

ENTO XX: Ecological Entomology
Spring, 2016, 3 credits
Department of Entomology, KSU

Instructor

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Course Description: DNA-sequence level variation enables powerful tests of hypotheses about how populations expand and contract, disperse, and diversify through neutral and selective processes. Moreover, the structure and dynamics of communities and other higher-order biological assemblages may also be inferred from sequence-level variation. With the advent of affordable and reliable DNA sequencing of entire genomes, ecologists and evolutionary biologists are now in a position to examine the above biological processes at larger scales and often with much greater confidence. In this course we will explore the current state of the field of 'ecological genomics', including sequencing technology, analytical tools, and applications in basic and applied systems. We will emphasize 'hands-on' learning, often applying hypothesis testing to real or manipulated data sets. We will not do bench work, instead focusing on concepts, data analysis and interpretation. Statistical modeling of data will be an important component, but this is not a statistics course and we will not be deriving or evaluating models, only applying them.

Learning outcomes:

The goal of the course is to develop a broad command of the topic and some technical skills related to data analysis, including the ability to:

1. Describe the different 'flavors' of sequencing technology and evaluate their suitability for various types of analyses.
2. Derive genomic tests for biological hypotheses related to population and community dynamics.
3. Apply statistical models to test hypotheses, within the context of available software packages.
4. Interpret and critically evaluate primary literature applying genomics to ecological questions.
5. Identify different sub-disciplines within ecological genomics, recognizing the breadth of biological questions that each field addresses.

Evaluation:

Performance in the course will be evaluated based on:

1. Participation in in-class discussions including demonstrating command of assigned readings.
2. Completion of 'hands-on', data analysis assignments.
3. Leading of one or more group discussions on a peer-reviewed scientific paper.
4. Completion of individual or group projects (TBD) that may either focus on a student's own data or on data mined from online genomic archives. Project topics will be agreed upon by students and the instructor.

Course Materials:

No text is required for this course. We rely on published primary studies and review articles for written material, and open source software to learn and perform analyses.

Prerequisites:

Ideally, students will have completed basic courses in genetics (including some basic population genetics and statistics). However, the course may be taken without these prerequisites upon instructor approval. Programming skills are helpful, but not necessary; we will learn as we go.

Tentative Course Schedule: (subject to student input)

Week 1	31 flavors of next-generation sequencing
Week 2	Population genetics – a brief review
Week 3	Calling DNA variants in populations
Week 4	Landscape genomics – dispersal and gene flow
Week 5	Phylogenomics
Week 6	Metagenomics
Week 7	Transcriptome-wide gene expression
Week 8	Plasticity in changing environments
Week 9	Epigenomics
Week 10	Co-evolution
Week 11	Speciation and genomic divergence
Week 12	Introgression and secondary contact
Week 13	Local adaptation
Week 14	Special topic: TBD
Week 15	Project presentations