



Course unit (module) title	Code
Transcriptomics	

Lecturer(s)	Department(s) where the course unit (module) is delivered
Coordinator: Gediminas Alzbutas, PhD Other(s): tutor from the Department of Human and Medical Genetics	Faculty of Mathematics and Informatics, Naugarduko st. 24, Vilnius Department of Human and Medical Genetics, Institute of Biomedical Sciences, Santariškių str. 2, Vilnius

Study cycle	Type of the course unit (module)
Second cycle	Compulsory

Mode of delivery	Period when the course unit (module) is delivered	Language(s) of instruction
Face-to-face, self-study Lectures, seminars and practice	2 nd semester	English

Requirements for students	
Prerequisites:	Additional requirements (if any):

Course (module) volume in credits	Total student's workload	Contact hours	Self-study hours
5	135	68	67

Purpose of the course unit (module): programme competences to be developed		
Aim of this course is to acquire knowledge about transcriptomic regulation of the genome and to develop competences in order to discuss and evaluate scientific arguments in transcriptomics and metabolomics fields, and analyse transcriptomic experimental data.		
Learning outcomes of the course unit (module)	Teaching and learning methods	Assessment methods
2.1; 2.2; 3.1; 5.1 Ability to identify the issues assessed in scientific publications and ability to propose solutions to the analysed problems	Group discussions, tutorials, self-study assignments, report preparation, exercises	Completion of exercises, performance in group discussions, written examination
2.1; 2.2; 3.1; 4.2 Ability to plan, to use techniques and technologies in transcriptomic experiments and to report, critically analyse, and interpret the obtained experimental data	Group discussion, tutorials, report preparation, database analysis, laboratory works, individual presentations	Two written reports (one report on experiment planning, one report on data analysis), performance in group discussions and during laboratory works, individual presentation, written examination

3.1; 5.1; Ability to operate with main transcriptomic processes underlying regulation of gene expression in living organisms				Lectures (problem-based teaching), group discussions, self-study assignments, database analysis				Completion of practical assignments (one written colloquium/test, completion of exercises), performance in group discussions, written examination	
Content: breakdown of the topics	Contact hours						Self-study work: time and assignments		
	Lectures	Tutorials	Seminars	Exercises	Laboratory work	Internship/work	Contact hours	Self-study hours	Assignments
1. Research areas and objectives of transcriptomics. G. Alzbutas, PhD	3						3	1	Passos, G. A., Part I, Section 1, p. 3-49.
2. Techniques and technologies in transcriptomics. G. Alzbutas, PhD	4						4	4	Wu, J. Section 1-2, p. 1-73. Transcriptomics and Gene Regulation
3. Role of transcriptomics in gene expression studies. G. Alzbutas, PhD	4		2	10			16	16	Database analysis-based self exercises, preparation for seminar topics
4. Transcriptomics and metabolomics. G. Alzbutas, PhD	3		1	6			10	13	Self-study of scientific papers provided by the tutor.
5. Integrative analysis of transcriptomics and proteomics data. G. Alzbutas, PhD	3		1	6			10	13	Database analysis-based self exercises, preparation for seminar topics
6. Single cell transcriptomic analysis with Python and designated Python libraries. Assoc. prof., E. Pranckevičienė				13			13	10	Understanding and locally performing single cell analysis with Python using Scanpy and other libraries. Guiding references and data: https://training.galaxyproject.org/training-material/topics/single-cell/
7. Data mining methods in transcriptomics. Deep analysis of classification and clustering methods widely used in single	2			10			12	10	Familiarizing and reviewing computational methods in references (Qi, Ren, et al and Zhao, Xinlei, et al , please see the Compulsary reading list). Preparing for discussion on practical applications using BioJupies portal https://amp.pharm.mssm.edu/biojupies/

cell sequencing data analysis. Review and discussion. Data mining algorithms in transcriptomics								Discussion and analysis on merits of available off-the-shelf tools https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/scrna-scanpy-pbmc3k/tutorial.html
Total	19		4	45			68	67

Assessment strategy	Weight,%	Deadline	Assessment criteria
1-5 topics			
Individual presentation and group discussions during seminars	15%	During the cycle	Activity during seminars, performance in group discussions, oral and written presentations on particular topics. <u>Presentation assessment criteria:</u> Clear selection of the papers (2 points); Quality of speech (clarity, distinction) (1.5 point); Eye contact with audience (2 points); Quality of visually presented material (1.5 point); Management of questions (quality of answers to the presented questions) (2 points); Management of time (is the time given for presentations used properly) (1 point).
Written assessment of theoretical knowledge	24 %	During the cycle after the corresponding lectures	The scoring for each test question is given. Maximum grade of the exam test is 10 points. The evaluation criteria of questions are presented to the students in writing at the lecture before the test.
2-5 topics			
Drawing conclusions from the results of transcriptome data analysis.	15%	During the cycle	The grade is based on the evaluation of capabilities to explain the designed transcriptome data analysis pipeline and on a written report in combination with presentation of findings.
6 topic			
Completion of problem sets in Python, including recreating published single-cell RNA sequencing data analyses	15 %	During the cycle	The grade is proportional to the number of correctly solved problem in problem sets.
7 topic			
Performing analysis of assigned transcriptomics dataset from NCBI Gene Expression Omnibus and interpretation of analysis results highlighting a most significant analysis approach that led to the conclusions.	15%	During lectures and seminars	4 points analysis + 6 points interpretation. Most significant assessment criteria is student's ability to rationalize what information is revealed by each analysis method/step, why it was applied and explain whether/why data normalization was required.
6-7 topics			
Written assessment of theoretical knowledge	16 %	During the cycle after the corresponding lectures	The scoring for each test question is given. Maximum grade of the exam test is 10 points. The evaluation criteria of questions are presented to the

			students in writing at the lecture before the test.
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Author	Year of publication	Title	Issue of a periodical or volume of a publication	Publishing place and house or web link
Compulsary reading				
Wu, Jiaqian (Ed.)	2016	Transcriptomics and Gene Regulation		Springer
Passos, Geraldo A. (Ed.)	2014	Transcriptomics in Health and Disease		Springer
Qi, R., Ma, A., Ma, Q., & Zou, Q.	2019	Clustering and classification methods for single-cell RNA-sequencing data		Briefings in bioinformatics 7, https://doi.org/10.1093/bib/bbz062
Zhao, X., Wu, S., Fang, N., Sun, X., & Fan, J.	2019	Evaluation of single-cell classifiers for single-cell RNA sequencing data sets.		Briefings in Bioinformatics, https://doi.org/10.1093/bib/bbz096
Optional reading				
https://hstalks.com/biosci/				
https://scanpy.readthedocs.io/en/stable/		Scanpy – python library for single cell RNA sequencing data analysis		
		The Snakemake workflow management system is a tool to create reproducible and scalable data analyses.		https://snakemake.readthedocs.io/en/stable/tutorial/tutorial.html
