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Statistical tests of association with rare variants

Kai Wang
University of Iowa, USA

Sequencing has become an important means in medical genetics research. In particular, it enables accurate identification of rare variants underlying complex human traits. Due to their rarity and their unknown biological role, statistical analysis of these variants has been challenging. The "burden test" approach typically has reduced power when the effects of the rare variants are of opposite direction. The C-alpha test addresses this issue. However, its inference is based either on an asymptotic distribution which often does not behave well or on a computation intensive permutation procedure. In addition, existing tests typically ignore the interaction effects of rare variants. To address these issues, we investigate ways to improve the accuracy of the C-alpha test. We also propose a method based on the multi-locus genotypes which is similar to the Kernel-Based Adaptive Cluster (KBAC). The utility of these methods are demonstrated using simulation studies.

Biography

Kai Wang obtained his Ph.D. degree in statistics in 1999 from University of Iowa. His research interest is in statistical genetics. His methodology research and collaborative work have appeared in many reputed journals.

kai-wang@uiowa.edu