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| Course Title | Bioinformatics | | | | |
| Course Code | MCB650 | | | | |
| Course Type | Elective | | | | |
| Level | Master's (2 nd cycle) | | | | |
| Year / Semester | 1 st Year / 2 nd Semester | | | | |
| Teacher's Name | TBA | | | | |
| ECTS | 10 | Lectures / week | 3 Hours | Laboratories / week | None |
| Course Purpose and Objectives | The main objective of the Bioinformatics course is for students to learn various bioinformatics tools and analysis methods and be able to apply them in the analysis of various cancer genomes. Upon completion of the course, students should be able to work with the vast amounts of genomic, transcriptomic and/or proteomic data and tools and apply this knowledge to their research or professional career. | | | | |
| Learning Outcomes | <p>Upon completion of the course, students will be able to:</p> <ul style="list-style-type: none"> • Apply computational tools to biological data with a focus on cancer genomes • Collect and interpret biological and cancer-related data from public databases • Apply statistical and non-statistical tools for multiple sequence alignment and alignment of reads from high-throughput sequencing technologies • Apply computational methods for the analysis of high-throughput DNA/RNA sequencing data • Utilize contemporary bioinformatics tools to address biological questions related to cancer and metastasis | | | | |
| Prerequisites | None | Required | None | | |
| Course Content | <p>Description:</p> <ul style="list-style-type: none"> • Presentation and practical use of various computational tools • Sequencing technology • Short read alignment • Pairwise Sequence alignment, multiple sequence alignment • Functional Genomics and Genome analysis • Mining of Biological and Cancer-related Data from Online Repositories (GEO, SRA, TCGA, ICGC etc) • Microarray data analysis (Gene expression analysis, microarray genotyping) • High-throughput DNA/RNA sequencing data analysis | | | | |

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| | <ul style="list-style-type: none"> • Genome re-sequencing and de novo sequencing/assembly • Gene expression analysis using RNA-sequencing (RNA-seq) • Chromatin immunoprecipitation sequencing (ChIP-seq): protein-DNA interactions • Epigenetic data analysis: histone modifications, chromatin accessibility, DNA methylation • Single-cell genomics • Enrichment analysis | | | | | | | | | | |
| Teaching Methodology | Face to face | | | | | | | | | | |
| Bibliography | <p>Bioinformatics: Sequence and Genome Analysis, David Mount, Latest Edition, ISBN 978-087969712-9</p> <p>Bioinformatics and functional genomics, Jonathan Pevsner, Latest Edition, ISBN: 978-1-118-58178-0</p> <p>Structural Bioinformatics. P. E. Bourne, H. Weissig, Latest Edition, Wiley-Liss ISBN 0471 20199 5</p> <p>Selected scientific articles in pdf format that will be provided in advance by the lecturer</p> | | | | | | | | | | |
| Assessment | <table> <tr> <td>Mid-Term Examination</td> <td>30%</td> </tr> <tr> <td>Final Examination</td> <td>40%</td> </tr> <tr> <td>Assignments</td> <td>20%</td> </tr> <tr> <td>Class participation</td> <td>10%</td> </tr> <tr> <td>Total</td> <td>100%</td> </tr> </table> | Mid-Term Examination | 30% | Final Examination | 40% | Assignments | 20% | Class participation | 10% | Total | 100% |
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| Class participation | 10% | | | | | | | | | | |
| Total | 100% | | | | | | | | | | |
| Language | English | | | | | | | | | | |