GDAŃSK UNIVERSITY OF TECHNOLOGY

Subject card

Subject name and code	Genomics and transcriptomics, PG_00070035		
Field of study	InfoBioChem		
Date of commencement of studies	February 2026	Academic year of realisation of subject	2025/2026
Education level	second-cycle studies	Subject group	Obligatory subject group in the field of study Subject group related to scientific research in the field of study
Mode of study	Full-time studies	Mode of delivery	at the university
Year of study	1	Language of instruction	Polish Lecture slides in English will be provided to familiarise students with terminology in the global scientific and technical literature.
Semester of study	1	ECTS credits	3.0
Learning profile	general academic profile	Assessment form	exam
Conducting unit	Department of Biotechnology and Microbiology -> Faculty of Chemistry -> Faculties of Gdańsk University of Technology		
Name and surname of lecturer (lecturers)	Subject supervisor	prof. dr hab. inż. Paweł Sachadyn	
	Teachers	prof. dr hab. inż. Paweł Sachadyn	

Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	0.0	45.0	0.0	60
	E-learning hours included: 0.0						

Learning activity and number of study hours	Learning activity	Participation in didactic classes included in study plan	Participation in consultation hours	Self-study	SUM
	Number of study hours	60	5.0	10.0	75

Subject objectives	The aim of the course is to present modern technologies of genome and transcriptome research, the possibilities and limitations of genomics and transcriptomics and their applications in diagnostics and scientific research.

Learning outcomes

Course outcome	Subject outcome	Method of verification
[K7_K02] is ready to work in a team, taking on various roles depending on the needs of the task.	The student is aware of the need to expand knowledge in the rapidly developing field of genomics and transcriptomics and the importance of their role in interdisciplinary projects.	[SK4] Assessment of communication skills, including language correctness [SK2] Assessment of progress of work
[K7_W02] has in-depth knowledge of omics science, including the principles of generating, analyzing, and interpreting omics data.	The student has knowledge of the structure of the genome and the functioning of the epigenome and transcriptome, methods and technologies of next-generation DNA sequencing, and applications of genome and transcriptome research in science and diagnostics.	[SW1] Assessment of factual knowledge [SW2] Assessment of knowledge contained in presentation
[K7_K01] is ready to determine the priorities of activities in the implementation of his/her own tasks or those assigned by others	The student is aware of the possibilities and limitations of genome and transcriptome research, as well as the ethical challenges arising from the development of genomics and transcriptomics.	[SK2] Assessment of progress of work [SK5] Assessment of ability to solve problems that arise in practice
[K7_U02] is able to use IT tools for operations on nucleotide and protein sequences.	The student can select methods of genomic and transcriptome analysis and critically interpret the obtained results.	[SU2] Assessment of ability to analyse information [SU5] Assessment of ability to present the results of task [SU3] Assessment of ability to use knowledge gained from the subject

Subject contents

Course content – lecture
The aim of the course is to present modern technologies of genome and transcriptome research, the possibilities and limitations of genomics and transcriptomics and their applications in diagnostics and science.

1-2. The human genome, epigenome, and transcriptome, and other model genomes basic information. 2 h
3. Genome and transcriptome research technologies hybridization arrays, shotgun sequencing, nanopore. 1 h
4-5. Genome research epigenomics: DNA methylation (MethylSeq) and other covalent DNA modifications. 2 h
5-6. Genome research epigenomics: chromatin remodeling ATAC-Seq and others. 2 h
9-10. DNA polymorphism SNPs and others in hereditary diseases and cancer. Sequencing of individual genomes and exomes. 2 h
11-12. Transcriptome research, RNAseq, and more. 3 h
13. Single-cell analysis. 1 h
14. Spatial transcriptomics. 1 h
15. Summary genomics and transcriptomics: importance, perspectives, and threats. 1 h

Course content – project
The aim of the project is to provide students with practical insights into the potential of genomics and transcriptomics in research and diagnostics, including applications, technological solutions, and data analysis through independent analysis of publications and datasets using modified criteria, a different analysis objective, an alternative strategy, or other bioinformatics tools. The project will provide hands-on experience with genomics, its applications, data analysis methods, and the development of their own creativity.

The course will consist of two parts: an introduction by the lecturer and student presentations corresponding to the three subsequent stages of the project, combined with a critical discussion.

INTRODUCTION 3 hours of class

Explanation of tasks, evaluation criteria, guidelines for genomic and transcriptomic databases, selection and critical evaluation of scientific articles.

STUDENTS TASKS 42 hours of class

A. Select a scientific article in the field of genomics and/or transcriptomics and a dataset (a supplement to this article) to prepare its presentation and perform your own analysis of genomic/transcriptomic data (e.g., based on different assumptions or using different tools than in the source article). Individual work only.

B. Prepare and show a short working presentation of the selected article and dataset for discussion in class of selected proposals, potential revisions and modifications (Presentation 1, 10-15 min). Approx. 3 hours of class.

C. Prepare and show a presentation and discussion of selected publications and datasets, including the objectives, methods, results, and conclusions, and propose your own analysis strategy (Presentation 2, 30-45 min). Approx. 15 hours of classes

D. Prepare and show a presentation of the methodology and results of analyses, highlighting novelty elements. (Presentation 3, approx. 60-90 min). Approx. 24 hours of classes

Prerequisites and co-requisites

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
Lecture exam in the form of a multiple-choice test	60.0%	50.0%
Evaluation of student presentations	60.0%	50.0%

Recommended reading

Basic literature	Lecture slides
Supplementary literature	Publications discussed in the lecture

	eResources addresses	

Example issues/ example questions/ tasks being completed	**Lecture: Transcriptome Analysis; RNAseq and others** **Transcriptome analysis methods before the ngs era** RT-qPCR, DNA microarrays, Northern blotting Limitations of these methods **RNAseq technology** RNA library preparation Sequencing (NGS Platforms) Read mapping and bioinformatics analysis Illumina vs. Aviti **RNAseq data analysis** Raw NGS data NGS data processing steps Identification of Differentially Expressed Genes (DEGs) Ontology analysis **Other RNA analysis approaches** Small RNAseq miRNA profiling Long-Read sequencing (e.g., Pacific Biosciences, Oxford Nanopore Technologies) **RNAseq applications in research** Potential Limitations Sources of errors **Medical applications of transcriptome analysis** Personalized medicine Disease biomarkers

	Transcriptomics in clinical trials Integration with proteomics and epigenomics **Exam Topics** Advantages and disadvantages of microarrays compared to RNAseq Main Steps of RNAseq Analysis What is Ontology Analysis and What Is It Used for? Specificity and applications of small-RNA sequencing Benefits of using RNAseq in personalized medicine What are the possibilities and limitations of RNAseq in scientific research?
Practical activites within the subject	Not applicable

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