Course Description

Bioinformatics studies biological problems using biological, computational, and mathematical methods. Computational biology studies computational techniques that can solve biological problems efficiently. This course covers some selected topics from Bioinformatics research.

Topics

The topics are drawn from the following lists:

- Pairwise sequence alignment with affine gap penalty.
- Multiple sequence alignment with affine gap penalty.
- Tree comparison algorithms.
- RNA structure alignment algorithms.
- Neighbour-joining algorithm for phylogenetic tree construction.
- Sequence assembly
- Hidden Markov models
- RNA secondary structure prediction by minimum energy folding.
- Protein peptide de novo sequencing.
- Normalized similarity and distance

Course work

There will be at least one assignment for the course. Each participant will be required to give a presentation on a topic chosen individually and approved by the instructor. Group projects may be required (depends on the enrolment). By the end of the semester each participant is required to hand in an essay of about fifteen pages. This should be either a survey paper on a research topic or a summary of current research. There will be no test for the course.

MMASc students enrolled in this class may have an alternate grading scheme which will form an addendum to the official course outline.

Prerequisite: Computer Science 3331, 3340.

Instructor

Dr. KaiZhong Zhang, 372 Middlesex College, Tel: 661-3826

Class Meetings

1:30-3:30pm Thursday, MC 320.