Statistical Methods for Association Analysis of Genome-wide Sequencing Studies for Rare Variants

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Abstract

High-throughput sequencing technology is quickly becoming available in genomic studies, e.g., to identify rare variants that are associated with diseases. Analysis of such data however presents substantial challenges. For example for finite samples, causal variants might not observed because they are rare and multiple variants are likely to causal.

We develop a weighted kernel machine method for genome-wide association studies using sequencing data. We show our method is powerful compared to the other existing methods.