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Genome Analysis Using Bioinformatics Tools (281954)

Course coordinator

Asst. Prof. Vladimir Brajković, PhD

Course description

The aim of this course is to introduce students to the application of next-generation sequencing technology by understanding the processes and formats involved in genome sequence processing and analysis. Students will learn how to install the Linux operating system on a personal computer and use basic command-line commands to install and apply bioinformatics tools for genome sequence processing, analysis, and interpretation of basic analyses. Additionally, students will be introduced to advanced computing services on remote computers/clusters provided by the University Computing Centre. For cluster usage, user accounts will be created for students, and they will learn how to connect to these systems, apply bioinformatics tools, and define the necessary resources for job queue execution in genome sequence processing and analysis.

ECTS: **4.00**

Teaching hours: 40
Lectures: 20
Auditory exercises: 20

Grading

Sufficient (2):
Good (3):
Very good (4):
Excellent (5):

Type of course

- Graduate studies / MS Courses taught in English (Elective course, 2 semester, 1 year)