

Statistical challenges in whole genome association studies

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Resumen The recent advances in genome-wide technology and the patterns of genome-wide variation provided by the HapMap project have facilitated that a large number of association studies are now being performed. Current association studies generally compare the single nucleotide polymorphism (SNP) data at individuals with a disease with the SNP data at individuals without the disease, aiming to find the genes that increase disease susceptibility. The analysis and interpretation of association studies relies heavily on Statistics, and despite the existence of many successful studies, there are still many interesting statistical challenges left. In this talk, which does not require previous knowledge of Genetics, I will give an overview of genome-wide association studies and describe some of the statistical challenges they present.