

SAMPLE COURSE OUTLINE

Course Code, Number, and Title:

BIOL 4315: Genomics and Transcriptomics

Course Format:

[Course format may vary by instructor. The typical course format would be:]

Lecture 4.0 h + Seminar 0.0 h + Lab. 2.0 h

Credits: 4.0

Transfer Credit: For information, visit bctransferguide.ca

Course Description, Prerequisites, Corequisites:

Students are challenged to think critically about genome scale data and to think creatively about how to best design and utilize powerful computational tools in their analyses. They learn how to work with large nucleic acid data sets and draw meaningful conclusions that can be applied in modern research, medicine, and industrial settings. Students explore fundamental concepts behind genomic and transcriptomic analyses and design and execute genomic and transcriptomic analyses of real datasets. This course prepares students for future work designing and creating original analyses of novel genomes and transcriptomes, and provides the foundation for diverse bioinformatics applications, such as personalized medicine, bioremediation assessment, industrial quality control, and even forensic science.

Prerequisites: A minimum "C" grade in BIOL 3315, 3430, and CPSC 3280

Corequisites: None

Priority registration given to students admitted to the BSc Bioinformatics program

Learning Outcomes:

Upon successful completion of this course, students will be able to...

- Explain the methods by which bioinformatics data is stored and shared
- Access bioinformatics databases to obtain large volumes of bioinformatics data
- Describe the core concepts of genomic construction and genome annotation and apply established genomics computational tools on novel bioinformatics datasets
- Work with large volumes of next generation sequencing data, from sequencing platforms such as Illumina and Ion Torrent
- Design and interpret real RT-PCR and RNA seq experiments in order to carry out transcriptomic analyses to provide insight into gene expression and for a variety of biological processes
- Apply computational tools to characterize and interpret metagenomic datasets
- Use genomic data to obtain insights into broader biological processes, such as evolution, as well as specific pathologies such as cancer

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Instructor(s): TBA

Office: TBA

Office Hours: TBA

Phone: (604) 323-XXXX

Email: TBA

Textbook and Course Materials:

[Textbook selection may vary by instructor. An example of texts and course materials for this course might be:]

Golding, B, Morton, D, Haerty, W. "Elementary Sequence Analysis". McMaster University. 2016.

For textbook information, visit https://mycampusstore.langara.bc.ca/buy_courselisting.asp?selTerm=318

Note: This course may use an electronic (online) instructional resource that is located outside of Canada for mandatory graded class work. You may be required to enter personal information, such as your name and email address, to log in to this resource. This means that your personal information could be stored on servers located outside of Canada and may be accessed by U.S. authorities, subject to federal laws. Where possible, you may log in with an email pseudonym as long as you provide the pseudonym to me so I can identify you when reviewing your class work.

Assessments and Weighting:

Final Project 20%

Other Assessments %

[An example of other assessments might be:]

Midterm Exam 20%

Quizzes 5%

Assignments: 20%

Lab Work: 20%

Project: 10%

Participation: 5%

Participation Format: In class assignments

Proportion of individual and group work:

Individual: 80%

Group: 20%

Grading System: Letter grade

Specific grading schemes will be detailed in each course section outline.

Passing Grade: D

Topics Covered:

[Topics covered may vary by instructor. An example of topics covered might be:]

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Introduction: What are gene sequences? How are they saved and stored? Review: Central Dogma of Biology.

First Generation Sequencing: The Sanger Method. What is the difference between DNA sequencing, RNA sequencing, and protein sequencing?

Alignment and Functional Inference. How were the first genomes sequenced and constructed?

Next generation Genomics. How do next gen sequencing technologies work? What are their advantages and disadvantages?

Microbial Genomics. How is sequencing microbes different than eukaryotes? What important features of microbial life have been revealed from sequencing genomes? How have they been applied to medicine and biotechnology?

Genome wide association studies. How are these done? What have they accomplished? How have they been disappointing?

Changing Genomes: Reconstructing major genomic events in evolutionary history. How was the genome changed over the course of mammalian evolution?

Ancient Genomes: How do we extract and sequence ancient DNA? What have we learned from ancient genomes?

Gene and Genome Duplication Events. How can we identify them? What is their significance?

Metagenomics. Can we use genomic sequencing to define an entire ecosystem? Should we move to a gene sequence centered definition of biodiversity?

First generation Transcriptomics. How can we measure gene expression? What insights have this level of information provided? Details of RT-PCR and PSQ pyrosequencing will be covered.

Next generation Transcriptomics. How can we integrate gene expression measurements across the entire genome? Details and examples of RNA-seq analysis will be covered.

Creating new life. What is synthetic biology and how are novel genomes constructed and modified?

As a student at Langara, you are responsible for familiarizing yourself and complying with the following policies:

College Policies:

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SAMPLE COURSE OUTLINE

[E1003 - Student Code of Conduct](#)

[F1004 - Code of Academic Conduct](#)

[E2008 - Academic Standing - Academic Probation and Academic Suspension](#)

[E2006 - Appeal of Final Grade](#)

[F1002 - Concerns about Instruction](#)

[E2011 - Withdrawal from Courses](#)

Departmental/Course Policies:

Information unavailable, please consult Department for details.

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