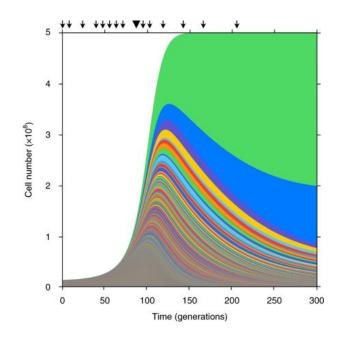Molecular Genetics
UNIVERSITY OF TORONTO

The Barcode-Sequencing Technology and its Application to Predicting Evolution

Presented by: Dr. Sasha Levy

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Next-generation measurement of biological function will rely on massively parallel experiments that convert functional differences into differences in nucleic acid sequence counts. This powerful approach, loosely defined as Barcode-Sequencing (Bar-Seq), has the potential to revolutionize a variety of areas in academics and industry, from functional genomics to protein engineering to synthetic biology. I will introduce current and future applications of Bar-Seq with a special emphasis on how we are using the technology to predict evolution. I will also discuss challenges that must be overcome to make Bar-Seq experiments as accessible, reliable, and shareable as RNA-Seq.

Host: Dr. Fritz Roth

Date: Monday, March 2nd, 2020
Time: 4:00 PM
Place: PGCRL Auditorium, 686 Bay Street