# Anticipated Learning Objectives

## Lecture 1: What is Ecological Genetics?

1) Introduce course content and structure.

## Lecture 2: Adaptation and why we study it

1) Cultivate an appreciation for the coolness of adaptation.
2) Develop a working definition of evolutionary fitness.
3) Understand the primary modes of natural selection: purifying (stabilizing) selection, directional selection. Be familiar with less common modes of selection: overdominance (heterozygote advantage), underdominance (heterozygote disadvantage), disruptive selection, negative frequency dependent or diversifying selection.
4) Realize that not all variation is necessarily adaptive. Use critical thinking and hypothesis-testing to identify adaptations.

## Lecture 3: The Null Hypothesis

1) A brief review of Hardy Weinberg Equilibrium and the assumptions that underlie it.
2) Develop an understanding of genetic drift as a process. Genetic will become both an evolutionary force (for example, in causing isolated subpopulations to genetically diverge) and a null hypothesis (for example, in tests for natural selection.
3) Understand the concept of effective population size.
4) Introduce the effects of population bottlenecks and demographic expansions on effective population size.

## Lectures 4-6: Phenotypic Adaptation

### Lecture 4

1) Understand how directional selection operates on phenotypic diversity, and how selection can change the phenotypic mean and variance in a population.
2) Understand how directional selection progressively becomes saturating selection. A classic example of this would be sexually selected traits such as exaggerated bird plumage or oversized antlers in artiodactyls, where selection drives an increase in the trait value due to enhanced reproductive success but an eventual cost of the bearing the trait will limit further increase in trait value.
3) Not all phenotypic variation has a genetic basis. Understand how environmental factors can contribute to phenotypes. Understand the concept of phenotypic plasticity. There can be natural selection without any genetic change in the population (therefore, no evolution).

## Lecture 5

1) Introduce the concept of heritability. Be able to apply the Breeder's equation R=*h*2S. Understand how selection can actually change the heritability of a trait over successive generations.

2) Develop an understanding of fitness functions. Directional selection has a linear fitness function. Other forms of function have non-linear fitness functions, sometimes termed "non-linear selection".

3) Understand how correlated traits respond to natural selection, and how selection on one trait can lead to a correlated response in another.

4) Understand the concept of "epistatic selection" (sometimes called by the misnomer "correlational selection").

## Lecture 6

1) Understand how to calculate estimated fitness from phenotypic data. Understand relative fitness among different genotypes.

2) Use recursion equations to calculate the rate of change in the frequency of a selected allele. Test the alternative hypothesis of 'natural selection' against the null hypothesis of 'genetic drift'.

3) Understand the balance between natural selection and genetic drift, and how the relative magnitudes of $N_e$ and $s$ determine whether natural selection or genetic drift is the stronger force. Understand the risk that even adaptive mutations may drift to loss when they are at low population frequencies, particularly when they are recessive.

## Lectures 7-9: Molecular Population Genetics and Molecular Evolution

## Lecture 7

1) Understand how directional selection alters the site frequency spectrum. Understand the basic of SFS-based tests such as Tajima's *D* and Fay and Wu's *H*.

2) Understand the concept of linkage disequilibrium, and how haplotype-based tests can be used to infer selection.

3) Introduce composite tests that use both SFS and haplotype distributions.

4) Note briefly that non-equilibrium demography and population structure can give SFS and haplotype signatures that mimic the signatures of selection.

## Lecture 8

1) Introduce the coalescent process. Recognize that forward-backward relationship between genetic drift and the coalescent.

2) Conceptually understand how to apply the coalescent to tests population genetic hypotheses.

3) Be familiar with the use of genome-wide population genetic analyses to identify genes that may be have experienced recent adaptation.

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### Lecture 9

1) Understand the basic $K_A/K_S$ test as a test for adaptive evolution over longer evolutionary time.

2) Be familiar with more powerful tests of $K_A/K_S$ (sometimes termed $\omega$) that use maximum likelihood tests to evaluate whether adaptive evolution has occurred on a subset of codons in a gene or a subset of lineages within a phylogeny, such as those implemented in PAML.

3) Understand the McDonald-Kreitman test, and more recent extensions of it.

4) Be familiar with application of molecular evolutionary tests at both single gene and genome-wide scales.

### Lecture 10: Life History Tradeoffs

1) Understand the concept of pleiotropy, and how it relates back to the concept of correlated responses to selection.

2) Life History Tradeoffs result from “antagonistic pleiotropy”. Understand LHT as a constraint on adaptation.

3) Know how to experimentally measure life history tradeoffs.

4) Understand the difference between “allocation” variation and “acquisition” variation.

5) Life history tradeoffs are condition dependent. The strength, and even direction, of correlations between traits may depend on environmental conditions or organismal context.

### Lecture 11: Introduction to Quantitative Genetics

1) Introduce basic concepts in quantitative genetics, including how genetic and environmental factors combine to generate the familiar “bell shaped curve”.

2) Understand how quantitative genetic variation can be decomposed into variance components. Recall the concept of phenotypic plasticity when discussing environmental variance and the concept of epistasis when discussing interaction variance.

3) Define broad-sense and narrow-sense heritability. Understand why selection acts most efficiently on narrow-sense heritability, recalling the breeder’s equation and phenotypic response to selection. Understand how environment contributes to heritability.

### Lecture 12: Introduction to Quantitative Genetic Mapping

1) Introduce the fundamental premise of genetic mapping through pedigrees.

2) Understand the Transmission Disequilibrium Test (TDT).

3) Begin to develop a conceptual understanding of QTL mapping, relating QTL mapping to other transmission and pedigree-based tests.

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### Lecture 13: QTL Mapping

1) Understand the conceptual basis for QTL mapping.
2) Understand how to reconstruct a linkage map from marker data, and how to estimate the amount of recombination that occurs between markers.
3) Understand how mapping resolution and accuracy is limited by the number of recombinations in the mapping panel and the density of markers typed.
4) Understand permutation tests.

### Lecture 14: Association Mapping

1) Understand the similarities and differences between Association Studies and QTL mapping.
2) Understand the power and limitations of candidate gene based association studies.
3) Understand genome-wide association studies (GWAS). Be familiar with common graphical representations like Manhattan plots and *q-q* plots.

### Lecture 15: "Truth" in Mapping

1) Understand the accepted standards for believability in quantitative genetic mapping. Have an appreciation for the rate of false positives and false negatives.
2) Develop a sense of the expected repeatability of mapping experiments.
3) Develop an appreciation for the importance of experimental validation of mapping results.
4) Understand the concept of "missing heritability" and some of its potential causes.

### Lecture 16: The Stickleback Model System

1) Explore stickleback fish as a case system illustrating many of the concepts in discussed in the Adaptation and Quantitative Genetics modules of the course.

### Lecture 17-18: Introduction to Population Structure

### Lecture 17

1) Develop the fundamentals concepts required for studying population substructure. Understand how populations may become subdivided, including through vicariance, innate barriers to gene flow, and founding of new populations.
2) Understand that divided subpopulations may diverge genetically both through genetic drift and through adaptation to local conditions. Understand the differences in expected genomic scale of divergence through local adaptation versus genetic drift.
3) Introduce migration as a force that erodes population differentiation.

4) Understand how phylogeography can give insight into historical population structure and migration routes.

### Lecture 18

1) Become comfortable calculating and interpreting the test statistic $F_{ST}$. Understand how Wright's F-statistics relate to inbreeding and genetic drift. Be able to calculate statistical significance of $F_{ST}$ by a chi-squared test or by permutation.

2) Establish the long-term equilibrium between drift and migration as predicted by $F_{ST}$. Know the assumptions of this equilibrium and when they are likely to be violated.

3) Briefly introduce other metrics of population structure, including sequence-based statistics such as $K_{ST}$ and phenotypic statistics such as $Q_{ST}$.

4) Discuss tests like STRUCTURE that do not rely on *a priori* hypotheses about how many subpopulations there are or which individuals belong to each. STRUCTURE also allows the detection of migration and identification of admixed individuals.

### Lecture 19: Structure and Adaptation

1) Understand how spatial variation in selective pressures can result in local adaptation. Understand that migration reduces the likelihood of local adaptation according to the rate of migration and the strength of selection. Be sure to distinguish genetic adaptation from phenotypic plasticity.

2) Understand the Levene model of synthetic overdominance across environments with different selective pressures. Establish the conditions under which local adaptation can maintain a global polymorphism.

3) Consider more advanced models of local adaptation, where reproduction occurs within the subpopulation.

### Lecture 20: Structure and Genetic Mapping

1) Understand how population structure complicates quantitative genetic mapping by introducing artificial correlations among traits and between traits and genotypes.

2) Introduce corrections and controls that allow mapping to be performed even in structured populations.

3) Admixture mapping is a mapping method that explicitly makes use of mixed population ancestry for efficient genetic mapping.

### Lecture 21: Speciation

1) Understand how long term population structure can lead to speciation both through divergence in reproductive timing or behavior, and through the evolution of reproductive incompatibilities.

2) Understand Dobzhansky-Muller incompatibilities.

3) Understand the process of reinforcement after secondary contact. Discuss empirical examples of mapping the genetic basis for reinforcement.

4) Be able to use the width of a hybrid cline to identify genes that are locally adapted geographically, or adapted to the background genome of parent species.

5) With enough time of separation, populations (species?) will evolve reciprocal monophyly by genetic drift. Reciprocal monophyly is accelerated by selection, and can be used to identify locally adapted genes.

## Lecture 22-23: Coevolution

### Lecture 22

1) Define coevolution as coordinate evolution between or among species. Understand mutualistic, antagonistic, and incidental co-evolution.

2) Distinguish between pairwise and diffuse co-evolution, and understand their differing evolutionary predictions and constraints.

3) Understand the genome evolution of pathogenic and symbiotic microbes. Understand how co-evolution can result in obligate mutualisms using symbiotic bacteria as an example.

### Lecture 23

1) Discuss host-pathogen interactions as a special case of co-evolved relationships. These can be specific or general (pairwise or diffuse).

2) Understand the evolutionary genetic predictions of different types of host-pathogen interactions. Know when to expect adaptive "arms races", "churning alleles", and balanced polymorphism.

3) Be able to relate host-pathogen interactions back to life history tradeoffs and constraints on both the host and the pathogen.

## Lecture 24-25: Community Genetics

### Lecture 24

1) Understand extended phenotypes, and how organisms alter their environments. These alterations shape the environment for other organisms, allowing the formation of ecosystems.

2) Understand how genetic diversity can impact ecosystem diversity, productivity, and stability.

### Lecture 25

1) Evolutionary change in one organism can alter the environment such that it changes selective pressures on other organisms in the environment. Evolutionary responses in those organisms can feed back onto the initial organism. Understand feedback loops.

2) Define community parameters like "community heritability". Understand where the analogy to genetic heritability within species holds, and where it breaks down. Be able to construct a cogent argument about whether community evolution is adaptive.

## Lecture 26: Conservation Genetics

1) Establish the role of genetics in conservation endeavors. Use genetic thinking to identify appropriate units for conservation: is it species, genetic variant, or ecosystem? Are some species more important to conserve than others?

2) Understand how population fragmentation can lead to population decline through inbreeding and genetic drift. Be able to discuss the merits and concerns associated with genetic reintroduction into at-risk populations.

## Lecture 27: Buffer/Make-up Lecture

1) TBD