

Rare variant association mapping in admixed populations

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An admixed population and its ancestral populations bear different burdens of a complex disease. The ancestral populations have different haplotypes of deleterious alleles and thus ancestry gene interaction can be associated with disease risk in the admixed population. Among admixed individuals, deleterious haplotypes and their ancestries are dependent and can provide non-redundant association information. In this talk, I will present a new local ancestry boosted genetic association test for identifying chromosomal blocks that harbor rare alleles. For such a stable ancestral block, the proposed test exploits ancestry-gene interaction and the number of rare alleles therein. Under the null of no genetic association, the new test statistic asymptotically follows a chi-square distribution with one degree of freedom (1-df). It properly controlled type I error rates under extensive simulations, suggesting that the asymptotic approximation is accurate for the null distribution of the test statistic. In terms of power for identifying rare variant associations, the proposed test uniformly outperformed several famed methods under four important modes of disease genetics over a large range of relative risks. In conclusion, exploiting ancestry-gene interaction provides an effective avenue to boost statistical power for rare variant association mapping in admixed populations.