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Covariate Modulated False Discovery Rate.

Large-scale hypothesis testing, such as genome-wide association studies (GWAS), is facing the challenge of properly controlling for type I error. Traditional multiple-comparison procedures tend to be underpowered. Procedures that control false discovery rate (fdr) are more powerful; yet most of proposed methods treat all hypothesis tests as exchangeable and independent, ignoring auxiliary covariates that may influence the distribution of the test statistics and ignore the prior knowledge of the correlations structures of Single nucleotide polymorphisms (SNPs). The current work incorporates Hidden Markov Random Field (HMRF) into a Bayesian two-group mixture model for a covariate-modulated local false discovery rate (cmfdr) on SNPs that are not independent. The simulations and real data application are carried out to compare the performance in terms of sensitivity, specificity and false discovery proportion (FDP) between the new method and the independent cmfdr, as well as the correlation-based fdr without covariates. (Received August 04, 2020)