. Alon, An Introduction to Systems Biology: Design Principles of Biological Circuits, Chapman & Hall/CRC, 2006.
5. MCK Khoo, Physiological Control Systems: Analysis, Simulation and Estimation, Willey-Black Well, 1999.