

Testing Gene-Environment Interactions with Nuclear Family Data

The widespread availability of genetic markers for samples of reasonable size has intensified interest in testing for gene-environment interactions with complex diseases. Both traditional case-control and family-based designs are used in genetic association studies, the latter having the advantage of eliminating problems due to population substructure, as well as sensitivity to modeling the genetic effect when testing for genetic effects alone. Here we address the issue of extending the family design to test gene-environment interactions. Robustness to population substructure can be maintained, but robustness to model specification is not. We also discuss joint-tests of gene-environment interaction which are generally more powerful, as well as completely robust to the genetic model and population substructure.