CMPT 829 - G100 Special Topics in Bioinformatics

Instructor(s): Kay C Wiese

Calendar Objective/Description:
Examination of recent literature and problems in bioinformatics. Within the CIHR graduate bioinformatics training program, this course will be offered alternatively as the problem-based learning course and the advanced graduate seminar in bioinformatics (both concurrent with MBB 829).

Instructor’s Objectives:
This course is open to interested graduate students from Computing Science, Math, Engineering, Biology, and MBB. It is also open to interested senior undergraduate students.

The first part of the course will review some of the basic and more advanced topics in bioinformatics. This will include select chapters from several reference text books, but also selected papers from the literature. The course will be offered in a mixed lecture style/seminar style format. Lectures are given by the instructor or a guest lecturer. The seminar part of the course will include student presentations on selected topics/papers/chapters.

Prerequisites:
permission of the instructor.

Topics:
- Exhaustive Search: Restriction Mapping, Profiles, Motif Finding, Search Trees
- Greedy Algorithms: Genome Re-arrangements, Reversal Sorting, Motif Finding
- Dynamic Programming: Edit Distance and Alignments, LCS, Local Alignment, Gap Penalties, Gene Predictions
- Divide and Conquer Algorithms: Space efficient Sequence Alignment, Block Alignment and Four Russians
- Graph Algorithms: DNA Sequencing, Shortest Superstring Problem, DNA Arrays, Fragment Assembly in DNA
- Combinatorial Pattern Matching: Repeat Finding, Exact Pattern Matching, Suffix Trees, Heuristic Search
- Clustering and Trees: Gene Expression Analysis, Evolutionary Trees, Parsimony Problem
- Hidden Markov Models: HMM Parameter Estimation, Profile HMM Alignment
- RNA secondary structure prediction, RNA Gene Finding, RNA Design
- RNA and Protein Visualization

Grading:
There will be assignments, student presentations, a project and an exam. Students will also be graded based on participation. Details of grading will be discussed in the first week of classes.

Students must attain an overall passing grade on the weighted average of exams in the course in order to obtain a clear pass (C- or better).

Required Books:
Reference Books:

- Biological Sequence Analysis, Durbin, Eddy, Krogh, and Mitchison, Cambridge, 1998, 9780521629713
- Computational Intelligence in Bioinformatics, Gary B. Fogel, David W. Corne, Yi Pan, IEEE Press/Wiley Interscience, 2008, 9780470105269
- Evolutionary Computation in Bioinformatics, Gary B. Fogel and David W. Corne, Morgan Kaufmann, 2003, 9781558607972

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).