COURSE DESCRIPTION

<table>
<thead>
<tr>
<th>Course No.</th>
<th>Course Type</th>
<th>Course Title</th>
<th>Coordinator</th>
</tr>
</thead>
<tbody>
<tr>
<td>CSC 526</td>
<td>Sel. Elect.</td>
<td>Bioinformatics</td>
<td>Francine Blanchet-Sadri</td>
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Sem. Hours: 3

Current Catalog Description:

Introduction to the problems and methods in Bioinformatics. Problem areas include restriction mapping, map assembly, sequencing, DNA arrays, and sequence comparison.

Textbook:


References:


Course Outcomes:

Upon successful completion of this course, a student should be able to:

1. **Understand** the basic theoretical models of problems in Bioinformatics such as the fragment assembly problem, the physical mapping problem, and the genome rearrangements problem. (CO1)
2. **Search** existing biological sequence databases. (CO2)
3. **Comprehend** and **apply** a number of algorithms such as the classic dynamic programming algorithm, the phylogenetic tree reconstruction algorithm, and the dynamic programming algorithms for RNA structure prediction. (CO3)
4. **Understand** that models for the fragment assembly problem shed light on the diverse computational aspects of the problem, although none of them completely addresses the biological issues. (CO4)
5. **Simulate** variants of the sequence comparison algorithm. (CO5)
6. **Apply** algorithms for the consecutive ones problem that plays an important role in physical mapping. (CO6)
7. **Access** ideas and results whose main aim is to solve quickly problems in Bioinformatics. (CO7)
Prerequisites by Topic:

Students must have
- permission of instructor.

Major Topics Covered in the Course:

- Sequence Comparison and Database Search
- Fragment Assembly of DNA
- Physical Mapping of DNA
- Phylogenetic Trees
- Genome Rearrangements
- Molecular Structure Prediction

Estimated Curriculum Category Content (Semester hours):

<table>
<thead>
<tr>
<th>Area</th>
<th>Core</th>
<th>Advanced</th>
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<td>Software design</td>
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