2018-2019 CSB Graduate Modules

Students enroll in CSB 1020H for Fall (F) 2018, Winter (S) 2019, or Summer 2019*, depending on the session the specific module is offered. This course code is used for all quarter-credit (0.25 FCE) CSB modules.
***Summer courses/modules cannot be requested on ACORN until March 18, 2019.**

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 (e.g. Fall 2018), 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 requirements.

Seminar and lab-based modules offered 2018-2019

Module: Basement membrane dynamics and human pathologies
CSB 1020H/F, Teaching Section LEC 0111
Coordinator: Professor M. Ringuette
Offered: Fall 2018 session, for six weeks starting Thursday, September 13th until October 18th.
Weight: One module (0.25 FCE)
Time: Thursdays, 2-4 pm
Location: St. George campus, Ramsay Wright Building (Room TBA)
Enrolment: Limited to 8 students

Description of the module:
Basement membranes (BMs) are specialized nanometer-thick, sheet-like extracellular matrices with developmental stage- and tissue-specific morphoregulatory and physiological functions, which include formation of tissue compartments and barriers, mechanical strength, cell-matrix adhesion, epithelial morphogenesis, growth factor chemotactic gradients, stem cell self-renewal and differentiation, and tissue filtration. Hence, BMs play indispensable roles in the formation, growth, regenerative capacity and homeostasis of tissues and organs throughout life. Mutations, excessive post-translational modifications and misexpression of BM components is the underlying cause of several congenital diseases that are often fatal during early stages of life.

Special emphasis will be placed on the structural organization, assembly into networks and functions of two key universal polymer-forming components of BMs: laminin and network-forming collagen IV. The contributions of perlecan and nidogen and other well characterized members of the BM proteome will be discussed when appropriate for the research topic being presented.

Schedule/Seminar topics: 2 hours/week

Week 1: Introductory lecture: BM assembly, topography, remodeling and function. Manuscript assignments.
Weeks 2-5: Student presentations and discussion (Two presentations/week)

- Kidney filtration: Alport syndrome and Goodpasteur syndrome
- Epidermolysis bullosa: Junctional, Dystrophic and Simplex
- Neuromuscular deficits, ocular abnormalities, sensorineural hearing loss, pulmonary fibrosis, and vascular hypertension
- Stem cell renewal and differentiation
- Epithelial cancer metastasis

Week 6: Summary Discussion

Evaluation:
Presentation: one presentation per student on a primary research paper.
30-minute presentation, 20-minute discussion (40%)
Presentation grading breakdown:
- Introduction (10%)
- Content: clarity, accuracy and effectiveness (10%)
- Comprehension of subject and technology and ability to answer questions (15%)
- Quality of slides and slide transition (5%)

Leading discussions/Participating in discussions (20%)
For each presentation, two students will be assigned the task of asking questions and leading the discussion.
News and Views: Three-page paper for one of the modules (40%)

Course: Readings in Genome Biology and Bioinformatics
Course Code: CSB 1482H/F, Teaching Section LEC 0101
Coordinator: *Professor A. Moses*
Offered: Fall 2018 session
Weight: Half credit (0.5 FCE)
Time: Mondays 11 am – 1 pm
Location: St. George campus, Earth Sciences Centre, Room 1014
Enrolment: Limited to 12 graduate students (minimum 8 reserved for CSB grads)

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 for Data Science
CSB1020H/F, Teaching Section LEC 0135
Coordinators: *Professor D. Guttman and Dr. Erica Acton*
Offered: Fall 2018 session (Sept. 18th – Oct. 23rd) for six weeks
Weight: One module (0.25 FCE)
Time: Tuesdays, 3:00 – 6:00 pm
Location: St. George campus, Earth Sciences Centre, room 3087
Enrolment: Limited to 20 students

Description:
This course is a beginner's introduction to R and R-Studio for students who do not have a computer science background. It is intended for the student who wants to develop the skills to analyze his or her own data. Students who complete this course will be able to 1) be comfortable with the R-Studio environment, data structures and data types, 2) import data into R and manipulate data frames, 3) transform a 'messy' dataset into a 'tidy' dataset, 4) make exploratory plots, 5) use string manipulation to clean data, and 6) perform basic statistical tests and run a regression model. The structure of the class is 'code-along' and students are expected to bring a laptop.

Evaluation:
Grades in this module will be determined by a combination of participation in in-class quizzes (6 x 5% = 30%), short assignments (5 x 10% = 50%), and a final project (20%). Short assignments require students to apply the material that they learned during each module with an emphasis on well-documented code that is concise. The final project brings together concepts from all modules by performing exploratory data analysis on a dataset of interest.

Pre-requisites for module:
1) Access to a laptop computer at each module.; 2) R and R-Studio installed (https://cloud.r-project.org/ and https://www.rstudio.com/products/rstudio/download/).

Reading materials:
As preparatory material for the course, students should install *swirl* (install.packages('swirl')) and complete R Programming 1: Basic Building Blocks, 3: Sequences of Numbers, 4: Vectors, 7: Matrices and Data Frames. A reference throughout the course will be *R for Data Science* (http://r4ds.had.co.nz/).

Website: All lesson materials and datasets for the course are found at https://github.com/eacton/CAGEF. Assignments will be submitted to a course Dropbox.

Module: Fundamentals of Genomic Data Science
CSB1020H/F, Teaching Section LEC 0131
Coordinators: *Professor D. Guttman and Dr. Marcus Dillon*
Offered: Fall 2018 session (Oct. 30th – Dec. 11th) for seven weeks
Weight: One module (0.25 FCE)
Time: Tuesdays, 3:00 – 6:00 pm
Location: St. George campus, Earth Sciences Centre, room 3087
Enrolment: Limited to 10 students

Description:
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 computer science. Students in the course will learn to perform a number of basic genomic data analyses using Galaxy, an open, web-based platform that incorporates multiple bioinformatics tools into an easy to use Graphic 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 work in a Unix terminal, install bioinformatics software, and connect to remote servers. They will become familiar with the common genomics file formats and use both Galaxy and command line tools to process these files and manipulate the data. They will learn how to perform *de novo* and reference-based genome assemblies, perform variant calling, and analyze RNA-seq data. The course will take advantage of some of the excellent online resources for

background material, while spending class time analyzing real data sets. Students will be expected to have at least a basic understanding of genomics and molecular biology. No prior computational knowledge is required, although students will be expected to have access to a laptop computer. Students who complete this course will have the foundation to approach genomic data analysis in a more efficient manner, enabling them to tackle more questions in less time.

Evaluation:
Grades in this module will be determined by a combination of attendance (25%), short assignments (6 x 5% = 30%), and a final project (45%). Short assignments require students to apply the material that they learned during each module to new problems and answer brief questions about their analyses. The final project is split into three parts, each worth 15%, covering the application of the three main genomics pipelines covered in this course to a new dataset: a) Assembly and annotation, b) Reference alignment and variant detection, and c) RNA sequencing analysis.

Pre-requisites for module: 1) Basic background in genetics and molecular biology; 2) Access to a laptop computer at each module.

Reading materials:
As preparatory material for the course, students will watch lectures from Coursera's Genomic Data Science Specialization. Specifically, preparatory lectures for this course come from "Introduction to Genomic Technologies", "Genomic Data Science with Galaxy", and "Command Line Tools for Genomic Data Science". There are also five reviews that are assigned as reading over the course of the module.

Website:
All documents and data are shared via a Dropbox account that is setup for the course. The section of the course that covers Galaxy is set up on a local server that can be accessed at http://142.150.214.76:8080/.

Module: Functional Genomics Using "Big" Data
CSB1020H/F, Teaching Section LEC 0103
Coordinator: *Professor J. Mitchell*
Offered: Fall 2018 session. Six weeks beginning Thursday September 20th, 2018
Weight: One module (0.25 FCE)
Time: Thursdays, 2:00 – 4:00 pm
Location: St. George campus, Ramsay Wright Building, Room TBA
Enrolment: Limited to 8 students

Description:
This is a seminar based course in which students will investigate the current knowledge of how complex genomes function. Data generated by massively parallel sequencing and system-wide approaches will be discussed and explored in the context of understanding how genomes and their protein products function in whole organisms.

The course will provide a forum for an interactive discussion between the instructor and students and will be based on a selection of current high impact primary research papers.

Schedule: 2h/week; 6 weeks
Week 1: Introductory lecture and reading assignments.
Weeks 2-5: Students presentations and discussion (2 talks/week)
Week 6: Summary Discussion

Evaluation:
Students will each present a PowerPoint style presentation based on a selection of primary research papers. Presentation dates and papers will be assigned; 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. Students will be required to write a "news and views" paper on a topic related to the course material but different from the one they presented.

Seminar: 2 x 20 min, and 60 min for discussion of both papers - 40%
Participation in Discussion: 2 students assigned as major questioners/talk - 20%
News & Views paper - 40%

Module: Current Techniques in Neuroscience
CSB 1020H/F, Teaching Section LEC 0124
Coordinators: *Professors M. Woodin and V. Tropepe*
Offered: Fall 2018 session, six meetings to be held on Mon. September 17th, Mon. October 1st, Wed. October 3rd, Wed. October 10th, Mon. October 15th, and Wed. October 17th
Weight: One module (0.25 FCE)
Time: 3 pm to 5 pm
Location: St. George campus, Ramsay Wright Building, Room TBA
Enrolment: Limited to 10 students

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 clonal analysis (e.g., Brainbow), genome engineering in the nervous system (e.g., CRISPR), next generation fluorescent indicators. 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: Theoretical and Applied Topics in Data Visualization for Genome Biology
CSB 1020H/F, Teaching Section LEC 0133
Coordinators: *Professor N. Provart and Dr. J. Waese*
Offered: Fall 2018 session, beginning in mid-October. A total of six two-hour meetings.
Weight: One module (0.25 FCE)
Time: Wednesdays from 9-11 am (tentative)
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

Course: Computational Genomics and Bioinformatics
Course Code: CSB 1472H/S, Teaching Section LEC 0101
Coordinator: *Professor N. Provart*
Offered: Winter 2019 session
Weight: Half credit (0.5 FCE)
Time: Wednesdays 10 am – 1 pm
Location: St. George campus, Ramsay Wright Building, Room 432
Enrolment: Limited to 10 graduate students (minimum 7 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 2019 session
Weight: Half credit (0.50 FCE)
Time: Tuesdays 12-4 pm
Location: St. George campus, Earth Sciences Centre Room 4076 & Ramsay Wright 109.
Enrolment: Limited to 2 or 3 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 ROSI, 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, shotgun library construction, PCR, DNA sequencing, expression profiling using microarrays, 2D-gel proteome analysis, mass spectrometry and associated bioinformatics analyses such as sequence analysis and assembly, and statistical analysis of microarray 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 (60%), lab performance (25%). 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: Neuroscience of Behavioural State Control
CSB 1020H/S, Teaching Section LEC 0123
Coordinator*: Professor J. Peever*
Offered: Winter 2019 session.
Weight: One module (0.25 FCE)
Time: January and February, dates and times TBA.
Location: St. George campus, Ramsay Wright Building, Room TBA
Enrolment: Limited to 6 students

Description:
This course will examine the latest advances in how the nervous system controls behavioural states such as sleep, arousal, daily rhythms, breathing and movement. It will consider leading hypotheses on the function of the cell systems, organ systems and at the whole organism level that lead to appropriate and pathological control of such behaviours.

Evaluation:
Students will present 2 seminars, one from each section of the course. They will write a brief synopsis of the presentation. Students will also participate in discussion. Seminars and discussion will focus on issues raised in a selection of primary research papers. Written assignment: students will write a "News and Views" style review article on a current "hot topic" within the field. The subject chosen will accommodate the specific research interests of each student but must be different from those discussed in seminars.

Seminar = 20% (x2 = 40% total)
Synopsis = 10% (x2 = 20%)
Discussion = 10% (x2 = 20% total)
News and Views = 20%

Prerequisites: None
Reading Materials: to be determined by the specific interests of the participating students.

Module: Protein homeostasis in regulating plant development and stress response
CSB 1020H/S, Teaching Section LEC 0121
Coordinators*: Professors R. Zhao and D. Riggs*
Offered: Winter 2019 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: Current Techniques in Gene Regulation
CSB 1020H/F (Summer 2019*), Teaching Section LEC 0134
Coordinator*: Professor Ho-Sung Rhee*
Offered: Summer 2019* session, from early May to mid-June for six weeks (plus an organizational meeting).
Weight: One module (0.25 FCE)
Time: TBA
Location: UTM campus, room TBA
Enrolment: Limited to 8 students

Description:
This course will examine cutting-edge techniques to study gene regulation. Techniques to be discussed include: cell (re)programming into specific cell types, production of embryonic stem cell-derived mouse models, current strategies for genome-editing in vivo and in vitro systems such as CRISPR-Cas9, isolating cell type-specific nuclear proteins in a few model organisms, and identifying functional gene regulatory elements throughout the genome using next-generation sequencing technologies. Lectures and seminars will involve presentation and discussion of current topics in gene regulation. Students will present recently published research articles, lead a discussion, and write a report.

Evaluation:
Presentation: 30%
Leading a discussion: 20%
Participation: 30%
Written assignment: 20%

Pre-requisites for module: None

*Summer courses cannot be requested on ACORN until March 18, 2019.

Module: Cell Biology of Gastrulation
CSB 1020H/S (Summer 2019*), Teaching Section LEC 0107
Coordinators*: Professors A. Bruce & R. Winklbauer*
Offered: Summer 2019* session, in June and July 2019 for six weeks (plus an organizational meeting in May).
Weight: One module (0.25 FCE)
Time: TBA, but likely Wednesdays 5-7 pm
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 migration, tissue rearrangement and spreading as well as tissue separation. In addition to discussing these cell behaviours in the context of gastrulation, we will explore other contexts in which these same or similar behaviours also occur.

Evaluation:
40% seminar (1 presentation per student on a primary research paper)
30% final presentation (group project)
10% write-up of final presentation (one per group)
20% participation in discussion

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

*Summer courses cannot be requested on ACORN until March 18, 2019.

Course: Advanced Microscopy and Imaging
Course Code: CSB 1018H (Summer 2019*), Teaching Section LEC 0101
Course Coordinators: *Professors R. Harrison, M. Terebiznik and B. Richards*
Offered: Summer 2019* session in May and June.
Weight: 0.5 FCE
Time: TBA
Location: University of Toronto, Scarborough campus
Enrolment: Limited to 20 students

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

Course Schedule and Structure:
We have 14 formal meetings. Each meeting is 3 hours, some sessions may not go that long. Lectures are for 1-2 hrs in most cases, then, if relevant, there is a demonstration of the particular equipment. By appointment, students arrange for training of specific equipment.

Meetings 1-10: Lectures, Demos and Practicum
Meetings 11-12: prarcticum examination
Meetings 12-13: student seminar presentations (Tuesday June 20th, 3 pm-8:15 pm)
Meeting 14: Final Exam: Wednesday June 28th, 3-6 pm

Grading Scheme:

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

	100%

Pre-requisites: None
Reading materials: TBA
Website: Quercus
*Summer courses cannot be requested on ACORN until March 18, 2019

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

PSY5110H/S Neurobiology of Social Behaviour
Instructor: *Professor Melissa Holmes* (melissa.holmes@utoronto.ca)
Offered: Winter 2019 session
Weight: (0.5 FCE)
Time: Mondays 10:00 AM -12:00 PM
Location: CCT-3000, UTM campus

Topics:
This course will focus on the development and adult organization of neurobiological mechanisms underlying the perception of social information and production of social behaviours in diverse species. Each week will focus on a unique topic (e.g., eusociality in hymenoptera; pair bonding in voles; face perception in humans; etc) incorporating a mix of lecture, primary literature, and group discussion.

Reading:
Articles will be assigned each week and posted on the course web site. No text will be used.

Marking scheme:
Class participation (10%); thought papers (20%); major presentation (30%); major research proposal (40%)

Website: Quercus