

# Abstract

The recent advance in technology and the strides made by scientists working on the Human Genome Project, have made available more detailed genetic marker maps than were available in the past. This has given fresh impetus to the challenge of discovering genetic causes of common diseases. The aim of this work was to review the most common statistical techniques for genetic linkage analysis and association, to study the behaviour of the test statistics used and to devise tests for association. We organize this thesis as follows. In chapter 2, following the introductory chapter, we recall the statistical background needed to tackle various hypothesis testing problems. Here the difficulties of hypothesis testing in the presence of unknown distributions are illustrated through discussions about the asymptotic distribution of likelihood-based statistics and of bootstrap statistics. In chapter 3, we present a concise review of statistical methods for linkage and association analyses. A test for association at two polymorphic loci is outlined in chapter 4. An Extension to the case of more than one associated allele at the marker is also developed. A new multi-point method based on the most associated haplotype (MAH) is proposed and studied in chapter 5. The method MAH is inspired by the Terwilliger (1995) paper. The results obtained are illustrated by figures and tables throughout this document. Numerical applications to actual and simulated data are presented. Simulation techniques are given in chapter 6. Important remarks and sample code are provided in appendices A and B following the discussion section.