2020-2021 CSB Graduate Modules

Students enroll in CSB 1020H or CSB1021H for Fall (F) 2020, Winter (S) 2021, or Summer 2021*, depending on the session the specific module is offered. These two course codes apply to all quarter-credit (0.25 FCE) CSB modules.
*Summer courses/modules cannot be requested on ACORN until March 15, 2021.

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

If you want to request two modules in the same session that have the same course code (e.g. CSB1021H/F, for Fall 2020), you may need to contact the CSB Graduate Office to arrange for enrolment in a second module.

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

<u>**Seminar and lab-based modules offered 2020-2021**</u>

Module: Introduction to Python
CSB1021H/F, Teaching Section LEC 0140
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),* Fall 2020 session.
Weight: One module (0.25 FCE)
Instructors:
Dr. David S. Guttman, CSB, CAGEF   david.guttman@utoronto.ca
Oscar Montoya, CAGEF Bioinformatics   oscar.montoya@utoronto.ca
Date: Thurs, 2:00-5:00, from September 10th to October 15th (6 weeks)
Enrollment: 20 graduate students; up to 40 auditors

Course Objectives:
This is a beginner's introduction to Python for data science applications for students who do not have a computer science background. It is intended for the students who want to develop the skills to analyze their own data. Students who complete this course will be able to: Perform data analysis in Python using the Jupyter Lab environment; understand data structures and data types; import data into Python and manipulate Python objects such as list, data frames, and dictionaries; transform a 'messy' dataset into a 'tidy' dataset and make exploratory plots; use flow control and use string manipulation to clean data. The structure of the class is 'code-along' and students are expected to bring a laptop.

Each class will consist of a short introductory lecture followed by 'code-along' hands-on learning. A homework assignment 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 using Bb-collaborate.

Course Availability:
This course will be presented online and will be available to all graduate students, postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN. Anyone wishing to audit the course should fill out the request form at https://bit.ly/3jMK0zk

Evaluation:

Item	Note	% Mark
Homework Assignments	6 weekly assignments x 12% each	72%
Term project	Due 2 weeks after the end of the course	28%

Pre-requisites: Access to a computer. 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
Syllabus

Class	Topic
1	**Intro to Python and Jupyter Lab:** Generalities about Python, Installing Python and JupyterLab, How to run Python code, The JupyterLab environment, Variables, Functions and 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, Writing data
4	**Flow control:** Flow control, for loops, Conditionals
5	**Regular Expressions:** Classes, Quantifiers, Operators, Patterns matching, String manipulation.
6	**User-defined functions:** Defining a function, Best practices in user-defined functions

Subject to change

Module: Introduction to R
CSB1020H/F, Teaching Section LEC 0135
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF),* Fall 2020 session
Instructors:
Dr. David S. Guttman, CSB, CAGEF   david.guttman@utoronto.ca
Oscar Montoya, CAGEF Bioinformatics   oscar.montoya@utoronto.ca
Dates: Tues, 2:00-5:00pm **from** September 22nd to November 3rd (7 weeks)
Enrollment: 20 graduate students; up to 40 auditors

Course Objectives:
This is a beginner's introduction to R and R-Studio for individuals with no prior experience or background. Individuals who complete the course will be able to: work in the R-Studio environment; understand data structures and data types; import data into R and manipulate data frames; transform a 'messy' dataset into a 'tidy' dataset; make exploratory plots as well as publication-quality graphics; use flow control; use string manipulation to clean data; and perform basic statistical tests and run a regression model.

Each class will consist of a short introductory lecture followed by 'code-along' hands-on learning. A homework assignment 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 using Bb-collaborate.

Course Availability:
This course will be presented online and will be available to all graduate students, postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN. Anyone wishing to audit the course should fill out the request form at https://bit.ly/3g5iTgS

Evaluation:

Item	Note	% Mark
Homework Assignments	6 weekly assignments x 12% each	72%
Term project	Due 2 weeks after the end of the course	28%

Pre-requisites: Access to a computer. No prior programming experience needed.
Reference Material: *R for Data Science* (http://r4ds.had.co.nz/)
Syllabus

Class	Topic
1	**Introduction to R an RStudio**: R and RStudio 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:** Wide and long formats, Importing text and Excel files, dplyr basic functions.
3	**Introduction to Tidy Data**: Wide versus long data formats, reshaping data with tidyverse.
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, Patterns matching, 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: Signal Transduction in Animal Cells
CSB1020H/F, Teaching Section LEC 0129
Coordinators: *Angela B. Lange, Ian Orchard and Jimena Leyria*
Offered: September 21, 2020 for initial meeting to discuss course and topics. Course will be offered on Mondays from 10am – 12 pm (via Zoom)
Weight: One module (0.25 FCE)
Duration of Module: 1 organizational meeting followed by 5-6 weeks
Enrollment: Maximum 6 students

Description:
This seminar-based module focuses on the intercellular communication and signal transduction events that mediate fundamental biological events in animals. Signal transduction involves the binding of extracellular signaling molecules or ligands to receptors located on the cell surface or inside the cell that trigger events inside the cell leading to a response. These responses can alter cell growth, metabolism, gene expression and many other processes.

Each student will prepare and present two seminars of their choice, preapproved by the instructors. Student seminar dates will be assigned during the first meeting to allow sufficient time for preparation. All students must read all the papers and will be expected to participate in a discussion of the topics. Students will also be assigned the task of being a critical reviewer of two of the seminars, i.e. they must prepare 2-3 critical questions/per paper in advance and lead the discussion. These questions will be used, in part, for starting the discussion period. A final critique paper will be expected as the final component of the course.

Evaluation:
2 Seminars (25-30 minutes; 15 minutes for questions/discussion)   50%
2-3 Critical Questions Submitted for two papers   10%
Contributing to the Discussion   10%
Final Critique/Report (to be discussed)   30%

Pre-requisites for module: None
Reading materials: None
Website: None

Module: Mass spectrometry for biological systems
CSB1021H/F, Teaching Section LEC 0137
Coordinator: *Professor Michael Phillips*
Offered: Fall 2020 session for 6 weeks, running September to December, 2020 (course meets once per week on alternate weeks), specific dates TBA*
Weight: One module (0.25 FCE)
Time: TBA
Location: Mississauga campus, room TBA with online/synchronous option.
Enrollment: limited to 15 students

Description:
This is a seminar based course that covers the theory and application of mass spectrometry in biological research. Initial lectures by the instructor will cover principles of chromatography, ionization and common mass analyzers (quadrupole, ion trap, magnetic sector, and time-of-flight) useful for the detection of small molecules. Students will give an oral presentation on a specific application of mass spectrometry and submit a term paper. Group discussion and practical training will introduce modern data analysis pipelines for metabolomics data sets.

Students will be assigned readings from the literature and Martin Smith's textbook "*Understanding Mass Spectra*" to accompany course lectures.

Schedule:
2-3 hours/week, 6 weeks (meets every other week from September through December)
Week 1-2: Introductory lectures and reading assignments
Weeks 3-5: Students presentations and discussion (2 talks/week)
Week 6: Summary Discussion

Evaluation:
Students will deliver an oral presentation on an application of mass spectrometry and then submit a term paper on this topic by end of term. The paper should incorporate discussion points following the oral presentation and show a synthesis of new ideas resulting from this discussion. 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 read all papers and participate in all discussions. The term paper is normally on the same topic as the oral presentation but students may choose to write on a different mass spectrometry subject if desired.
Seminar: 20 min + 60 min for discussion of the paper   40%

Participation during discussion period of oral presentations 20%
Term paper   40%

Pre-requisites: None, but two semesters of organic chemistry or one semester of analytical chemistry is strongly recommended.

Course delivery: In person delivery with social distancing is anticipated to be the primary mode of course delivery. A zoom link will be provided each session for students who choose to opt out of in person delivery. Virtual attendance must be synchronous and videos of presentations and lectures will not be provided. Student presentations will not be recorded except by request of the speaker.

Course: Foundational Discoveries in Genome Biology and Bioinformatics
Course Code: CSB 1482H/F, Teaching Section LEC 0901
Coordinator: *Professor Alan Moses*
Offered: Fall 2020 session
Weight: Half credit (0.5 FCE)
Time: Tuesdays 11 am – 1 pm
Location: Online
Enrolment: Limited to 5 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 471H1F. Graduate students should NOT request this course as CSB471H1F on ACORN because it would not count toward graduate credit.

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

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

Pre-requisites: Instructor approval

Module: Current Techniques in Neuroscience
CSB1020H/F, Teaching Section LEC 0124
Coordinator: *Dr. Baohua Liu*
Offered: Fall 2020 session, 6 classes
Weight: One module (0.25 FCE)
Location: Online
Enrolment: Limited to 10 graduate students

Schedule: Tentative, all online
Thursday, Oct 22th 2020, 9-11pm
Thursday, Oct 29th 2020, 9-11pm
Thursday, Nov 5th 2020, 9-11pm
Thursday, Nov 12th 2020, 9-11pm
Thursday, Nov 19th 2020, 9-11pm
Thursday, Nov 26th 2020, 9-11pm

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: Fundamentals of Genomic Data Science
CSB1020H/F, Teaching Section LEC 0131
Offered by the *Centre for the Analysis of Genome Evolution & Function (CAGEF)*.
Fall 2020 session
Instructors:
Dr. David S. Guttman, CSB, CAGEF   david.guttman@utoronto.ca
Oscar Montoya, CAGEF Bioinformatics   oscar.montoya@utoronto.ca
Date: Thurs, 2:00-5:00 from November 5th to December 17th (7 weeks)
Enrollment: 20 graduate students; up to 40 auditors

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 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 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. No prior computational knowledge is required. Students who complete this course will have the foundation to approach data

analysis in a more efficient manner, enabling them to tackle more questions in less time.

Each class will consist of a short introductory lecture followed by 'code-along' hands-on learning. A homework assignment 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 using Bb-collaborate.

Course Availability:
This course will be presented online and will be available to all graduate students, postdocs, staff, and faculty, although only registered students will be evaluated. The course will count as a single module (0.25 credits) for CSB graduate students. All graduate students interested in taking the course for credit should enroll through ACORN. Anyone wishing to audit the course should fill out the request form at https://bit.ly/3fb4rTq

Evaluation:

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

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

Syllabus

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

Subject to change

Course: Computational Genomics and Bioinformatics
Course Code: CSB 1472H/S, Teaching Section LEC 0901
Coordinator: *Professor Nicholas Provart*
Offered: Winter 2021 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 8 graduate students (CSB grads with priority)

*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.

Module: Neuroscience of Behavioural State Control
CSB 1021H/S, Teaching Section LEC 0123
Coordinator: *Professor John Peever*
Offered: Winter 2021 session, starting in January
Weight: One module (0.25 FCE)
Time: Winter session, dates and times TBA
Location: St. George campus, Ramsay Wright Building, Room TBA (or online)
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: Current Techniques in Gene Regulation
CSB1021H/S, Teaching Section LEC 0134
Instructor: *Professor Ho Sung Rhee* (hosung.rhee@utoronto.ca)
Offered: Winter 2021 (six weeks, Feb. 25th – April 1st, 2021)
Schedule: 3:10 PM – 6:00 PM, Thursdays
Weight: One module (0.25 FCE)
Location: UTM campus, Room TBA
Enrolment: Limited to 8 graduate students

Description:
This course will examine cutting-edge techniques to study regulation of gene expression. Techniques to be discussed include: cell reprogramming into specific cell types, high-resolution protein-DNA interaction analysis, current strategies for genome-editing and screening in vivo and in vitro systems such as CRISPR-Cas9, isolating cell type-specific nuclear proteins in model organisms, and identifying gene regulatory networks at the single-cell level using next-generation sequencing technologies such as single-cell RNA-seq. 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: 50%
Discussion: 10%
Participation: 20%
Written assignment: 20%

This course consists of about 50% of lectures and 50% of seminar presentations. Lectures will provide an overview of techniques to study gene regulation and fundamental concepts related to mammalian gene expression studies. Students are expected to give two seminar presentations (30 minutes long). The discussion will be addressed during the presentation. The 1st presentation will focus on the basic background and details of the selected method/system and related techniques related to gene regulation studies. The 2nd presentation would focus on findings and applications of selected methods/systems using the published research articles.

Pre-requisites: None

Reading materials: Required readings will be primary research articles and reviews, and will be provided during class.

Website: https://q.utoronto.ca

Course Delivery: In-person class will be offered in a large classroom at the UTM campus, but it may be changed to a remote class under certain circumstances.

Module: Topics in Cell and Developmental Biology: Genetic strategies in the analysis of animal development
CSB 1020H/S, Teaching Section LEC 0104
Coordinator: *Professor Dorothea Godt*
Offered: Winter 2021 session. The module starts at the end of February 2021 with an informal meeting to discuss the course, which is followed by 6 weeks of seminars (March to April).
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus, Ramsay Wright Building, room 601
Enrolment: Limited to 9 students

Description: Strategies to manipulate genes and gene activity and to detect and measure changes in gene expression have become exceedingly sophisticated and are no longer restricted to a few model organisms. In this reading course, we will discuss recent articles focusing on how genetic analysis contributes to revealing mechanistic insight into developmental processes, such as cell differentiation, stem cell activity, cell polarity, and tissue morphogenesis.

Graduate students will present and discuss primary research articles, will guide group discussions, and write a critical review about a scientific manuscript deposited in BioRxiv.

Grading:
30% Presentations (a short and long presentation)
20% Leading a discussion
20% Participation in discussions
30% Written report

Module: Cell Biology of Gastrulation
CSB 1020H/S (Summer 2021*), Teaching Section LEC 0107
Coordinators: *Professors Ashley Bruce & Rudi Winklbauer*
Offered: Summer 2021* session, between May and July 2021 for six weeks (plus an organizational meeting in May).
Weight: One module (0.25 FCE)
Time: TBA
Location: St. George campus, Ramsay Wright Building, room TBA
Enrolment: Limited to 8 students

Description:
Gastrulation in different animals, including invertebrates and vertebrates, is used to illustrate biological processes and to discuss basic concepts in animal development. This course will explore cell behaviours that occur during 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 15, 2021.

Course: Advanced Microscopy and Imaging
Course Code: CSB 1018H (Summer 2021*), Teaching Section LEC 0101
Course Coordinator: *Professor R. Harrison*
Offered: Summer 2021* session in May and June (exact time TBA)
Weight: 0.5 FCE
Time: TBA
Location: University of Toronto, Scarborough campus
Enrolment: Limited to 10 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: practicum examination
    Meetings 12-13: student seminar presentations
    Meeting 14: Final Exam

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 15, 2021

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

CHM1448H/F, Modelling of Biochemical Systems (0.5 FCE, 12 weeks)
Instructor: *Professor David McMillen*
This course will be offered entirely online, in the Fall 2020 term. Days/times TBA.

CHM1448H/F, Modelling of Biochemical Systems. An introduction to mathematical modelling of complex biological systems, with a focus on biochemical kinetic models, their numerical simulation, and methods for analytically and computationally studying their behaviour. This is a one-term independent-study project course: students will be given a set of directed readings, then assisted in selecting an existing model from the literature. After reproducing existing results, students will be tasked with extending the model in a direction of their own choosing; this can include exploring different parameter regimes, incorporating new or different aspects of the underlying biology, or applying different analytical techniques. Students will work with the instructor to select a suitable project, matching their background and interests. Formal lectures will be replaced with a series of weekly meetings with the instructor to discuss progress and plans. (The nature of the course is such that it can be tailored to students without an extensive mathematical background, as long as they are willing to learn to work with computational software.)