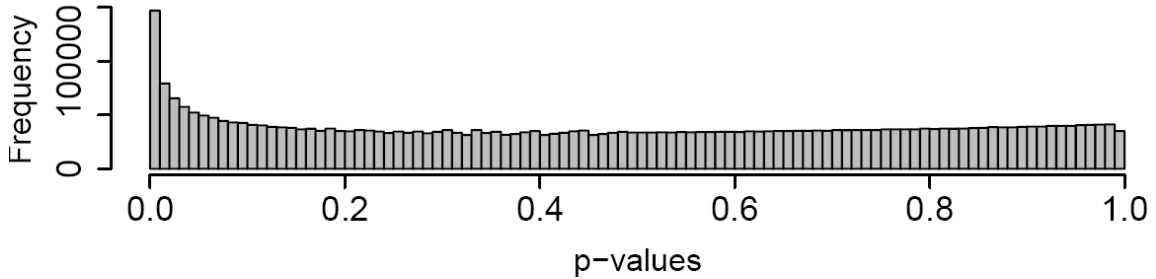
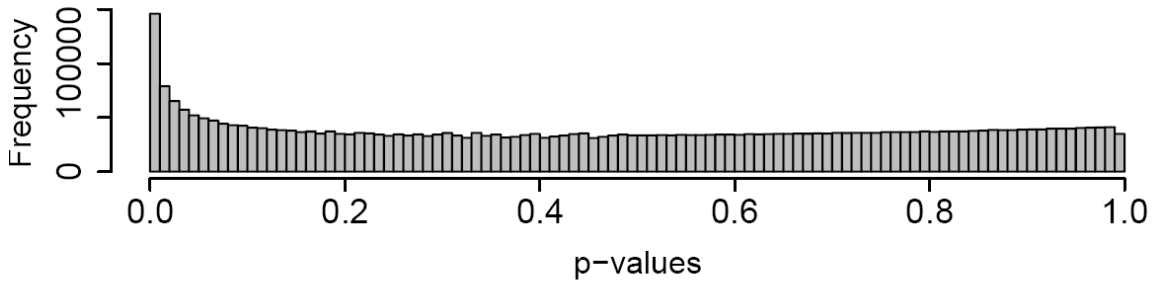


Figure 1 - Histogram of p-values for linkage of SNPs to gene expression traits

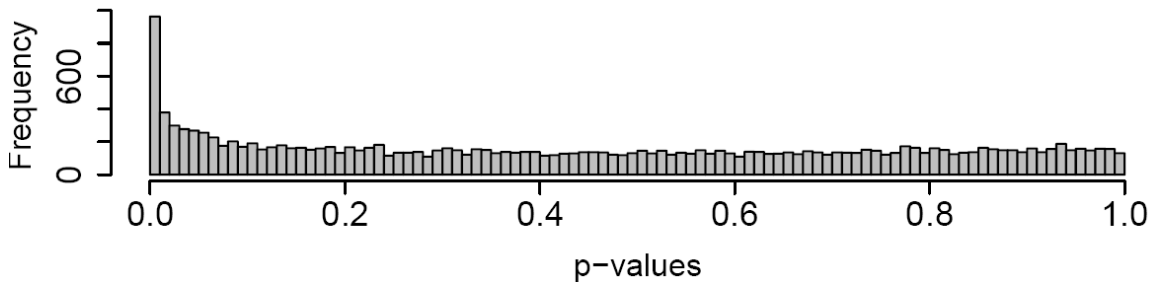
(a) all 3,855,428 tests



(b) 3,839,410 tests in trans

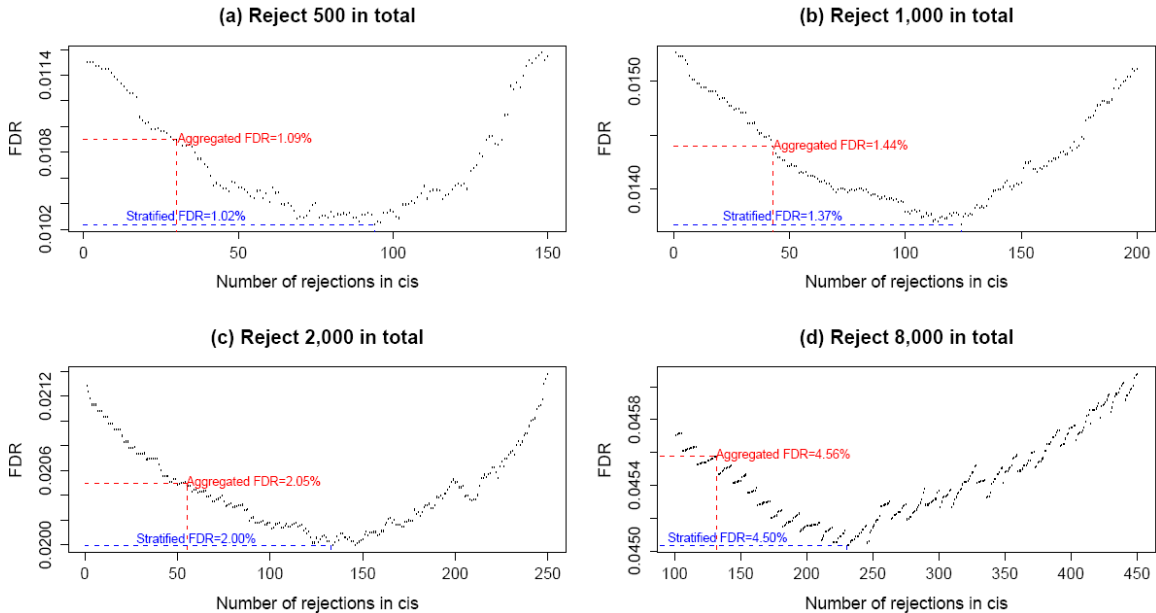


(c) 16,018 tests in cis



Distributions of the aggregated p-values and partitioned p-values in trans and cis strata were roughly uniform. Comparing distributions of p-values in *trans* and *cis*, we can see that the cis stratum contains a relatively higher proportion of true signals than the trans stratum,

Figure 2 - FDR vs. number of rejections in the *cis* stratum under framework III



For different total numbers of rejections, we could always find the optimized number of rejections in *cis* which gives us the lowest overall FDR.

(a): with 500 rejections, $F\hat{D}R = 1.09\%$ under aggregation and $F\hat{D}R = 1.02\%$ under the optimized stratification assigning 30 rejections to *cis* and 470 to *trans*;

(b): with 1000 rejections, $F\hat{D}R = 1.44\%$ under aggregation and $F\hat{D}R = 1.37\%$ under the optimized stratification assigning 43 rejections to *cis* and 957 to *trans*;

(c): with 2000 rejections, $F\hat{D}R = 2.05\%$ under aggregation and $F\hat{D}R = 2.00\%$ under the optimized stratification assigning 55 rejections to *cis* and 1945 to *trans*;

(d): with 8000 rejections, $F\hat{D}R = 4.56\%$ under aggregation and $F\hat{D}R = 4.50\%$ under the optimized stratification assigning 132 rejections to *cis* and 7868 to *trans*;