# BIOL-UA 45 Biostatistics and Human Genetics 

Instructor:<br>David Gresham

## Course Description:

Deciphering the information encoded in the human genome is one of the greatest (and most exciting) challenges of the 21st century. This course will provide an introduction to studying and interpreting the human genome with a focus on the statistical methods required for its study. Fundamental concepts in human genetics will be introduced including inheritance of mendelian disease, population genetics, multifactorial disease and functional genomics. Accompanying each topic will be an introduction to the statistical concepts and tools that are required to study inheritance, genes and gene function. These include probability, hypothesis testing, ANOVA, regression, correlation and likelihood. Hands on experience will be provided through weekly assignments using the statistical programming language, R. Prior experience with statistics and genetics is not required

## Pre-requisites:

Principles of Biology II (BIOL-UA 12).
Molecular and Cell Biology I (BIOL-UA 21)
Molecular and Cell Biology II (BIOL-UA 22)
Textbook and Required Materials:
Introduction to Genetic Analysis, $10^{\text {th }}$ Edition
Griffiths, Wessler, Carrol, Doebley
The Analysis of Biological Data
Whitlock \& Schluter
Grading:
Assignments: 50\%
Quizzes: $\quad 10 \%$
Midterm: $\quad 15 \%$
Final Exam: $\quad 20 \%$
Attendance/Participation: 5\%

## Topics:

An introduction to using $R$ and Rstudio
Using Rmarkdown for reproducible research
Genetics: Distributions of human phenotypes
Statistics: Descriptive Statistics
Genetics: Samples from populations
Statistics: Uncertainty, sampling distributions, standard error
Genetics: Mendel's experiments and expected phenotypic proportions
Statistics: Probability
Genetics: Independent assortment, introduction to linkage
Statistics: chi square, contingency tables, hypothesis testing
Genetics: Mendelian inheritance in humans I, penetrance
Statistics: Conditional probability, Relative risk
Genetics: Mendelian inheritance in humans II, Segregation ratios
Statistics: Binomial distribution
Genetics: Linkage, recombination, three factor cross
Statistics: Probability

Genetics: Interference, Genetic variation in humans, Mapping functions<br>Statistics: Poisson distribution<br>Genetics: Linkage analysis in human pedigrees<br>Statistics: Likelihood<br>Genetics: Human Linkage Analysis, Refined genetic mapping<br>Statistics: Likelihood, LOD scores<br>Genetics: Genetic testing<br>Statistics: Law of total probability, conditional probability; Bayes Theorem<br>Genetics: Gene frequencies in populations<br>Statistics: Hardy-Weinberg equilibrium<br>Genetics: Inbreeding<br>Statistics: Recursive calculations<br>Genetics: Genetic drift, Selection<br>Statistics: Binomial sampling, simulation<br>Genetics: Genetic diversity, Linkage disequilibrium, mutation-drift equilibrium<br>Statistics: Computational simulation<br>Genetics: Distribution of quantitative traits<br>Statistics: Normal distribution, z-scores, Central limit theorem<br>Genetics: Sampling quantitative phenotypes<br>Statistics: Student's t-test, confidence intervals<br>Genetics: Comparison of quantitative phenotypes between two populations<br>Statistics: Two sample t-test<br>Genetics: Comparison of quantitative traits in more than two populations<br>Statistics: ANOVA<br>Genetics: Broad sense heritability<br>Statistics: Covariance, correlation<br>Genetics: Narrow sense heritability<br>Statistics: Linear regression I<br>Genetics: Narrow sense heritability and prediction<br>Statistics: Linear regression II: significance and variance explained<br>Genetics: Genome-wide expression analysis<br>Statistics: Non-parametric methods<br>Genetics: eQTL mapping<br>Statistics: Randomization and Bootstrapping<br>Genetics: Genome-wide association studies<br>Statistics: Odds ratio, multiple hypothesis testing

