**BCB725 Introduction to Statistical Genetics**

**(offered Fall every even year)**

**Course Description**

This is an introductory course for graduate students in Computational Biology, Bioinformatics, Biostatistics, Genetics, Statistics, Computer Science, Epidemiology, and other related quantitative disciplines. The course will cover statistical methods for the analysis of modern genetic and genomic data. Topics will include basic principles in population genetics, commonly adopted statistical methods in genetic studies (e.g., likelihood based inference, EM algorithm, and hidden Markov models), genetic association analysis, haplotype inference, genotype imputation, meta-analysis, rare variant association analysis, and methods for massively parallel genomic sequencing data. Students will be exposed to the latest statistical methodology and computational tools on gene mapping for complex human disease.

Other topics that might be covered include gene-set or pathway‐based analysis, admixture mapping, analysis of copy number variations, methods for bulk and single cell transcriptome sequencing, analysis of genome-wide chromatin conformation capture (e.g, derived from Hi-C and alike technologies), and multi-omics integrative analysis. We may also have guest lecturers covering the fundamentals of mice genetics; and other special topics.

**Instructors**

Yun Li, PhD

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**Prerequisites**

Introductory graduate‐level courses in statistics or biostatistics (e.g., BCB720, Bios660 or 661) or permission of the instructor.

**When and Where**: MW 2:40- 3:55PM in McGavran-Greenberg PH-Rm 2304

**Recommended Textbooks (optional)**

1. The Fundamentals of Modern Statistical Genetics. Nan M. Laird, Christoph Lange. (2011). (UNC ebook available)
2. Handbook on Analyzing Human Genetic Data: Computational Approaches and Software. Edited by Shili Lin and Hongyu Zhao. (2010) (UNC ebook available)
3. A Statistical Approach to Genetic Epidemiology: Concepts and Applications. Andreas Ziegler, Inke R. Koenig (2006).