MMG1328H
Course Title: Advanced 'omics methods, paired analysis principles, and their applications Course
Location: Room 1062 Mt. Sinai Hospital
Course Time and Date: Tuesdays 2-4pm, April 8 - May 6, 2025 (no class on April 29)
Course Instructor(s): Hartland Jackson, Aleksandrina Goeva
Instructor Contact Information (email): hjackson@lunenfeld.ca; aleksandrina.goeva@utoronto.ca
Additional Lecturers (list name, email, Department): TBD
Maximum Number of Participants: 10
Prerequisites: MMG1004H, preference will be given to students who have completed MMG1344H

Course Overview:
Quantitative high-dimension technologies continue to rapidly revolutionize the study of molecular biology. With increasing parameters, resolution, dimensions, and new modalities, paired computational analysis is necessary to properly utilize these methods. Covering the current standard and state of the art in single cell and spatial transcriptomics, their analysis, and utilization with other 'omics technologies including proteomics, this course will detail how to use these technologies from experimental workflows through to paired analysis pipelines. Furthermore, we will discuss cutting-edge applications, the limitations of current systems, and a framework to develop new experimental and analysis methods. The course will feature a combination of lectures, discussion of recent publications, guest speakers and student presentations.

Course Objectives:
- Learn about sequencing and proteomics technologies and their various applications
- Understand the data processing and analysis of such datasets
- Discuss frameworks and principles for the development of new experimental and analysis methods
- Practice critical thinking skills in the evaluation of published articles and the choice of technologies for various applications

Marking Scheme:
- Attendance 10%
- Participation in discussions 20%
- Assignment 40%
- Final presentation 30%

If you anticipate missing a class you must let the instructor know in advance, given the weight on participation and the fact that there are only six classes. Providing that you had a legitimate reason for missing the class, you will be expected to catch up on the reading for that week that you can use to make up for the lost class.

The basic outline for what will be covered in the six weeks is below. Assigned reading will be sent out the week in advance. All students are expected to read the assigned articles and comment in class. These articles are meant to provide context for the accompanying lecture.

Week 1: Single cell. Why and How?
Week 2: Single cell analysis: workflow, limitations, and examples.
Week 3: Spatial transcriptomics. Why and How?
Week 4: Spatial transcriptomics analysis: workflow, limitations, and examples.
Week 5: What's next? Frontiers and methods development.
Week 6: Show and Tell: Assignment Presentation