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Title: Quantitative trait mapping methods with complex data sets

Recent developments in association mapping methods along with improvements in sequencing technology have made it possible to link locations along the genome (single nucleotide polymorphisms, or SNPs) with quantitative traits. Although this goal is central in the biological sciences, progress has been limited by the inability of existing methods to consider complex, but relevant, scenarios such as the simultaneous influence of genetic and external effects on quantitative trait(s) under study. Regression-based methods are computationally feasible and perform well in detecting external effects, but may miss weaker genetic signals since they fail to consider uneven evolutionary relatedness among samples. Previous work has shown promise in improving detection of associated SNPs by using the uneven relatedness within a SNP to estimate the underlying covariance structure among trait values. Here, a method is proposed to search for genetic and external effects on a quantitative trait.