

BIOL436/FNH436: Integrated Functional Genomics (3 credits)

Term 1, 2016W Tues and Thurs 11:00-12:30 pm (Hugh Dempster Pavilion 201)
Prerequisite: BIOL 335 or 338

Instructor: Dr. Jae-Hyeok Lee (jae-hyeok.lee@botany.ubc.ca)

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Course Website: <http://www.elearning.ubc.ca/connect/>

Course design and main objectives:

Lectures and in-class tutorials will provide practical exercises suited for those who prepare or just begin graduate-level study in genomics-enabled research environment. This course intends to introduce students to

1. Modern functional genomics research involving genome-wide mutant collections, high-throughput mutation identification, and investigation of a gene's function using omics approaches including gene-expression/ proteome analysis.
2. Essential software tools used in genomics-level studies and their practical training.
3. Exercises on planning and presenting a research project utilizing genome-wide approaches.

Some of the specific learning objectives:

1. To learn about random mutagenesis, natural variation, indexed gene knock-out resources and targeted gene modification methodologies for preparing for a functional genomics project.
2. To learn ways to identify a newly introduced mutation by obtaining flanking-sequence-tags (FSTs) or whole genome sequencing.
3. To analyze sequencing-based genome-wide expression data by fold-difference and clustering.
4. To relate sequence homology to functional homologs by protein sequence analysis and phylogenetic inference.

Tutorial design to provide:

1. Hands-on practices focused on big-data analysis and bioinformatics tools that are frequently used in genomics-enabled research projects.
2. Group activities that help students to elaborate what they have learned in class and during homework.

Learning Outcomes: Students will

1. Achieve a good working knowledge of the high throughput technologies used in biological research laboratories.
2. Be able to critically evaluate published literature in the field of functional genomics.
3. Be able to integrate different high-throughput technologies to design a graduate-level genomics project to address specific biological questions.

Evaluation:

Students will be assessed on their knowledge of the materials covered in the lectures, course participation ranging from in- and out-class activities such as group discussion and project, and ability to analyze genomics data to produce biologically meaningful conclusions. Two midterms will be a written test (two-stage exam) in class on the knowledge-base, and the final will consist of take-home questions/tasks similar to tutorial exercises.

The mark breakdown is shown below:

Class participation: 20%

- At-home participation (10 pre-reading quizzes, on-line submission): 5%
- In-class participation (10 tutorial worksheet*): 10%
- (*Use of carbon-copy sheets allowing late submission)
- Term project submissions (4 components + 2 proposals): 5%

Two midterms: 40%

Final take-home exam: 20%

Group activities: 20%

- 5-min mini-lecture on two topics (ML): 5%
- Max 5-page term paper: 5%
- 5-min individual presentation: 10%

Term project() overview as group activities**

- Focused on the Chlamydomonas system (a soil-borne green alga)
- Each student will choose up to three subject areas of their interests.
- Group (4-5) will be assigned based on the subject areas.
- For a subject chosen from the given list (10 choices with specific review papers).
- Each student will generate one-page summary about the updated knowledge and remaining questions in the subject area (**component 1**).
- Each student will propose a novel genetic screen in the subject area. It should be hypothesis-driven and contain a high-throughput component (**screening proposal**).
- Individual screens will be peer-reviewed in the presence of a graduate student helper assigned to each group (**component 2**)
- Each student will choose a group of genes that are known or potentially involved in the subject area, whose mutations are likely uncovered in the chosen screening project (**Target gene proposal**).
- The target genes are analyzed by phylogenomics and co-expression analysis that will be learned during tutorial session, in order to provide likelihood contexts of the targets to be associated with the subject matter (**component 3**).
- Based on the analysis results, students will refine their hypothesis and present them in individual 5-min thesis presentation (Max 5 slides, **component 4**). During the preparation of individual presentation, students will have expert's help from the assigned graduate student helper.

What you need in class (during tutorial):

A laptop or an equivalent device that can run various on-line and off-line software, including Ugene, JMP, and EXCEL.

What you will expect to do outside class:

Average 3 hours preparation per each class for pre-readings and assignments.

Tentative Class Schedule

Date	Class theme	Tutorial	Term project and etc.
Week 0 (9.8)	Introduction to functional genomics. Group survey	What is a functional genomics project ?	n.a.
Week 1 (9.13-15)	Do we still need a model system? Model systems and genomics resources: <i>Arabidopsis/Chlamydomonas</i>	How to read papers? Peer teaching (NGS technology) . Online-survey tool.	Web resources for NGS technology. How to read papers.
Week 2 (9.20-22)	Phenotypes: High-throughput characterization by reporters, non-invasive techniques. Study design concept.	Excel software for science. Brainstorm about term project (subject review).	Subject submission.
Week 3 (9.27-29)	Mutations- induced (lecture), natural, indexed (papers)	Guest presentations by graduate students (2 per each day)	Component 1 Due
Week 4 (10.4-6)	Mutation identification: genetics and sequencing. ML1 (Application of CRISPR)	Sequence-based analysis for cloning (ugene or others)	Screening proposal due
Week 5 (10.11-13)	ML2 (FST detection methods), Mid-term 1 (Thu. wk1-4+ML1-2)	JMP and IGV software. Group discussion about proposed screening.	Component 2 Due (Sun)
Week 6 (10.18-20)	Phylogenomic analysis. INTERPRO-scan Mid-term 1 review.	What is 3-min or 5-min thesis? Multiple sequence alignment (MEGA or other analysis)	Target gene proposal due (Thu).
Week 7 (10.15-27)	Expression-based analysis: RNA-seq and modeling. ML3 (sequencing-based analysis)	Q-PCR analysis. RNA-seq analysis (1-2)	Target gene approval (Tue).
Week 8 (11.1-3)	Protein-based analysis: Mass spectrometry.	Target-gene analysis Statistics by JMP (1-2)	Component 3 Due (Sun)
Week 9 (11.8-10)	Genome-wide analysis toward system biology (summary)	IGV for visualization. Modeling software. Presentation prep.	Component 4 due (5 min presentation draft, Sun)
Week 10 (11.15-17)	Mid-term 2 (Thu. wk6-9)	Special presentation on 'R'	
Week 11 (11.22-24)	5-min thesis competition followed by peer evaluation 1,2	Peer review and guest judges	Common introduction as an option to take.
Week 12 (11.29-)	5-min thesis competition followed by peer evaluation 3,4	Peer review and guest judges	
Final Exam	Take home exam as a review of tutorial exercises.		Final and term paper submission due on 12.12 midnight