

A Bayesian framework for generalized linear mixed modeling identifies new candidate loci for late-onset Alzheimer's disease

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Article Summary

Genetic association studies are commonly carried out in structured populations, often have categorical variables as phenotypes, and increasingly use high-resolution sequencing technologies. We have developed an approach, *Bayes-GLMM*, that addresses these analytical complications. Implemented in the Stan programming environment, our Bayesian linear mixed model approach enables fast and flexible genetic association analysis. We used *Bayes-GLMM* to identify four novel, non-coding variants that affect Alzheimer's disease risk in whole-genome sequencing data from the Alzheimer's Disease Sequencing Project.