2025-2026 CSB Graduate Modules

Students enroll in CSB 1020H or CSB1021H for Fall (F) 2025, Winter (S) 2026, or Summer 2026*, 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 mid-March, 2026.**

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.

In very rare cases where a student wants to request two modules in the same session that have the same course code (e.g. CSB1021H/F, for Fall 2025), 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 2025-2026

Course: Foundational Discoveries in Genome Biology and Bioinformatics
Course Code: CSB 1482H/F, Teaching Section LEC 0101
Coordinator: *Professor Alan Moses*
Offered: Fall 2025 session
Weight: Half credit (0.5 FCE)
Time: Tuesdays 11 am – 1 pm
Location: St. George campus, AP-120 (Anthropology Building)
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: Introduction to R
CSB1020H/F, Teaching Section LEC 0142
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),*
Fall 2025 session
Instructors:
Dr. David S. Guttman, CSB, CAGEF david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics calvin.mok@mail.utoronto.ca
Time**:**
Tuesday, September 2 – Tuesday, October 14 (7 weeks)
1:00 - 4:00 pm
Earth Sciences Centre 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 RStudio and Markdown 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 using the University of Toronto JupyterHub and its RStudio server.

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 and EEB 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://forms.gle/Evc6E6cYtrw4bZBKA

Evaluation

Item	Note	% Mark
Completed R Markdown 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, RStudio and R Markdown Notebooks**: R and R Markdown 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 2025 session, tentatively scheduled for 6 weeks from late September to November, 2025 (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: 9 am – 12 pm (tentative)
Location: UTM campus, room TBA. Check Quercus for links.
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). Course material will focus on the detection of small molecules, although peptide mass spectrometry will also be discussed in the context of proteomic analysis. 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. Free software will be available for analysis of data files, and students will utilize online platforms for statistical analysis of processed data sets.

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 **(every week beginning late September through the first week of November, 2025).** Week 1-3 consist of introductory lectures by instructor and discussion of reading assignments. Week 4-5 will feature students presentations and discussion. Week 6 is a writing workshop to discuss term paper drafts as well as finishing any remaining student presentations. Preliminary dates are listed below (to be confirmed prior to start date in September).

Date	Topic	Reading
Sep 22	Lecture 1: Mass spec theory and application	Smith chs. 1+2
Sep 29	Lecture 2: Mass spec theory and application	Smith ch 3
Oct 6	Lecture 3: Mass spec theory and application	Smith ch 4
Oct 20	Student presentations 1	
Oct 27	Student presentations 2	
Nov 3	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 on a different topic than the oral presentation. Students must write and speak on topics not directly related to their thesis work.

Seminar: 20 min oral presentation + 20 min. discussion	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: Plant Bioinformatics
CSB1021H/S, Teaching Section LEC 0139
Coordinator: *Professor Nicholas Provart*
Offered: Fall 2025, from mid-October to late November
Weight: One module (0.25 FCE)
Time: TBA
Location: Earth Sciences Centre. St. George campus (room TBA)
Enrollment: Limit of 8 students

The past 15 years have been exciting ones in plant biology. Hundreds of plant genomes have been sequenced, RNA-seq has enabled transcriptome-wide expression profiling, and a proliferation of "-seq"-based methods has permitted protein-protein and protein-DNA interactions to be determined cheaply and in a high-throughput manner. These data sets in turn allow us to generate hypotheses at the click of a mouse. For instance, knowing where and when a gene is expressed can help us narrow down the phenotypic search space when we don't see a phenotype in a gene mutant under "normal" growth conditions. Coexpression analyses and association networks can provide high-quality candidate genes involved in a biological process of interest. Using Gene Ontology enrichment analysis and pathway visualization tools can help us make sense of our own 'omics experiments and answer the question "what processes/pathways are being perturbed in our mutant of interest?"

Structure: each of the 6 classes will draw on material from Prof. Provart's two Plant Bioinformatics courses running on Coursera.org - Plant Bioinformatics and the Plant Bioinformatics Capstone. Tools explored will include those listed below. We expect to cover around 2 “modules” (in the Courserian sense) per class, with the classes towards the end taken up with capstone presentations.

Module 1: GENOMIC DBs / PRECOMPUTED GENE TREES / PROTEIN TOOLS. Araport, TAIR, Gramene, EnsemblPlants Compara, PLAZA; SUBA4 and Cell eFP Browser, 1001 Genomes Browser
Module 2: EXPRESSION TOOLS. eFP Browser / eFP-Seq Browser, Araport, Genevestigator, TravaDB, NCBI Genome Data Viewer for exploring RNA-seq data for many plant species other than Arabidopsis, MPSS database for small RNAs
Module 3: COEXPRESSION TOOLS. ATTED II, Expression Angler, AraNet, AtCAST2
Module 4: PROMOTER ANALYSIS. Cistome, Athena, ePlant
Module 5: GO ENRICHMENT ANALYSIS AND PATHWAY VIZUALIZATION. AgriGO, AmiGO, Classification SuperViewer, TAIR, g:profiler, AraCyc, MapMan (optional: Plant Reactome)
Module 6: NETWORK EXPLORATION. Arabidopsis Interactions Viewer 2, ePlant, TF2Network, Virtual Plant, GeneMANIA

Grading will be based on participation (20%), a tools presentation (20%), a written report (capstone paper; 35%), and a final presentation (25%).

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 2025 session
Instructors:
Dr. David S. Guttman, CSB, CAGEF david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics calvin.mok@mail.utoronto.ca
Dates:
Tuesday, October 28th – Tuesday, December 9th 2025 (7 weeks)
10:00 am - 1:00 pm
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 and EEB 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://forms.gle/EG992rHreFjmdguBA

Evaluation

Item	Note	% Mark
Homework Assignments	7 weekly assignments x 9% each	63%
Term project	Due 2 weeks after the end of the course	37%

Pre-requisites**:** Access to a modern laptop (no more than 3 years old, if possible). 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 2026 session
Weight: Half credit (0.5 FCE)
Time: Wednesdays 11 am – 1 pm
Location: St. George campus, Bahen Centre, room 2155
Enrolment: Limited to 6 graduate students (at least 4 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 2026 session
Weight: Half credit (0.50 FCE)
Time: Tuesdays 12 - 4 pm
Location: St. George campus, Earth Sciences Centre, room 4076.
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 2026 session.
Instructors:
Dr. David S. Guttman, CSB, CAGEF — david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics — calvin.mok@mail.utoronto.ca
Dates:
January 6 – Feb 17 (7 weeks)
Tuesdays, 10:00 am - 1:00 pm
Earth Sciences Centre 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 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 and EEB 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://forms.gle/XWnGtgbwvJFdwQ5RA

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: Current Topics in Systems Neuroscience
CSB1020H/S LEC0152
Coordinator: Dr. Qian Lin (neuroqian.lin@utoronto.ca)
Offered: Winter 2026 session, starting in January or February
Weight: One module (0.25 FCE)
Schedule: TBA
Location: St. George campus, Ramsay Wright Building, Room TBA (or online)
Enrolment: Limited to 10 graduate students

Description:
How do neurons cooperate and coordinate to produce flexible and adaptive behaviors? Using various animal models, this course aims to provide quantitative and causal links between neural circuits/networks and perception, behavior, and cognition at the systems level. Through presentation and writing assignment, students will learn about the popular animal models with simpler brains (such as fly, zebrafish, rodents, and primates), and interpret the neural mechanisms from multiple perspectives, to acquire a quantitative understanding. Particularly, this course will emphasize interdisciplinary technology, such as large-scale optical neural recording and advanced computational tools. Students will take actively roles, present recently published research articles, participate in discussions, and write a report.

Evaluation:
Class participation and discussion: 20%
Seminar presentation: 30%
Writing assignment #1: 20%
Writing assignment #2: 30%

Pre-requisites: None
Reading materials: Required readings will be primary research articles and reviews, and will be provided during class.

Module: Neuroscience of Behavioral Control and Methodology
CSB1021H/F, Teaching Section LEC 0153
Instructor*: Professor J. Fraigne*
Offered: Winter 2026 session
Weight: One module (0.25 FCE)
Time: March and April, dates and times TBA
Location: St. George campus, Ramsay Wright Building, Room TBA
Enrolment: Limited to 6 students
Description:
This course aims to review the latest neuroscience methods and how they can be used to reveal how the nervous system controls behaviours such as sleep, daily rhythms, breathing,

motivation and movement. Part of the course is focused on describing methodology such as optogenetics, chemogenetics, magnetogenetics, large-scale population dynamics, genetically-encoded fluorescent sensors, and circuit-mapping transcriptomic. The other part of the course will focus on the function of cells, neurotransmitter systems, neural circuits, organs and the whole organism level to control behavioural states.

Evaluation:
Students will present two seminars based on primary research articles, one from each aspect of the course (i.e., Method and Behavioral control). They will write one brief research proposal related to their own work 1) using methodologies discussed in the course, and 2) focusing on an aspect of behavioral control. Students will also participate in the discussion. Seminars and discussions will focus on issues raised in a selection of primary research papers depending on students' interests.

Seminar = 50% (two seminars @ 25% each)
Proposal = 30%
Discussion/Participation = 20%

Prerequisites: None
Reading Materials: Primary research paper selected by Prof. Fraigne and based on the interests of the participating students.
Website: Quercus

Module: Protein homeostasis in regulating plant development and stress response
CSB1020H/S, Teaching Section LEC 0121
Coordinator*: R. Zhao*
Offered: Winter 2026 session (6 weeks, 2h/week)
Weight: One module (0.25 FCE)
Time: TBA
Location: UTSC campus, Room TBA
Enrolment: Limited to 8 students

Description: Plant development and stress response pathways often depend on protein functions that are tightly regulated at post-translational level. In this seminar course, students will investigate particularly how regulated protein folding, trafficking and degradation impact plants under normal and stress conditions. The presentation and discussion will be based on selected high impact and recent primary research papers. Students need to read all selected papers, submit 2-3 critical questions/per paper in advance and participate in the discussion. A final written proposal following his/her presentation is required.

Schedule:
2h/week; 6 weeks
Weeks 1-2: Introductory lecture and choice of primary literature.
Weeks 3-6: Students presentations and discussion.
Week 6: Summary and discussion of final proposal writing.

Evaluation:

Seminar	40%
2-3 Critical Questions	15%
Contribution to the Discussion	15%
Proposal	30%

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 2026 session.
Instructors:
Dr. David S. Guttman, CSB, CAGEF david.guttman@utoronto.ca
Dr. Calvin Mok, CAGEF Bioinformatics calvin.mok@mail.utoronto.ca
Dates:
March 3 – April 14, 2026 (6 lectures)
Tuesdays, 10:00 am - 1:00 pm
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 to run an RStudio server for 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 and EEB 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://forms.gle/iUGQxfgzXFm7yH3M6

Evaluation

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

Pre-requisites**:** CSB1020 *Introduction to R* (or equivalent) with a good understanding of data wrangling using the tidyverse package. 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 Markdown Notebooks**: R and RStudio basics, setting up R Markdown 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: Current Techniques in Neuroscience
CSB1020H/F, Teaching Section LEC 0124
Coordinator: *Dr. Arbora Resulaj*
Offered: Summer (F) 2026 session, 6 classes
Weight: One module (0.25 FCE)
Location: Online
Enrolment: Limited to 10 graduate students
Schedule: Six weeks from mid-April through May, dates TBA

Description:
This course will examine emerging cutting-edge techniques that are revolutionizing fundamental neuroscience research. Techniques to be investigated include: optogenetics, chemogenetics, current strategies for cell-type-specific transgene expression and virus-based circuit tracing, large scale electrophysiology, next generation fluorescent indicators, new imaging techniques such as two photo imaging and super-resolution microscopy. Students will take an active role in researching these techniques and presenting their theoretical foundations as well as practical applications, including advantages and disadvantages, to the class.

Evaluation:
Presentation 60%
Participation 40%

Pre-requisites for module: Background in Neuroscience
Reading materials: Required readings will be primary research articles and reviews, and will be provided during the first week of class
Website: Quercus

Module: Scientific Writing
CSB1021H/F, Teaching Section LEC 0157
Instructor: Dr. Cosima Porteus
Offered: Offered Summer 2026, 6 classes, from early May through June
Weight: One module (0.25 FCE)
Schedule: Fridays (3-hour class), in person at UTSC
Duration of Module: 6 weeks

Description of the module:
Students taking the course must have a data set that has been analyzed and already graphed. Students will take this data set and will produce a first draft of a manuscript with guidance from the course instructor and following Joshua Schimmel's "Writing Science" book. The purpose is to learn about how to structure a manuscript, improving sentence and paragraph structure, and learn how to make a compelling story. Students will be assigned weekly writing exercises that reinforce the writing skills covered during class. These exercises will build towards a first draft of a manuscript. Students will also provide weekly peer feedback to other students and discuss papers from the primary literature to see how concepts discussed in class are used by other scientists. The final assignment is a draft of their manuscript that uses the elements discussed in class and will be evaluated on how well they use these in their own scientific writing.

Evaluation:
Weekly Assignments: 6 x 6% each
Peer review: 6 x 2% each
In-class participation during discussions: 6 x 2% each
Final draft: 40%

Enrollment limitations: 12

Pre-requisites for module:
Students taking the course must have a data set that has been analyzed (statistical analysis completed) and ideally already graphed.

Reading materials:
Joshua Schimmel "writing Science: How to write paper that get cited and proposals that get funded" plus required readings that will be provided ahead of the first day of class.

Website: Quercus