

# **Backward Haplotype Transmission Association (BHTA) Algorithm--A Fast Multi-point Screening Method for Complex Traits**

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## **Abstract:**

Family-based association methods have shown great promise in detecting genetic factors for complex traits of common human diseases during the past decade. Yet the success in identification of disease susceptibility genes has been restricted largely to simple Mendelian cases. This is because complex diseases such as diabetes, asthma and heart disease, usually involve multiple, interacting genetic determinants, which can be distributed widely across our genome. Current genome scans for the susceptibility loci of complex diseases, involving hundreds of markers, usually carry out hundreds to thousands of individual marker-wise tests, which fail to take into account the possible interactions among the disease susceptibility loci, and the significance is also difficult to establish due to the small sample size and the effects from multiple comparisons. As a result, researchers are calling for haplotype-based methods, which should be more informative and cost-efficient. At the same time, current haplotype algorithms can only possibly deal with small number of markers, say 4-5, due to the computation-intensive nature of these methods. This is far from enough to fulfill the needs in the field.

In my talk, I will introduce an original haplotype-based algorithm--Backward Haplotype Transmission Association Algorithm, which we proposed to address some of the current issues in the field of association mapping. It could help researchers identify a small set of "important" markers from the original large set of markers at many candidate regions. The mechanism of this algorithm will be discussed in details and the performance of this method will be demonstrated using a couple of computational examples, using both real medical data and simulated data under a newly found complex disease model.