

Statistical advances and challenges for analyzing correlated high dimensional SNP data in genomic study for complex diseases

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Abstract

Recent advances of information technology in biomedical sciences and other applied areas have created numerous large diverse data sets with a high dimensional feature space, which provide us a tremendous amount of information and new opportunities for improving the quality of human life. Meanwhile, great challenges are also created driven by the continuous arrival of new data that requires researchers to convert these raw data into scientific knowledge in order to benefit from it. Association studies of complex diseases using SNP data have become more and more popular in biomedical research in recent years. In this paper, we present a review of recent statistical advances and challenges for analyzing correlated high dimensional SNP data in genomic association studies for complex diseases. The review includes both general feature reduction approaches for high dimensional correlated data and more specific approaches for SNPs data, which include unsupervised haplotype mapping, tag SNP selection, and supervised SNPs selection using statistical testing/scoring, statistical modeling and machine learning methods with an emphasis on how to identify interacting loci.



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Liang, Yulan, Kelemen, Arpad, Statistical advances and challenges for analyzing correlated high dimensional SNP data in genomic study for complex diseases, *Statistics Surveys*, , (), 43-60 (electronic). DOI: 10.1214/07-SS026.

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