

Comparing F test with permutation test

Simulations are performed with $E = 0, 0.3, 0.5$ when $P_0 = 0.2$ and $d = 0$ under simulation scenario 1. For each E value, the simulation is repeated 1,000 times. The permutation tests are performed by randomly permute the SNP genotype codes across individuals, this is because permuting SNP codes can take both SNP-GE association and genotype frequency difference between populations into account simultaneously. For each SNP-GE data, the null hypothesis ($H_0: GS = 0$) is rejected if the original F value (calculated from the non-permuted data) is larger than 95 percent of the permuted F values (calculated from 1,000 permutation). Results show that permutation approach (green bar) has lower probabilities of rejecting the null hypothesis in comparison with those using non-central F distribution (red bar). In addition, the rejection probabilities of these two methods are both inflated as the E value increases.

