The human genome project in conjunction with the rapid advance of high throughput technology has transformed the landscape of health science research. The genetic and genomic era provides an unprecedented promise of understanding genetic underpinnings of complex diseases or traits, studying gene-environment interactions, predicting disease risk, and improving prevention and intervention, and advancing personalized medicine. A large number of genome-wide association studies conducted in the last ten years have identified over 1000 common genetic variants that are associated with many complex diseases and traits. Massive next generation sequencing data as well as different types of ‘omics data have become rapidly available in the last few years. These massive genetic and genomic data present statisticians with many exciting opportunities as well as challenges in data analysis and result interpretation. They also call for more interdisciplinary knowledge and research, e.g., in statistics, machine learning, computational biology, molecular biology, genetic epidemiology and clinical science. In this talk, I will discuss some of these challenges, such as analysis of rare variants in next generation sequencing association studies; integrative genomics, which integrates different types of ‘omics data and environmental data; and reproducible research. I will also discuss thoughts of training next generation quantitative genomic scientists at the interface of statistical genetics and genomics, computational biology and genetic epidemiology, to meet these challenges.