

## **Biochemistry Graduate Courses**

### **9501: Scientific Writing (0.25 credits)**

This course prepares students for the writing of scientific documents such as abstracts, manuscripts, and grant applications. During class, students are expected to actively participate in the critique of writing samples provided by the instructors and to create writing samples for in-class assignments.

The course comprises three sections:

- Mechanics of writing (punctuation and word usage) and style of writing (effective words, sentences, and paragraphs) – session 1
- Scientific writing, including editing, writing for a lay audience, and creating a scientific paper - sessions 2-5
- Career choices and designing effective CVs - session 6

### **9511: Systems and Synthetic Biology (0.25 credits)**

The overall theme of this course will be directed towards investigation of the latest developments in the field of Synthetic Biology. Synthetic Biology is a vast area of study that can be loosely described as those efforts, which seek to make biology easier to engineer. Many recent advances in Chemistry, Biology, Computer Science and Engineering put this area of Biology at the **cutting edge** of promising new developments for improved products across many *industries* such as medicine, energy and the environment. Emerging avenues across the field of Synthetic Biology will be highlighted within the context of current efforts being made in the Human Genome Project – Write, specifically with emphasis on Genome Synthesis and Assembly, DNA Storage (information/biological function), DNA Delivery (genome transplantation), DNA Editing (Crisper etc) and Ethics.

### **9522: Applied Proteomics (0.25 credits)**

This course is targeted to students who will need to use proteomics approaches in their research project. The goal is to provide a more detailed understanding of the various technologies in proteomics so that the optimal protocol will be taken to carry out their experiments (sample preparation, instrument, data analysis). Students will be asked to actively participate in the course by giving a formal presentation (20-30 minutes depending on the number of registered students) on recent developments or applications as well as asking questions after presentations. Assignments and final exam will provide the remaining marks.

### **9545: Bioinformatics I (0.25 credits)**

1. RNA-seq experiments: from theory to costing. High throughput sequencing, an introduction to data types in high throughput sequencing. Designing HTS experiments for maximum power and minimum cost.
2. PCA, compositional biplots, and correlations
3. Introduction to the Barton RNA-seq dataset. Initial exploration of the data using PCA. Finding outliers. Implications for experimental design.
4. Removing outliers. Count normalization and data transformations. Why, how, when.
5. Differential abundance using edgeR, DESeq2 and ALDEx2. Comparing and contrasting the results.
6. Pathway analysis of differential abundance results (KEGG, GO)
7. Generalizing to microbiome, metatranscriptome and other data types.

### **9546 Bioinformatics II (0.25 credits)**

1. An introduction to RMarkdown, functional note taking and reproducible data analysis, plain text.
2. More R! data types, installing packages, simple plots, exploring data
3. Making a function() and running it.
4. An introduction to Bayesian thinking. Monte Hall and Bertrand's box, Regression to the mean, Gambler's fallacy
5. Common statistical errors when designing and interpreting biomedical experiments; or why the p-value is what you get, but the effect size is what you want.
6. An introduction to high throughput sequencing and data types generated in high throughput sequencing. The error structure and correlations in high throughput sequencing. Counts, or the idea of a lattice.

### **9549: High Throughput Transcriptomics (0.5 credits)**

High Throughput Transcriptomics: Technologies & Data Interpretation provides the fundamental knowledge necessary for students to make use of state-of-the-art transcriptomic technologies and available datasets. This course will cover currently available technologies, experimental design considerations, obtaining publicly available data and how to analyze and interpret the results. This is a graduate-level course offered by Western University through the Department of Biochemistry. This course is suitable for life sciences students with interests in generating or using transcriptomic data in their projects as well as students with backgrounds statistics, mathematics or computer science/engineering interested in developing new methods for the analysis of transcriptomic data.

### **9552: Quantitative Approaches in the Biomedical Sciences (0.5 credits)**

Quantitative approaches are now ubiquitous used throughout biomedical research and it has become increasingly important for biomedical researchers to include training in advanced statistics, computation and data science in order to maintain modern research programs. This course is designed to provide biochemistry graduate students with the opportunity to efficiently learn quantitative tools and techniques relevant to their research regardless of their prior training background. Topics include programming, software development, permutation and randomization testing, stochastic modelling, machine learning, artificial intelligence, generative modelling, data cleaning, and visualization.

### **9703: Chemical Biology (0.25 credits)**

This course will begin with a broad overview of chemical biology with special emphasis on topics, including protein synthesis with non-canonical amino acids, probing cellular functions and protein-protein interactions with small molecules, and chemical genetic approaches to drug discovery. Following the course lectures, each student will have the opportunity to lead a Journal Club and discussion session. Students will be expected to write a 1-page 'news & views' article about any area of chemical biology.

### **9509: Protein Structure Determination: Theory, Practice, Analysis and Validation Synopsis (X-ray crystallography emphasis) (0.25 credits)**

This course is targeted to students who use X-ray and/or NMR structures in their work, and the goal is to provide a deeper understanding of the methods as well as a more comprehensive knowledge of how to analyze and validate structures in the Protein Data Bank. Approximately 40% of the course will cover the theory and fundamentals of experimental structure determination by X-ray crystallography (9509S) or NMR spectroscopy (9510S); note that the two courses will be delivered on alternate years. This part of the course will cover practical aspects including protein preparation, data collection and analysis, structure solution and refinement. Common aspects of the courses (approximately 60%) will cover the use of both NMR and X-ray derived structures: understanding how chemical restraints are used in the structure solution; how to evaluate structure quality and reliability; location and analysis of problem areas

or ambiguities; and comparison of related structures. Some complementary methods will also be discussed, and may include homology modelling, CD spectroscopy, calorimetry, X-ray and/or light scattering, analytical ultracentrifugation.

### **9510: Protein Structure Determination: Theory, Practice, Analysis and Validation Synopsis (NMR spectroscopy emphasis) (0.25 credits)**

This course is targeted to students who use X-ray and/or NMR structures in their work, and the goal is to provide a deeper understanding of the methods as well as a more comprehensive knowledge of how to analyze and validate structures in the Protein Data Bank. Approximately 40% of the course will cover the theory and fundamentals of experimental structure determination by X-ray crystallography (9509S) or NMR spectroscopy (9510S); note that the two courses will be delivered on alternate years. This part of the course will cover practical aspects including protein preparation, data collection and analysis, structure solution and refinement. Common aspects of the courses (approximately 60%) will cover the use of both NMR and X-ray derived structures: understanding how chemical restraints are used in the structure solution; how to evaluate structure quality and reliability; location and analysis of problem areas or ambiguities; and comparison of related structures. Some complementary methods will also be discussed, and may include homology modelling, CD spectroscopy, calorimetry, X-ray and/or light scattering, analytical ultracentrifugation.

### **9516: Cancer Biology (Precision Oncology) (0.25 credits)**

The overall theme of this course will be directed towards investigation of the biochemical and mechanistic basis underlying the development and application of specific molecular-targeted therapies that can be employed for precision cancer medicine. Both proven examples of molecular-targeted therapies and emerging avenues for the development of new molecular-targeted therapies will be highlighted. A central focus will be on constituents of signal transduction pathways (for example, protein kinases) and the development of strategies for targeting these constituents for the treatment of cancer. Following an introductory lecture, Journal Club/Discussion sessions will be led by student participants. This course will draw on the primary literature to provide examples for discussion. Students will also be expected to complete a Knowledge Translation Assignment that is comprised of a News & Views Article, a Press Release and an Invention Disclosure based on a recent advance in the field. A short presentation highlighting the News & Views Article, Press Release and/or Invention Disclosure will also be required.

### **9551: Artificial Intelligence for Genome Data Science (0.5 credits)**

Artificial Intelligence for Medicine provides the basic knowledge necessary for students to pursue biomedical research using machine-learning methods. The course will focus on concepts necessary for applying machine learning to multiomic high-throughput data and their applications to topics relevant to human health. This is a graduate-level course offered by Western University through the Department of Biochemistry. This course is suitable for life sciences students with interests in applying machine learning in analyses of omics data sets (e.g. next-generation DNA and RNA sequence, epigenetic data, proteomic) or students with a background in statistics, mathematics or computer science/engineering interested in developing new methods for the analysis of omics data.