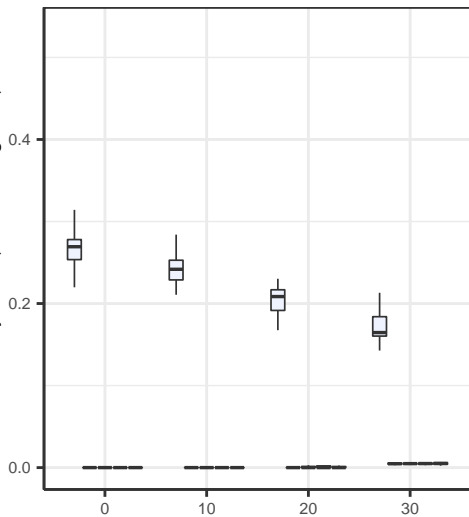


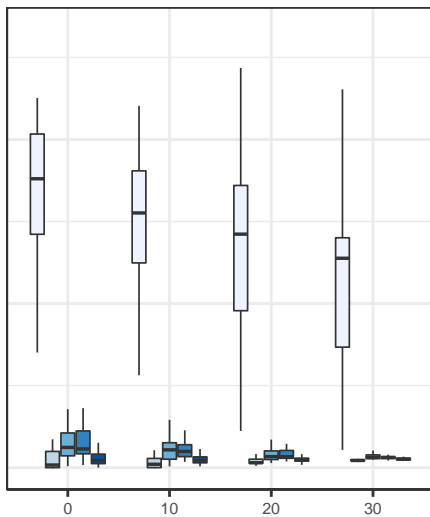
Var. by Confounder 0 %

Var. by Confounder 50 %

Discovery Rate (out of 10k genes)



Variance Caused by Disease Effect (%)



neighbours

