Project Narrative

An enormous amount of effort has been expended over the last decade in identifying genetic variants associated with complex genetic disease, yet a comprehensive understanding of how we should expect disease prevalence and the distribution of genetic risk among individuals and across the genome remains lacking. I will develop mathematical models of complex disease evolution in human populations and statistical techniques to determine what we can learn from presently available data about how these diseases have evolved. The results will be useful as a guide for designing future studies of disease, and will be informative about the nature of disease more broadly.