Haplotype-association analysis.

Submitted by nliu on Mon, 09/08/2014 - 3:28pm

Title: Haplotype-association analysis.
Publication Type: Journal Article
Year of Publication: 2008
Authors: Liu, N, Zhang, K, Zhao, H
Journal: Adv Genet
Volume: 60
Pagination: 335-405
Date Published: 2008
ISSN: 0065-2660
Keywords: Genetic Techniques, Haplotypes, Humans, Models, Genetic, Pedigree

Abstract: Association methods based on linkage disequilibrium (LD) offer a promising approach for detecting genetic variations that are responsible for complex human diseases. Although methods based on individual single nucleotide polymorphisms (SNPs) may lead to significant findings, methods based on haplotypes comprising multiple SNPs on the same inherited chromosome may provide additional power for mapping disease genes and also provide insight on factors influencing the dependency among genetic markers. Such insights may provide information essential for understanding human evolution and also for identifying cis-interactions between two or more causal variants. Because obtaining haplotype information directly from experiments can be cost prohibitive in most studies, especially in large scale studies, haplotype analysis presents many unique challenges. In this chapter, we focus on two main issues: haplotype inference and haplotype-association analysis. We first provide a detailed review of methods for haplotype inference using unrelated individuals as well as related individuals from pedigrees. We then cover a number of statistical methods that employ haplotype information in association analysis. In addition, we discuss the advantages and limitations of different methods.

DOI: 10.1016/S0065-2660(07)00414-2
PubMed ID: 18358327
Grant List: GM 074913 / GM / NIGMS NIH HHS / United States
GM 57672 / GM / NIGMS NIH HHS / United States
GM 59507 / GM / NIGMS NIH HHS / United States