CMPT 711 - G100 Bioinformatics Algorithms

Instructor(s): Leonid Chindelevitch

Calendar Objective/Description:
Fundamental algorithmic techniques used to solve computational problems encountered in molecular biology. This area is usually referred to as Bioinformatics or Computational Biology. Students who have taken CMPT 881 (Bioinformatics) in 2007 or earlier may not take CMPT 711 for further credit.

Instructor’s Objectives:
The goal of this course is to provide a solid foundation in the algorithmic techniques, such as dynamic programming, graph theory and probabilistic modeling, that computational biologists use on a daily basis, as well as to create exposure to the practice of computational biology through the analysis of a biological dataset. The course targets both graduate and advanced undergraduate students in computing science, molecular biology, biochemistry, biophysics, mathematics and biostatistics with minimal or no background in computational biology. However, a basic knowledge of algorithm design and analysis is required.

Prerequisites:
None

Topics:
- Sequence alignment: global, local and multiple alignment
- Probabilistic models: hidden Markov models, stochastic context-free grammars
- Secondary structure prediction: RNA and proteins
- Phylogenetics: inferring and analyzing evolutionary trees

Grading:
10% participation, 20% midterm, 30% assignments (best 3 out of 4), 40% team project. The team project will involve the analysis of a biological dataset provided by a life sciences faculty member. It will be evaluated via an oral presentation and a written report.

Recommended Books:

Academic Honesty Statement:
Academic honesty plays a key role in our efforts to maintain a high standard of academic excellence and integrity. Students are advised that ALL acts of intellectual dishonesty will be handled in accordance with the SFU Academic Honesty and Student Conduct Policies (http://www.sfu.ca/policies/gazette/student.html).