**CSB 352H1S – BIOINFORMATIC METHODS**

6L, 18P

**Lecturer:**

Prof. N. Provart nicholas.provart@utoronto.ca

**Prerequisite:** BIO230H1/255H1, BIO260H1/HMB 265H1

Large-scale biology projects such as the sequencing of the human genome and gene expression surveys using microarrays or RNA-seq have created a wealth of data for biologists. However, the challenge facing scientists is analyzing and even accessing these data to extract useful information pertaining to the system being studied. This course focuses on employing existing bioinformatics resources - programs and databases - to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on. Topics covered include multiple sequence alignments, transcriptome data analysis, and protein interaction networks. This course is useful to any student considering graduate school in the biological sciences, as well as students considering molecular medicine. The grading is based on lab reports, quizzes and participation.

**Syllabus**

Each 2-hour session is a hands-on tutorial/computer laboratory session. A 20-25 minute overview of the concepts behind the bioinformatic field in focus is provided as an **online streamed lecture**. Extensive use will be made of computer-based resources and learning material. Research assignments submitted as 2 formal lab reports, are based on material covered in the separate modules of Sequence Alignment, Phylogenetics / Proteins, Transcriptome Analysis (space delimited below).

No programming will be required, however, command line programs are extensively used. Students interested in learning programming and more about the theoretical underpinnings of the programs are encouraged to take CSB472H.

Lab Topic (\*quiz at start of class)

1 NCBI/Blast I

2 Blast II/Comparative Genomics

3 Multiple Sequence Alignments

4\* Phylogenetics

5 Selection Analysis

 *Reading week*

6 'Next Gen' Sequence Analysis / Metagenomics

7\* Protein motifs

8 Protein-protein interactions

9 Protein structure

10\* Transcriptome data analysis I

11 Transcriptome data analysis II

12\* Cis regulatory elements

**Grading**

Lab reports 60% (2) Due at the start of Labs 7 and 12.

Quizzes 30% (4) At the start of Labs 4, 7, 10, 12

Participation 10% (12) For work completed during each lab