

**Course Title:** An introduction to statistical genetics

**Instructor:** Amy D. Anderson, Western Washington University

In this two-day course, we will look at the methodology behind gene-mapping studies, considering both population-based and family-based designs. In our first session, we will begin with an introduction to genetics and genetic data, then explore background topics including Hardy-Weinberg equilibrium and linkage disequilibrium. Once we are comfortable with the structure of genetic data, we will briefly discuss gene-mapping methods applicable to population-based association studies on binary (case-control) and quantitative traits.

Our second set of lectures begins with a more in-depth look at association studies including practical issues such as data quality, population structure, and multiple testing. We then turn our attention to some of the classic methods for gene-mapping using data collected from families of individuals. In particular, we will look at the transmission disequilibrium test (TDT) and its relative, the Quantitative transmission disequilibrium test (QTDT).

The course will finish with a lab session in which we use the JMP Genetics portion of the JMP Genomics statistical package to run some of the analyses we have discussed. If time permits, we may also, depending on student interest, cover additional topics such as model-free linkage (e.g. affected sib pair designs, Haseman-Elston Regression and Variance Component methods), multiple-stage designs (as a way to reduce genotyping costs), or the statistics behind forensic DNA profiling.