

COURSE CATALOGUE

Courses for the

Biodata Analysis

Online Post-graduate Certificate
Program

2023-24

Pázmány Péter Catholic University
Faculty of Information Technology and Bionics

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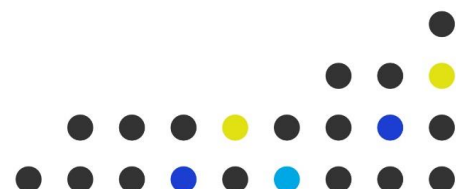
Advanced Structural Bioinformatics

P-ITOBA-0120

ECTS / semester	6 credits / spring
Course classification	Elective
Prerequisite course(s)	Introduction to Structural Bioinformatics
Assessment	Project work
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Additional lecturer(s)	Martti Tolvanen, PhD
Recommended reading	Gu, J & Bourne, P.E. (eds, 2009): Structural bioinformatics, 2nd ed. Wiley-Blackwell Gáspári Z (ed. 2020): Structural bioinformatics: Methods and Protocols. Humana Press

Course description:

- Advanced concepts and tools in biomolecular structure analysis
- Assigning secondary structural elements from 3D coordinates
- The concept of domains: definitions based on structural and sequence features
- Origins and uses of global and local similarity in structures
- Structure classification and functional assignment
- Prediction of structural features from sequences
- Full 3D structure prediction
- Protein: ligand docking
- Ensemble-based structural models to represent protein internal dynamics
- Analysis of the structure of nucleic acids



Biological Data Analysis with R

P-ITOBA-0060

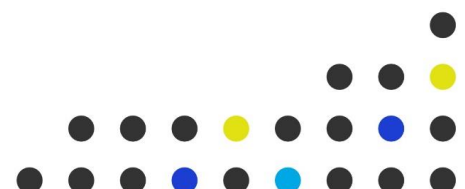
ECTS / semester	6 credits / fall
Course classification	Compulsory
Suggested background knowledge	essentials of molecular biology, essentials of evolution, usage of command line, knowledge about biological database
Assessment	Assignments + online tests
Subject coordinator	Balázs Ligeti, assistant professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Ortutay & Ortutay (2017): Molecular Data Analysis Using R. ISBN: 978-1-119-16502-6. , Wiley-Blackwell

Course description:

The purpose of this course is to teach how the R statistical environment can be applied for biological data analysis.

- Introduction to R: Installation, package management, basic operations
- Sequences and sequence analysis
- Annotating gene groups: Ontologies, pathways, enrichment analysis
- Proteomics: mass spectrometry
- Reconstructing gene regulation networks
- Network analysis: iGraph

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Biological Databases and Online Analysis Tools

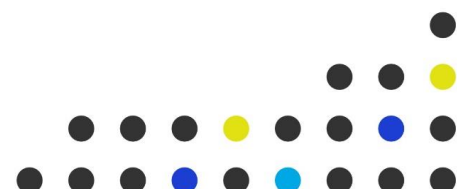
P-ITOBA-0010

ECTS / semester	5 credits / fall
Course classification	Compulsory
Suggested background knowledge	basic biochemistry and molecular biology
Assessment	Project work
Subject coordinator	Attila Csikász-Nagy, full professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Pevzner, P. (2011): Bioinformatics for biologists, Cambridge University Press; Lesk, A.M. (2005): Introduction to bioinformatics, Oxford University Press
Course URL	http://www.bioinfoacademy.com/IntroBioinfo

Course description:

An overview of the major biological databases and an introduction of the basic sequence analysis methods

- Biological databases with the main focus on DNA and protein sequences
- Comparison and alignment of sequences, similarity-based searches in databases
- Discovery of protein sequence motifs and sequence features; metabolic pathway data
- Genome browsers and sources of gene expression data; gene lists and the concept of enrichment
- Micro-RNAs and their targets; protein visualization



Enrichment Analysis

P-ITOBA-0100

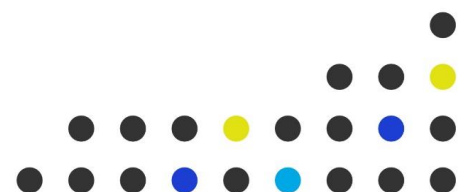
ECTS / semester	3 credits / spring
Course classification	Elective
Suggested knowledge background	basics about high throughput gene expression experiments
Assessment	Questionnaire
Subject coordinator	Attila Csikász-Nagy, full professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD

Course description:

Introduction of the two most frequently applied approaches to locate the common features of large gene lists.

- Enrichment analysis: an overview
- Over-representation Analysis
- Gene Set Enrichment Analysis

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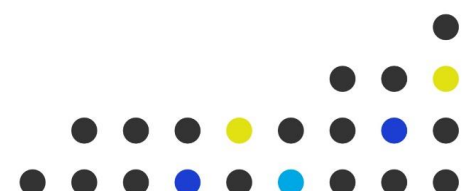
Genomics, Transcriptomics and Proteomics

P-ITOBA-0050

ECTS / semester	5 credits / fall
Course classification	Compulsory
Suggested background knowledge	basic biochemistry and molecular biology
Assessment	Project work
Subject coordinator	Attila Csikász-Nagy, full professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Campbell, A.M. & Heyer L.J. (2006) Discovering Genomics, Proteomics and Bioinformatics, 2nd ed.. Benjamin Cummings Press

Course description:

Familiarity with Internet sources for genome-wide data; basic skills in using tools at these web sites; understanding how modern high-throughput methods generate sequence data and gene and protein expression data; practical skill of using genome browsers to access genome data and genome comparison data; understanding gene prediction and genome annotation pipelines; skill of performing individual gene predictions; understanding different levels of variation in human genomes; understanding basic workflows of microarray data analysis and next-generation sequencing data analysis; basic knowledge of experimental methods in proteomics and metabolomics which enables understanding data analysis in these fields; skill of identifying proteins from mass spectroscopic data.



Heatmaps for Analyzing Gene Expression Data

P-ITOBA-0110

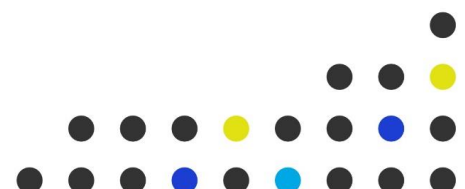
ECTS / semester	3 credits / spring
Course classification	Elective
Suggested background knowledge	Basics about high throughput gene expression experiments
Assessment	Questionnaire
Subject coordinator	Attila Csikász-Nagy, full professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	
Course URL	

Course description:

Introduction of the frequently applied approaches to create heatmap plots from gene expression data using online and local software tools

- Theoretical background of heatmap analysis
- Methodological overview including statistics and software aspects
- Practice with the heatmap tool at Gene Expression Omnibus
- Optional practice: How to create heatmaps with R?

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High Throughput Data Analysis with R

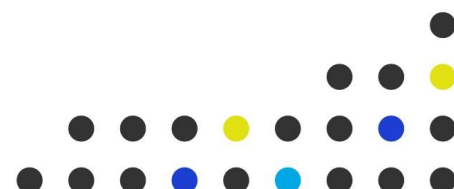
P-ITOBA-0070

ECTS / semester	6 credits / spring
Course classification	Compulsory
Prerequisite course(s)	Biological Data Analysis with R
Assessment	Assignments + online tests
Subject coordinator	Balázs Ligeti, assistant professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Ortutay & Ortutay (2017): Molecular Data Analysis Using R. ISBN: 978-1-119-16502-6. Wiley-Blackwell

Course description:

- Flow cytometry: counting and sorting stained cells
- Next-generation sequencing: introduction and genomic applications
- Quantitative transcriptomics: qRT-PCR
- Advanced transcriptomics: gene expression microarrays
- Next-generation sequencing in transcriptomics: RNA-seq experiments
- Analysis of DNA-protein interactions: chromatin immunoprecipitation

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Introduction to Bio-statistics

P-ITOBA-0020

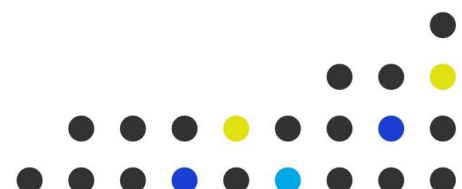
ECTS / semester	5 credits / fall
Course classification	Compulsory
Suggested background knowledge	basic biochemistry and molecular biology
Assessment	Project work
Subject coordinator	Sándor Pongor, full professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Aho Ken A. (2014) Foundational and applied statistics for biologists using R. CRC press

Course description:

An application oriented course focusing on how statistical methods can be used to address common problems in the analysis of results from molecular biology experiments.

- Comparing simple groups: hypothesis testing
- Multiple groups: ANOVA and related concepts
- Hypothesis testing in complex experimental settings: Randomized complete block design
- Dose and response: regression models
- Handling low sample sizes with General Linear Models
- Planning optimal sample sizes: how many animal do I need?

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Introduction to Programming in Python

P-ITOBA-0030

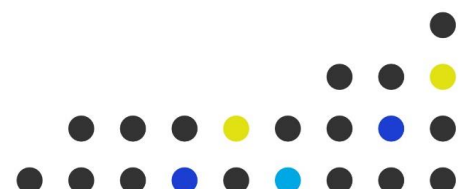
ECTS / semester	3 credits / fall
Course classification	Compulsory
Assessment	Questionnaire
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Additional lecturer(s)	Dániel Györffy, PhD
Recommended reading	Lutz, M (2011): Programming Python. O'Reilly

Course description:

Programming for beginners, using the Python language:

- Concepts in programming, fundamentals of algorithms
- Basic variable types & data structures
- Program organization, loops and conditional statements
- Basics of file input/output
- Parsing text files
- Basics of GUI programming

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Introduction to Structural Bioinformatics

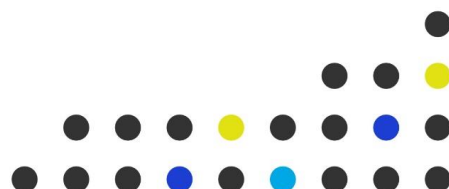
P-ITOBA-0040

ECTS / semester	5 credits / fall
Course classification	Compulsory
Suggested background knowledge	basic biochemistry and molecular biology. Ability of downloading and installing the free UCSF Cimer software
Assessment	Project work
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Additional lecturer(s)	Martti Tolvanen, PhD
Recommended reading	Gu, J & Bourne, P.E. (eds, 2009): Structural bioinformatics, 2nd ed. Wiley-Blackwell Gáspári Z (ed. 2020): Structural bioinformatics: Methods and Protocols. Humana Press
Course URL	http://www.bioinfoacademy.com/StructBioi

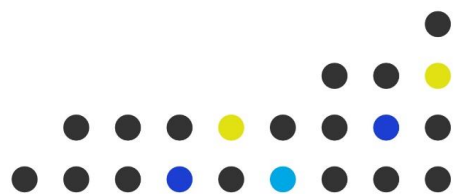
Course description:

Basics of search, manipulation and analyses of structures of large biological molecules, especially proteins.

- Basics of protein structures and structure determination. Simple validation of models by Ramachandran plots. Basic use of molecular graphics software
- Molecular graphics: illustrating and highlighting molecular details on screen and print; generating molecular surfaces
- Comparison of structures: overlaying molecules and measuring their structural similarity



- Molecular animations
- Theory of protein modeling and protein dynamics
- Validation and analysis of models



Java Programming for Bionics

P-ITOBA-0130

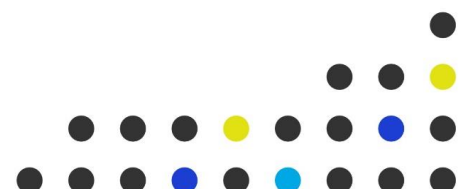
ECTS / semester	3 credits / spring
Course classification	Elective
Suggested background knowledge	basic biochemistry and molecular biology
Assessment	Questionnaire
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Recommended reading	H.M. Deitel, P.J. Deitel. (2005) Java: how to program. Pearson/Prentice Hall

Course description:

Introduction to the Java programming language:

- Basics of object-oriented programming in Java
- Classes, interfaces, inheritance, function overloading
- Basics of file input/output
- Basics of GUI programming
- Concept of threading in Java
- Use of external APIs to solve bioinformatics-related tasks

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Phylogenetics with R

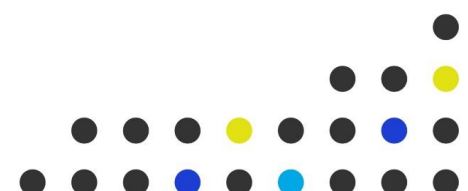
P-ITOBA-0080

ECTS / semester	6 credits / spring
Course classification	Compulsory
Prerequisite course(s)	Biological data analysis with R
Assessment	Project work
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Additional lecturer(s)	Csaba Ortutay, PhD
Recommended reading	Wiley, E.O. & Lieberman, B.S. (2011) Phylogenetics: Theory and Practice of Phylogenetic Systematics, 2nd. ed. Wiley-Blackwell

Course description:

Phylogenetics is the taxonomical classification of organisms based on how closely they are related in terms of evolutionary differences. The course will familiarize students with different phylogenetics algorithms and practical software applications for biological problems.

- Introduction to phylogenetics, and essentials of evolution as background
- Data types for phylogenetic analysis and parsimony
- Distance based methods, distance matrices, nucleotide substitution models
- Model based methods: maximum likelihood and Bayesian phylogenetics
- Auxiliary methods: bootstrapping, consensus trees, tree comparison
- Visualization of phylogenetic trees



Sequence Analysis with BioPython

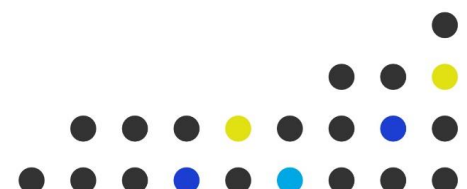
P-ITOBA-0090

ECTS / semester	4 credits / spring
Course classification	Compulsory
Prerequisite course(s)	Introduction to Programming in Python
Assessment	Questionnaire
Subject coordinator	Zoltán Gáspári, associate professor, PhD
Additional lecturer(s)	Dániel Györffy, PhD
Recommended reading	Stevens, T.J. (2015): Python Programming for Biology : bioinformatics and beyond. Cambridge University Press Libeskind- Hadas, R & Bush E. (2014): Computing for biologists : python programming and principles. Cambridge University Press

Course description:

The Biopython Project adopts the flexibility and easy to code features of Python to classic bioinformatics projects. After this course students will be able to use Python to address the following problems:

- Parsing FASTA and GenBank sequence files
- Parsing multiple sequence alignment files
- Creating multiple sequence alignments
- Accessing BLAST services programmatically



Thesis Work

P-SZD-ISTI-ABA

ECTS / semester	12 credits / spring
Course classification	Compulsory
Assessment	Thesis work
Subject coordinator	Zoltán Gáspári, associate professor, PhD



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