Introduction to statistical quantitative genetics

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This course will cover quantitative genetic analysis of complex trait genetics with emphasis on the use of molecular markers spanning the entire genome. We will discuss statistical methodologies for connecting phenotypes with high-dimensional genomic information to better understand polygenic traits from both prediction and inference perspectives. Topics will include genomic relatedness, linkage disequilibrium, population stratification, genomic heritability, genome-wide association study, genomic prediction, causal inference, and statistical learning. The course will use R/Bioconductor software for statistical computing tools.

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