

Results for the simulations under H_0

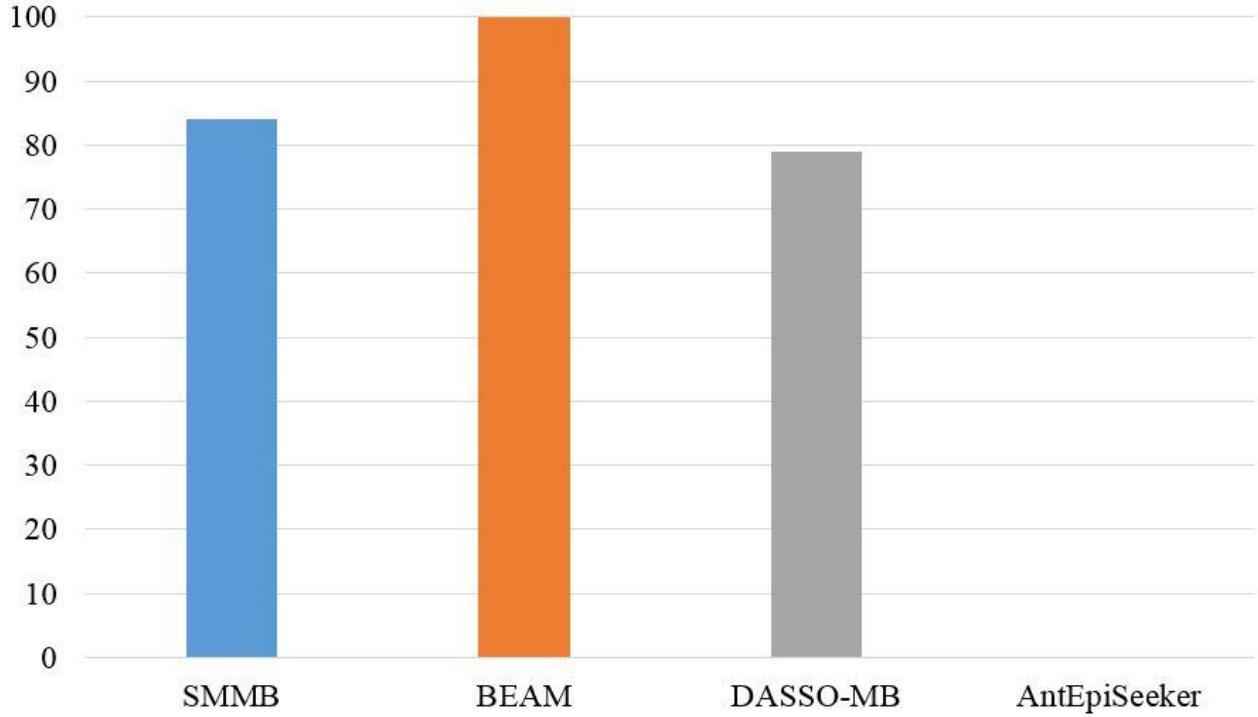


Figure 1. Comparison of true negative rates between SMMB, BEAM, DASSO-MB and AntEpiSeeker, for the data simulated under hypothesis H_0 . The true negative rate is defined as the percentage of datasets for which no epistasis interaction has been identified ($TNR = \#TN / (\#TN + \#FP)$). Simulated data: 4000 individuals, 100 SNPs, MAFs in $[0.05, 0.5]$, number of datasets replicated = 100. Parameters for SMMB: $t = 1000$, $r = 100$, $m = 30$, $K = 10$, $k = 3$, $\alpha = 0.05$. Parameters for BEAM: nb iterations for burn-in phase: 1000, nb iterations for stationary phase: 10000. Parameters for DASSO-MB: $\alpha = 0.05$. Parameters for AntEpiSeeker: 450 iterations, 1000 ants, $\alpha = 0.01$.

Comments

With around 16% of false positives, SMMB ranks second behind BEAM (0% of false positives). DASSO-MB shows 21% of false positives. AntEpiSeeker output a false positive for each of the 100 simulated datasets.