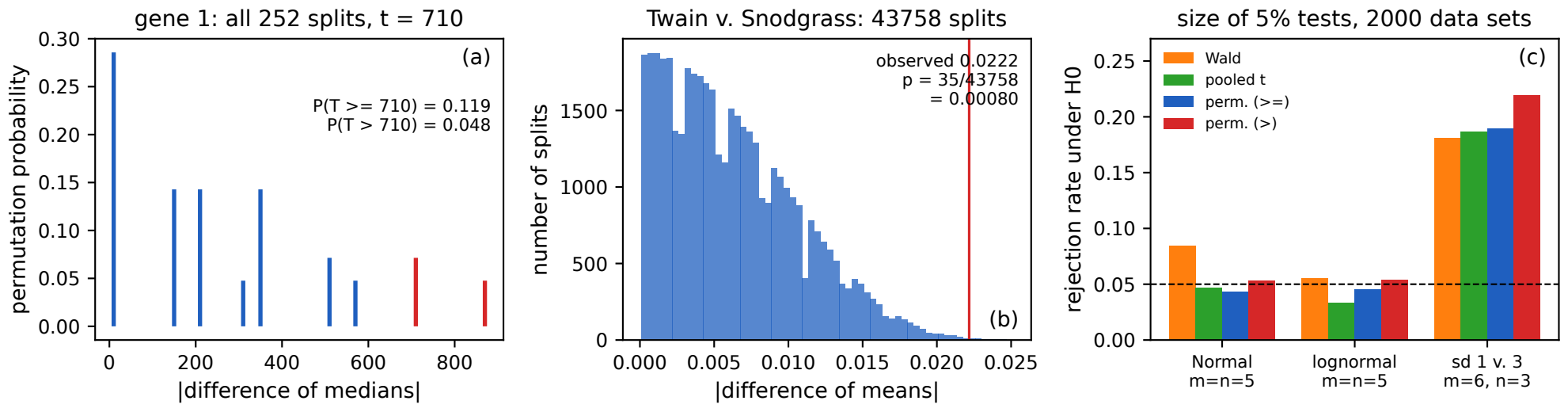

gene 1: all 252 splits, t = 710
(a)
P(T >= 710) = 0.119
P(T > 710) = 0.048
permutation probability
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0
200
400
600
800
|difference of medians|
Twain v. Snodgrass: 43758 splits
observed 0.0222
p = 35/43758
= 0.00080
(b)
number of splits
1500
1000
500
0
0.000
0.005
0.010
0.015
0.020
0.025
|difference of means|
size of 5% tests, 2000 data sets
(c)
Wald
pooled t
perm. (>=)
perm. (>)
rejection rate under H0
0.25
0.20
0.15
0.10
0.05
0.00
Normal
m=n=5
lognormal
m=n=5
sd 1 v. 3
m=6, n=3