COURSE RECORD

Code	**ECE 563**
Name	**Computational Genomics**
Hour per week	3 (3 + 0)
Credit	3
ECTS	10
Level/Year	Graduate
Semester	Fall-Spring
Type	Elective
Location	
Prerequisites	
Special Conditions	
Coordinator(s)	Burcu Bakır Güngör, Ph.D. , Assistant Professor
Webpage	
Content	Following the Human Genome Project, the recent revolution in genomic technologies has enabled the generation of massive amounts of "omics" data. The challenge in this new era is to develop computational methods for integrating different data types and extracting complex patterns accurately and efficiently from a large volume of data. This course will discuss computational issues arising from high-throughput techniques recently introduced in genomics, including next-generation sequencing data analysis, genome-wide association study data analysis, the identification of genomic variations and their functional effects, biological networks, pathway analysis, epigenome analysis, cancer genomics. Throughout the course, the current computational genomics approaches that are used to understand disease development and progression mechanisms will be covered. Along this line, two newly emerging disciplines, i.e. personalized medicine and pharmacogenomics will be discussed in this course.
Objectives	This course aims to teach: • main computational problems in genomics, epigenomics and cancer genomics, • next-generation sequencing data analysis, "omics" data analysis algorithms which are also widely used in many other engineering fields, • network and pathway based computational approaches that can integrate several multi-layered "omics" data, • how to use genomic data in translational medicine, personalized medicine and pharmacogenomics studies.
Learning Outcomes	LO1.　An ability to convert data into biological, genomic or medical knowledge. LO2.　Understanding massively parallel sequencing technologies. LO3.　Obtaining skills to develop novel statistical approaches to analyze association studies and other problems in computational genomics. LO4.　Critiquing the existing methodologies for the analysis of various biological high throughput datasets. LO5.　Understanding methods to discover sequence motifs, polymorphisms and miRNAs. LO6.　Understanding biological networks and their utility in genomics. LO7. Obtaining the knowledge of the current challenges and open issues in computational genomics.
Requirements	Expected requirements of the course.
Reading List	Shugart, Yin Yao (Ed.), Applied Computational Genomics, Springer, 2012. Mayer B., Bioinformatics for Omics Data: Methods and Protocols, Humana Press, 2011.
Ethical Rules and Course Policy	

LEARNING ACTIVITIES *Please, use this one as a reference for your course*

Activities	Number	Weight (%)
Lecture	3	25%
Group Works	8	25%
Presentations	7	25%
Site Visits	1	25%
	Total	100

ASSESSMENT

Evaluation Criteria	Weight (%)
Quizzes	10%
Weekly Assignments	10%
Group Project Assignments & Presentations	20%
Midterm	20%
Final Exam/Submission	40%
Total	100%

For a detailed description of grading policy and scale, please refer to the website https://goo.gl/HbPM2y section 28.

COURSE LOAD *Please, use this one as a reference for your course*

Activity	Duration (hour)	Quantity	Work Load (hour)
In class activities	2	14	28
Lab	1	7	7
Group work	2	12	24
Research (web, library)	2	12	24
Required Readings	2	10	20
Pre-work for Presentation	2	7	14
Lab reports	1	7	7
		General Sum	**124**

ECTS: 4 (Work Load/25-30)

CONTRIBUTION TO PROGRAMME OUTCOMES*

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PO13	PO14
LO1														
LO2														
LO3														
LO4														

* Contribution Level: 0: None, 1: Very Low, 2: Low, 3: Medium, 4: High, 5: Very High

WEEKLY SCHEDULE

W	Topic	Outcomes
1	Introduction to Computational Genomics, basic concepts	LO1, LO7
	Lab/ Activity:	
2	Sequencing the Human Genome, Human Genome Project, Turkish Genome Project	LO2
	Lab/ Activity:	
3	Medical diagnostics using Single Nucleotide Polymorphisms	LO1, LO5
	Activity:	
4	Analysis of Genome-wide Association Study (GWAS) Datasets	LO3, LO4
	Activity:	
5	Network Based Genomics, Analysis of miRNA Regulatory Networks	LO6, LO7
	Activity:	
6	Sub-network identification in protein-protein interaction networks using simulated annealing and genetic algorithms	LO6, LO7
	Activity:	
7	Gene Set Enrichment Analysis (GSEA), Pathway Based Genomics	LO1, LO6
	Activity:	
8	Epigenomics	LO1, LO7
	Activity:	
9	Gene discovery using Hidden Markov Models, metagenomics	LO1, LO5
	Activity:	
10	Discovering Gene Regulatory Signals: Expectation Maximization, Gibbs sampling and related approaches	LO3, LO5
	Activity:	
11	Cancer Genomics	LO1, LO4, LO7
	Activity:	
12	From GWAS to Next-Generation Sequencing on Human Complex Diseases: The Implications for Translational Medicine and Therapeutics	LO1, LO2, LO7
	Activity:	
13	Trans-omic data analysis	LO1, LO2, LO7
	Activity:	
14	Personalized Medicine, Pharmacogenomics	LO1, LO2, LO7
	Activity:	

Prepared by

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Date
27.04.2018