POZNAN UNIVERSITY OF TECHNOLOGY

EUROPEAN CREDIT TRANSFER AND ACCUMULATION SYSTEM (ECTS)

COURSE DESCRIPTION CARD - SYLLABUS

Course name
Phylogenetic Analysis [S2Bioinf1>AFIL]

Course

Field of study	Year/Semester
Bioinformatics	2/4
Area of study (specialization)	Profile of study
–	general academic
Level of study	Course offered in
second-cycle	polish
Form of study	Requirements
full-time	compulsory

Number of hours

Lecture	Laboratory classes	Other (e.g. online)
15	15	0
Tutorials	Projects/seminars	
0	0	

Number of credit points

2,00

Coordinators

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Lecturers

Prerequisites

Students shall know basis of evolutionary processes, molecular biology, algorithms and data structures, machine learning, optimization and statistical data analysis.

Course objective

The main course objective is to equip students with knowledge and skills needed to preform phylogenetic analysis. Students will learn theoretical concepts and practical use of modern methods, algorithms and tools that are crucial in phylogenetic tree reconstruction and analysis.

Course-related learning outcomes

Knowledge:
1. Student possess theoretical knowledge about phylogenetic and is able to use it in order to solve biological problems based on real data.
2. Student understands essential methods and algorithms in phylogenetic analysis, including statistical analysis of phylogenetic trees.
3. Student has knowledge about chosen tools and algorithms that are used in phylogenetic analysis. Student understands phylogenetic techniques and research problems in sequence similarity.

4. Students knows advanced concepts in phylogenetic analysis and is able to use them while planning and designing phylogenetic analysis for different organisms. Student incorporates knowledge about molecular evolution and genomics while solving phylogenetic problems.
5. Student is familiar with databases, tools and modern methods in phylogenetic analysis and knows trends in this discipline.

Skills:
1. Student is proficient in use of selected computer tools in phylogenetic analysis. Student understands phylogenetic techniques and is able to use it properly in sequence similarity analysis. Student can select proper tools, algorithms and methods to solve specific biological problem related to phylogenetics (in scope of this course).
2. Student is proficient in use of statistical methods and tools that perform phylogenetic tree analysis and evaluation.
3. Student is able to analyze phylogenetic problem and pick the best approach to solve it.
4. Student knows how to formulates phylogenetic hypotheses and perform relevant analysis to test them.

Social competences:
1. Student understands the need for lifelong learning and sees practical usage of gained knowledge in phylogenetics (students will learn about phylogenetic analysis of viruses during epidemics and will be presented selected publications about new approaches in phylogenetic analysis).

Methods for verifying learning outcomes and assessment criteria
Learning outcomes presented above are verified as follows:

Learning outcomes presented above are verified as follows:
Students will have to complete the final test from material covered on lectures.
During laboratories students will be evaluated by their activity and reports (each class will have specific exercises to perform and problems to solve).

Programme content

Lectures on Phylogenetic analysis can be divided into 7 parts.
First part of the lectures is meant to introduce students to phylogenetics. During this part some crucial problems and needs of phylogenetic analysis will be covered. Moreover, students will be introduced to elements of biological systematics of prokaryotic and eukaryotic organisms. The importance of reliable systematics, taxonomy and phylogenetics in biological and medical research will be highlighted.
Second part of lectures will concentrate on mechanisms guiding evolution on molecular level and genomic diversity. In this part most common difficulties and problems in phylogenetic analysis will be covered such as misuse of biological data and data imperfections or inaccessibility. In scope of this part terms and definitions for crucial concepts will be presented including: homoplasy, homology, use of morphological and other various types of data as phylogenetic analysis support. Methods and criteria for traits and biological sequence proper choice will be given for different problems with phylogenetic analysis close and distant related biological taxa (molecular markers). During this part concept of molecular clock will be presented and problems related to it.
Third part of lectures will cover different types of phylogenetic trees and graph representations of similarity. Moreover, methods for data transformation and processing will be presented as well as natural and artificial taxa and phylogenetic tree rooting.
Fourth part of the lectures will focus on algorithms and tools that are used in phylogenetic tree reconstruction. Students will be introduced to general concept of clustering and data labeling. Chosen and most widely used methods in phylogenetic analysis will be presented, that is distance approaches, parsimony approaches, maximum likelihood approaches and Bayesian approaches. Chosen tools in phylogenetics will be briefly characterized in addition to this part.
The fifth part of lectures will concentrate on statistical analysis of phylogenetic trees and results of analysis. Methods for tree sampling and branch support will be covered as well as terms such as phylogenetic signal, Bremer index, bootstrap, aLTR, posterior probability. In addition some methods for divergent time analysis and consensus tree construction will be presented.
Sixth part of lectures will focus on heuristic approach to phylogenetic analysis and analysis and visualization of results. During this part methods for scoring and validation of phylogenetic trees will be presented.

Last part of lectures will be covering applications of phylogenetic analysis to modern biological research. Chosen methods for phylogenetic analysis of proteins will be presented, but also analysis and monitoring of viruses evolution during epidemics.
Laboratory part of the course will focus on development practical skills in phylogenetic analysis by problem solving. During each laboratory classes students will work with set of tools, algorithms and databases in order to learn how to perform end-to-end phylogenetic analysis. Students will practice different ways to construct, analyze, visualize and score phylogenetic trees. Moreover, student will learn how to monitor evolution of viruses during epidemics.

Teaching methods

1. Lecture – multimedia presentation with examples presented on blackboard.
2. Labolatories - activity on classes and reports.

Bibliography

Basic
Hall B., Łatwe drzewa filogenetyczne, WUW, Warszawa, 2008
Additional
Felsenstein J., Inferring phylogenies, Sinauer Associates, , 2004
Warnow, T., Computational Phylogenetics: An Introduction to Designing Methods for Phylogeny Estimation. Cambridge, Cambridge University Press, 2017
Xia, X. A Mathematical Primer of Molecular Phylogenetics, Apple Academic Press Inc., 2020

Breakdown of average student's workload

	Hours	ECTS
Total workload	50	2,00
Classes requiring direct contact with the teacher	30	1,00
Student's own work (literature studies, preparation for laboratory classes/ tutorials, preparation for tests/exam, project preparation)	20	1,00