

# **“Statistical Methods for Detecting Associations of Rare Variants with Complex Diseases”**

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## **Abstract:**

Recent studies have demonstrated that complex diseases can be due to multiple functional variants which are rare in population. Although whole genome association studies using tagSNPs are a powerful approach for detecting common variants, they are underpowered to localize rare variants. An effective alternative is through direct sequencing of candidate genes/regions to identify rare variants. Due to the extreme allelic heterogeneity in a gene with multiple rare variants, methods for association studies of common variants may not be optimal. In this study, new statistical approaches to detect associations of rare variants with complex diseases are proposed and their performances are compared with methods frequently used for common variants.