

Course Outline (W2025)

BME808: Computations in Genetic Engineering

Instructor(s)	Adam Lim [Coordinator] Office: TBA Phone: TBA Email: adam.lim@torontomu.ca Office Hours: Wednesday 11am - 12pm Virtual
Calendar Description	Discusses the theory and practice of molecular database searching and sequence alignment in genetic engineering. Covers databases and Internet access, sequence homology searching, and multiple alignment and sequence motif analysis, and protein structure and function.
Prerequisites	BME 501 and BME 532 and MTH 410
Antirequisites	None
Corerequisites	None
Compulsory Text(s):	1. Exploring Bioinformatics, A Project-Based Approach, Second Edition by Caroline St. Clair & Jonathan E. Visick Jones & Bartlett Learning 2015.
Reference Text(s):	1. Sequence and Genome Analysis, D.W. Mount, Cold Spring Harbor Laboratory Press, 2004, ISBN 978-087969712-9 Data Mining, I..H. Witten, E. Frank, M.A. Hall, Morgan Kaufmann, 2011. 2. Reproducible Bioinformatics with Python, Ken Youens-Clark, Released July 2021, Publisher(s): O'Reilly Media, Inc. ISBN: 9781098100889 3. Bioinformatics with Python Cookbook, 2nd Edition Paperback November 2018
Learning Objectives (Indicators)	<p>At the end of this course, the successful student will be able to:</p> <ol style="list-style-type: none"> 1. Apply specialized engineering knowledge to predict functional regions in genetic data, such as exon-intron borders and promoter regions. (1d) 2. Appraise the validity/reliability of bioinformatics sequence data relative to the degrees of error and limitations of sequence analysis theory and measurement. (3a) 3. Apply selection/decision-making techniques to determine the relative value of feasible alternatives or proposed solutions in a complex sequence analysis problem. (4c) 4. Design and develop simple software to perform given tasks as required by the problem, evaluate skills and tools to identify their limitations with respect to the project needs, and evaluate results using several skills and tools to determine the one that best explains reality. (5a) 5. Gain a working knowledge of the literature of sequence analysis in the field of bioinformatics and how sequences are produced, annotated and analyzed. (12b) <p>NOTE: Numbers in parentheses refer to the graduate attributes required by the Canadian Engineering Accreditation Board (CEAB).</p>

Course Organization	3.0 hours of lecture per week for 13 weeks 1.0 hours of lab per week for 12 weeks 1.0 hours of tutorial per week for 12 weeks														
Teaching Assistants	Daniel Genkin (daniel.genkin@torontomu.ca) Mukhesh Reddicherla (mukhesh.reddicherla@torontomu.ca)														
Course Evaluation	<table border="1"> <thead> <tr> <th colspan="2">Theory</th> </tr> </thead> <tbody> <tr> <td>Midterm</td> <td>25 %</td> </tr> <tr> <td>Final</td> <td>45 %</td> </tr> <tr> <th colspan="2">Laboratory</th> </tr> <tr> <td>Research Project</td> <td>10 %</td> </tr> <tr> <td>Labs/Tutorials</td> <td>20 %</td> </tr> <tr> <td>TOTAL:</td> <td>100 %</td> </tr> </tbody> </table> <p>Note: In order for a student to pass a course, a minimum overall course mark of 50% must be obtained. In addition, for courses that have both "Theory and Laboratory" components, the student must pass the Laboratory and Theory portions separately by achieving a minimum of 50% in the combined Laboratory components and 50% in the combined Theory components. Please refer to the "Course Evaluation" section above for details on the Theory and Laboratory components (if applicable).</p>	Theory		Midterm	25 %	Final	45 %	Laboratory		Research Project	10 %	Labs/Tutorials	20 %	TOTAL:	100 %
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Midterm	25 %														
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Examinations	Midterm exam in Week 8, 2.0 hours, closed book (covers Weeks 1-6 of lecture, assignment and laboratory material). Final exam, during exam period, 3.0 hours, closed book (covers all the course material).														
Other Evaluation Information	<p>Labs: From Week 2 onward.</p> <p>Participation: Based on in-class exercises and in-class presentations of recent advances in biotechnology.</p> <p>Research Project: Review and presentation of a scientific paper. The research project combines two separate components: a written component and an oral presentation component. The objective of this project is to study a specific topic in bioinformatics literature and to become familiar with the research community and history of bioinformatics. You must select a publication that presents either a specialized bioinformatics algorithm or its application. A 12 minute presentation and a two page technical report will be used to evaluate your project, as well as the technical merit and the skill with which the student communicates his or her message. Papers in (peer-reviewed) journals and conference proceedings are the main resources for this project.</p>														
Other Information	None														

Course Content

Week	Hours	Chapters / Section	Topic, description
1	3	Exploring Bioinformatics Chapters 1 2	Introduction to Bioinformatics and Computational Genomics: Structure of nucleic acids DNA RNA Role of mRNA tRNA and ribosome Gene transcription translation protein genetic code Bioinformatics Databases
2	3	Exploring Bioinformatics: Chapter 8	DNA Sequencing: Deep sequencing of clinical samples Assembly and Mapping Algorithm for determining largest overlap Next generation sequencing Methods: Sanger Shotgun 454 Illumina Solid Introduction to the Greedy Algorithm
3	3	Exploring Bioinformatics: Chapters 3 5	Sequence Alignment: Fundamentals of sequence Alignment Scoring Alignments Substitution matrices and scoring Dynamic Programming Alignment algorithms Needleman-Wunsch Algorithm Sequence similarity databases Alignment score significance: probability Longest overlap algorithm using Python
4	3	Exploring Bioinformatics: Chapters 4 5	Sequence Alignment: Smith-Waterman Algorithm Dot-Matrix method Multiple sequence alignment: Global and local sequence alignments Word or k-tuple method ClustalW BLAST Introduction to protein sequence Alignment:
5	3	Exploring Bioinformatics: Chapters 9 D. Mount: Chapter 9	Gene Prediction Part-1: Structure of genes in Prokaryotes vs. Eukaryotes Consensus sequences in Prokaryotes vs. Eukaryotes Alignment-Based Algorithms Sequence-Based Algorithm Pattern Matching Algorithm using Python Content-Based Algorithm introduction Probabilistic Algorithm introduction

			Protein sequence Alignment: Sequence Alignment using Substitution matrices Hydrophobicity matrix PAM Matrix BLOSUM matrix
6	3	Exploring Bioinformatics: Chapters 10	Gene Prediction Part-2: Content-Based Algorithm CpG Island Prediction Algorithm using Python Probabilistic Algorithm Exon-intron boundaries Hidden Markov Model (HMM) Neural Networks introduction
7	0		Study week - No class Groups assigned for Final Project
8	2	Midterm Exam	Midterm-exam
9	3	Exploring Bioinformatics: Chapter 11 D. Mount: Chapter 10 (pp 417-434)	Hidden Markov Models (HMM): Predicting Exon-Intron Boundary Setting up Viterbi matrices Hidden Markov Models Evaluation problem Hidden Markov Models Learning problem Hidden Markov Models Decoding problem
10	3	Exploring Bioinformatics: Chapter 11 D. Mount: Chapter 10 (pp 435-467)	Proteins: Primary, secondary and Tertiary Structures Protein databases Homology modeling Threading Chou-Fasman Algorithm Chou-Fasman: find alpha Chou-Fasman: find beta-strand Chou-Fasman: find beta-turn
11	3	Exploring Bioinformatics: Chapter 12 D. Mount: Chapter 8	Nucleic Acid Structure Prediction: Stem and loop structures Folded Structure Secondary Structure Nussinov-Jacobson Algorithm

12	3	Phylogenetics	Phylogenetics
13	3	Presentation	Students will present their course research project

Laboratory(L)/Tutorials(T)/Activity(A) Schedule

Week	L/T/A	Description
2	LAB 1: Exploring bioinformatics database on the internet	Students will be familiarized with key features of the bioinformatics databases.
3	LAB 2: Assembly of sequence data	Students will familiarize themselves with Python and use it to write simple bioinformatics applications. Greedy Algorithm using Python
4	LAB 3: Sequencing	Gaining experience with DNA sequencing data and software that analyzes it. Example: the human gut metagenome in NCBI trace archives.
5	LAB 4: Dynamic programming algorithm Pairwise Sequence Alignment	Students will implement the dynamic programming algorithm. Needleman-Wunsch and Smith-Waterman
6	LAB 5: Primer Design	Students will utilize their learnings of Multiple Sequence Alignment to develop primer sequences for identifying SARS-CoV-2 virus variants
9	LAB 6: CpG Algorithm	Implementation of CpG approach to finding the promoter region.
10	LAB 7: Gene Annotation	Implementation of the Pattern algorithm which is good for gene annotation in prokaryotes.

11	LAB 8: RNA Secondary Structure	Explore a web application which deals with prediction of RNA secondary structure. Also write python code for generating complement and reverse complements of nucleic acid strands.
12	LAB 9: Chou Fasman Algorithm	Python implementation and testing of Chou-Fasman algorithm
13	LAB 10: Nussinov Jacobson Algorithm	Python implementation and testing of Nussinov Jacobson algorithm

University Policies & Important Information

Students are reminded that they are required to adhere to all relevant university policies found in their online course shell in D2L and/or on [the Senate website](#)

Refer to the [Departmental FAQ page](#) for further information on common questions.

Important Resources Available at Toronto Metropolitan University

- [The Library](#) provides research [workshops](#) and individual assistance. If the University is open, there is a Research Help desk on the second floor of the library, or students can use the [Library's virtual research help service](#) to speak with a librarian.
- [Student Life and Learning Support](#) offers group-based and individual help with writing, math, study skills, and transition support, as well as [resources and checklists to support students as online learners](#).
- You can submit an [Academic Consideration Request](#) when an extenuating circumstance has occurred that has significantly impacted your ability to fulfill an academic requirement. You may always visit the [Senate website](#) and select the blue radio button on the top right hand side entitled: **Academic Consideration Request (ACR)** to submit this request.

For Extenuating Circumstances, Policy 167: Academic Consideration allows for a once per semester ACR request without supporting documentation if the absence is less than 3 days in duration and is not for a final exam/final assessment. Absences more than 3 days in duration and those that involve a final exam/final assessment, require documentation. Students must notify their instructor once a request for academic consideration is submitted. See Senate [Policy 167: Academic Consideration](#).

- If taking a remote course, familiarize yourself with the tools you will need to use for remote learning. The [Remote Learning Guide](#) for students includes guides to completing quizzes or exams in D2L Brightspace, with or without [Respondus LockDown Browser and Monitor, using D2L Brightspace](#), joining online meetings or lectures, and collaborating with the Google Suite.
- Information on Copyright for [Faculty](#) and [students](#).

Accessibility

- Similar to an [accessibility statement](#), use this section to describe your commitment to making this course accessible to students with disabilities. Improving the accessibility of your course helps minimize the need for accommodation.
- Outline any technologies used in this course and any known accessibility features or barriers (if applicable).
- Describe how a student should contact you if they discover an accessibility barrier with any course materials or technologies.

Academic Accommodation Support

Academic Accommodation Support (AAS) is the university's disability services office. AAS works directly with incoming and returning students looking for help with their academic accommodations. AAS works with any student who requires academic accommodation regardless of program or course load.

- Learn more about [Academic Accommodation Support](#).
- Learn [how to register with AAS](#).

Academic Accommodations (for students with disabilities) and Academic Consideration (for students faced with extenuating circumstances that can include short-term health issues) are governed by two different university policies. Learn more about [Academic Accommodations versus Academic Consideration and how to access each](#).

Wellbeing Support

At Toronto Metropolitan University, we recognize that things can come up throughout the term that may interfere with a student's ability to succeed in their coursework. These circumstances are outside of one's control and can have a serious impact on physical and mental well-being. Seeking help can be a challenge, especially in those times of crisis.

If you are experiencing a mental health crisis, please call 911 and go to the nearest hospital emergency room. You can also access these outside resources at anytime:

- **Distress Line:** 24/7 line for if you are in crisis, feeling suicidal or in need of emotional support (phone: 416-408-4357)
- **Good2Talk:** 24/7-hour line for postsecondary students (phone: 1-866-925-5454)
- **Keep.meSAFE:** 24/7 access to confidential support through counsellors via [My SSP app](#) or 1-844-451-9700

If non-crisis support is needed, you can access these campus resources:

- **Centre for Student Development and Counselling:** 416-979-5195 or email csdc@torontomu.ca
- **Consent Comes First - Office of Sexual Violence Support and Education:** 416-919-5000 ext 3596 or email osvse@torontomu.ca
- **Medical Centre:** call (416) 979-5070 to book an appointment

We encourage all Toronto Metropolitan University community members to access available resources to ensure support is reachable. You can find more resources available through the [Toronto Metropolitan University Mental Health and Wellbeing](#) website.