# BIOCHEMISTRY 4010/5010
# Bioinformatics


Lecturers: **Andrew Roger (coordinator)**, Rm 8B4, Sir Charles Tupper Medical Building, tel: 494-2620, email: andrew.roger@dal.ca
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**Morgan Langille**, Mona Campbell Building, 1459 Le Marchant St., Faculty of Computer Science tel: 433 5094,
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**Dan Gaston**, Rm 11D4, Sir Charles Tupper Medical Building,
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**Sergio Hleap Lozano (teaching assistant)**, Rm 4233, Mona Campbell Building, 1459, Le Marchant St., email: jshleap@dal.ca


Time: Tuesday and Thursday 1:00 – 2:30 pm

Place: Tupper L10
Teaching lab 1 – Rm 4001, Rowe Bldg (Faculty of Management – see schedule for times).

Subject: This class presents methods and applications of bioinformatics, computational molecular biology, genetics and evolution. The lectures will introduce diverse topics of bioinformatics, with an emphasis on molecular evolutionary analysis. Topics covered include sequence similarity, database searching and retrieval of molecular sequences, alignment, profile analysis, gene prediction, machine learning, next-gen sequencing and phylogenetic reconstruction.

Lectures and labs: The attached schedule of lectures indicates the approximate order in which topics will be discussed in the course.

Workshops: Occasional workshops or student presentations may be organized during the term at mutually agreed upon locations and times.

References: There is no required textbook for this course. However, the following book provides a good all-round inroduction to bioinformatics and is recommended:
***Understanding Bioinformatics* by M. Zvelebil and J. O. Baum, (2008) Garland Science (Taylor and Francis Group) ISBN 0-8153-4024-9**

There are several other books at the Killam library which are relevant to parts of the course including: "Fundamentals of Molecular Evolution" (2nd edition) by Graur and Li (Sinauer Associates, 2000), Phylogenetic trees made easy by Hall (Sinauer Associates, 2001) and "Molecular evolution, a phylogenetic approach" by Page and Holmes (Blackwell Science, 1998).

Course Evaluation:

| Items | BIOC4010 | BIOC5010 |
|---|---|---|
| Examination #1 | 30% | 25% |
| Assignments | 40% | 35% |
| Graduate student project* | -- | 15% |
| Examination #2 | 30% | 25% |

*Note: Special Project is an essay written up in the format of a scientific review paper on the use of a particular bioinformatic method or tool to make inferences about evolution or biochemical/biological function. Topics will be given in class.

Other Notes:
Students may request accommodation as a result of barriers related to disability, religious obligation, or any characteristic under the Nova Scotia Human Rights Act. Students who require academic accommodation for either classroom participation or the writing of tests and exams should make their request to the Advising and Access Services Center (AASC) prior to or at the outset of the regular academic year. Please visit www.dal.ca/access for more information and to obtain the Request for Accommodation - Form A. A note taker may be required as part of a student's accommodation. There is an honorarium of $75/course/term (with some exceptions). If you are interested, please contact AASC at 494-2836 for more information. Please note that your classroom may contain specialized accessible furniture and equipment. It is important that these items remain in the classroom, untouched, so that students who require their usage will be able to participate in the class.

## Schedule of lectures/labs for BIOC 4010/5010 – Bioinformatics

| Date | Course | Instructor |
|---|---|---|
| Jan 8th | Intro. to molecular evolution and pairwise sequence alignment | Andrew Roger |
| Jan 10th | Pairwise sequence alignment and database searching | Andrew Roger |
| Jan15th | BLAST and FASTA | Andrew Roger |
| Jan17th | **Lab 1 – Database searching and homology** | Hleap / Roger |
| Jan 22nd | BLAST, FASTA, Multiple alignment | Andrew Roger |
| Jan 24th | **Lab 2 – Multiple sequence alignments** | Hleap / Roger |
| Jan 29th | Mutiple alignment, Profiles | Hleap / Roger |
| Jan 31st | Hidden Markov Models | Andrew Roger |
| Feb 5th | Genome Assembly | Morgan Langille |
| Feb 7th | **Lab 3 – Introduction to Scripting** | Hleap / Langille |
| Feb 12th | Gene Prediction | Morgan Langille |
| Feb 14th | **Lab 4 – Gene Prediction** | Hleap / Langille |
| Feb 19th | Environmental Sequencing and Metagenomics | Morgan Langille |
| Feb 21st | **Mid-term examination** | Roger / Langille |
| Feb 26th | Study break | |
| Feb 28th | Study break | |
| Mar 5th | Next-generation sequence analysis for biomedical applications | Dan Gaston |
| Mar 7th | Next-generation sequence analysis and biomedical applications 2 | Dan Gaston |
| Mar 12th | Protein Structure | Morgan Langille |
| Mar 14th | **Lab 5** | Hleap / Langille |
| Mar 19th | Introduction to Phylogenetics | Andrew Roger |
| Mar 21st | Phylogenetics 1 – distance and parsimony methods | Andrew Roger |
| Mar 26th | Phylogenetics 2 – Tree-searching/intro maximum likelihood | Andrew Roger |
| Mar 28th | **Lab 6 – Phylogenetics** | Hleap / Roger |
| April 2th | Phylogenetics 3 – maximum likelihood/Bayesian analysis | Andrew Roger |
| April 4th | Phylogenetics 4 – bootstrapping and uses. | Andrew Roger |

## Department of Biochemistry & Molecular Biology
## Policy on Plagiarism

***What is plagiarism?***

"Dalhousie University defines plagiarism as the presentation of the work of another author in such a way as to give one's reader reason to think it to be one's own. Plagiarism is a form of academic fraud."† The Department is committed to protecting honest students against the devaluation of their work by students who resort to plagiarism.

Some examples of plagiarism include (but are not restricted to):

- Submitting as your own work any material created, in whole or in part, by someone else, **including material created in collaboration with other students**, unless specifically allowed by the course instructor and credited appropriately.
- Paraphrasing extensively or copying from sources such as the Internet, journal articles, or books (including textbooks) without crediting the original author or source.
- Using another student's laboratory data, unless specifically allowed by the course instructor and credited appropriately.
- Submitting, in whole or in part, any work that has been submitted in another course, or re-submitting the same work in different years of the same course.

***How can plagiarism be detected?***

If required by the Instructor, work submitted for credit must be submitted in electronic as well as hard copy form. Submissions may be screened by one or both of the following methods:

- A pattern recognition program that compares all submissions with one another as well as submissions from previous years. Every individual has a unique pattern of writing. This program will detect submissions that are derived from a common source, even if words or phrases have been changed.
- A third-party computer-based assessment system that compares submissions against a large database including previous submissions and Internet sources.

***What are the consequences of plagiarism?***

"Plagiarism is a serious academic offence which may lead to loss of credit ['F' in a course], suspension or expulsion from the University, or even the revocation of a degree."† **At Dalhousie University, the Department is obligated to refer any cases of suspected plagiarism to the Senate Discipline Committee**, which will then conduct a hearing to evaluate the innocence or guilt of students alleged to have committed an act of plagiarism.

***How can accusations of plagiarism be avoided?***

You can avoid accusations of plagiarism by:

- Preparing all submissions independently and ensuring that they are expressed in your own unique writing style.
- Never sharing any written or electronic material with other students. You may discuss ideas with other students but you may not work with another student while preparing materials you are planning to hand in.
- Acknowledging any material paraphrased extensively or copied from sources such as the Internet, journal articles or textbooks. Paraphrasing of short phrases from the course textbook need not be acknowledged.
- Guarding all your work, both drafts and final submissions, to ensure that no one else can copy it. If you provide access to your work and someone copies it, then you may have to appear before the Senate Discipline Committee to establish that you are the original creator of the work. If you suspect that someone has taken any of your work, notify your course instructor immediately.
- Using only laboratory data that you actually collected in the lab. Altering laboratory data is not permitted. If your data are unusable, you must still report your own data along with any explanation as to why the data are unusable. You may then use data supplied by the lab instructor for analysis, but you must acknowledge such use.

† Dalhousie University Undergraduate Calendar, 2005/2006, p. 21.

**FOR ANDREW ROGER'S SECTION**

To get to lectures, problem sets, and labs during the course, the following URL is where you should go:

http://rogerlab.biochem.dal.ca

Follow the links to Teaching, then to the bioinformatics course.

Most materials there are password protected. The username/password you will need is:

Username: bioc
Password: bioinf4010