2023-2024 CSB Graduate Modules

Students enroll in CSB 1020H or CSB1021H for Fall (F) 2023, Winter (S) 2024, or Summer 2024*, depending on the session the specific module is offered. These two course codes apply to all quarter-credit (0.25 FCE) CSB modules.
***Summer courses/modules cannot be requested on ACORN until March 11, 2024.**

Please note that each quarter-credit module has a unique teaching section, and that code must be entered when requesting a specific module on ACORN.

If you want to request two modules in the same session that have the same course code (e.g. CSB1021H/F, for Fall 2023), you will need to contact the CSB Graduate Office to arrange for enrolment in a second module.

For students in graduate programs outside of CSB, any single quarter credit module may not help complete any of your graduate program coursework requirements.

Seminar and lab-based modules offered 2023-2024

Course: Foundational Discoveries in Genome Biology and Bioinformatics
Course Code: CSB 1482H/F, Teaching Section LEC 0101
Coordinator: *Professor Alan Moses*
Offered: Fall 2023 session
Weight: Half credit (0.5 FCE)
Time: Tuesdays 11 am – 1 pm
Location: St. George campus, Sidney Smith Hall, Room 2120
Enrolment: Limited to 6 graduate students (minimum 3 reserved for CSB grads)

*CSB 1482H/F is a half-credit course that takes place during the full Fall session. It is the equivalent of two modules. This course is also offered to undergraduate students as CSB 471H1S. Graduate students should NOT request this course as CSB471H1S on ACORN because it would not count toward graduate credit.

Description:
This course will focus on close reading and detailed discussion of landmark papers in genome biology and bioinformatics. Focus will be on the context of the paper, technological developments exploited (or reported) and impact on the field. Topics include: comparative, population and functional genomics, single cell genomic technologies, genome browsers, alignment and clustering algorithms. Evaluation will be focused on class discussion and presentations.

Evaluation:
Class participation (30%)
In-class presentation (35%)
Written report (35%)

Pre-requisites: Instructor approval

Module: Current Techniques in Gene Regulation
CSB1020H/F, Teaching Section LEC 0134
Instructor: *Professor Ho Sung Rhee* (hosung.rhee@utoronto.ca)
Offered: Fall 2023 session. Six classes will be scheduled between September 7th and October 20th, 2023. The first organizational meeting will be on Thursday, September 7th @ 3:00 PM (location at UTM TBA).
Schedule: TBA. The course details (e.g., schedule, classroom, syllabus) will be announced on the Quercus website. If you have questions, email hosung.rhee@utoronto.ca
Weight: One module (0.25 FCE)
Location: UTM campus, room TBA
Enrolment: Limited to 8 graduate students

Description:
This course will cover cutting-edge techniques to study transcription, epigenetics, and genome architecture. Lectures and seminars will involve presentations and discussions of contemporary topics and techniques in gene regulation. Techniques to be discussed include cell (re)programming and differentiation, CRISPR genome editing (e.g., knock in, knock out, knock down), single-cell sequencing technologies (e.g., scRNA-seq, snATAC-seq), protein-DNA interaction analysis using nuclease (e.g., CUT&Tag), and long-range chromatin interaction analysis. Students will also present recently published research articles, lead a discussion, and write a report.

Evaluation:
1st seminar presentation: 30%
2nd seminar presentation: 30%
Class participation and discussion: 20%
1st written assignment: 10%
2nd written assignment: 10%

Pre-requisites: None
Reading materials: Required readings will be primary research articles and reviews, and will be provided during class.
Website: Quercus - https://q.utoronto.ca

Module: Introduction to R
CSB1020H/F, Teaching Section LEC 0142
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),*
Fall 2023 session
Instructors:

Dr. David S. Guttman, CSB, CAGEF	david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics	calvin.mok@mail.utoronto.ca

Time:
September 13 – October 25 (7 weeks)
Wed, 1:00 - 4:00pm
Earth Sciences Centre 3087
Enrollment:
20 graduate students
Audit spaces based on availability
Weight: One module (0.25 FCE)

Course Objectives
This is a beginner's introduction to R and the Jupyter Notebook environment for individuals with no prior experience or background. Individuals who complete the course will be able to:

- Work with the Jupyter Notebook environment and navigate the R programming language.
- Understand data structures and data types.

- Import data into R and manipulate data frames.
- Transform ‘messy’ datasets into ‘tidy’ datasets.
- Make exploratory plots as well as publication-quality graphics.
- Use string searching and manipulation to clean data.
- Perform basic statistical tests and run a regression model.
- Use flow control and build branching code.

Throughout the course we’ll work with a set of data that takes us through the various steps of analysis from importing to data wrangling to statistical analysis and visualization. Each class will consist of a short introductory section followed by ‘code-along’ hands-on learning that will gradually build up the lecture’s topic(s). Students are expected to have access to a computer during class and are encouraged to ask questions while coding-along with the instructor. A homework assessment will be assigned after each class to reinforce the skills learned and a final project will test overall knowledge and application. The course materials will be provided through Quercus and lectures will be held in-person.

Course Availability
This course will be held in-person (unless otherwise determined) and will be available to graduate students in CSB and EEB. Auditor spaces will be based upon available space to postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN.
Anyone wishing to audit the course should fill out the request form at https://bit.ly/475zufA

Evaluation

Item	Note	% Mark
Completed Jupyter Notebook	7 lectures x 2% each*	14%
Homework Assignments	6 weekly assignments x 6% each	36%
Term project	Due 2 weeks after the end of the course	50%

* a 3.5% bonus (0.5% per lecture) will be awarded for submitting notebooks within 24 hours of lecture completion.

Pre-requisites**:** Access to a computer. No prior programming experience required.

Reference Material: *R for Data Science* (http://r4ds.had.co.nz/)

Syllabus

Class	Topic
1	**Introduction to R and Jupyter Notebooks**: R and Jupyter Notebook basics, best coding practices, functions and syntax, data types and structures, mathematical operations with R objects, installing R packages, getting help.
2	**How to read, write, and manipulate your data:** Importing text and Excel files, the dplyr package and functions to manipulate tabular data.
3	**Introduction to Tidy Data**: Wide versus long data formats, reshaping data with the tidyverse package.
4	**Data visualization with ggplot2**: The grammar of graphics; scatter, line, box, bar, and density plots, among other types of graphics.
5	**Data cleaning with regular expressions (RegEx):** Introduction to RegEx; inspecting, cleansing, and data wrangling using RegEx; classes, quantifiers, operators, pattern-matching, and string manipulation.
6	**Linear regressions**: Simple and multiple linear regressions, ANOVA, ANCOVA, model selection.
7	**Flow control**: for loops, conditional statements (if, while, repeat, next, and break); troubleshooting loops.

Subject to change

Module: Mass spectrometry for biological systems
CSB1021H/F, Teaching Section LEC 0137

Coordinator: *Professor Michael Phillips*
Offered: Fall 2023 session for 6 weeks from late October to December, 2023 (course meets once per week for six 3 hour sessions). Final dates and meeting room on UTM campus will be posted to Quercus.
Weight: One module (0.25 FCE)
Time: TBA
Location: UTM campus, room TBA.
Enrollment: limited to 15 students

Description:
This is a mixed lecture and seminar-based course that covers the theory and application of mass spectrometry in biological research. Initial lectures by the instructor will cover principles of mass spectrometry, chromatography, ionization and design of modern mass analyzers (quadrupole, ion trap, orbitrap, and time-of-flight). Although peptide mass spectrometry will be discussed in the context of proteomic analysis, course theory will focus on the detection of small molecules. Students will participate in discussions, give an oral presentation on one application of mass spectrometry, and submit a term paper on another. Students will acquire practical training in data analysis by working with targeted and untargeted sample data sets provided to the students.

Textbook
Students will be assigned readings from the primary literature and chapters from Martin Smith’s textbook “*Understanding Mass Spectra*”, which is available for free online in PDF form. Readings are intended to prepare students for upcoming lectures. It is therefore essential that students complete readings beforehand. The following primary literature readings have been assigned in previous years, and additional readings will be assigned during lecture.

Ricci, Fiorentino, Piccolella, D’Abrosca, Pacifico and Monaco “Structural discrimination of isomeric tetrahydrofuran lignan glucosides by tandem mass spectrometry” (2010) *Rapid Comm Mass Spec*
Cajka and Fiehn “Toward merging untargeted and targeted methods in mass spectrometry-based metabolomics and lipidomics” 2016 *Anal chem*
Ma, Li, Van den Heuvel and Claeys “Characterization of Flavone and Flavonol Aglycones by Collision-induced Dissociation Tandem Mass Spectrometry” 1997 *Rapid Comm Mass Spec*
Es-Safi, Kerhoas and Ducrot “Application of positive and negative electrospray ionization, collision-induced dissociation and tandem mass spectrometry to a study of the fragmentation of 6-hydroxyluteolin 7-O-glucoside and 7-O-glucosyl-(1-3)-glucoside” (2005) *Rapid Comm Mass Spec*

Schedule**:**
Six meetings of 3 hours **(meets every week beginning end of October and first week of December, 2023).** Weeks 1-3 consist of introductory lectures by instructor and discussion of reading assignments. Weeks 4-5 will feature students presentations and discussion. Week 6 is the writing workshop to discuss term paper drafts as well as finishing any remaining student presentations.

Date	Topic	Reading
tbd	Lecture 1: Mass spec theory and application	Smith chs. 1+2
tbd	Lecture 2: Mass spec theory and application	Smith ch 3
tbd	Lecture 3: Mass spec theory and application	Smith ch 4
tbd	Student presentations 1	
tbd	Student presentations 2	
tbd	Student presentations 3 & writing workshop	

Evaluation**:**

Students will deliver an oral presentation on one application of mass spectrometry and submit a term paper on another by end of term. A list of suggested topics will be provided, and presentation dates and papers will be assigned the first day of class. Students are expected to complete all readings assignments before the corresponding lecture and participate in all discussions. Students must attend all lectures and seminars for full participation credit. The term paper is normally on the same topic as the oral presentation, but students may choose to write on a different mass spectrometry subject if desired.

Seminar: 20 min + 60 min for discussion of the paper	40%
Participation during discussion period of oral presentations	10%
Term paper	35%
Practice data sets	10%
Attendance	5%

Pre-requisites: None. Two semesters of organic chemistry or one semester of quantitative analysis, analytical chemistry or instrumental analysis is strongly recommended.

Course delivery: This course is delivered exclusively in person on the UTM campus. Attendance at all meetings is mandatory.

Module: Fundamentals of Genomic Data Science
CSB1021H/F, Teaching Section LEC 0131

Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF)*.
Fall 2023 session
Instructors:

Dr. David S. Guttman, CSB, CAGEF	david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics	calvin.mok@mail.utoronto.ca

Dates:
November 1st – December 20th (7 weeks)
Wednesdays, 1:00 - 4:00pm
Earth Sciences Centre 3087
Enrollment:
16 graduate students
Audit spaces based on availability
Weight: One module (0.25 FCE)

Course Objectives

The rise of next-generation genomics has changed the way we think about, study, and employ genetic data, enabling applications that were, until recently, merely the stuff of science fiction. These advances have dramatically increased both the size and scope of biological datasets, and consequently, increased the need for basic computational literacy for nearly all biologists.

This course is designed to serve as an introduction to genomic data science for students who do not have a background in bioinformatics. Students in the course will learn to perform several basic genomic data analyses using Galaxy, an open, web-based platform that incorporates multiple bioinformatics tools into a friendly Graphical User Interface (GUI). Students will then learn to scale up these genomic analyses using the Unix command line to tackle larger and more complex datasets. During the course, students will learn how to:

- Use Galaxy and command line tools to process and manipulate data
- Use the Integrative Genomics Viewer to visualize genomes
- Work in a Unix terminal
- Install bioinformatics software
- Connect and work on remote servers
- Understand common genomics file formats
- Perform de novo genome assembly, reference-based genome assembly, genome annotation, variant calling, and RNA-seq data analysis.

The course will take advantage of online resources for background material, while spending class time analyzing real data sets. Students are expected to have a basic understanding of genomics and molecular biology, but no prior computational knowledge is required.

Each class will consist of a short introductory section followed by 'code-along' hands-on learning that will gradually build up the lecture's topic(s). Students are expected to have access to a computer during class and are encouraged to ask questions while coding-along with the instructor. A homework assessment will be assigned after each class to reinforce the skills learned. The course materials will be provided through Quercus and lectures will be held in-person.

Course Availability

This course will be held in-person (unless otherwise determined) and will be available to graduate students in CSB and EEB. Auditor spaces will be based upon available space to postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN.
Anyone wishing to audit the course should fill out the request form at https://bit.ly/3QbC1i7

Evaluation

Item	Note	% Mark
Homework Assignments	7 weekly assignments x 10% each	70%
Term project	Due 2 weeks after the end of the course	30%

Pre-requisites**:** Access to a computer. No prior programming experience needed.

Syllabus:

Class	**Topic**
1	Introduction, Exploring Genomic File Formats
2	Galaxy Platform: Navigation, Quality Control, De Novo Assembly, Annotation
3	Galaxy Platform: Reference Alignment, Variant Detection, RNA-Seq
4	Galaxy Platform: RNA-Seq Command Line: Navigation, File management & manipulation, Accessing remote servers
5	Command Line: Downloading & installing software, $PATH, Testing software
6	Command Line: Quality Control, De Novo Assembly, Annotation, BLAST
7	Command Line: Reference Alignment, Samtools, Variant Detection, RNA-Seq

Subject to change

Course: Computational Genomics and Bioinformatics
Course Code: CSB 1472H/S, Teaching Section LEC 0101
Coordinator: *Professor David Guttman*
Offered: Winter 2024 session
Weight: Half credit (0.5 FCE)
Time: Wednesdays 10 am – 12 pm
Location: St. George campus, Bahen Centre, room 2175
Enrolment: Limited to 7 graduate students (6 reserved for CSB grads)

*CSB1472H/S is a half-credit course that takes place during the full Winter session. It is the equivalent of two modules. Graduate students should NOT request the course using the undergraduate course code CSB472H1S, because it would not count toward graduate credit.

Description:
Recent technological advances have driven a revolution in genomics research that has had a direct impact on both fundamental research as well as direct application in nearly biological disciplines. These advances have made the generation of genomic data relatively straightforward and inexpensive; nevertheless, the data are meaningless if they cannot be properly analyzed. Computational genomics and bioinformatics are the tools we use to extract biological information from complex genomic data.

CSB1472 will teach you the fundamentals of analyzing genomic data. This course emphasizes understanding how core bioinformatic analyses work, the strengths and weaknesses of related methods, and the important parameters embedded in these analyses. CSB1472 is not an applied methods course, nor a course to for developing new bioinformatic tools, but rather a course designed to provide you with a basic understanding of the principles underlying genome analyses. We will examine the fundamentals of sequence alignment, phylogenetic analyses, genome annotation, gene prediction, and gene expression data analysis. Theoretical, applied, and statistical issues will be addressed.

Recommended text: Jonathan Pevsner, *Bioinformatics and Functional Genomics*, 3rd edition (2015)

Course: Methods in Genomics and Proteomics
Course Code: CSB 1025H/S, Teaching Section LEC 0101
Coordinator: *Dr. Pauline Wang*
Offered: Winter 2024 session
Weight: Half credit (0.50 FCE)
Time: Tuesdays 12-4 pm
Location: St. George campus, Earth Sciences Centre 4076 & labs in Lash Miller (rooms TBA).
Enrolment: Limited to 2 CSB graduate students

Students who are interested in taking this course should contact Dr. Pauline Wang at pauline.wang@utoronto.ca. The course requires instructor approval, after it is requested on ACORN.

*CSB 1025H/S is a half-credit course that takes place during the full Winter session. It is the equivalent of two modules. This course is also offered to undergraduate students as CSB 474H1S. Graduate students should NOT request this course as CSB474H1S on ACORN, because it would not count toward graduate credit.

Description:
Genomics and proteomics have revolutionized biological research. It is now theoretically possible to fully characterize the structure, organization, regulation and interaction of all genes, proteins and small bioactive molecules in an organism. CSB 1025H/S is an intensive and rigorous laboratory course that will teach students how to produce and analyze data that are central to the fields of genomics and proteomics. The course is divided into three modules, the first of which focuses on genomics, the second on transcriptomics, and the third on proteomics. Each module begins with at least two wet labs where students generate data and end with computer labs where students analyze the data. In this way students will learn how to conduct an experiment from beginning to end. Techniques taught include DNA and RNA extraction, Next Generation sequencing library construction, Illumina DNA sequencing, expression profiling using RNASeq, 2D-gel proteome analysis, mass spectrometry and associated bioinformatics analyses such as sequence analysis and assembly, and statistical analysis of gene expression and mass spectrometry data. This is an advanced laboratory and computer-based course, and assumes a strong background in molecular genetics and some prior laboratory experience.

Required Text: No required textbook. Information will be provided through lectures presented in the first wet lab and first computer lab of each module.

Evaluation: Three quizzes (15%), three lab reports (45%), lab performance (20%). Graduate students have an additional grant proposal (20%).

Prerequisite: BIO 260H1/HMB 265H1 (Genetics), BIO 255Y1/CSB 330H1/350H1 or by permission of the instructor. Recommended Preparation: BCH 311H1/CSB 349H1/MGY 311Y1

Module: Introduction to Python
CSB1021H/S, Teaching Section LEC 0140
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),* Winter 2024 session.
Instructors:

Dr. David S. Guttman, CSB, CAGEF	david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics	calvin.mok@mail.utoronto.ca

Dates:
January 11 – Feb 22 (7 weeks)
Thursdays, 1:00pm-4:00pm
Earth Sciences Centre 3087
Enrollment:
20 graduate students
Audit spaces based on availability
Weight: One module (0.25 FCE)

Course Objectives
This is a beginner's introduction to Python for data science applications. The course is intended for students with no computer science background who want to develop the skills needed to analyze their own data. Students who complete this course will be able to:

- Perform data analysis in Python using the Jupyter Notebook environment.
- Understand Python data structures and data types.
- Manipulate Python objects such as lists, data frames, and dictionaries.
- Import data into Python and transform 'messy' datasets into 'tidy' datasets.
- Use flow control to develop branching code.
- Use regular expression and string manipulation to explore and clean data.
- Make exploratory plots.

Throughout the course we'll work with a set of data that takes us through the various steps of analysis from importing to data wrangling to visualization. Each class will consist of a short introductory section followed by 'code-along' hands-on learning that will gradually build up the lecture's topic(s). Students are expected to have access to a computer during class and are encouraged to ask questions while coding-along with the instructor. A homework assessment will be assigned after each class to reinforce the skills learned and a final project will test overall knowledge and application. The course will be provided through Quercus and lectures will be held in-person.

Course Availability

This course will be held in-person (unless otherwise determined) and will be available to graduate students in CSB and EEB. Auditor spaces will be based upon available space to postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN.
Anyone wishing to audit the course should fill out the request form at https://bit.ly/3OuWcGl

Evaluation

Item	Note	% Mark
Completed Jupyter Notebook	7 lectures x 2% each*	14%
Homework Assignments	7 weekly assignments x ~5% each	36%
Term project	Due 2 weeks after the end of the course	50%

* a 3.5% bonus (0.5% per lecture) will be awarded for submitting notebooks within 24 hours of lecture completion.

Pre-requisites**:** Access to a computer and internet. No prior programming experience needed.

Reference Material**:** 2016. Severance, Charles. Python for Everybody: Exploring Data Using Python 3. http://do1.dr-chuck.com/pythonlearn/EN_us/pythonlearn.pdf

Course Tools**:** University of Toronto Jupyter Hub, DataCamp, Zoom.

Syllabus

Class	Topic
1	**Intro to Python and Jupyter Notebooks:** Basics about Python, using Jupyter Notebooks, how to run Python code, as well as an introduction to Python variables, functions, modules, best coding practices, data types, missing data, code debugging and getting help.
2	**Python data structures, Numpy and Pandas:** List, Dictionaries, Tuples, Sets, Series, mathematical operations with Python objects, Introduction to NumPy and Pandas.
3	**How to Read, Write, and Manipulate Your Data:** The wide and long formats, reading in data, data wrangling with Pandas, and writing data.
4	**Data visualization with seaborn:** The grammar of graphics; scatter, line, box, bar, and density plots, among other types of graphics.
5	**Flow control:** Flow control, for loops, Conditionals
6	**Regular Expressions:** Classes, quantifiers, operators, pattern-matching, String manipulation.
7	**User-defined functions:** Defining a function, best practices in user-defined functions, and web scraping

Subject to change

Module: Structural Biology in Drug Development & Biotechnology
CSB1021H/S, Teaching Section LEC 0144

Instructor: *Professor Mark Currie* (mark.currie@utoronto.ca)
Offered: Winter 2024 (nine weeks, starting Tuesday, January 9th)
Schedule: 6:00 PM – 9:00 PM, Tuesdays
Weight: One module (0.25 FCE)
Location: UTM campus, room TBA
Enrolment: Limited to 12 graduate students

Description:

Biological, disease, and drug mechanisms are all determined by the three-dimensional arrangement of atoms within biological macromolecules. Therefore, knowledge of molecular structure is fundamental to protein engineering and the development of new therapeutics and vaccines. This course will cover the application of structural biology methods to drug development and biotechnology. Students will be introduced to the modern tools of protein structure determination including Cryo electron microscopy, X-ray crystallography, and NMR through lectures and tutorials. Lectures will focus on theory, techniques, and the advantages and limitations of each method. The applications of these methods to the pharmaceutical and biotechnology industries including protein engineering, target selection and drugability, lead identification and optimization, rational drug design, and drug mechanism of action will be explored through student presentations and discussions.

Evaluation:

Presentations: 30%
Participation: 25%
Report: 20%
Tutorials: 15%
Quizzes: 10%

Module: Advanced Bayesian statistics for genomics
CSB 1021H/S, Teaching Section LEC 0150

Coordinator: *Professor Guillaume Filion*
Offered: Winter 2024 session, in January and February for a total of six meetings.
Weight: One module (0.25 FCE)
Time: TBA
Location: Remote
Enrolment: Limited to 10 students

Description:

This course is an in-depth introduction to Bayesian inference with the variational inference method using the programming language Pyro. It covers the basic theory of variational inference and consists of practical applications to concrete problems (vaccine efficiency, mutation rates, single-cell transcriptomics). The content consists of video lectures explaining how to use Pyro and Pytorch, and in-person lectures with laptop computers to work on practical applications. This course requires some familiarity with statistics and working knowledge of the Python programming language.

Evaluation:

The evaluation consists of a take-home exam to solve problems similar to those addressed in class.

Pre-requisites for module: No particular classes are required, but the students should be familiar with statistics and standard distributions (Poisson, binomial normal, etc.) and have working knowledge of the Python programming language.
Reading materials: None
Website: TBA

Module: Theoretical and Applied Topics in Data Visualization for Genome Biology

CSB 1020H/S, Teaching Section LEC 0133

Coordinator: *Professor Nicholas Provart*
Offered: Winter 2024 session, in January and February for a total of six meetings.
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus, Room TBA
Enrolment: Limited to 10 students

Description:
The past decade has seen a vast increase in the amount of data available to biologists, driven by the dramatic decrease in cost and concomitant rise in throughput of various next-generation sequencing technologies. While access to data is no longer limiting, manipulating and interpreting those data has become a bottleneck. One important aspect of interpreting data is data visualization. This graduate course module will provide a theoretical perspective on data visualization for biological applications, along with a hands-on component to provide practical training for students. The format of the course will be six 2-hour modules, each consisting of a short theory lecture of around 40 minutes followed by a discussion of 2-3 assigned papers/online resources per week, with students taking turns to present the papers/resources. The last 30-45 minutes of each module will encompass a hands-on session where students will use various data visualization packages (such as Tableau, D3, Plotly, ggplot, etc.) to explore biological data sets.

Evaluation:
20% - Contribution to discussion
20% - Presentation of assigned paper or online data resource (15-minutes)
60% - Project

The project will be to tell a story with data. You may use any technique you like (e.g., poster, interactive tool, video, etc.). It should combine data analysis, data visualization and a narrative to contextualize the findings. It should be accessible and engaging to anyone with an interest in biology.

Pre-requisites for module: Familiarity with molecular biology
Reading materials: TBA
Website: TBA

Module: Current topics in evolutionary medicine

CSB 1020H/S, Teaching Section LEC 0149

Coordinator: *Professor Maxwell Shafer*
Offered: Winter 2024 session, in January and February for a total of six meetings.
Weight: One module (0.25 FCE)
Time: TBA
Location: Room TBA
Enrolment: Limited to 10 students

Description:
Evolutionary medicine is the application of insights and knowledge from the fields of evolution and ecology to biomedical research. For example, a better understand of why humans are susceptible to certain diseases can be gained by studying our evolutionary history, and novel treatments can be found through examination of 'extreme' physiological adaptations across the tree of life. This course will cover a wide range of topics including research in non-model organisms, neuroscience and behavior, cell biology and cancer, host/pathogen interactions, and human biology, with a focus on emerging methodologies and evolutionary principles. Students will engage with each other and the instructor through presentation and discussion of current primary literature and preparation of a written component.

Evaluation:
Each session will be devoted to one of the above topics, with 1-2 students (depending on enrollment) summarizing primary literature per session. Additionally, each student will write a short Letter of Intent (LOI) proposing a research project related to their presentation topic due at the end of the module.
40% Presentation (one presentation per student)
40% Written component
20% Participation in discussions

Pre-requisites for module: None
Reading materials: Primary literature will be disseminated during an organizational meeting.
Website: TBA

Module: Data Visualization and Advanced Graphics in R

CSB1020H/S, Teaching Section LEC 0141

Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),*
Winter 2024 session.
Instructors:

Dr. David S. Guttman, CSB, CAGEF	david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics	calvin.mok@mail.utoronto.ca

Dates:
March 7 – April 11, 2024 (6 weeks)
Thursdays, 1:00pm-4:00pm
Earth Sciences Centre 3087
Enrollment:
16 graduate students
Audit spaces based on availability
Weight: One module (0.25 FCE)

Course Objectives
This is an intermediate to advanced level introduction to R and the packages associated with visualizing large or complex data sets. Participants are strongly encouraged to have prior experience in R (i.e., Introduction to R, CSB1020). Individuals who complete the course will be able to manipulate and prepare large datasets to produce publication-quality graphics. The goal of this course is to introduce the proper use and interpretation of simple, popular, and complex data visualizations. Topics will include

- A deep dive into building relatable figures with the ggplot package.
- Analysis and visualization of large datasets from differential expression experiments.
- Popular visualization methods and packages for genes and genome analysis.

Each class will consist of a short introductory section followed by 'code-along' hands-on learning that will gradually build up the lecture's topic(s). Students are expected to have access to a computer during class and are encouraged to ask questions while coding along with the instructor. A homework assessment will be assigned after each class to reinforce the skills learned. The course materials will be provided through Quercus and class lectures will be held in-person while using the University of Toronto JupyterHub for lecture and assessment.

Course Availability
This course will be held in-person (unless otherwise determined) and will be available to graduate students in CSB and EEB. Auditor spaces will be based upon available space to postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN.

Anyone wishing to audit the course should fill out the request form at https://bit.ly/476fyJd

Evaluation

Item	Note	% Mark
Homework Assignments	6 weekly assignments ranging from 15-20% each	100%

Pre-requisites**:** CSB1020 *Introduction to R* (or equivalent). Access to a computer.

Reference Material: *R for Data Science* (http://r4ds.had.co.nz/)

Syllabus

Class	Topic
1	**Re-Introduction to R, RStudio, and Jupyter Notebooks**: R and RStudio basics, setting up R for Jupyter Notebooks, installing R packages, best practices for producing graphs, best coding practices, functions and syntax, data types and structures, importing and exporting data, tidy data formatting, saving data and plots.
2	**The grammar of graphics with ggplot:** box-, violin-, beeswarm-, and jitter plots, combining layers in ggplot, kernel density plots, and parallel coordinate plots.
3	**Finishing touches for ggplot**: themes, aesthetics, color palettes, mathematic annotation with expression() and bquote(), scaling data, error bars, handling outliers, and multi-panel plots.
4	**Visualizing differential expression data**: heatmaps, volcano plots, side-by-side boxplots, dotplots, and Upset plots.
5	**Common visualization methods for data classification/partitioning:** clustering, principal component analysis, multidimensional scaling, and linear projection with t-SNE plots and UMAP.
6	**Simplifying Genes and genomes:** sequence logos, phylogenetic trees, network graphs, Manhattan plots, Gviz, GenomeGraphs, gene model plots and other helpful packages.

Subject to change

Course: Advanced Microscopy and Imaging
CSB 1018H/S (Summer 2024*), Teaching Section LEC 0101
Coordinator*: Professor Rene Harrison*
Offered: Summer 2024* session, likely between May and June 2024 for eight weeks (plus a final exam)
Weight: Half credit (0.50 FCE)
Time: TBA
Location: UTSC campus, room TBA. Lectures could be in hybrid format for off-campus students, but weekly microscope demos and practicums will be held in person at UTSC and are mandatory.
Enrolment: 24 students

Description:
This graduate course will cover theory and practical demonstrations of current light, fluorescent and electron microscopy. The first four weeks of classes will have lectures and demonstrations on brightfield, epifluorescent, confocal and scanning and transmission microscopy. As well, consideration will be given to specimen preparation. Student presentations will occur in the remaining three weeks of formal classes.

Course Schedule and Structure:
Each meeting is 3 hours, some sessions may not go that long. Lectures are for 1-2 hours in most cases and then, if relevant, there is a demonstration of the particular equipment. By appointment, students arrange for training of specific equipment.

Tentative Grading Scheme:

Participation	10%
Seminar	25%
Microscopy Technical Sheet	10%
Practicums (4)	20%
Final Exam	35%

	100%

Pre-requisites: None
Reading materials: TBA
Website: Quercus

***Summer courses cannot be requested on ACORN until March 11, 2024.**

Other courses that may be of interest to Cell and Systems Biology graduate students, instructed by CSB Graduate Faculty

PHY2711HS - Biophysical Techniques
Co-Instructor: Prof. Joshua Milstein
Offered: Winter 2024 session
https://www.physics.utoronto.ca/graduate/graduate-courses/biophysical-techniques/
Weight: 0.5 FCE