CMPT 441 - D100 Computational Biology

Instructor(s): Leonid Chindelevitch

Calendar Objective/Description:
This course introduces students to the computing science principles underlying computational biology. The emphasis is on the design, analysis and implementation of computational techniques. Possible topics include algorithms for sequence alignment, database searching, gene finding, phylogeny and structure analysis.

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 modelling, that computational biologists use on a daily basis, as well as present a sampling of applications to the analysis of metabolites, proteins, genes, and their interactions. 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.

Prerequisites:
CMPT 307. Students with credit for CMPT 341 may not take this course for further credit.

Topics:
- Sequence alignment, global and local
- Phylogenetics - inferring evolutionary trees
- RNA secondary structure prediction
- Biological networks analysis

Grading:
Option 1: 10% participation, 30% assignments (best 3 out of 4), 20% midterm, 40% final exam Option 2: 100% final exam
While I highly recommend option 1, you will automatically get the higher of the two grades.

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).