

Biochemistry 9545B  
Macromolecular Informatics

January 2012

Course Co-ordinator: Dr. Greg Gloor, [ggloor@uwo.ca](mailto:ggloor@uwo.ca)

Day and Time: to be determined

Location: C1 MBL

The course will cover the design and analysis of high-throughput sequencing for ChIP-seq and RNA-seq

The course will start with a self-study literature review of technologies (i.e., course co-ordinator will assign each student several papers to read and critique). Then we will move on to learning analysis methods.

Course Co-ordinator plans on covering the following:

Planning the experiment

Collecting the data

Generating the input tables (This will require some bash and Perl)

Analysis using Differential expression tools (This will require some R)

Testing hypotheses with the output

It is anticipated that the course will run over the term, with some concentration early on learning UNIX, bash, Perl and R and later stuff showing practical uses of these tools

Evaluation:

Based on the assignments students complete.

**Academic/Scholastic Offences:**

Scholastic offences are taken seriously and students are directed to read the appropriate policy, specifically, the definition of what constitutes a Scholastic Offence, at the following Web site:

[http://www.uwo.ca/univsec/handbook/appeals/scholastic\\_discipline\\_grad.pdf](http://www.uwo.ca/univsec/handbook/appeals/scholastic_discipline_grad.pdf) Academic Handbook, Exam, Course Outlines Page 4 Issued: 2011 02

All required papers may be subject to submission for textual similarity review to the commercial plagiarism-detection software under license to the University for the detection of plagiarism. All papers submitted for such checking will be included as source documents in the reference database for the purpose of detecting plagiarism of

papers subsequently submitted to the system. Use of the service is subject to the licensing agreement, currently between The University of Western Ontario and Turnitin.com (<http://www.turnitin.com>).