This syllabus is a general representation of the course as previously offered and is subject to change.

BIOL/FNH 436 – Integrated Functional Genomics

General Course Syllabus (as of November 2019)

About the Course:

Course Description: This course is suited for those who are preparing for or just beginning graduate-level studies in a genomics-facilitated research environment. This course aims to introduces students to:

1. Modern biological research that aims to discover the genetic basis of phenotypes.
2. High-throughput technology used in research at the genome-wide level.
3. Theories and practices on RNA-seq analysis (R-language and big-data analysis).

Course topics include: high-throughput genetics workflow using model systems, genome-wide analysis for global transcript and protein profiling and their integration; applications focused on cell biology questions and biotechnologies to mitigate climate crisis due to increased atmospheric CO2.

Course Format: Lecture (Note: 25 minutes of lecture time per class will be set aside for tutorial sessions with hands-on exercises and group activities)
Credits: 3
Co-requisites: One of BIOL 335, BIOL 338.

Course Learning Outcomes:

By the end of this course, students will be able to:

- Design a gene-discovery study using genomics approaches for a given biological question.
- Collect candidate genes of interests by analyzing gene expression or other quantitative data using R.

Textbooks and Additional Resources:

Students will need:

- A laptop or an equivalent device that can run various on-line and off-line software including EXCEL and R-studio, for use in-class.
- iClicker for in-class participation.
- Access to course website on Canvas (canvas.ubc.ca) for course information and suggested readings.

Evaluation:

Students will be assessed on:

1) Their knowledge about the materials covered in the lectures/tutorials.
2) Course participation ranging from tutorials worksheets and pre-reading quizzes.
3) Their ability to analyze genomics data to produce biologically meaningful conclusions.

The mark breakdown is shown below:

Assessment	**Weight**
Midterms (two-stage exam): 2 x 20%	40%
Final - project design (5%), paper submission (group work, 5%), and take-home quiz (10%)	20%
R-Tutorial worksheets 6 x 2.5%	15%
Home-tutoring preparation 4 x 2.5%	10%
Pre-reading quizzes 4 x 2.5%	10%
Participation in class and surveys	5%

Two midterms will be an in-class written test on the knowledge-base. It has a two-stage exam structure where each midterm will contain one or two questions that can be revisited for group discussion. The second-stage exam answers will be used to revise the individual exams only for improvement.

The final will consist of a group project (to design and analyze a mock RNA-seq experiment using a real-world dataset) and take-home questions pertaining to the tutorial exercises and the group project.

Tutorial sessions will provide hands-on practice using R and group activities that help students to elaborate what they have learned in class and during homework.

Home tutoring: Students will collect information about specific technologies and theorems and share it with the group members during tutorial sessions.

Schedule of Topics:

A sample schedule from 2019W1 is below:

Week	Lecture Topic	Tutorial topic (HT = Home Tutoring)
1	Introduction to functional genomics	T0. Why R?
2	Genetics workflow using model systems/*Chlamydomonas* model Mutational resources	T1. R-studio set-up
3	High-throughput techniques for genetic screening – Mutation profiling, Phenotyping with molecular probes	T2. R- Data types/handling **HT1. CRISPR**
4	Quantitative PCR Differential expression	T3. R- qPCR analysis
5	Basics of genome-wide analysis: problems and solutions R-day 1; review of basic functions	T4. R- Plotting (1) **HT2. Advanced sequencing protocols**
6	Case study 1: genetic screening, gene expression, probe development, proteomics Case study 2: genomics in plant research	T5. R- Plotting (2) **HT3: How many seq-techniques are invented so far?**
7	**Midterm exam 1** Overview of RNA-seq workflow	T6. RNAseq – Data structure
8	Differential expression analysis and linear modeling Principal component analysis	T7. RNAseq – Quality control (Normalization, correlation) **HT4. Math theories relevant to biology**
9	Clustering/time series analysis	T8. RNAseq – Differential expression (Statistics, Fitting)
10	Hot trend: High-throughput scRNA-seq	T9. RNAseq – Analysis design, Visualization (Venn diagram)
11	**Midterm exam 2** Introduction to the group project (Case study 3)	T10. RNAseq – Group work
12	Help sessions for the group project	Help sessions for the group project
13	Group project presentation	Feedback to the group project
	Final exam (take-home)	

University Policies:

UBC provides resources to support student learning and to maintain healthy lifestyles but recognizes that sometimes crises arise and so there are additional resources to access including those for survivors of sexual violence.

UBC values respect for the person and ideas of all members of the academic community. Harassment and discrimination are not tolerated nor is suppression of academic freedom.

UBC provides appropriate accommodation for students with disabilities and for religious, spiritual and cultural observances.

UBC values academic honesty and students ae expected to acknowledge the ideas generated by others and to uphold the highest academic standards in all of their actions.

Details of the policies and how to access support are available on the UBC Senate website.