



2024-2025 CSB Graduate Modules

Students enroll in CSB 1020H or CSB1021H for Fall (F) 2024, Winter (S) 2025, or Summer 2025*, 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, 2025.

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 unusual 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 2024), 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 2024-2025

Course: Foundational Discoveries in Genome Biology and Bioinformatics

Course Code: CSB 1482H/F, Teaching Section LEC 0101

Coordinator: Professor Alan Moses

Offered: Fall 2024 session

Weight: Half credit (0.5 FCE)

Time: Tuesdays 11 am – 1 pm

Location: St. George campus, University College, room 67

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: Self/Non-self-Recognition in Plants

CSB 1020H/F, Teaching Section LEC 0106

Coordinators: Professors Daphne Goring and Keiko Yoshioka

Offered: Fall 2024 session for six weeks on Sept. 11th and 25th, Oct. 2nd, 16th, 23rd, and 30th.

Weight: One module (0.25 FCE)

Time: Wednesdays 1 pm - 3 pm

Location: St. George campus, Earth Sciences Centre, Room TBA

Enrolment: Limited to 9 students

Seminar topics:

Week 1: Introductory lecture and reading assignments.

Weeks 2-6: Students presentations and discussion (2 presentations/week, 1 on week 6)

Week 6: Summary Discussion

Description:

The molecular and cellular basis of self/non-self-recognition is an active area of research for a number of key biological processes in plants. This module focuses on two broad areas: self/non-self-recognition in pollen-pistil interactions (compatible pollen acceptance, incompatible pollen rejection) and plant-microbe interactions (immunity, beneficial interactions). In this seminar course, students will investigate the current knowledge of self/non-self-recognition of plants. The course will provide a forum for an interactive discussion between the instructors and students and will be based on a selection of current high impact primary research papers.

Evaluation:

Each student will present a PowerPoint style presentation based on an assigned topic using a selection of primary research papers. A written summary on one key research article will also be due at the end of the module. The written summary on the primary research article will follow a format similar to a *Science Perspective/Nature News & Views/Cell Preview* which not only explains and provides context of the research to a broader audience, but also poses questions and future directions for this research. Students are expected to read all papers and participate in all discussions. However for each presentation, two students will be assigned the task of asking questions and leading the discussion.

Grading: 50% Presentation (one presentation per student on a primary research paper)
25% Leading discussions/Participating in discussions
25% Written Summary

Pre-requisites for module: undergraduate courses in molecular and cell biology

Reading materials: TBA

Website: Quercus

Module: Introduction to R

CSB1020H/F, Teaching Section LEC 0142

Offered by the Centre for the Analysis of Genome Evolution & Function (CAGEF),

Fall 2024 session

Instructors:

Dr. David S. Guttman, CSB, CAGEF

david.guttman@utoronto.ca

Dr. Calvin Mok, CAGEF Bioinformatics

calvin.mok@mail.utoronto.ca

Time:

September 4 – October 16 (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 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/JAJFK76vKcWA6kKD7>

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: Plant Bioinformatics

CSB1021H/S, Teaching Section LEC 0139

Coordinator: Professor Nicholas Provart

Offered: Fall 2024, 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: Regenerative Medicine
CSB1020H/F, Teaching Section LEC 0154

Coordinator: Professor Penney Gilbert (penney.gilbert@utoronto.ca)

Offered: Fall 2024, from late October to late November (Fridays from October 25th to November 29th)

Weight: One module (0.25 FCE)

Time: 10 am – 12 pm

Location: Ramsay Wright Building, St. George campus (room TBA)

Enrollment: Limit of 14 students

Description:

In this course we will delve into the innovative world of regenerative medicine; a translation-forward research field that aims to restore function to aged, injured, and diseased tissues. Our journey will begin by highlighting foundational discoveries in stem cell biology that opened up new regenerative medicine possibilities, followed by tracking the path forged by subsequent researchers to overcome hurdles impeding the translation of the initial discovery to clinical practice. Curated journal articles and videos, and break-out activities will frame our discussions of stem cell biology, biomaterials, tissue engineering, and gene therapy approaches to restore function to blood, heart, and skeletal muscle tissues, while we also consider the ethics and the translational hurdles associated with regenerative medicine therapies. Canada is the proud birthplace of the discovery of stem cells, and much of the research we will draw upon was developed by scientists in Canada.

Course Format:

This is a participatory course, meaning that we will learn through our interactions with one another in class. Each week on Quercus there will be required pre-class readings and other materials to review to prepare the student for the upcoming class. The class component of the course, comprised of class discussions, break-out activities, and short knowledge check quizzes, will be delivered synchronously and in person.

Evaluation:

| | |
|-------------------------|------|
| Knowledge Check Quizzes | 30% |
| Participation | 30% |
| *Rabbit Hole Assignment | 40% |
| Total | 100% |

*Regen Med "Rabbit Hole" Assignment

To encourage curiosity and independent learning, this course has a Rabbit Hole written assignment. Professor Gilbert will provide a list of possible Rabbit Hole topic areas for students in the class to choose from. The topics will be related to the course materials, but are not directly covered within the course content. Each student will choose one of the topic areas for which to conduct their independent inquiry. With few exceptions, no two students may work on the same topic area. Rabbit Hole assignments are due on the final day of class. Additional details of this assignment can be found in the Rabbit Hole Assignment module on Quercus.

Website: Quercus

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 2024 session

Instructors:

Dr. David S. Guttman, CSB, CAGEF

david.guttman@utoronto.ca

Dr. Calvin Mok, CAGEF Bioinformatics

calvin.mok@mail.utoronto.ca

Dates:

October 30th – December 11th (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 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/ECKFqmoQ85YLeZo8>

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

Module: Neuroscience of Behavioral Control and Methodology CSB1021H/F, Teaching Section LEC 0153

Instructor: Professor J. Fraigne

Offered: Fall 2024 session

Weight: One module (0.25 FCE)

Time: November and December, dates and times TBA.

Location: St. George campus, Ramsay Wright Building, Room TBA

Enrolment: Limited to 8 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 two brief research proposals 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 = 40% (two seminars 20% each)

Proposal = 40% (two proposals 20% each)

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

Course: Computational Genomics and Bioinformatics Course Code: CSB 1472H/S, Teaching Section LEC 0101

Coordinator: Professor David Guttman

Offered: Winter 2025 session

Weight: Half credit (0.5 FCE)

Time: Wednesdays 10 am – 12 pm

Location: St. George campus, Bahen Centre, room 2195

Enrolment: Limited to 7 graduate students (5 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 2025 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 2025 session.

Instructors:

Dr. David S. Guttman, CSB, CAGEF
Dr. Calvin Mok, CAGEF Bioinformatics

david.guttman@utoronto.ca
calvin.mok@mail.utoronto.ca

Dates:

January 9 – Feb 20 (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 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/KYevNYXWWDhHdco7>

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 evolutionary medicine
CSB 1020H/S, Teaching Section LEC 0149

Coordinator: Professor Maxwell Shafer

Offered: Winter 2025 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: Theoretical and Applied Topics in Data Visualization for Genome Biology
CSB 1020H/F, Teaching Section LEC 0133

Coordinator: Professor Nicholas Provart

Offered: Winter 2025 session in January and February 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: Advanced Bayesian statistics for genomics
CSB 1021H/S, Teaching Section LEC 0150

Coordinator: Professor Guillaume Filion

Offered: Winter 2025 session, in January and February for a total of six meetings.

Weight: One module (0.25 FCE)

Time: TBA

Location: Remote or UTSC campus, room TBA

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

Advanced Techniques in Microscopy
CSB1021H/S, Teaching Section LEC 0147

Instructors: Professors Ulrich Tepass, Heather McFarlane, and Sergey Plotnikov

Offered: Winter 2025 session from late February to mid-April for eight meetings.

Weight: One module (0.25 FCE)

Time: TBA

Location: St. George campus, Ramsay Wright Building, Room TBA

Enrolment: Limited to 8 students

Description:

This course will provide an introduction to light microscopy and digital imaging in the biological sciences. The course consists of lectures, discussions, and presentations that will enable the students to obtain and interpret high quality microscope data and to understand and assess potential artifacts. The course also places a strong emphasis on appropriate sample preparation and advanced microscopy usage (e.g., confocal microscopy, total internal reflection fluorescence (TIRF) microscopy, fluorescence resonance energy transfer (FRET) imaging, and multiphoton microscopy). Particular emphasis will be placed on 'picking the right tool for the job'.

Topics to be covered include:

- Basic principles of microscope design, digital image recording, image resolution and contrast;
- Fluorescence microscopy techniques – fluorescent probes, fluorescent biosensors, TIRF, FRET, and FRAP;
- Confocal and multiphoton microscopy;

Each class will consist of two 12 min student presentations covering the fundamentals of light microscopy followed by an in-depth presentation of an imaging technique with an example of its biological application.

Evaluation:

This is a flipped classroom course, so students will learn theory through an assigned independent reading of the resource materials, review articles, and primary research papers. The in-class activities will be devoted to presentations and student-led discussions.

| Item | Note | % Mark |
|--|---------------------------------------|--------|
| Short (12min) presentation on imaging fundamentals | 2 individual presentations x 20% each | 40% |
| Group presentation of an imaging technique | 2 group presentations x 20% each | 40% |
| Participation in discussions | Weekly 2.5% x 8 weeks | 20% |

Prerequisites for module: Some background in cell/developmental biology. Prior experience in imaging is desired, but not essential.

Reading materials:

- Nechyporuk-Zloy, V. (2022). *Principles of Light Microscopy*. Springer International Publishing AG. This book is available online at the UofT library website.
- *MicroscopyU: the Source of Microscopy Education*. <https://www.microscopyu.com> (similar online recourses from Zeiss and Olympus can be used)
- iBiology: Microscopy Series. <https://www.ibiology.org/online-biology-courses/microscopy-series/>
- Review articles and research papers

Website: Quercus

Module: Animal Models of Human Conditions CSB1021H/S, Teaching Section LEC 0155

Coordinator: Professor Laura Corbit

Offered: Winter 2025 session in March and April for a total of six meetings.

Weight: One module (0.25 FCE)

Time: TBA, likely Monday afternoons or Thursday mornings

Location: St. George campus, Ramsay Wright Building, Room TBA

Enrolment: Limited to 10 students

Description:

Animal models can be a powerful way to study both basic mechanisms and pathologies related to human capabilities and diseases. But the data produced are only as good as the model used to generate them. This course will cover what makes a good animal model, some of the common frameworks used for generating models, as well as limitations of this research approach. In addition to these general principles, students will have the opportunity to focus on a model of a specific process (cortical development, learned fear) or disease (e.g., Alzheimer's disease) through their work related to an in-class presentation and paper that critically evaluate the strengths and weakness of a specific model of their choice. The topic relate to their own research, but does not have to be. Attendance and participation in class discussions are an important component of the class.

*Specific Topics will be decided in an organizational meeting based on student interests

Evaluation:

Paper proposal: 10%

Presentation (of a research article): 30%

Paper (critical evaluation of an animal model): 50%

Participation: 10%

Prerequisites for module: None

Reading materials: Readings (journal articles) will be assigned throughout the course, some based on student topic selections

Website: Quercus

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 2025 session.

Instructors:

Dr. David S. Guttman, CSB, CAGEF

david.guttman@utoronto.ca

Dr. Calvin Mok, CAGEF Bioinformatics

calvin.mok@mail.utoronto.ca

Dates:

March 6 – April 10, 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 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/zAdzVYN3SUKNdTpE8>

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 <code>expression()</code> and <code>bquote()</code> , 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) 2025 session, 6 classes

Weight: One module (0.25 FCE)

Location: UTM campus, room TBA

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