

Description of the Bioinformatics Option

Members of the McGill Centre for Bioinformatics (MCB):
R. Beech, M. Blanchette, D. Bryant, K. Dewar, L. Glass, M. Hallett,
P. Harrison, R. Kearney, M. Mackey, R. Nadon, M. Stromvik.

February 1, 2005

The goal of this document is to provide an overview of the graduate option in Bioinformatics. General information regarding Bioinformatics at McGill is accessible at <http://www.mcb.mcgill.ca>.

Bioinformatics, which is the application of computer science, mathematical, statistical and engineering techniques to problems in the medical and biological sciences, extends in many directions: instrumentation and real-time control for data acquisition, the construction of large-scale software and databases for organizing and extracting meaning from the data, the design and analysis of algorithms for interpreting biological data, and the modeling and identification of cellular and subcellular functions. The rapid development of this field has been fueled by large-scale, international and inter-disciplinary projects in genomics, proteomics, and other areas of medical and pharmacological research. In turn, developments in Bioinformatics have accelerated these projects and opened up broad new paradigm shifts in biology and medicine. The shift to *in silico* research (i.e. computer-based analyses and modelling) offers enormous opportunities both intellectually and financially. Nationally and provincially, Bioinformatics has been singled out as one of the most important growth areas (see for example “La Bio-informatique au Québec: un levier essentiel du développement des bio-industries”; Conseil de la science et de la technologie, Québec), in part to produce the highly qualified personnel needed by industry and to develop the area as a focus of academic research excellence.

The intention of the Bioinformatics Option is to train graduate students to become researchers in the area, by helping them develop the necessary skills including the following:

1. strategies for experimental design (e.g., how microarray studies should be performed from initial setup to the analysis of particular datasets),
2. tools to analyze datasets (e.g., the development of software to analyze conserved sequences between species),
3. modeling techniques (e.g., using dynamical systems for protein expression),
4. tools to acquire, manage, and make accessible datasets (e.g., data generated by high-throughput genomics, proteomics, and metabolic biotechnologies),
5. integration of biological databases (e.g., construction and maintenance of biological databases), and
6. algorithms and statistics (e.g., the construction of de novo algorithms for evolutionary biology).

The focus of the Bioinformatics Option, however, is for students that are serious about incorporating Bioinformatics approaches into their research programs. Upon graduation, students will

1. be fluent in the basic concepts, language, and approaches of Bioinformatics;
2. have preliminary skills towards developing independent research programs that include the development of Bioinformatics tools;
3. know solid, relevant approaches to answering biological hypotheses via Bioinformatic approaches; and
4. understand the limitations and major open research areas in Bioinformatics.

The Bioinformatics Option will cross-train students in computer science, mathematics, engineering, biology, biochemistry, human genetics, and physiology to ensure that they have the background needed to understand Bioinformatics. For example, biochemists will understand the basic structure of how BLAST works at a level where they know how to set parameters correctly and possibly to modify the software if the need arises in their research; or mathematicians will understand the basic principles of regulatory genetics so that they can formulate good algorithms, statistics and software for developing approaches to locating regulatory elements.

The Bioinformatics Option is intended for graduate students in participating departments who have a significant Bioinformatics portion to their thesis. The program is not designed for students who may be interested in Bioinformatics, but are not actively using/developing Bioinformatics. Although there are a significant number of courses and a seminar, a large portion of the training these students receive will be motivated by their particular research problems. The courses/seminar are not alone sufficient for students to achieve all of the skills described above.

All students in the Option must be registered in one of the participating departments; their home department. The students need not be supervised by a member of the MCB or even by someone teaching within Bioinformatics Option. Upon acceptance to McGill, graduate students are responsible for submitting a completed application to the Bioinformatics Option Program Advisory Committee (PAC), detailing their background, a brief description of why they want to register in the Option, a letter of consent from their supervisor, and a letter of consent from their home department.

The PAC will review the document and make relevant recommendations. The intention is to help guide students to the appropriate courses needed to do Bioinformatics related research in their field. For example, if a student is judged to have insufficient background in the biological sciences, the PAC may recommend that the student complete one or more appropriate courses before they are allowed to join Bioinformatics Option. The PAC will also provide advice to students and supervisors about the composition of students' progress committees,, subject to their home department's regulations, to ensure that students have access to the expertise they need to help them develop their understanding of Bioinformatics and to integrate it into their research.

Seminar

The seminar, which will run weekly (1.5 hours long) throughout the fall and winter terms, will include presentations and discussion and will accomplish three goals:

1. The seminar will ensure that all the students with different backgrounds meet at regular times. The students will be required to register for the seminar for two semesters, but will be encouraged to attend for the full duration of their studies.
2. The seminar will provide a forum for Bioinformatics researchers, possibly including those from outside McGill, as well as researchers who are doing work that is closely related to Bioinformatics to present their work, which will provide students with a full picture of research in the area..
3. Ph.D. students will be required to give a full seminar regarding their research, which will prepare them to communicate with researchers outside of their field.

 student has completed an M.Sc. in Bioinformatics Option and they want to continue towards a Ph.D. in the Bioinformatics Option, they will be requested to take an additional Bioinformatics Option course (total of 3 over their studies for credit) and the seminar for at least 2 semesters (no additional credit initially).

Courses

The courses offered by the Bioinformatics Option are intended for students enrolled in the option, although exceptions can be made. The courses are meant to be truly interdisciplinary, and taught by instructors from many

departments. They are meant to provide occasions for students and researchers from different departments to discuss basic ideas, strategies, and techniques from Bioinformatics and to allow them to develop more precise criticisms of the field.

The courses do not have prerequisites, given the broad diversity of the students in the Bioinformatics Option. Instead, the courses will be geared to all students, but will also challenge them to learn material from the “other side.” However, it is realistic for every student to understand the material to a level where they can use existing tools properly and where they can learn more about the particular concepts if need be. For example, a biologist may have little problem understanding the models of gene regulation presented in the Bioinformatics: Functional Genomics course, but it will be challenged to understand normalization strategies such as d-Chip and RMA commonly used in microarray analysis.

There are also many Bioinformatics courses beyond the Bioinformatics Option that would be appropriate for students with specific backgrounds. Thus, our students will be able to master particular parts of Bioinformatics at a detailed level. For example, COMP-462, which is intended for Computer Science students, covers the advanced statistics and algorithms of BLAST. Graduate students in the Bioinformatics Option in Plant Sciences will gain greatly from taking courses in that department to learn how to design an experiment using BLAST properly and how to gather the necessary information from heterogeneous databases..

The list of (initially proposed) Bioinformatics Option Bioinformatics courses is detailed below in Section 14. A complete list of Bioinformatics courses at McGill can be found at <http://www.mcb.mcgill.ca/academics/courses.php>.

Participating Units

The following units have shown a strong interest in participating in Bioinformatics Option, but this list may change. Units denoted with an  risk are currently contributing instructors to the program.

Agriculture and Environmental Sciences:

- Department of Plant Sciences*
- Institute of Parasitology

Medicine:

- Department of Anatomy and Cell Biology
- Department of Biochemistry
- Department of Biomedical Engineering
- Department of Biostatistics and Epidemiology
- Department of Human Genetics*
- Department of Immunology and Microbiology
- Department of Pharmacology
- Department of Physiology*
- Department of Medicine

Science:

- Department of Mathematics*
- School of Computer Science*
- Department of Biology*

Other departments that may be interested:

- Department of Physics (Science)
- Department of Chemistry (Science)