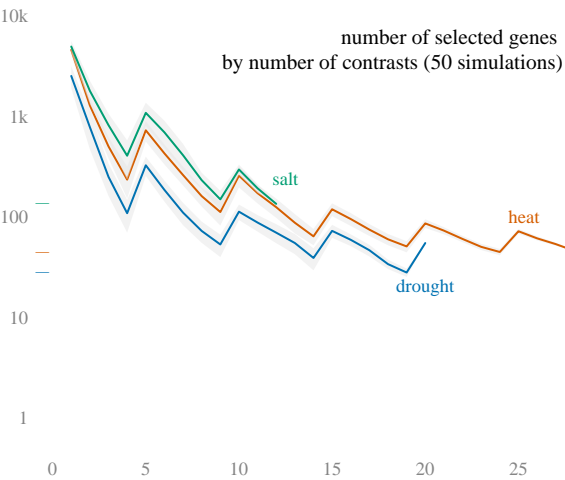
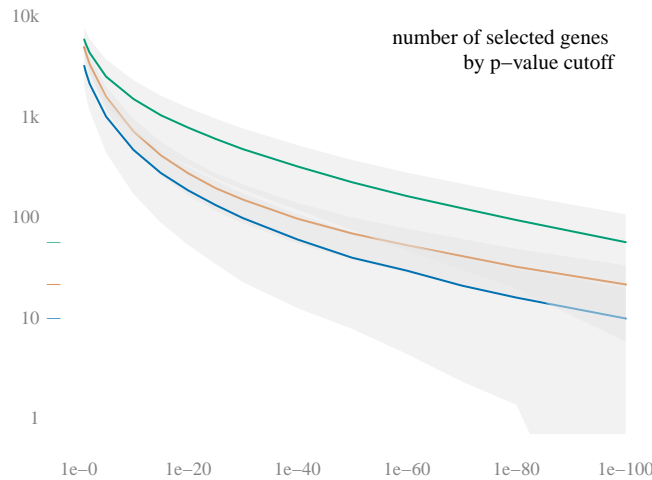


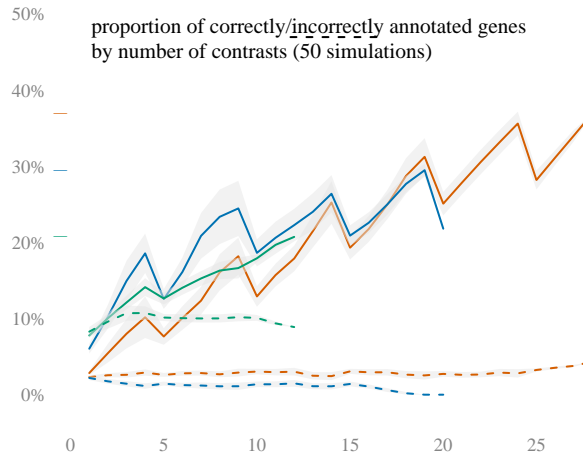
number of selected genes
by number of contrasts (50 simulations)



number of selected genes
by p-value cutoff



proportion of correctly/incorrectly annotated genes
by number of contrasts (50 simulations)



proportion of correctly/incorrectly annotated genes
by p-value cutoff

