Population Genetics & Genomics
BIL 551 | BIL 651 | MBE 529 | MBE 629
Tue & Thu 4:00-5:30 PM
SLAB 114 (RSMAS)
Spring 2017

Instructor:
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Textbook:
Nielsen, R. and M. Slatkin. 2013. An Introduction to Population Genetics: Theory and Applications. Sinauer Associates, Sunderland, Massachusettes, USA.

Course Description:
This course provides an introduction to population genetics, which examines the evolutionary processes that affect the allele frequencies of natural populations: mutation, genetic drift, natural selection, and gene flow. Population genetics has had a long mathematical tradition and is rich in theory and empirical data. In this course, we will examine all aspects through mathematical models, methods of measuring genetic variation, and readings of published empirical studies. Taxonomic focus will be broad and will include both model and non-model organisms. With the genomics revolution, population genetics theory has renewed relevance for understanding genomic-scale patterns of genetics diversity, as a means to identify genes of importance for human disease, agricultural diseases and breeding, and for developing conservation and management strategies.

Student Learning Objectives:
By the end of this course students will have a solid foundation in the mechanisms of evolution, population genetic theory, and mathematical applications. For undergraduate students, this course will prepare you for an entre into fields of bioinformatics, population genetics and genomics, including applications in agriculture, biotechnology, and medical fields. For graduate students, this course is meant to be a beginning. It will offer an opportunity to integrate an aspect of population genetic and evolutionary thinking into your current research and will give you perspective for future forays in the field.

Schedule of Lecture Topics

Lecture Topic	**Nielsen & Slatkin**
History of Population Genetics	Intro
Allele Frequencies, Genotype Frequencies, & Hardy-Weinberg Equilibrium	1
Genetic Drift & Mutation	2
Coalescent Theory	3
Maximum Likelihood, Bayesian Statistics, Markov Chain Monte Carlo	B,C
Population Subdivision	4
Inferring Population History & Demography	5
Mid-term Exam	**TBA**
Linkage Disequilibrium & Gene Mapping	6
Selection 1	7
Selection in a Finite Population	8
Neutral Theory & Tests of Neutrality	9
Selection 2: Interactions & Conflict	10
Quantitative Genetics	11
Conservation Genetics	--
Final Exam	**TBA**
Software presentations	
Software presentations	

Course Format:
The course will be interactive, a hybrid between traditional lecture and flipped format. Each Tuesday there will be a formal lecture presented by the professor, followed by student-led discussion of assigned readings the following Thursday. Students will be expected to prepare for each class section by completing the assigned readings, thinking about previous lecture topics, and preparing questions for the instructor and their classmates. During the semester, each student will choose an analytical software package to learn, analyze a data set, and demonstrate to the class at the end of the semester with a 20-min powerpoint presentation. There will be one mid-term exam following spring break and a final exam.

Grading:

Participation	10%
Problem sets	10%
Exam 1	30%
Exam2	30%
Software presentation	20%

Participation: You are signing up for a course called "Population Genetics & Genomics" so I assume you are self motivated to learn the material. I expect everyone to show up for every class unless you are sick or have an acceptable excuse. "Participation" doesn't mean just showing up, though. This is a small class, so participation means engaging in the material, asking relevant questions, and providing insights that others do not see. Most class sessions will follow a discussion format and we also will work through problem sets together. You should also take notes as you read so that you are prepared for a discussion part. We will review the answers to these questions during our discussion, but you should also strive to come up with some of your own questions regarding the readings. So…. participation means being fully engaged and prepared for class.

Problem Sets: To help you synthesize and learn to apply the issues covered in lecture and discussion sections, problem sets will be assigned some weeks. These will be due the one week after they are assigned. You may work on the homework problem sets independently or in groups, but if you work in a group you should contribute equally and write up and turn in your answers separately. Late problem sets will be marked down 10% for each week they are late.

Exams: Two exams will be assigned, a mid term and a final. These will differ somewhat for graduate and undergraduate students.

Software Presentation: Many software programs have been developed in the fields of population genetics and molecular evolution. Each student will be asked to review and present the utility and functionality of one of these programs at the end of the term. Which program you will present will be determined in consultation with me. A list of some of the many softwares you might choose from is provided on the last page of your syllabus.

Exam Make-up and Incomplete Policy:
Make-up exams are discouraged. If circumstances are such that you are unable to take the exam, please contact me by e-mail (kevin.g.mccracken@gmail.com) in advance of the exam. Incomplete grades will only be authorized under special circumstances. Your participation in the course will factor into this decision.

Student Code of Conduct:
Students are subject to the UM Student Honor Code. The *existence or even the appearance* of plagiarism, cheating, or any other forms of academic dishonesty will not be tolerated, and will result in immediate failure of the course (not just the assignment). Students that *participate or appear to participate* in these types of activities will receive a F as the final recorded grade, be withdrawn from the course, and may be referred to the Dean of Students. Participation in this course implies that these terms are mutually agreed upon.

Other Policies:
Needs of students with disabilities will be accommodated following university policies and all applicable federal laws. Please talk to the instructor if you require assistance. The Office of Disability Services in the Academic Resource Center, N201, Whitten University Center provides disability services. Student athletes and members of the U.S. military should coordinate their absences with the instructor in advance.

Additional Texts:

There are several other good books in the field of population genetics. You might find some of these helpful.

Avise J.C. 2004. Molecular Markers, Natural History, and Evolution. 2nd edition. Sinaur Associates.

**Avise's book is a classic in molecular ecology.*

Gillespie J.H. 2004. Population Genetics; A Concise Guide, 2nd edition. Johns Hopkins University Press.

**A classic guide to fundamental population genetics concepts*

Hartl D.L., Clark A.G. (2007) Principles of Population Genetics, 4th edition. Sinauer Associates.

**A great textbook covering population genetics. Descriptions of population genetic principles are lucid.*

Halliburton R. 2004. Introduction to Population Genetics. Pearson Prentice Hall.

**Another excellent population genetics textbook.*

Wakeley J. 2008. Coalescent Theory: An Introduction, 1st edition. W.H. Freeman.

**A advanced population genetics text dealing with coalescent theory.*

Li W.-H.1997. Molecular Evolution. Sinaur, Sunderland, MA.

**This is probably the best reference text for molecular evolution, but it can be very mathematical and difficult at times. It is now out of print. The text covers phylogenetics, coalescent theory, and higher level mechanisms for molecular evolution such as gene duplication and transposition.*

Population Genetics/Genomics Softwares:

Pop Gen Softwares

G-PhoCS
Heylab Software
IMgc
Hudson Lab
LAMARC
BEAST
dadi
msBayes
Pritchard Lab
Structure Harvester
Stephens Lab
CMPG Lab
ATGC: Montpellier Bioinformatics
Arlequin 3.5
DnaSP
IBD Web Service
Felsenstein Software Site
Rambaut Lab
Network
SplitsTree4
DensiTree
Posada Lab
MrBayes
PhyML
PAUP* 4.0
INCA
bgc
BayeScan
SweepFInder
SweeD
Gompert Lab
Buerkle Lab
MGLTools
ClineFit
Abbababa
Cn3D
PyMOL
DINO
SWISS-MODEL Workspace
GOLD
HaploBlock
Haploview
LDhat
Rarefaction Calculator
OligoCalc
Lat/Long GPS distance
GEOPORTAL-SERNANP
phrapl - O'Meara Lab
ImageJ
STRING: Funct Prot Assoc Networks
NewHybrids

NGS Tools

FASTX-Toolkit
PRINSEQ @ SourceForge.net
VCFtools
PLINK
PLINK/SEQ
Ultraconserved Elements (UCEs)
Genome Analysis Toolkit
SOAPdenovo
RNA-Seq De novo Assembly Using Trinity
PGDSpider
rna-star
Stacks
MaSuRCA
ALLPATHS-LG
Roche NimbleGen
MYcroarray