Genetics and Genomics PhD

Name: _____   Date: _____

Entry Term and Year: _____   Expected Graduation Date: _____   Current GPA: _____

POSC completed: YES / NO   Major Prof: _____   Prelim date: _____

Prerequisites – must be taken by end of their 4th semester (summer included)	BBMB 404	STAT 401/STAT 587	**GR ST 565** **(1 credit)** End of first year to meet NIH and NSF requirements must have a "B" or better (F,S)
IG Core Courses grade of "B" or better Required (12 credits)	**Genetics, Bioinformatics, and Statistical Genetics** **Circle the class taken:** ANS 556 COM S 551 STAT 516, 581 BCB 544, 546X, 567, 568, 569, 570 EEOB 561	**Evolution, Population and Quantitative Genetics** **Circle the class taken:** ANS/Agron 561 EEOB 507, 540X, 562, 563, 566, 567 GDCB/STAT 536	**GDCB 511** Advanced Molecular Genetics	**GDCB 510** Transmission Genetics
Seminars (9 credits)	**Workshop in Genetics (F)** GENET 591 GENET 591	**Conceptual Foundations of Genetics (F)** GENET 692	**Graduate Student Seminar (F,S)** GENET 690 GENET 690 GENET 690	**Faculty Seminar in Genetics (F)** GENET 691 GENET 691
Elective courses	Course: Credit:	Course: Credit:	Course: Credit:	Course: Credit:
Research GENET 699				
Use research credits to fill to meet 72 and 32 course credit requirement Contact Program Coordinator for reference number for your major professor's GENET 699 Research credits do not count towards grade GPA Minimum research credits for MS is 3; for Ph.D. is 10. There is no maximum.				
Total (72 credits)				

- **AN S 556: Current Topics in Genome Analysis**   *(3-0) Cr. 3. Alt. S., offered even-numbered years. .Prereq: BBMB 405 or GDCB 510*
  Introduction to principles and methodology of molecular genetics useful in analyzing and modifying large genomes.
- **AN S 561: Population and Quantitative Genetics for Breeding**   *(Cross-listed with AGRON). (4-0) Cr. 4. F. Prereq: STAT 401*
  Population and quantitative genetics for plant and animal genetics. Study of the genetic basis and analysis of variation in quantitative traits in domestic or experimental populations using phenotypic and molecular marker data, including estimation of heritability and other genetic parameters, linkage analysis and mapping of quantitative trait loci, and the impact of inbreeding, heterosis, and genotype-by-environment interaction.
- **BCB 544: Fundamentals of Bioinformatics**   *(Cross-listed with COM S, CPR E, GDCB). (4-0) Cr. 4. F.Prereq: MATH 165 or STAT 401 or equivalent*
  A practical, hands-on overview of how to apply bioinformatics to biological research. Recommended for biologists desiring to gain computational molecular biology skills. Topics include: sequence analysis, genomics, proteomics, phylogenetic analyses, ontology enrichment, systems biology, data visualization and emergent technologies.
- **BCB 546X/EEOB 546X. Computational Skills for Biological Data.**   (Cross-listed with EEOB 546X). (1-2) Cr. 3. S. *Prereqs: Graduate student status or permission of the instructor.*

  Computational skills necessary for biologists working with big data sets. UNIX commands, scripting in R and Python, version control using Git and GitHub, and use of high performance computing clusters. Combination of lectures and computational exercises.
- **BCB 567: Bioinformatics Algorithms**   *(Cross-listed with COM S, CPR E). (3-0) Cr. 3.Prereq: COM S 228; COM S 330; credit or enrollment in BIOL 315, STAT 430*

  Biology as an information science. A review of the algorithmic principles that are driving the advances in bioinformatics and computational biology.
- **BCB 568: Statistical Bioinformatics***(Cross-listed with COM S, GDCB, STAT). (3-0) Cr. 3. S. Prereq: BCB 567 or (BIOL 315 and STAT 430), credit or enrollment in GEN 409*

  Statistical models for sequence data, including applications in genome annotation, motif discovery, variant discovery, molecular phylogeny, gene expression analysis, and metagenomics. Statistical topics include model building, inference, hypothesis testing, and simple experimental design, including for big data/complex models.
- **BCB 569: Structural Bioinformatics**   *(Cross-listed with BBMB, COM S, CPR E, GDCB). (3-0) Cr. 3. F. Prereq: BCB 567, BBMB 316, GEN 409, STAT 430*
  Molecular structures including genes and gene products: protein, DNA and RNA structure. Structure determination methods, structural refinement, structure representation, comparison of structures, visualization, and modeling. Molecular and cellular structure from imaging. Analysis and prediction of protein secondary, tertiary, and higher order structure, disorder, protein-protein and protein-nucleic acid interactions, protein localization and function, bridging between molecular and cellular structures. Molecular evolution.
- **BCB 570: Systems Biology***(Cross-listed with COM S, CPR E, GDCB, STAT). (3-0) Cr. 3. S. Prereq: BCB 567 or COM S 311, COM S 228, GEN 409, STAT 430*
  Algorithmic and statistical approaches in computational functional genomics and systems biology. Analysis of high throughput biological data obtained using system-wide measurements. Topological analysis, module discovery, and comparative analysis of gene and protein networks. Modeling, analysis, and inference of transcriptional regulatory networks, protein-protein interaction networks, and metabolic networks. Dynamic systems and whole-cell models. Ontology-driven, network based, and probabilistic approaches to information integration.
- **COM S 551: Computational Techniques for Genome Assembly and Analysis**   *(3-0) Cr. 3. Prereq: COM S 311 and some knowledge of programming*
  Introduction to a big data research area in bioinformatics. Focus on applying computational techniques to huge genomic sequence data. These techniques include finding optimal sequence alignments, generating genome assemblies, finding genes in genomic sequences, mapping short sequences onto a genome assembly, finding single-nucleotide and structural variations, building phylogenetic trees from genome sequences, and performing genome-wide association studies.
- **EEOB 507: Advanced Animal Behavior**   *(3-0) Cr. 3. S. Prereq: Graduate standing, BIOL 354, or permission of instructor*
  Analysis of current research in animal behavior. Topics covered may include behavioral ecology, mechanisms of behavior, evolution of behavior, applications of animal behavior to conservation biology, and applications of animal behavior to wild animals in captivity.
- **EEOB 561: Evolutionary and Ecological Genomics***(3-0) Cr. 3. Alt. S., offered even-numbered years. Prereq: Permission of nstructor; BCBIO 444 recommended.*
  Use of genomic and other "omic" data in evolution and ecology. Review of data-generation platforms, computational methods, and examples of how phylogenomics, metagenomics, epigenomics, and population genomics are transforming the disciplines of evolution and ecology.
- **EEOB 562: Evolutionary Genetics**   *(3-0) Cr. 3. Alt. S., offered even-numbered years. Prereq: Permission of instructor*
  Seminar/discussion course covering the genetic basis of evolutionary processes in multicellular organisms.
- **EEOB 563: Molecular Phylogenetics**   *(2-3) Cr. 3. S. Prereq: BIOL 313 and BIOL 315*
  An overview of the theory underlying phylogenetic analysis and the application of phylogenetic methods to molecular datasets. The course emphasizes a hands-on approach to molecular phylogenetics and combines lecture presentations with computer exercises and discussion of original scientific literature.
- **EEOB 566: Molecular Evolution**   *(3-0) Cr. 3. Alt. F., offered even-numbered years. Prereq: Permission of instructor*
  Seminar/discussion course covering the fundamentals of molecular evolution. Emphasis is placed on original scientific literature and current topics, including rates and patterns of genetic divergence; nucleotide and allelic diversity; molecular clocks; gene duplications; genome structure; organellar genomes; polyploidy; transposable elements; and modes and mechanisms of gene and genome evolution.
- **EEOB 567: Empirical Population Genetics**   *(3-0) Cr. 3. Alt. F., offered irregularly. Prereq: Permission of instructor*
  An overview of fundamental population genetic theory and the ecological and evolutionary factors underlying the distribution of genetic variation within and among natural populations. Emphasis on the analysis of inbreeding, breeding systems, parentage, relatedness, spatial autocorrelation, effective population size, hierarchial population models, and phylogeography.
- **GDCB 510: Transmission Genetics**   *(3-0) Cr. 3. F. Prereq: GEN 410 or graduate standing*
  In-depth investigations of modern research practices of transmission genetics. Designed for students interested in genetic research. Topics include: Mendelian genetic analysis, analysis of genetic pathways, mutational analysis of gene function, chromosomal mechanics, genetic mapping, epigenetic inheritance, human genetic analysis.
- **GDCB 511: Advanced Molecular Genetics**   *(Cross-listed with MCDB). (3-0) Cr. 3. S. Prereq: BIOL 313 and BBMB 405*
  Mechanisms of molecular genetic processes in eukaryotes and prokaryotes, including DNA replication and repair, transcription, translation and regulation of gene expression. Critical evaluation and discussion of current primary literature, methodologies and experimental data.
- **GDCB 536: Statistical Genetics**   *(Cross-listed with STAT). (3-0) Cr. 3. Prereq: STAT 401, STAT 447; GEN 320 or BIOL 313*
  Statistical models and methods for genetics covering models of population processes: selection, mutation, migration, population structure, and linkage disequilibrium, and inference techniques: genetic mapping, linkage analysis, and quantitative trait analysis. Applications include genetic map construction, gene mapping, genome-wide association studies (GWAS), inference about population structure, phylogenetic tree construction, and forensic and paternity identification.
- **STAT 516: Statistical Design and Analysis of Gene Expression Experiments**   *(3-0) Cr. 3. Prereq: STAT 500; STAT 447 or STAT 542*
  Introduction to high-throughput technologies for gene expression studies (especially RNA-sequencing technology): the role of blocking, randomization, and biological and technical replication in the design of gene expression experiments; normalization methods; methods for identifying differentially expressed genes including mixed linear model analysis, generalized linear model analysis, generalized linear mixed model analysis, quasi-likelihood methods, and empirical Bayes analysis; procedures for controlling false discovery rate for multiple testing; clustering problems for gene expression data; testing gene categories; emphasis on current research topics for statistical analysis of high dimensional gene expression data.
- **STAT 581: Analysis of Gene Expression Data for the Biological Sciences**   *(3-0) Cr. 3. S. Prereq: STAT 401 or STAT 587*
  Introduction to high-throughput technologies for gene expression studies (especially RNA-sequencing technology): the role of blocking, randomization, and biological and technical replication in the design of gene expression experiments; normalization methods; methods for identifying differentially expressed genes including mixed linear model analysis, generalized linear model analysis, generalized linear mixed model analysis, quasi-likelihood methods, empirical Bayes analysis, and resampling based approaches; procedures for controlling false discovery rate for multiple testing; clustering and classification problems for gene expression data; testing gene categories; emphasis on practical use of methods. May not be used for graduate credit in the Statistics MS and PhD degree programs. Credit in STAT 416 or STAT 581, but not both, may be applied toward graduation.