COURSE DESCRIPTION CARD - SYLLABUS

Course name

Population Genomics [S2Bioinf2>GENP]

Course

Field of study Bioinformatics	Year/Semester 1/1
Area of study (specialization) –	Profile of study general academic
Level of study second-cycle	Course offered in Polish
Form of study full-time	Requirements compulsory

Number of hours

Lecture	Laboratory classes	Other (e.g. online)
30	30	0
Tutorials	Projects/seminars	
0	0	

Number of credit points

5,00

Coordinators	Lecturers
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Prerequisites

The student starting this course should have a basic knowledge in basic computer programming. He/she should possess skills in solving basic problems that computer science deals with and the ability to acquire information from specific. They should also have basic knowledge of molecular biology, molecular genetics and statistics.

Course objective

1. To provide students with basic knowledge in the field of population genomics, in particular: genetic and phenotypic variability and its organisation, influence of factors such as genetic drift, mutation, Darwinian selection. 2. To get students acquainted with bioinformatic tools, approaches and analyses used in population genomics research. 3. To get students acquainted with currently used methods of computational analysis in bioinformatics of nucleic acids on the example of RNA.

Course-related learning outcomes

Knowledge:

1. The student has a knowledge, with theoretical basis in bioinformatics in approaches, research and analyses concerning broadly defined population genomics and bioinformatics of nucleic acids on the

example of RNA.
2. Knows the application of computer tools and programs in analysis of genetic data in population genomics and bioinformatics of nucleic acids.
3. Knows methods, techniques and tools used in the process of solving bioinformatics complex tasks, mainly of engineering character.
4. Has advanced knowledge and understanding of topics in mathematics, statistics, optimization, and artificial intelligence methods useful for modeling and analyzing biological processes.
5. Knows principles of planning reasearch in bioinformatics field.

Skills:
1. Is able to retrieve and interpret the information from a variety of sources concerning scientific literature and the Internet.
2. Knows and is able identify, choose and apply in practice appropriate approaches and software for carrying out population genomics analysis. They will be able to interpret and discuss the results obtained by such analysis.
3. Is able to apply advanced techniques and computer tools to solve biological problems and evaluate their usefulness.
4. Is able to prepare a written report in Polish presenting the results of conducted analyses, as well as discuss them.
5. Formulates and tests hypotheses connected with bioinformatics problems.

Social competences:
1. Is ready to prioritize tasks defined by himself/herself or others and to take actions aimed at accomplishing them in an entrepreneurial manner.
2. Is ready to demonstrate a creative approach in professional and social life and to consciously fulfill the social role of a university graduate, including caring for the public interest.

Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

Forming evaluation
a) in lectures verifying established effects of the education is being carried out through:
• filing the written test with 5-10 questions / tasks to solve - every task 0-4 pt (tasks can consist of a few subsections - there is a then set fragmentary score for every subsection). In order to get the credit one should score at least half of the points plus one.
• Completion of a review on a topic covered in the lectures, as specified by the lecturer, presenting it, and receiving a positive grade for it.
The final grade is the average of the review grade (including the presentation) and the written exam.
b) in laboratories:
The final evaluation is determined on the average evaluations of the exercies and practical laboratories.

Programme content

This course is devoted to a theoretical and practical introduction to the field of population genomics. The following issues will be discussed during the lectures: historical background, importance of population genomics and its basic concepts; genetic and phenotypic variation (e.g. single and multiple inheritance, DNA polymorphism and its significance, molecular population genetics); organisation of genetic variation (e.g. e.g. Hardy-Weinberg's law, its extensions and testing methods, linkage disequilibrium and its causes); genetic drift (e.g. Wright-Fisher drift model, effective population size, founder and bottleneck effects, gene trees and coalescence); mutation and neutral theory (e.g. types of mutations, model of infinite number of alleles and sites, linkage to genetic drift and recombination); Darwinian selection (e.g. types of selection, selection in haploid and diploid organisms, link to mutation, equilibrium states); inbreeding and migration (e.g. divided populations, inbreeding and selective mating, types of migration and its models); molecular population genomics; evolutionary quantitative genetics; transposable elements; The topics will be illustrated with examples.
Laboratories will consist of the analysis of biological and biomedical data, with a focus on geting to know programs, tools and approaches related to the topics discussed in the lecture and their applications.

Course topics

This course introduces research in the field of population genomics.
The lectures cover:

- Historical background, the importance of population genomics, and basic concepts.
- Genetic and phenotypic variation (e.g. inheritance, DNA polymorphism).
- Organisation of genetic variation (Hardy-Weinberg law, genetic drift).
- Mutations and neutral theory.
- Darwinian selection.
- Inbreeding, migration.
- Evolutionary quantitative genetics, transposons.

The topics will be illustrated with examples.
Laboratories: analysis of biological and biomedical data, learning bioinformatics tools.

Teaching methods

Lecture illustrated by a multimedia presentation enriched with numerous examples
Laboratories: practical exercises in population genomics and dedicated RNA analysis, group work, discussion and problem analysis.

Bibliography

Basic:
Hartl D.I., Clark A.G., "Principles of Population Genetics", 2009

Additional:
1. Avise J.C., "Molecular Markers, Natural History and Evolution", 2008
2. Baxevanis A.D., Ouellette B.F.F., "Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins", 2005

Breakdown of average student's workload

	Hours	ECTS
Total workload	125	5,00
Classes requiring direct contact with the teacher	60	2,50
Student's own work (literature studies, preparation for laboratory classes/ tutorials, preparation for tests/exam, project preparation)	65	2,50