Xiong, Sican; Hu, Guikai; Ruan, Zhou Sheng
Applying group Lasso to map the quantitative trait loci for recombinant inbred intercrosses lines derived from collaborative cross mice. (Chinese. English summary) Zbl 07366772

Summary: The recombinant inbred intercrosses derived from the collaborative cross (CC-RIX) have many merits, especially the higher mapping power in quantitative trait loci (QTL) for complex disease. Based on the existing studies, the paper establishes a linear mixed model that only includes the main founder effects to map the QTLs. The group Lasso penalized method has been applied to solve the model, and the iteratively re-weighted least-squares algorithm was used to find the optimal estimation. By doing that, some problems, such as the singularity of the design matrix, the computational cost, and so on, have been overcome. The simulation results show that our proposed method can identify the QTLs fast and correctly for CC-RIX lines with a high true positive rate (TPR) and low false-positive rate (FPR).

MSC:
62P10 Applications of statistics to biology and medical sciences; meta analysis
62J07 Ridge regression; shrinkage estimators (Lasso)

Keywords:
quantitative trait loci; group Lasso; iteratively re-weighted least-squares algorithm