## Subject card

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|---|---|---|---|
| Subject name and code | Bioinformatics - applications , PG_00153621 | | |
| Field of study | Biotechnology | | |
| Date of commencement of studies | October 2024 | Academic year of realisation of subject | 2024/2025 |
| Education level | postgraduate studies | Subject group | Obligatory subject group 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 |
| Semester of study | 2 | ECTS credits | 2.0 |
| Learning profile | academic | Assessment form | |
| Conducting unit | Intercollegiate Faculty of Biotechnology UG-MUG -> Rektor | | |
| Name and surname of lecturer (lecturers) | Subject supervisor | dr hab. Małgorzata Waleron | |
| | Teachers | dr hab. Małgorzata Waleron | |

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|---|---|---|---|---|---|---|---|
| Lesson types | Lesson type | Lecture | Tutorial | Laboratory | Project | Seminar | SUM |
| | Number of study hours | 0.0 | 0.0 | 30.0 | 0.0 | 0.0 | 30 |
| | E-learning hours included: 0.0 | | | | | | |

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| 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 | 30 | 5.0 | 15.0 | 50 |

**Subject objectives**

- Acquainting students with knowledge in the field of bioinformatics, allowing to consciously use bioinformatics methods and tools applied in biotechnology.
- Students will acquire an ability to use scientific information, in particular databases containing information indispensable in carrying out operations in bioinformatics analyses
- Students will get practical skills to collect and analyze the gathered data with the use of the publicly available software and preparing newly gathered data for deposition in public databases. Students will acquire an ability to design experiments in silico.

**Learning outcomes**

| Course outcome | Subject outcome | Method of verification |
|---|---|---|
| [BIOTECHMU2_W05] The graduate knows and understands the methods used in science and natural sciences necessary to understand biological phenomena and processes at the molecular level | The student has knowledge of the methods used in bioinformatics. | [SW4] test/exam - oral or written |
| [BIOTECHMU2_U02] The graduate is able to collect and interpret empirical data; use statistical methods and IT tools in data analysis; formulate conclusions based on empirical data | The student can collect sequence data, perform analyses using bioinformatics tools, and draw conclusions based on obtained results. | [SU2] presentation/project/paper/report<br>[SU5] implementation of a problem task |
| [BIOTECHMU2_U04] The graduate is able to use scientific information fluently, including English-language information on biotechnology; analyse and select information critically; use electronic sources; use appropriate databases | The student can use publicly available bioinformatics databases to retrieve the desired information and critically analyse it. | [SU2] presentation/project/paper/report<br>[SU5] implementation of a problem task |

<table>
<tr><td>Subject contents</td><td colspan="3">
<ul>
<li>Browsing through sequential databases and popular bioinformatics servers.</li>
<li>Review of the most popular sequence formats, with typical bioinformatics software requirements accounted for.</li>
<li>Searching for similar sequences in databases. Search parameters and statistical analysis of results (BLAST).</li>
<li>Sequence analysis by means of various software (Chromas, Bioedit, Geneious, Ugene, Bionumerics).</li>
<li>Comparing sequences (comparing sequence pairs, comparing many sequences) by means of various programs e.g. Clustal, Bioedit, MEGA, Geneious, Bionumerics).</li>
<li>Comparing similarities between nucleotide and amino acid sequences.</li>
<li>Phylogenetic analysis: selection of the model of nucleotide and amino acids substitution, construction of phylogenetic trees by means of various methods: maximum parsimony genetic distance, maximum Bayesian probability and reasoning, verification of the correctness of phylogenetic trees (Geneious, MEGA, and other software)</li>
<li>Assembling bigger fragments of sequence and searching for readout open frameworks (ORF-Finder)</li>
<li>Designing starters by means of various software: PRIMER3, PrimerQuest, OligoAnalyzer,</li>
<li>RFLP in silico</li>
<li>Analysis of sequences obtained from clone library (with mothur software). Searching for chimeric sequences (with Bellerophon software).</li>
<li>Metagenomics: Determination of the operational taxonomic unit (OTU) and AVS (K-base)</li>
<li>Genome assembling and annotation (RAST, Geneious, KEGG, BioCyc)</li>
<li>Searching for the gene clusters encoding secondary metabolites (antiSMASH platform)</li>
<li>Searching for plasmids (plasmidfinder software), prophages (Phaster), mobile genetic elements ( ICEfinder) in NGS data</li>
<li>Basic comparative genomics (constructing phylogenetic profiles, searching for genome plasticity regions with using various platforms: Integrated Microbial Genomes - IMG, Microbial Genome Annotation & Analysis Platform, Edgar 3, K-base, KEGG).</li>
<li>Computation of overall genome relatedness indices (OGRI) methods: DNA-DNA in silico (TYGS), ANI (platform Jspecies)</li>
<li>Pangenomic analysis - pangenome, core genome and dispensable genes, pangenomics with using various platforms: Integrated Microbial Genomes - IMG, Microbial Genome Annotation & Analysis Platform, Edgar 3, K-base)</li>
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<tr><td>Prerequisites and co-requisites</td><td colspan="3"></td></tr>
<tr><td rowspan="4">Assessment methods and criteria</td><td>Subject passing criteria</td><td>Passing threshold</td><td>Percentage of the final grade</td></tr>
<tr><td>The skills acquired will be validated in a work involving self-performed bioinformatics analysis, interpretation of the results obtained and their presentation as a report.</td><td>0.0%</td><td>60.0%</td></tr>
<tr><td>Reports from all classes will be required in order to pass the course.</td><td>0.0%</td><td>20.0%</td></tr>
<tr><td>Knowledge acquired in class will be verified by a test</td><td>0.0%</td><td>20.0%</td></tr>
<tr><td rowspan="3">Recommended reading</td><td>Basic literature</td><td colspan="2">
<ul>
<li>Applied Bioinformatics - An Introduction, Paul M. Selzer Richard J. Marhöfer, Oliver Koch. Second Edition.2018</li>
<li>Bioinformatics. A Practical Guide to the Analysis of Genes and Proteins. Redakcja naukowa: A.D. Baxevanis, B.F.F. Ouellette.</li>
<li>Bioinformatics and Molecular Evolution. Paul G. Higgs, Teresa K. Attwood.</li>
</ul>
</td></tr>
<tr><td>Supplementary literature</td><td colspan="2">
<ul>
<li>Bioinformatics. Sequence and genome analysis". D.W. Mount. 2001.</li>
<li>The students independently search for course material using, among other things, electronic information sources.</li>
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</td></tr>
<tr><td>eResources addresses</td><td colspan="2">Adresy na platformie eNauczanie:</td></tr>
<tr><td>Example issues/ example questions/ tasks being completed</td><td colspan="3"></td></tr>
<tr><td>Work placement</td><td colspan="3">Not applicable</td></tr>
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