**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:
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<thead>
<tr>
<th>Grade</th>
<th>Percentage Range</th>
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<tbody>
<tr>
<td>A</td>
<td>92% - 100%</td>
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<tr>
<td>A-</td>
<td>89% - 91%</td>
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<td>B+</td>
<td>84% - 88%</td>
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<td>80% - 83%</td>
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<td>B-</td>
<td>76% - 79%</td>
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<td>C-</td>
<td>64% - 67%</td>
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<td>F</td>
<td>0 - 63%</td>
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