

NAME OF THE COURSE		Genomics and Molecular Genetics of Eukaryotes				
Code	PMB702	Year of study	1			
Course teacher	Vesna Boraska Perica, Maja Barbalić, Ivica Šamanić, Jasna Puizina	Credits (ECTS)	7			
Associate teachers	Dean Kaličanin, mag. biol. et oecol. mar.	Type of instruction (number of hours)	L	S	E	F
			30	15	30	
Status of the course	Obligatory	Percentage of application of e-learning	10			
COURSE DESCRIPTION						
Course objectives	The course provides practical and theoretical skills to explore genome structure and gene function, from classical genetics methods to the latest high-throughput technologies. The use of computers in biological data analysis is an essential component of this course where students will be trained to use online tools and databases to assemble sequences, analyze gene expression and genome-wide data. The application of genomics in biotechnology and medicine will be presented.					
Course enrolment requirements and entry competences required for the course	Knowledge of the basics of genetics and molecular biology. Knowledge of basics of statistics, R programming language and Linux operating system can be useful.					
Learning outcomes expected at the level of the course (4 to 10 learning outcomes)	<p>Upon successful completion of the course students will be able to:</p> <ul style="list-style-type: none"> • explain the basics of the structure of the human genome and eukaryotic model organisms • understand the terminology, fundamental principles, strategies and technical methodology for genome research, such as GWAS, genome and transcriptome sequencing, genome annotation methods, and functional gene characterization • design and experimentally implement a smaller project in the field of functional genomics • use online tools and databases to analyze and visualize genomic data • apply bioinformatics tools for computerized analysis of genomic data • interpret the results of scientific research in the field of genomics 					
Course content broken down in detail by weekly class schedule (syllabus)	<p>Lectures (30 hours)</p> <ol style="list-style-type: none"> 1. Introduction, an overview of genome architecture and involvement of genetic variants with complex and monogenic diseases (3 hrs) 2. GWAS - Design, biological and clinical significance of genome-wide association studies (2 hrs) 3. Comparative genomics, exome and personalized genomics, (2 hrs) 4. Whole genome sequencing methods: shotgun sequencing and next-generation sequencing; whole-genome-sequence assembly (contigs, scaffolds) (3hrs) 5. Design and clinical application of next generation sequencing, (2 hrs) Maja 6. Genetic tests in clinical practice (2 hrs) 7. Cancer genomes (3 sata) 8. Functional genomics and reverse genetics, (2 hrs) 9. The Dynamic Genome: retrotransposons and transposons, (3 hrs) 10. Mutation, Repair and Recombination (3 hrs) 					

	<p>11. RNA biology and gene regulation (3 hrs) 12. Genetic control of development (2 hrs)</p> <p>Seminars (15 hrs) Students self-evaluate original genomics and publicly present their work (includes a Power Point presentation and discussion). Additional literature search is needed from sources that are not covered in sufficient detail by the textbook, given the rapidly changing field of genomics with the accumulation of new scientific data. The goal is to enable the student to clearly formulate and briefly and concisely present scientific issues (15 minutes), integrate the knowledge gained during the course through critical thinking and conclusion during the discussion on the topic of seminar work.</p> <p>Exercises (30 hrs) 1. Review of genomic databases (4 hours), 2. Classification of genetic variants according to their clinical significance (4 hours), 3. Application of genetic tests in biotechnology and medicine (4 hours), 4. Next Generation Sequencing Methods (NGS); hands-on demonstration of library preparation, sequencing, data storage (8 hours), 5. Bioinformatic processing of sequences obtained by next-generation sequencing; whole genome sequencing results of the Allium genus (or some other dana) and repeating sequence analysis using Repeat Explorer, application of 16S rRNA gene sequencing to identify bacterial species (Review of bioinformatics tools for taxonomic identification and diversity analysis of microbial communities from a metagenomic sample from the environment): data standards and storage, untreated processing data compilation, database review (4 hours), 6. Student project in molecular genetics (6 hours)</p>					
Format of instruction	<input checked="" type="checkbox"/> lectures <input checked="" type="checkbox"/> seminars and workshops <input checked="" type="checkbox"/> exercises <input type="checkbox"/> <i>on line</i> in entirety <input type="checkbox"/> partial e-learning <input type="checkbox"/> field work		<input type="checkbox"/> independent assignments <input type="checkbox"/> multimedia <input checked="" type="checkbox"/> laboratory <input type="checkbox"/> work with mentor <input type="checkbox"/> (other)			
Student responsibilities	Attend lectures, exercises and seminarina, prepare and present a seminar, keep a diary of work, prepare a laboratory report.					
Screening student work (<i>name the proportion of ECTS credits for each activity so that the total number of ECTS credits is equal to the ECTS value of the course</i>)	Class attendance	1	Research		Practical training	
	Experimental work	1	Report		(Other)	
	Essay		Seminar essay	1	(Other)	
	Tests		Oral exam	1	(Other)	
	Written exam	1	Project	1	(Other)	
Grading and evaluating student work in class and at the final exam	Assessment methods • Laboratory report					

	<p>All laboratory reports must include a complete and detailed overview of the experimental procedures, a description of the results, accompanied by analysis and interpretation of the data.</p> <ul style="list-style-type: none"> • Quizzes Quizzes include knowledge testing from a previous laboratory exercise as well as material for a subsequent experiment (data is based on theory and protocols from a laboratory manual) • Practical application of computers in biological data analysis In the computer classroom, students must demonstrate the skill of using bioinformatics tools to analyze genomic data. With the help of online tools and databases, it is necessary to enter genomic study data, show proper analysis and answer specific questions • Presentation of seminar work Students will need to prepare a presentation that presents an overview of the scientific issue they are dealing with. The presentation will be judged by the content of the presentation (keywords, critical review of the literature, presentation of scientific results), format, innovation and linguistic competence. • Regular attendance will also be part of the assessment. • Knowledge gained in lectures will be assessed through a written exam (essays and multiple choice questions). <p>The final grade is based on the total points for each rating category.</p>		
Required literature (available in the library and via other media)	Title	Number of copies in the library	Availability via other media
	A.J.F. Griffiths, S.R. Wessler, S.B. Carroll, J. Doebley (2015) Introduction to genetic analysis (11th edition), W.H. Freeman and Company, New York, USA	1	
	Arthur Lesk (2017) Introduction to Genomics (3rd edition), Oxford University Press		
Optional literature (at the time of submission of study programme proposal)	<p>Robert C. Elston (eds.) (2017) Statistical Human Genetics (Methods and Protocols), (2nd edition), Humana Press Jonathan Pevsner (2015) Bioinformatics and Functional Genomics (3rd edition), Wiley-Blackwell</p>		
Quality assurance methods that ensure the acquisition of exit competences	<p>Personal consultations, students survey for the evaluation of the subject and teacher, evidence of the presence on the classes, analysis of the success rate on the partial and final tests.</p>		
Other (as the proposer wishes to add)			