

Course unit (module) title	Code
Transcriptomics	

Lecturer(s)	Department(s) where the course unit (module) is delivered
<b>Coordinator: Gediminas Alzbutas, PhD</b>  <b>Other(s): Rasa Sabaliauskaitė, PhD; Juozas Nainys, PhD; Rapolas Žilionis, PhD; Justina Žvirblytė; Erinija Pranckevičienė, PhD, Eglė Preikšaitienė, PhD; Evelina Siavrienė, PhD</b>	Life Sciences Centre Saulėtekio ave. 7  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 <sup>nd</sup> semester	English

Requirements for students	
<b>Prerequisites:</b>	<b>Additional requirements (if any):</b>

Course (module) volume in credits	Total student's workload	Contact hours	Self-study hours
10	260	120	140

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 Practical skills to work with specialized and basic equipment of modern laboratory in compliance with safety requirements	Laboratory works	Performance during laboratory works
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 placement	Contact hours	Self-study hours	Assignments
1. Research areas and objectives of transcriptomics. G. Alzbutas, PhD	3						3	5	Passos, G. A., Part I, Section 1, p. 3-49.
2. Techniques and technologies in transcriptomics. G. Alzbutas, PhD	5						5	6	Wu, J. Section 1-2, p. 1-73. Transcriptomics and Gene Regulation
3. Novel functional RNA discovery in transcriptomics and their use in diseases treatment. Rasa Sabaliauskaitė, PhD	2		5				7	9	Wu, J. Section 5, p. 115-141. Wu, J. Section 7, p. 161-181. Database analysis-based self exercises, preparation for seminar topics
4. Role of transcriptomics in gene expression studies. G. Alzbutas, PhD	8		2	9			19	21	Database analysis-based self exercises, preparation for seminar topics
5. Transcriptomics and metabolomics. G. Alzbutas, PhD	4		2	7			13	15	Self-study of scientific papers provided by the tutor.
6. Integrative analysis of transcriptomics and proteomics data. G. Alzbutas, PhD	6		2	7			15	18	Database analysis-based self exercises, preparation for seminar topics
7. Single-cell and spatial transcriptomics. J. Nainys, PhD			7				7	8	Self-study of scientific papers provided by the tutor.
8. Single-cell transcriptomic data analysis with Python. R. Žilionis, PhD, J. Žvirblytė				32			32	35	Solving transcriptomic data-related analytical problems with Python.
9. Data mining methods in transcriptomics. Deep analysis of classification and clustering methods widely used in single cell sequencing data analysis. Review and discussion. Data mining algorithms in transcriptomics Assoc. prof., E. Pranckevičienė	2			9			11	12	Familiarizing and reviewing computational methods in references (Qi, Ren, et al and Zhao, Xinlei, et al , please see the Compulsory reading list). Preparing for discussion on practical applications using BioJupies portal <a href="https://amp.pharm.mssm.edu/biojupies/">https://amp.pharm.mssm.edu/biojupies/</a> Completing exercise in Galaxy preceding a discussion and analysis on merits of available off-the-shelf tools <a href="https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/scrna-scanpy-pbmc3k/tutorial.html">https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/scrna-scanpy-pbmc3k/tutorial.html</a>

10. Omics integration at patient level. E. Preikšaitienė, E. Siavrienė			6				6	7	Analysis of omics data provided by tutors
Examination	2						2	4	Preparation for examination
<b>Total</b>	<b>32</b>		<b>24</b>	<b>64</b>			<b>120</b>	<b>140</b>	

Assessment strategy	Weight,%	Deadline	Assessment criteria
<b>1-3 topics</b>			
Individual presentation and group discussions during seminars	10%	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).
Completion of exercises and performance during laboratory works	5%	During the cycle	Pass/ fail
<b>5-7 topics</b>			
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.
<b>8-9 topics</b>			
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. Half of the points from topics 8-9 are earned by correctly answering final exam questions, which will be based on lecture material AND discussions during seminars.
<b>10 topic</b> 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%		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.
Written examination	40%	At the end of the course	Test type written exam. The scoring for each exam question is given. Maximum grade of the exam test is 10 points. The evaluation criteria of exam questions are presented to the students in writing at the last lecture.

Author	Year of publication	Title	Issue of a periodical or volume of a publication	Publishing place and house or web link
<b>Compulsary reading</b>				
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, <a href="https://doi.org/10.1093/bib/bbz062">https://doi.org/10.1093/bib/bbz062</a>
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, <a href="https://doi.org/10.1093/bib/bbz096">https://doi.org/10.1093/bib/bbz096</a>
<b>Optional reading</b>				
<a href="https://hstalks.com/biosci/">https://hstalks.com/biosci/</a>				
<a href="https://scanpy.readthedocs.io/en/stable/">https://scanpy.readthedocs.io/en/stable/</a>		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.		<a href="https://snakemake.readthedocs.io/en/stable/tutorial/tutorial.html">https://snakemake.readthedocs.io/en/stable/tutorial/tutorial.html</a>

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