

Syllabus for ABT 785 Applications of Bioinformatics

NOTE: This syllabus document contains the basic information of this course. The most current syllabus is available in the full course.

Course Description

Explore and apply existing bioinformatic tools, including implementation of pre-coded solutions to data acquisition, wrangling, analysis, visualization, and structural modeling problems. Students will complete a final project that generates a multi-system workflow to solve bioinformatic problems.

Prerequisite(s)

ABT 720, ABT 730.

Course Outcomes

Upon completing this course, you will be able to do the following:

- Identify existing databases for genomic, transcriptomic, proteomic, and metabolomics analysis
- Describe construction and limitations for existing databases
- Identify existing tools for sequence analysis
- Identify and critique methods and tools for annotation of genomes
- Identify and critique methods and tools for phylogenetic analysis
- Identify and critique methods for assigning protein structure and function
- Identify and critique methods for identifying and assembling metabolite profiles
- Describe best practices in adapting and editing existing tools
- Identify methods for developing multi-tool workflows
- Build, analyze, and critique functional workflows

Course Requirements/Components

The following assignment types will account for your overall grade in this course.

- 5% Quizzes
- 65% Tutorials and Exploratory Assignments
- 30% Final project

Grading

The following grading scale will be used to evaluate all course requirements and to determine your final grade:

Grade	Percentage Range
A	92% - 100%
A-	89% - 91%
B+	84% - 88%
B	80% - 83%
B-	76% - 79%
C+	72% - 75%
C	68% - 71%
C-	64% - 67%
F	0 - 63%