MOLECULAR GENETICS

BIOL 361 - A01 (20365) January 6-April 4, 2025

COURSE OUTLINE

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Lectures: Engineering Comp Sci Bldg 125 Mon & Thurs: 8:30 am – 9:50 am

COURSE DESCRIPTION. We will study connections between **genes and phenotypes**. The course includes wrinkled and round peas, cystic fibrosis, and stickleback fins. We will also study microsatellites, SNPs, exomes and whole genomes. There will be some unusual examples of gene duplication and divergence, and of genes emerging from non-coding sequences (*de-novo* genes). The course ends with Genome Wide Association Studies (GWAS) and Genome Prediction.

EVALUATION

1. ASSIGNMENTS: (30%)
    a) Reading assignment: Experiments in Plant Hybridization (10%)
    b) BLAST/Topiary Assignment (20%)

2. MID-TERM EXAM: (30%)

3. FINAL EXAM: (40%)

Grading scheme: A+ (90%-100%), A (85-89.9%), A- (80-84.9%), B+ (77-79.9), B (73-76.9%), B- (70-72.9%), C+ (65-69.9%), C (60-64.9%), D (50-59.9%), F (<50%), N (max. 49%) = Failure to complete one or more of the following: Mid-term exam, Assignment 2, Final exam. N = F as far as your GPA is concerned.

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Lecture schedule

1	Jan. 6	Wrinkled and Round Peas Part 1	Start Assignment 1
2	9	Wrinkled and Round Peas Part 2	
3	13	Tall and Dwarf Peas	Assignment 1 due
4	16	Purple and White Peas	
5	20	Cystic Fibrosis Part 1	
6	23	Cystic Fibrosis Part 2	
7	27	Stickleback Part 1 (msats)	
8	30	Stickleback Part 2 (genome sequence)	
9	Feb. 3	Stickleback Part 3 (chromosomes)	
10	6	Gene-Environment Interactions	
11	10	Review	
	13	**Midterm Exam (30%)**	
	17	*Reading Break*	
	20	*Reading Break*	
12	24	Genes and Behaviour (incl. dogs) ***Last day to drop class****	
13	27	BLAST/Topiary	
14	Mar. 3	Phylogenetics	Start Assignment 2
15	6	De-Novo genes	
16	10	Ultra Conserved Elements	
17	13	Gene Duplication	
18	17	Opsin genes	Assignment 2 due
19	20	Transcriptomes	
20	24	Exomes	
21	27	GWAS	
22	31	Genome Prediction	
23	Apr. 3	Review	
		Final Exam (40%)	

**** I cannot remove you from the course, you must do this yourself.***

Academic Integrity

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Learning Objectives

1. Students will gain experience extracting information from scientific papers.
2. Students will learn about a diversity of molecular tools, from RFLPs in family pedigrees to PHATE analyses of millions of SNP loci.
3. Students will be able to describe how coding and non-coding mutations that influence phenotypes are discovered.
4. Students will learn how to reconstruct and then interpret phylogenies.