2022-2023 CSB Graduate Modules

Students enroll in CSB 1020H or CSB1021H for Fall (F) 2022, Winter (S) 2023, or Summer 2023*, 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 13, 2023.**

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 2022), you may 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 requirements.

Seminar and lab-based modules offered 2022-2023

Module: Introduction to R
CSB1020H/F, Teaching Section LEC 0142

Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF)*,
Fall 2022 session
Instructors:
Dr. David S. Guttman, CSB, CAGEF david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics calvin.mok@mail.utoronto.ca
Time:
September 7 – October 19 (7 weeks)
Wednesdays, 1 pm – 4 pm in Earth Sciences 3087
Enrollment:
16 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://bityl.co/DXRg

Evaluation

Item	Note	% Mark
Completed Jupyter Notebook	7 lectures x 2% each*	14%
Homework Assignments	6 weekly assignments x 9% each	54%
Term project	Due 2 weeks after the end of the course	32%

* a 4.9% bonus (0.7% per lecture) will be awarded for submitting notebooks on the day of lecture.
Pre-requisites**:** Access to a computer. No prior programming experience needed.

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: Plant Phenotyping, Phenomics and Monitoring Vegetation Dynamics to better understand plant adaptation to drought and heat

CSB1021H/F, Teaching Section LEC 0146

Instructor: *Professor I. Ensminger* (ingo.ensminger@utoronto.ca)
Offered: 2022 Fall (middle of term) for six weeks. Wednesday mornings (Time TBD). Coordination meeting and assignment of topics during first week of October, room and time TBD. Coordination meeting will be online, if majority of students prefers an online format during the coordination meeting, the entire module can be delivered as a synchronous course via zoom.
Enrolment: Limited to 10 students
Weight: One module (0.25 FCE)

Description: Climate change is impacting the yield of cultivated plants for food production, is impacting growth of trees and is causing large-scale tree mortality putting natural and managed forests at the risk of extinction. This seminar-based grad module will focus on high throughput plant phenotyping and phenomics approaches and methods for monitoring vegetation dynamics, which are aimed at assessing morpho-physiological and physico-chemical traits to understand heat and drought tolerance of plants. The use of phenotyping and phenomics approaches will help understand the performance of a genotype or a species in a given environment.

Evaluation: Student evaluation is based on i) Seminar - A PowerPoint style presentation (each student) based on a primary research paper. Presentation dates and papers will be assigned at the coordination meeting; students are expected to read all papers presented during the module and participate in all discussions. ii) News & Views paper - Students will be required to write a “news and views” paper on their presentation topic or another of their choosing. iii) Participation and contribution to discussion

Seminar: 30 min presentation and 30 min for discussion	40%
News & Views paper:	40%
Participation in Discussion: 2 students assigned as discussion leaders	20%

Seminar Grading:

- Verbal clarity and understanding of subject matter (10%)
- Critical thinking and ability to answer questions (10%)
- Slide quality and effectiveness (10%)
- Scientific content and appropriateness (10%)

Content and Format
Seminars and Papers should not focus on the students own work. Critical reviews are encouraged, but comments must be accurate and well-reasoned. In general, seminar presentations and papers should have three components:

- a short overview of the background of the reviewed paper
- a critical data-based review of the key findings
- a brief summary of the significance of the paper

*The seminar must offer more than a summary of what was stated in the original article. For example, it might provide a more in-depth explanation of a new technique used in the paper, important caveats or interpretations that the author did not mention, or a distinct interpretation of the results in the context of work that the author did not discuss (e.g., important findings published in the last couple of months). Focus should be on the most important results – there is rarely reason to discuss every figure.
*Seminars and papers must be concise. The length of the paper is limited to about 1500 words. References are limited to approximately 7.
*Papers should be written in a style that is understandable to all participants in the course.
*Avoid using jargon and unnecessary abbreviations.
*Titles should be informative; no word play.
*The paper can use up to two schematic or explanatory figures. The figure caption must appear in the main document, after the references. Do not duplicate figures that were in the reviewed paper –links to any figures you cite can be placed in the paper. In the text, refer to the cited figures with the author's name, e.g., "(Author et al., Figure 1A)".
Include a title page in your paper and include: Course title, citation of article being reviewed, author (student) affiliation (university/research institute etc.; for graduate students, the affiliation should be listed as the Graduate Program or Department), author's contact information (address, phone, and email address), abbreviated title, keywords (a minimum of six), and acknowledgments (optional).
Pre-requisites: None
Reading materials: TBD at the beginning of the module
Website: Will use Quercus

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

CSB 1020H/F, Teaching Section LEC 0133

Coordinators: *Professor Nicholas Provart and Dr. Jamie Waese*
Offered: Fall 2022 session, beginning late October for a total of six meetings.
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus, Earth Sciences Centre, 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: Fundamentals of Genomic Data Science
CSB1021H/F, Teaching Section LEC 0131

Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF)*.
Fall 2022 session
Instructors:

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

Dates:
October 26 – December 7 (7 weeks)
Wednesdays, 1 pm - 4 pm
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://bityl.co/DXRY

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 2023 session
Weight: Half credit (0.5 FCE)
Time: Wednesdays 10 am – 12 pm
Location: St. George campus, University College, Room 87
Enrolment: Limited to 8 graduate students (minimum 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.

The material is presented as an inverted course. Lectures are pre-recorded and available prior to class. Class time is devoted to review of the lecture material, discussion of the primary literature related to the course material, and hands-on analysis laboratories.

Recommended text: Zvelebil & Baum 2008 Understanding Bioinformatics. Garland Science, New York.

Course: Methods in Genomics and Proteomics
Course Code: CSB 1025H/S, Teaching Section LEC 0101
Coordinator: *Dr. Pauline Wang*
Offered: Winter 2023 session
Weight: Half credit (0.50 FCE)
Time: Tuesdays 12-4 pm
Location: St. George campus, Earth Sciences Centre Room 4076 & Ramsay Wright 107.
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

Course: Foundational Discoveries in Genome Biology and Bioinformatics
Course Code: CSB 1482H/S, Teaching Section LEC 0101
Coordinator: *Professor Alan Moses*
Offered: Winter 2023 session
Weight: Half credit (0.5 FCE)
Time: Thursdays 3 pm – 5 pm
Location: St. George campus, Earth Sciences Centre, Room 3087
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 Winter 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: Human Genomics
CSB1021H/S, Teaching Section LEC 0108
Instructor: *Professor Tim Westwood*
Offered: Start date - January 9, 2023
End date: February 17, 2023 (final graduate presentations may be given the week of Feb. 20)
Weight: One module (0.25 FCE)
Enrollment limitations: 3 students (possibly 1 or 2 more, based on availability)
Schedule:
UTM MN3170
(Monday 9:00 AM - 11:00 AM – this lecture will be recorded and not be held in person so students can attend virtually)
Tuesday 1:00 PM - 3:00 PM (in person)
Note - This course will be offered at the UTM campus in parallel with BIO477.

Description of the module:
This course examines the biology of the human genome. Topics include: the human genome project, regulation of the human transcriptome, genome wide association studies, pharmacogenomics, high throughput sequencing technologies. Lectures and seminars will also involve presentation and discussion of recently published research articles.

Evaluation:

Assignment 1	5 %
Assignment 2	5 %
Oral Presentation	15 %
Written questions (2 x 2.5%)	5 %
In class quizzes (2 x 2.5%)	5%
Term project	30 %
Final Exam (open book)	30%
Participation	5 %
	100 %

Pre-requisites for module:
Third year level Molecular Biology Course.
Exclusion: BIO477H

Reading materials: Assigned Chapters from- Molecular Biology of the Cell, 7th ed. (2022). Alberts et al.
Assigned articles and reviews.

Website: There will be a Quercus site for this course (i.e. associated with BIO477 course site at the UTM campus)

Module: Introduction to Python
CSB1021H/S, Teaching Section LEC 0140

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

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

Dates:
January 10 – Feb 17 (7 weeks)
Tuesdays, 10 am - 1 pm
Enrollment:
16 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://bityl.co/DdBX

Evaluation

Item	Note	% Mark
Completed Jupyter Notebook	7 lectures x 2% each*	14%
Homework Assignments	6 weekly assignments x 9% each	54%
Term project	Due 2 weeks after the end of the course	32%

* a 4.9% bonus (0.7% per lecture) will be awarded for submitting notebooks on the day of lecture.

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 plotnine:** 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 context managers

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 2023 (nine weeks, January 10th – March 14th, 2023)
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: Molecular Biology of Cancer
CSB1020H/S, Teaching Section LEC 0109

Instructor: *Professor Tim Westwood*
Offered: Start date: Feb. 27, 2023
End date: April 10, 2023 (plus final exam in exam period). Final graduate presentations may be given the week of April 10.
Weight: One module (0.25 FCE)
Enrollment limitations: 3 students
Schedule:
UTM MN3170
(Monday 9:00 AM - 11:00 AM – this lecture will be recorded and not be held in person so students can attend virtually)
Tuesday 1:00 PM - 3:00 PM (in person)
Note - This course will be offered at the UTM campus in parallel with BIO477.

Description:
This course examines the molecular and genetic basis of Cancer including the role of oncogenes, tumor suppressor genes and cell cycle regulating proteins in the development of this disease. Functional genomics approaches to understanding the mechanisms of cancer will also included as well as personalized genomics. Lectures and seminars will also involve presentation and discussion of recently published research articles.

Evaluation:

Assignment 1	5 %
Assignment 2	5 %
Oral Presentation	15 %
Written questions (2 x 2.5%)	5 %
In class quizzes (2 x 2.5%)	5%
Term project	30 %
Final Exam (open book) Date TBA	30%
Participation	5 %
	100 %

Pre-requisites: Third year level Molecular Biology Course. Exclusion: BIO477H

Reading materials: Assigned Chapters from- Weinberg, R. Biology of Cancer, 2nd ed. (2013). Assigned articles and reviews.

Website: There will be a Quercus site for this course (i.e. associated with BIO477 course site at the UTM campus)

Module: Topics in Cell and Developmental Biology: Biology of Adherens Junctions
CSB 1020H/S, Teaching Section LEC 0145

Coordinator: *Professor Ritu Sarpal*
Offered: Winter 2023 session. The module will begin with an organizational meeting at the end of February, followed by six weeks of seminars from March to April.
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus - Ramsay Wright Building, Room TBA. Could be online depending on circumstances.
Enrolment: Limited to 8 students

Description:
Understanding how epithelial cells stick together to form tissues and organs, how they withstand mechanical forces, and how the loss of this adhesion leads to diseases such as cancer and its metastasis, are important fundamental questions in biology with significant implications for human health. Adherens junctions (AJs) are known to be dynamic plasma-membrane structures that mediate cell-cell adhesion and promote tissue integrity. In this course, we will discuss research articles to understand how AJs facilitate multicellular development and how they impact disease.

Evaluation:
Two Seminars: 60% (2 X 30%)
Participation in discussions: 20%
Written report: 20%

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 2023 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 (6 weeks)
Tuesdays, 10 am - 1 pm in Earth Sciences 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://bityl.co/DdBs

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

Module: Cell Biology of Gastrulation
CSB 1020H/S (Summer 2023*), Teaching Section LEC 0107

Coordinators*: Professors Ashley Bruce & Rudi Winklbauer*
Offered: Summer 2023* session, likely between May and June 2023 for six weeks (plus an organizational meeting in May).
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus, Ramsay Wright Building, room TBA
Enrolment: Limited to 8 students

Description:
Gastrulation in different animals, including invertebrates and vertebrates, is used to illustrate biological processes and to discuss basic concepts in animal development. This course will explore cell behaviours that occur during gastrulation, such as invagination, intercalation, migration, spreading and tissue rearrangement.

Evaluation (subject to change)
- 20% seminar 1 (presentation per student)
- 20% seminar 2 (presentation per student)
- 40% final presentation (group project but marked individually)
- 20% participation in discussion

Pre-requisites for module: Some background in developmental biology as well as a strong interest in the topic.

Reading materials: Primary research articles and 1-2 reviews - TBD

***Summer courses cannot be requested on ACORN until March 13, 2023.**