In the relatively short time span of less than 10 years, association analysis has become the primary study design for finding genes underlying complex disorders. Genome Wide Association Studies have discovered hundreds of new genetic markers which predict disease. Early successes with association analysis (Macular Degeneration and Crohn’s Disease) led to great excitement about the promise of GWAS for understanding the genetic basis of complex disease.

Although the number of GWAS studies has proliferated rapidly, replications are often disappointing and Meta-Analysis has become an essential part of the process of gene discovery. This talk will review some features of GWAS that offer challenges and opportunities for Biostatisticians.