Exam 1 Info

Date: February 28th, 2019

Location: Normal classroom (HLL-009, Busch Campus)

Time: In-class (5:00-6:20 pm)

Notes:

1. Calculators and other electronic devices are **prohibited**. All calculations will be able to be completed by hand.
2. I will hold extra office hours on Wednesday (February 27th). I plan to be in my office from 1:30 pm - 4 pm (Hill 216). Feel free to stop by at any time in that interval (no need to email beforehand) with any questions you have. If this does not work for you, and you'd like to meet at some other time, please feel free to contact me via email, and I'm sure we can set something up.
3. You are allowed to bring **one** sheet of **handwritten** notes as a reference during the exam. I will not allow any typed sheets to be used, including the lecture notes (i.e. the main text).

Suggestions:

1. Read over covered sections in the textbook, as well as notes from class.
2. Understand all assigned homework questions and quizzes. Solutions to both are available on Sakai.
3. Do the review problems posted on the course site.
3. Solve other (unassigned) homework questions from the same section of the textbook.

Material:
The exam will cover Chapters 1-3 of the Professor Ocone's notes, as well as the basic epidemiological and death process models introduced early in the semester. Note that this does NOT include Section 3.3 on Wright's Fixation Index, as I did not cover this in class. Chapter 2 serves primarily as a review of techniques from probability theory, and I will not focus heavily on pure probability theory for the exam. Similarly, Chapter 1 gives a biological background, which you are responsible for, and serves as the basis for most models in Chapter 3. Some key topics to review are given below. But be aware: this list is **not** exhaustive, and anything covered could appear on the exam. See the Course Calendar on the website for a complete schedule of the material covered.

Biological Background (Chapter 1)

(a) Basics of Mendelian genetics. How traits are passed down, and quantitative techniques to predict outcomes of mating experiments (e.g. pea plant color and texture, etc.)

(b) Biological basis of Mendelian genetics. Genes, chromosomes, mitosis and meiosis. Basic definitions (eukaryote, prokaryote, zygote, autosomal chromosomes, recombination, monoecious, dioecious, etc.)

(c) Relation between genotype and phenotype (e.g. what is known, what isn't).

(d) Basics of DNA. How does DNA make proteins. Why are proteins significant? RNA as well. How it all fits together, at least at a high level (heredity to genotype to phenotype through DNA and meiosis, etc).

Probability Background (Chapter 2)

(a) Definition of a probability space. Basic examples (coin flip, colored urns in boxes, etc.): be able to identify sample space, events, and probability measure.

(b) Calculations using axioms of probability space. Computing probabilities of events, especially for discrete spaces (set of outcomes is finite or countable). Basic combinatorics.

(c) Independence of events. Conditional probability. Law of total probability (Bays' Theorem).

(d) Random variables. Definition and calculation. Be able to recognize *standard* random variables (Bernoulli, binomial, geometric, normal, exponential, etc.)

(e) Expectation, variance, etc.

(f) Random sampling. Computing probabilities of random samples. How is the probability space defined?

(g) Law of Large Numbers, and how it is used in the Infinite Population Assumption.

Population Genetics for Large Populations (Chapter 3)

(a) Allele and genotype frequencies. Basic definitions, and how to calculate for a finite population. Basic relations between them. For example, for a single locus with two alleles A and a,

$$f_A + f_a = 1$$
$$f_A = f_{AA} + \frac{1}{2} f_{Aa}$$

(b) Random mating. Most models discussed assumed that parents where chosen randomly from the population. What does this mean precisely? How does this relate frequencies to probabilities?

(c) Infinite Population Assumption. Again, what does this mean, **precisely**? What is the biological statement, and what does it translate to mathematically? Know where and when it is used precisely in deriving models.

(d) Other assumptions, such as how generations overlap, the difference between a monecious vs. dioescious species, mutation, migration, etc.

(e) Much of the time we studied the case of a single locus with two alleles. How would our analysis generalize if there were more alleles? What if we considered more than one locus?

(f) Understand the derivation and analysis of all models, both with and without selection. **This is very important!**

(g) What does Hardy-Weinberg equilibrium mean, both biologically and mathematically? When do you expect to see it, and how does it arise (e.g. after one, two, etc. generations, in a limit, never, etc.) Understand the different forms of Hardy-Weinberg that arise in different models with different assumptions (e..g monecious vs. dioecious, non-mutations vs. mutations, possibly overlapping generations, etc.).

(h) Be able to analyze and solve linear first- or second-order difference equations.

(i) Derivation and analysis of models with selection. What does selection mean, and how do we implement mathematically? Again, understanding derivations is very important.

(j) Analysis of nonlinear first-order difference equations. Fixed points, cobwebbing, etc.

Basic Death Process and Epidemiology (Miscellaneous)

(a) Know the basic death stochastic process introduced. What were the assumptions, and what results did we derive?

(b) Basics of SIS epidemiological model of diseases spread. Basic analysis and connection with ODE model.

(c) Most important part for these topics is the modeling, and not necessarily the mathematical techniques.