

MCB WINTER SESSION 2020

The courses below are open to all MCB graduate students and to qualified upper-level MCB undergraduates. Please contact Elaine Mirkin (elaine.mirkin@uconn.edu) with any questions. Information on Winter Session 2020 dates and graduate-level course fees can be found [here](#). Please note: semester GA tuition waivers do not apply to intersession courses.

MCB 5671-1 Advanced Theory and Practice of Laboratory Techniques in Microbiology – Advanced Liquid Handling and Sample Processing

1 credit

Enrollment Limit 4

Instructor: Joerg Graf

Room BPB 401 and BPB 402B

January 6, 2020: 9 a.m. to 5 p.m.

January 7, 2020: 9 a.m. to 5 p.m.

January 8, 2020: 9 a.m. to 12 p.m.

Instructor Consent Required

Class Notes - Contact elaine.mirkin@uconn.edu for permission number. Prerequisite is MCB 5427

Introduction to Molecular Biology Techniques or permission of instructor. Participants will learn how to program and use Eppendorf's EpiMotion 5073. In addition, students will learn how to use a fluorescent plate reader and a capillary gel electrophoresis system (QIAxcel). Students will also be trained in using multi-channel and electric hand-held pipettes.

MCB 5671-2 Advanced Theory and Practice of Laboratory Techniques in Microbiology – Microbial Genome Sequencing, Assembly and Annotation

2 credits

Enrollment limit 6

Instructors: Joerg Graf, Ahmad Hassan, and Kathleen Kyle

Room BCH 202, BCH 204, BCH 205

January 9, 2020: 9 a.m. to 5 p.m.

January 10, 2020: 9 a.m. to 5 p.m.

January 13, 2020: 9 a.m. to 5 p.m.

January 14, 2020: 9 a.m. to 5 p.m.

January 15, 2020: 9 a.m. to 5 p.m.

Instructor Consent Required

Class Notes - Contact elaine.mirkin@uconn.edu for permission number. Prerequisite is MCB 5427

Introduction to Molecular Biology Techniques or permission of instructor. In this module, each student will sequence, assemble and annotate a bacterial genome. The sequencing will be done using the MinION from Oxford Nanopore Technologies. The data analysis will include de novo assembly as well as annotation. The data analysis will be done using a range of freely available and commercially available software.