Cornell courses relevant to Population, Comparative & Evolutionary Genomics

Assembled by the Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu)
Available as a PDF downloadable from the 3CPG web site under “For Current Grads & Postdocs”, “For Undergrads”, and “For Prospective Grad Students & postdocs”

Please send corrections or updates to Chip Aquadro (CFA1@cornell.edu)

SPRING 2019 COURSES
(check Class Roster and Courses of Study for updates)

BIOMG 1290 Personal Genomics and Medicine – Chip Aquadro
3 credit. Preference given to freshman & sophomores, no prerequisites. Capped at 130
MWF 11:15 am – 12:05 pm (lectures M & W, discussions F)
Charles (Chip) Aquadro (MBG)
Are you curious about your family ancestry? How, and why, might your genetic ancestry have influenced the diseases to which you are susceptible? Do you have allergies to milk or wheat? Does a relative suffer from a genetic disease, and you wonder if you might also be at risk? How will medicine and insurance be impacted by DNA testing? How will your own future, your quality of life, your decisions regarding children be impacted with this information available to anyone with as little as $99 and a saliva sample? What are the scientific, ethical, legal and social challenges obtaining and using this information? This course will introduce you to the challenges and opportunities of DNA testing that is rapidly becoming part of our future.

NTRES 2830 DNA, Genes, and Genetic Diversity – Matt Hare
4 credits. Prerequisites: BIOEE 1780 or permission of instructor. Letter grades only.
Lecture: MWF 9:05 – 9:55 AM Lab Sections: Th 9:05 – 11:00 AM, F 2:30-4:25 PM
Do genes make us who we are? What are the rules of inheritance and when don’t they apply? How does a genome carry enough information to code for a complex organism? Can we keep an endangered species from going extinct based on information in its genome? This introductory genetics course is distinct from others at Cornell by devoting 1/3 of the semester to population-level topics including heritability, population connectivity, genetic rescue, evolutionary capacity and the factors determining levels of genetic diversity. These topics build upon a foundation of Mendelian transmission genetics (rules of inheritance) and molecular genetics (processes leading from genes to phenotype). Lab activities include use of DNA databases, bioinformatic tools, simulations, model construction, debate and role play. Useful for advanced courses in conservation biology and evolution.

NTRES 3400: Molecular tools for ecology, conservation, and natural resource management – Nina Overgaard Therkildsen
3 credits, Lectures Tues, Thurs 09:05 - 09:55, Lab Sections: Mon 02:00 - 04:25. Prerequisites: One semester of introductory genetics (e.g. BIOMG 2800 or NTRES 2830) is recommended, but not required. Target audience is Sophomores and Juniors in the EES and Biology majors, though others are welcome. Molecular genetics has become one of the fastest growing fields in the life sciences, and application of molecular methods has spread to virtually all fields of modern biology. In this course, we will examine how DNA analysis and modern ‘omics’ technologies can be used to address important issues in ecology, conservation, and natural resource management such as identification of species, populations, and individuals, reconstruction of phylogenetic and kinship relationships, and inference of migration patterns, behavior, and abundance. The focus will be on practical applications, and students will develop both a theoretical understanding of the methods and hands-on experience with all steps from sample collection, molecular biology laboratory techniques, data analysis, and communication of results. Students will learn to identify the major types of genetic variation, their function in the genome, and their utility for molecular ecological analyses; to explain and perform basic molecular biology laboratory techniques such as DNA extraction, polymerase chain reaction (PCR), and gel electrophoresis; to analyze raw molecular sequence and genotyping data and interpret the results in an applied context; to summarize the strengths and limitations of molecular ecological methods and identify scientific questions in ecology, conservation, and natural resource management that can be addressed with a molecular approach.

BIOEE/MATH 3620 - Dynamic Models in Biology – Steve Ellner and Elizabeth Wesson
Next offered Spring 2019
4 credits. Prerequisite: two majors-level biology courses and completion of mathematics requirements for biological sciences major or equivalent, or consent of the instructor.
Lecture TR 1:25 – 2:40 pm, computer lab F 12:20 - 2:15pm
Introduction to the development, computer implementation, and applications of dynamic models in biology. Case-study format covering a broad range of application areas such as gene regulatory networks, neurobiology, infectious disease management, and conservation of endangered species. Students also learn how to study dynamic model of biological systems on the computer using the R scripting and graphics environment.

PLBIO 4000 / 6000 Concepts and Techniques in Computational Biology – Gaurav Moghe  
Spring. 4 credits. Letter grades only.  
Prerequisites: Biology courses: BIOMG 2800 or PLBRG 2250 and PLBRG 3250, BIOMG 3320 or BIOMG 3350, or equivalent. Computational courses: CS 1110 or equivalent. Statistics courses: BTRY 3010, STSCI 2150, or equivalent. Prerequisites may be waived with the permission of the instructor. Co-meets with PLBIO 6000.  
This course is geared towards graduate students and advanced biology undergraduates seeking a better understanding of computational biology. Lectures will be a combination of presentations, paper discussions and hands-on sessions. Labs and paper discussions will have a significant component of plant science, but students from non-plant fields are also encouraged to register. Students will learn to work in a Unix environment, code using Python/R, and deploy tools for genome assembly, RNA-seq data analysis, local and global sequence alignment, protein domain searching using Hidden Markov Models, phylogenetic reconstruction, metabolomic analysis, and machine learning. Lectures will cover the algorithmic concepts underlying popular tools. The students will also learn practical aspects of implementing these tools in their own research using facilities available at Cornell.

BTRY 4381/6381 - Bioinformatics Programming – Haiyuan Yu  
3 credits. Letter grades only.  
Lecture Tues 2:55PM - 04:10PM, Lab Thursday 2:55 – 4:10 pm  
Prerequisite: at least one introductory course in computer programming (any language) and one in statistical methods, or permission of the instructor.

A higher level programming course using Perl and available bioinformatics tools and techniques for the analysis of molecular biological data, including biosequences, microarrays, and networks. This course emphasizes practical skills rather than theory. Topics include advanced Perl programming, R and Bioconductor, sequence alignment, MySQL database (DBI), web programming and services (CGI), microarray analysis, and methods for inferring and analyzing regulatory, protein-protein interaction, and metabolite networks.

BIOMG 4390 - The Molecular Basis of Disease – Charles Danko and Hojoong Kwak  
3 credits. Student option grading.  
Lecture Tues/Thurs 10:10 - 11:25 am.  
Prerequisites: BioMG3300, or BioMG3310 and BioMG 3320, or BioMG3320, or BioMG 3350, and BioMG2800  
This course will examine how changes in the normal expression, structure, and activity of gene products caused by genetic mutations and environmental agents lead to disease in humans and other animals. The material will focus on how proteins with modified structures and biochemical activities cause alterations in normal cellular processes, as well as the physiological consequences of these changes. Topics will be selected from hormone insensitivity syndromes, gene fusions resulting in hybrid proteins, gene amplification, gene inactivation, disruption of signaling pathways, genetic variation in non-coding transcriptional regulatory elements, and the molecular actions of environmental poisons and toxins. The methods used to identify the underlying biochemical and genetic basis of diseases, as well as possible pharmaceutical and genetic therapies for treating the diseases, will be presented.

BIOLP 4400 / ENTOM 4400 Phylogenetic Systematics – Kevin Nixon  
4 cr, Tu/Th 10.10-11 am and a biweekly computer lab, for a total of 5 lab hours per week (lab times TBA)  
This course covers basic and advanced theory and methods of phylogenetic analysis. Introduces students to phylogenetic analysis using parsimony, maximum likelihood and Bayesian analysis methods. Allows students to gain hands-on experience with computer programs which analyze both morphological and molecular data. Topics also include applications of phylogenetic methods to biogeography and evolutionary studies. Provides the fundamentals of understanding and interpreting phylogenetic analyses to any student using phylogenetic trees in their current or future research.

BIOLP 4470 Molecular Systematics – Jeff Doyle  
Lecture, MW 8:40 – 9:55 am, 3 credits. Lec. [offered alternate years, next offered Spr 2020]  
Theory and practice of using molecular evidence, particularly DNA sequence data, for addressing diverse systematic and evolutionary questions. Emphasis is on phylogeny reconstruction, particularly in eukaryotic
systems. The organization and evolution of nuclear and organelar genomes is described from the standpoint of their suitability for systematic and evolutionary studies.
Prerequisites: BIOEE 1780 or BIOMG 2810 or BIOMG 3300, or BIOMG 3320, or permission of instructor.

BIOEE4530 / BIONB3530 Speciation: Genetics, Ecology, and Behavior – Kerry Shaw
Spring. 4 credits. Limited to 40 students. Prerequisites: BIOEE 1780 and BIOMG 2810 or equivalents, or permission of instructor. S-U or letter grades.
TR 10:10 – 11:25 am; Offered alternate years. [offered Spring 2019]
Advanced course in evolutionary biology focusing on the pattern and process of speciation and the nature and origin of behavioral, morphological, physiological and ecological traits that form the intrinsic barriers to gene exchange. Lecture topics include species concepts and definitions, the history of ideas about speciation, the biological basis of intrinsic barriers to gene exchange, current models for the origin of such barriers, genetic architecture of speciation, rates of speciation. Emphasis is on developing a rigorous conceptual framework for discussing speciation and on detailed analysis of a series of case histories.

BIOMG 4610 Development & Evolution – Mariana Wolfner
TR 2:55-4:10; 3 credits, letter grade only. Every other year (odd-number years); next offered Spring 2019.
Prerequisites: genetics, molecular biology and evolution (e.g. BioMG2810, BioMG3320 (or 3300 or 3330), BioEE1780 or their equivalents).
Have you ever wondered what makes animals develop to look so different? Amazingly, the same fundamental pathways regulate many aspects of development across the animal kingdom, but over the course of evolution they have been modified in different lineages to cause striking variation in form and function. This course addresses the ways in which these fundamental pathways have changed during evolution, and how this results in the dazzling diversity seen in the animal kingdom. Class meets twice a week to explore the fascinating, new and current field of "EvoDevo" through readings of papers in the current scientific literature, and lecture and in-class discussion. The course material requires background in Genetics, Evolution and Molecular Biology - usually acquired through the prereq courses.

ENTOM 4610 - Model-Based Phylogenetics and Hypothesis Testing – Corrie Moreau (first offered 2020)
3 credits. Student option grading. (first offered Spr 2020, Corrie Moreau arriving Jan 2019)
Prerequisite: BIOEE 1780 or BIOMG 2800 or equivalent, or permission of instructor.
A variety of disciplines in biological research address questions that rely on a phylogenetic framework for hypothesis-testing, including the fields of ecology, epidemiology, behavior, physiology, evolution, and genomics. This course will provide an advanced undergraduate/graduate level introduction to model-based methods of phylogenetic analysis including maximum likelihood and Bayesian methods. The emphasis will be on DNA sequence data and issues associated with reconstructing phylogenetic trees from multiple gene loci. In addition, the course will cover how phylogenies can be used in the context of evolutionary hypothesis testing (including fossil-calibrated phylogenies, character mapping, detecting diversification rate shifts, ancestral state reconstruction, and historical biogeography) using rigorous statistical methods. The course will include a computer laboratory for performing analyses using real data sets. Beginning skills in R programming will be introduced, and students will build an independent dataset to analyze using the techniques introduced in class.

BIOEE 4640: Macromutation – Amy McCune [will not be offered 2019 and possibly not 2020]
4 credits. Lecture TTh 10:10-11:25, Discussion section to be arranged. Limited to 35 students. Offered alternate springs. next offered spring 2018. [will not be offered 2018 and possibly not 2020]
Prerequisite: BIOEE 1780 or permission of instructor.
Advanced course in evolutionary biology centered on large-scale features of evolution. Areas of emphasis include phylogeny reconstruction, using phylogenies, patterns and processes of speciation, the origin of evolutionary novelties, causes of major evolutionary transitions, and patterns of diversification & extinction in the fossil record. Discussion of these topics requires integration of genetics, morphology, systematics, paleobiology, development and ecology.

ENTOM 4700 / BIOEE 4800 – Ecological Genetics [of Infection and Disease] – Brian Lazzaro
4 credits, Offered odd-year spring semesters; Offered Spr 2019
Prereq: BioEE 1780 or permission of instructor. Familiarity with genetics and basic statistics is recommended. Satisfies major requirements in Entomology and Ecology and Evolutionary Biology.
Special offering of Ecological Genetics. The standard Ecological Genetics course focuses on the application of population genetic concepts in ecological or applied contexts, with emphases on measuring adaptation in natural populations, detecting the effects of population demography, and determining the genetic basis of quantitative
traits. In this special offering, the contextual examples will be related to host-microbe interactions and the establishment and spread of infectious disease in natural populations of animals and plants. Illustrative examples will be drawn from the primary research literature to demonstrate experimental techniques and methods of data analysis on single-gene, multi-locus and genome-wide scales. Although the examples used in class will focus on infection, resistance, and host-pathogen co-evolution, the experimental and methodological approaches can also be applied to other ecologically relevant traits and processes. Outcome 1: You will be introduced to basic models of genetic evolution, and shown how they can be applied and tested in real biological scenarios. There will be heavy reliance on case examples from the primary scientific literature, in addition to lecture-based presentation of abstract concepts. Outcome 2: You will learn how to conduct population and quantitative genetic tests on real data sets, and to interpret test results to yield plausible biological interpretation. Outcome 3: You will apply a diversity of tests to the same or related example data sets, and will draw logical conclusions from the joint results of all tests applied. You will interpret specific data and results in the context of broader concepts covered in the course to reach reasonable biological conclusions. You will employ "scientific thinking" to solve problems that mirror real-life experimental scenarios.

BTRY 4820 / BTRY 6820 Statistical Genomics: Coalescent Theory and Human Population Genomics – Alon Keinan
4 credits, Letter grade or S/U.
Lecture: Tues/Thurs, 10:10-11:25am; Discussion: Thurs, 12:20-1:10 pm
Prerequisite: MATH 1110 or equivalent. At least one previous course in statistical methods and at least one involving programming, or permission of instructor.
Statistical methods of genomic data, emphasizing coalescent theory and molecular population genetics and genomics. Topics include derivation of coalescent theory, tests of natural selection, population structure, and statistical inference, with a focus on the population genomics of human populations.

BTRY 4830 / BTRY 6830 Quantitative Genomics and Genetics – Jason Mezey
4 credits, Lecture: Tues, Thurs 8:40 - 9:55 am, plus computer Friday lab (time varies from year to year)
Available via Video-conferencing between at both Ithaca and Weill Medical College campuses.
Prerequisites: BTRY 3080 and Introductory Statistics or equivalent
A rigorous treatment of analysis techniques used to understand complex genetic systems. This course will cover the fundamentals of statistical methodology with applications to the identification of genetic loci responsible for disease, agriculturally relevant, and evolutionarily important phenotypes. Data focus will be genome-wide data collected for association, inbred, and pedigree experimental designs. Analysis techniques will focus on the central importance of generalized linear models in quantitative genomics with an emphasis on both frequentist and Bayesian computational approaches to inference.

VTPMD 6250, Evolutionary Genomics of Bacteria – Michael Stanhope
Credits: 1; Letter or S/U, Meets: Tuesday and Thursday, 1:00 – 2:15 pm
An overview of comparative evolutionary genomics of bacteria, with an emphasis on pathogens. Principles and concepts will be stressed, although methodology and bioinformatics tools will also be addressed. The course involves a combination of lectures and discussion of primary scientific literature. There will be three classes devoted to bioinformatics tools for studying bacterial genomics, including a lecture, an open tutorial session, and a group presentation of the assigned bioinformatics exercises.

BioMG 6870, Genetic analysis of biological pathways: Tricks of the trade: how to use genetics to dissect cell, molecular, and developmental pathways – Mariana Wolfner and Michael Goldberg
Spring. Offered alternate years. Next offered Spr 2020
3 credits. Letter or S/U grade options are both available.
Tues/Thurs. 2:55-4:10pm
Prerequisites: Prior courses in Genetics & Genomics (BioMG2800 or equivalent) and in Molecular Biology (BioMG 3300, 3320, 3330, 3350, or equivalent). Prior course exposure to Developmental Biology and/or Cell Biology is helpful but not required.
The explosion of new genetic/genomic methods, including the availability of genome sequences and CRISPR-based genome editing, provides new elegant tools and approaches with which to discover and dissect the pathways that mediate cell function, development, and other biological processes. This course presents and examines these approaches, with examples showing their use to determine the time/place/partners/actions of important genes. We focus primarily on multicellular organisms, including (but not only) model systems like fruit flies, nematodes, and mice. Lectures, class discussion, and problem sets are based on important papers in the current scientific literature, and some older “classics” where relevant. After completing this course, you will:
Outcome 1: Possess a working knowledge of advanced genetic methods and logic that are used to work out and analyze biological pathways. Outcome 2: Be familiar with, and able to interpret and analyze critically, the latest and “classic” ideas, results, papers and hypotheses in genetics through readings, problem sets, and lecture/discussion of scientific research papers. Outcome 3: Be able to communicate orally or (briefly) in writing the ideas, results and concepts in advanced genetic analysis of gene function and pathways. Outcome 4: Have made intellectual connections across the content of this course with information that you learned in other biology courses.

**BTRY 6890: Current Topics in Population Genetics – Philipp Messer**
1 credit. S/U only. Prerequisite: BIOMG 4810, BTRY 4810 or permission of instructor.
Graduate seminar on current topics in population genetics. Readings are chosen primarily from current scientific literature. Participation in discussion and presentation of at least one paper required for course credit.

**NTRES 6940: Current Topics in Non-Model Genomics – Nina Overgaard Therkildsen and David Toews**
1 credit, SX option only. Meeting time TBD. - Next offered Spring 2020
This graduate seminar will take the form of a journal club that meets weekly to discuss the burgeoning literature on non-model genomics, focusing on applications of next-gen sequencing to address ecological and evolutionary questions in non-model organisms (i.e. without the benefit of a high-quality well-annotated reference genome or extensive species-specific annotation information and genomic resources). The topics covered will be determined based on student interest and will include both novel results and methodological questions.

**BTRY 7200: Statistical and Computational Genomics – Amy Williams**
1 credit. S/U only. Prerequisites/Corequisites Prerequisite: BTRY 4840/BTRY 6840 or permission of instructor.
Fridays 12:20 – 1:10 pm Weekly seminar series on recent advances in computational genomics. A selection of the latest papers in the field are read and discussed. Methods are stressed, but biological results and their significance are also addressed.

**BTRY 7210: Topics in Quantitative Genomics – Jason Mezey**
1 credit. S/U only. Prerequisites: BTRY 4830/BTRY 6830 or permission of instructor.
Weekly seminar series on recent advances in quantitative genomics. A selection of the latest papers in the field is read and discussed. Methods are stressed, but biological results and their significance are also addressed.

**NTRES 7283 Molecular Genetic Approaches to Study of Ecology & Evolution – Matt Hare**
1 credit Seminar, S/U. During Spring 2019 this seminar will focus on the capacity for adaptive responses to environmental change; theoretical predictions, measuring adaptive capacity, identifying constraints in general and for specific cases, and managing adaptive capacity with assisted gene flow or genetic rescue. Specific topics covered will be determined based on student interest and may include both novel results and methodological questions.

**BIOEE 7600 - Introduction to Modeling in Ecology and Evolutionary Biology – Steve Ellner**
3 Credits, S/U Only, Even numbered years, next offered Spring 2020
This course is aimed at grad students in E&EB and related fields with no prior exposure to modeling. Students taking the course will learn to "read" dynamic models and identify the underlying assumptions; build their own process-based models; simulate models on the computer using R; and use computational methods to study the behavior of simple models. The class is in "bootcamp" format (75 min lecture and 3 hr computer lab each day, for about 3 weeks). Most class meetings will occur prior to the start of the semester in January 2018. Students interested in enrolling should contact Patty Jordan (pj17) by midway through fall semester. Grades are based on computer exercises that will be completed in-lab, and a term project involving a modest extension of published research using an ecological or evolutionary model. Prior knowledge of R is not required. The course is especially suitable for early (1st and 2nd year) grad students wishing to acquire modeling skills that can be used in their thesis research.

**BTRY 6890 Current Topics in Population Genomics – Alon Keinan**
1 credit, S/U, Currently Not Offered.
Graduate seminar on current topics in population genetics. Readings are chosen primarily from current scientific literature. Participation in discussion and presentation of at least one paper required for course credit.

**PLBRG 7170 - Quantitative Genetics in Plant Breeding – Kelly Robbins**
Spring (offered alternate years starting Spr 2020). 3 credits. Letter grades only.
Prerequisite: PLBRG 4030 and BTRY 6010 or equivalent. The core principles of quantitative genetics, outlined in the work of Fisher and Wright in the beginning of the 20th century, have long been the foundation of plant and animal breeding. Despite the passing of time since the foundational work of Fisher and Wright, quantitative genetics is as relevant today as it has ever been. Quantitative genetics is a science that has continually evolved, and with the development of new technologies in high-throughput genomics, metabolomics and phenomics, it is increasingly incorporating elements of computer science. A strong understanding quantitative genetics is key to understanding the science of plant and animal breeding. This course will provide students with a solid foundation in quantitative genetics theory, as applied to the field of plant breeding, and introduce students to modern day applications in genomic selection and genome-wide association mapping. While the methodologies of plant and animal breeding are distinct in many ways, the core principles are the same and this course will attempt to cover topics in a way that is inclusive of animal breeding applications. Although this course will cover a wide range of topics it is by no means an exhaustive coverage quantitative genetics, and students are strongly encouraged to compliment the principles learned in the class with introductory courses in statistical methods and experimental design.

BIO MG 8340 - Quantitative Biology for Molecular Biology & Genetics – Jeff Pleiss Next offered spr 2020 2 credits. Limited to 1st year Ph.D students in the grad fields of BMCB and GGD. We will examine topics in modern molecular biology and genetics focusing on the quantitative tools necessary for analyzing experimental data. Classes will be both lecture- and discussion-based including critical readings of current literature. Students will use computational statistical packages to individually and collaboratively re-evaluate data from the primary literature.

FALL 2019 COURSES (check Class Roster and Courses of Study for updates)

NS 2750 Human Biology and Evolution (also ANTHR 2750) -- Zhenglong Gu 3 credits. Prerequisite: college biology. Lec MW 10:10-11:00, Disc selected times R or F. S–U or letter grades. Examines the theories and mechanisms of modern evolutionary biology as they apply to present-day humans and their hominid ancestors. Lectures and discussions of molecular and paleontological evidence of human evolution, the causes and consequences of contemporary human biological diversity, and biological and behavioral modes of human adaptation to past and present natural and cultural environments.

ENTOM 3310/3311 - Insect Diversity and Evolution — Bryan Danforth Fall. 3 credits. Offered alternate years (offered Fall 2019) Prerequisite: ENTOM 2120. Co-requisite: ENTOM 3311. Insects are the dominant terrestrial organisms on planet earth both in terms of the number of species as well as in biomass. This course will provide a detailed look at insect diversity, phylogeny, natural history, and the insect fossil record. We will examine what is known about insect higher level relationships based on morphology and DNA sequence data and explore how phylogenies can be used to examine the evolution of behavior, life history, ecology, and natural history. Students will come away from the class with a deeper understanding of insect biodiversity, evolution, natural history, and phylogeny.

NTRES 3500 Computational Skills for Efficient Data Processing and Analysis – Nina Therkildsen 3 credits. Lecture: Tu/Thur 9:05-9:55, Lab Wed 2:00-4:25pm. Prerequisite: One college-level statistics course (e.g. NTRES 3130, STSCI 2150, or AEM 2100) and basic familiarity with the R statistical computing environment, or permission of the instructor. As data sets grow larger and more complex, computational skills are now in high demand across all areas of science. This course introduces a series of practical tools that enable scientists to spend less time wrestling with software and more time getting research done in efficient and powerful ways. Topics covered include 1) formatting, visualizing, and filtering complex datasets, 2) automating repetitive tasks and combining tools for implementing analysis pipelines, 3) basic programming for building and testing custom tools, and 4) best practices for reproducible science workflows. We will primarily work in R and the Unix command line environment, and the course will be structured around hands-on (the keyboard) learning.

Prerequisites: CALS math requirement; introductory genetics; NTRES 2830, NTRES 3100 or equivalent or permission of instructors. Satisfies major requirements in Ecology and Evolutionary Biology concentration. Decision making in conservation biology requires measurement and analysis of variation at the genetic, population, and landscape or system levels. Emphasis in this course is on quantitative tools for the formal analysis of variation at all three levels and principles guiding maintenance and management of biological and genetic diversity to promote population persistence.

**BioNB 4200:001 Genomics and Social Evolution – Michael Sheehan**
2 credit seminar. Students will read, present and discuss the current and historical primary literature at the interface of genomics and social evolution. In the first part of the semester, we will read papers dealing with the genomic changes that accompany the origin and elaboration of sociality, focusing mainly on comparative genomic approaches. In the second part of the semester, we will read papers examining the effects of social behavior on genetic variation within populations.

**PLBIO 4220 Comparative Plant Development: Evo-Devo -- Adrienne Roeder and Michael Scanlon**
2 credits. Student option grading. Tuesday Thursday 11:15 AM to 12:05 PM in Plant Sciences Building 141. Prerequisites/Corequisites: BIOMG 2800 or PLBRG 2250 and PLBRG 3250 and PLBIO 2410 or permission of instructor.
A comparative analysis of the developmental-genetic mechanisms contributing to the evolution of plant morphological structure and diversity.

**BTRY 4810 / BIOMG 4810: Population Genetics – Philipp Messer**
4 credits. Prereq: BIOMG 2810, BIOEE 1780, or equiv., Lec MWF 10:10 – 11:00am, plus disc.
Population genetics is the study of the transmission of genetic variation through time and space. This course explores what the patterns and dynamics of genetic variation in populations can teach us about the processes that underlie evolution. Topics include the quantification of genetic variation, mutation, selection and fitness, genetic drift, migration, population structure, multilocus models, quantitative traits, and adaptation at the molecular level. We will also discuss efforts to connect genotype with phenotype and ultimately fitness. Emphasis is placed on the interplay between theory, computer simulations, and data from natural as well as experimental populations. Specific case studies include the evolution of drug resistance, experimental evolution of microbes and insects, breeding techniques in plants and animals, the evolution of cancer, and the genetic structure and evolution of human populations.

**BTRY 4840: Computational Genetics and Genomics – Amy Williams**
4 credits. Prerequisite: BTRY 3010 and CS 2110 or equivalents.
Lecture TR 10:10am – 11:25 pm plus discussion F 12:2 – 1:10pm.
Computational methods for analyzing genetic and genomic data. Topics include sequence alignment, hidden Markov Models for discovering sequence features, motif finding using Gibbs sampling, phylogenetic tree reconstruction, inferring haplotypes, and local and global ancestry inference. Prior knowledge of biology is not necessary to complete this course.

**BIOMG 4870: Human Genomics – Andy Clark**
3 credits. Prerequisite: BIOMG 2810. Lec.Tues/Thurs 8:40-9:55 am.
Applies fundamental concepts of transmission, population, and molecular genetics to the problem of determining the degree to which familial clustering of diseases in humans has a genetic basis. Emphasizes the role of full genome knowledge in expediting this process of gene discovery. Stresses the role of statistical inference in interpreting genomic information. Population genetics, and the central role of understanding variation in the human genome in mediating variation in disease risk, are explored in depth. Methods such as homozygosity mapping, linkage disequilibrium mapping, and admixture mapping are examined. The format is a series of lectures with classroom discussion. Assignments include a series of problem sets and a term paper.