

“Detecting Haplotype Associations When the Important SNPs May Not Have Been Typed”

Dr. Dmitri Zaykin

NIEHS, National Institute of Environmental Health Sciences

Abstract:

We consider an association mapping scenario where scored haplotypes are either linked to causal variants via linkage disequilibrium (LD), or represent only a subset of all causal polymorphisms. In both cases, trait variances among the observed haplotypes may differ from each other. Such haplotypic variance contrast can be estimated, and incorporated into haplotypic tests for association for unphased data.

The inference involves simultaneous estimation of haplotypic effects, their frequencies, and haplotype-specific variances. The approach provides additional power under models where only a subset of functional polymorphisms has been scored, as well as under heterogeneity models, where multiple unobserved mutations are linked to non-functional observed polymorphisms via LD. A pronounced variance contrast may indicate such involvement of additional factors that influence the trait.