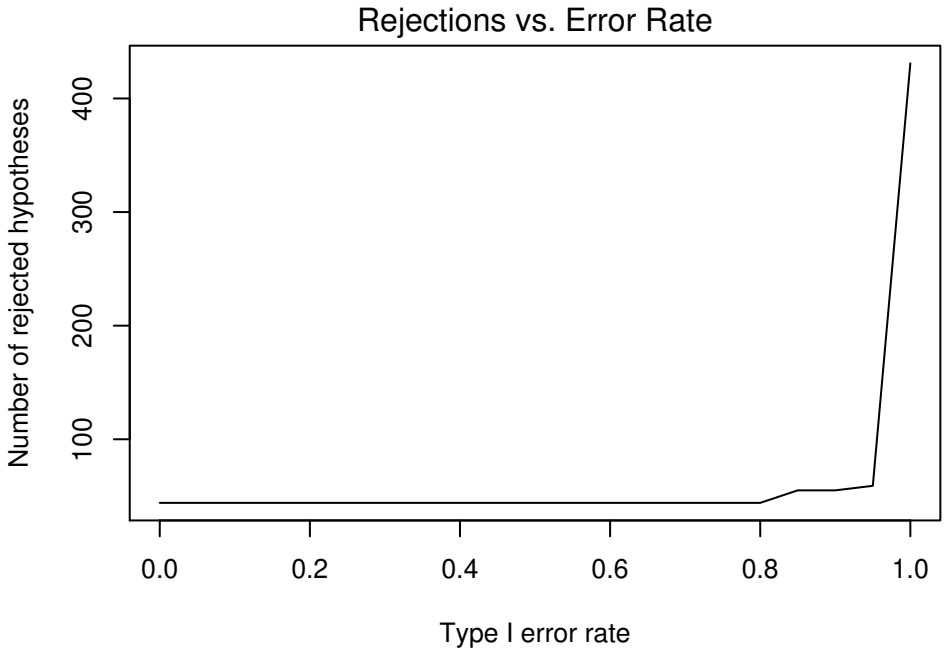
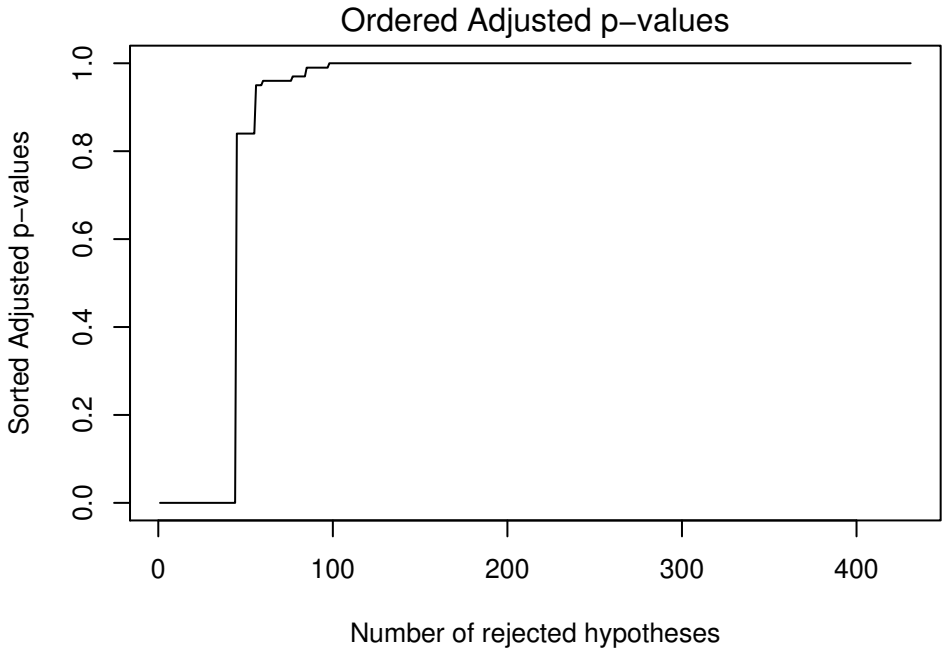
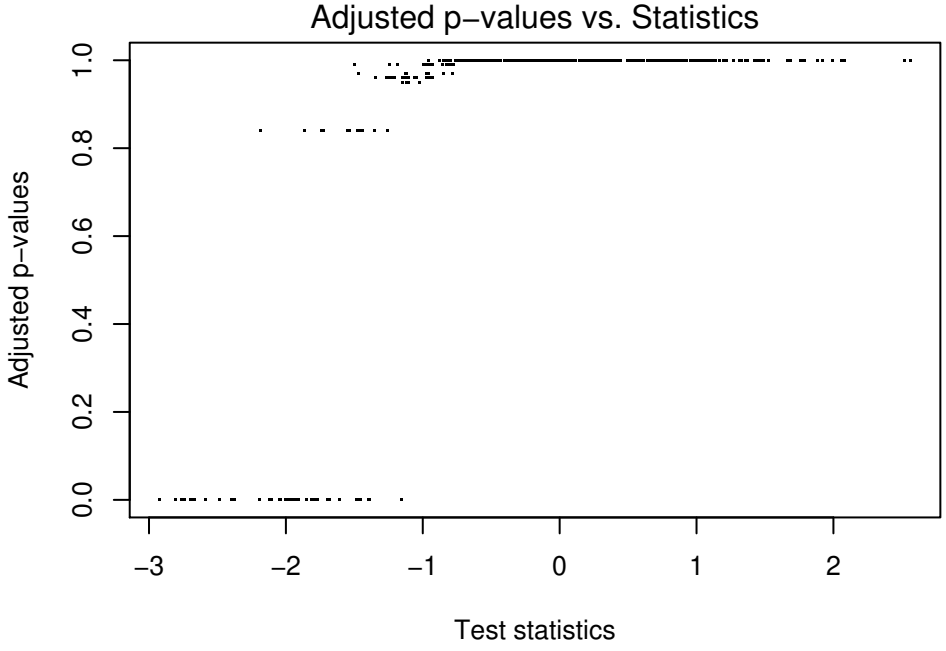
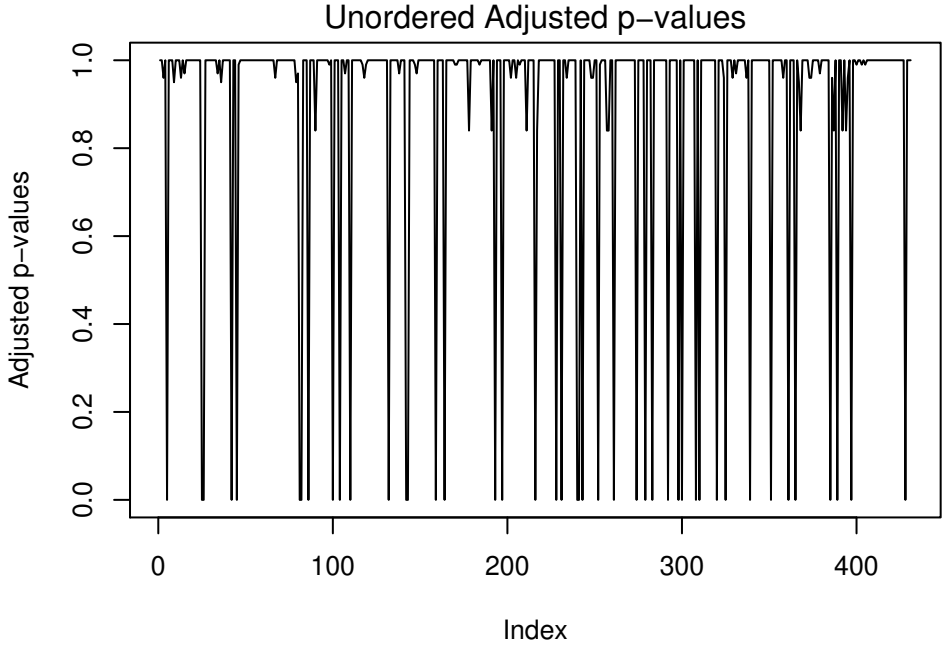
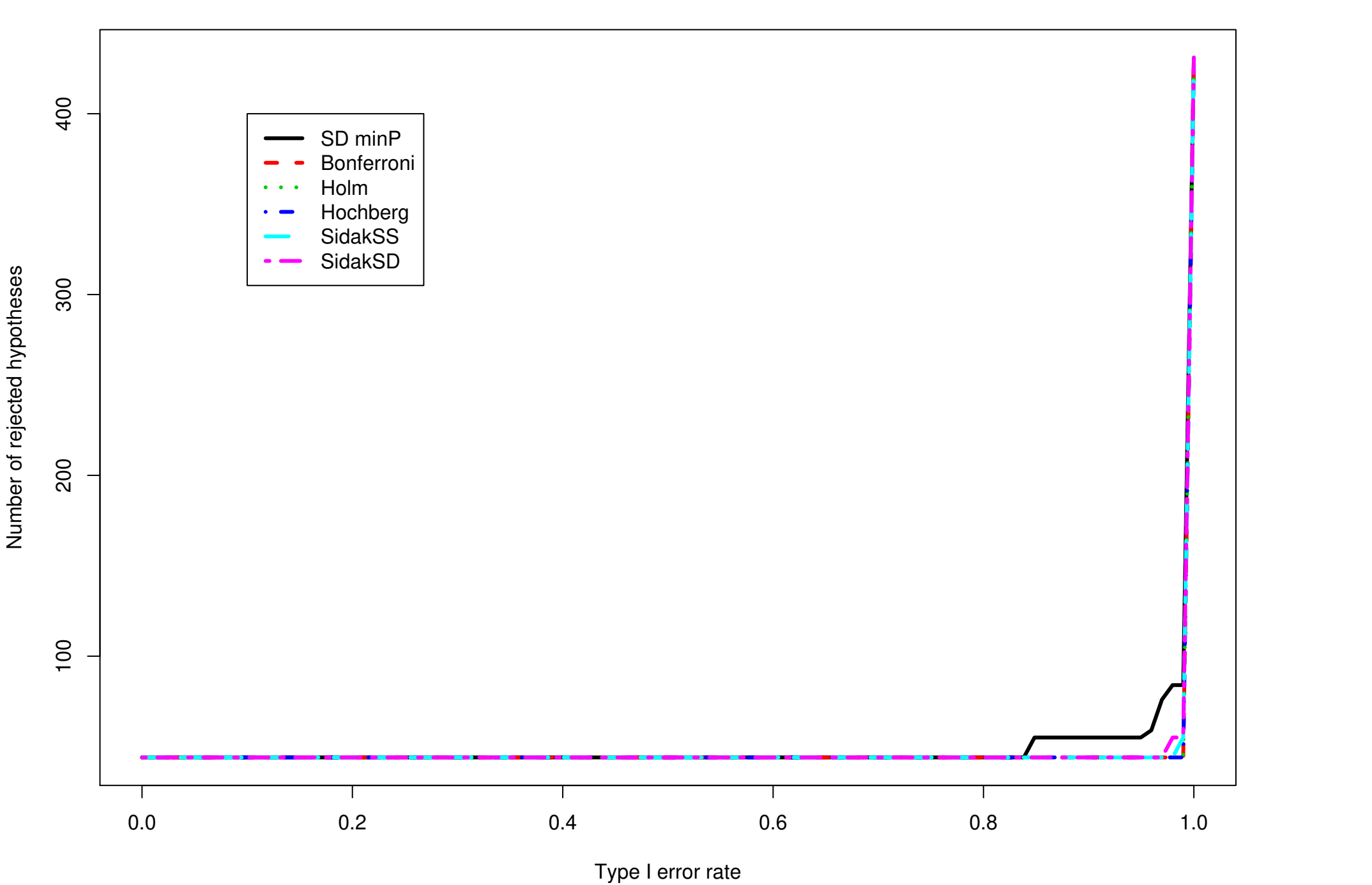
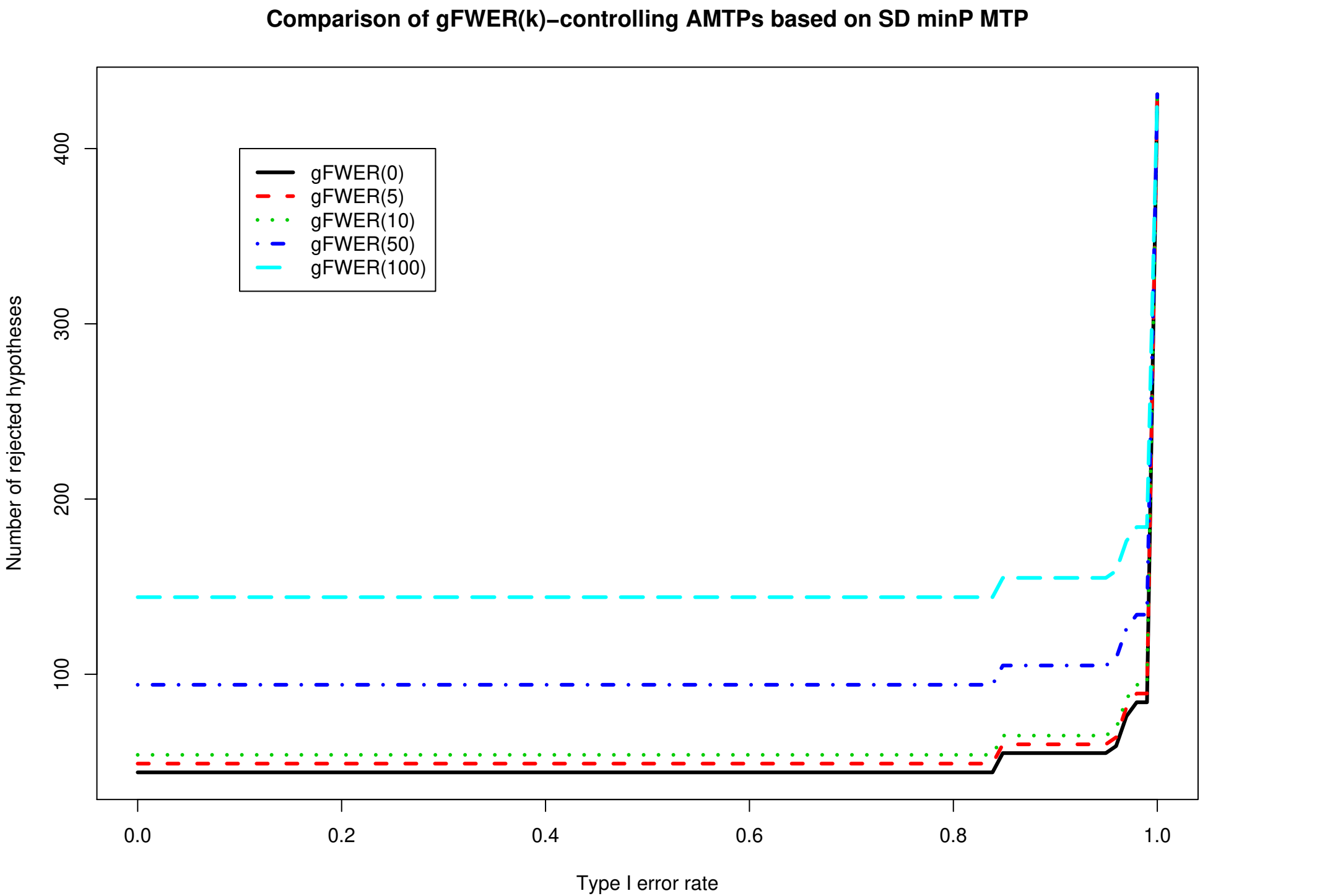

Rejections vs. Error Rate
Number of rejected hypotheses
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0
Type I error rate

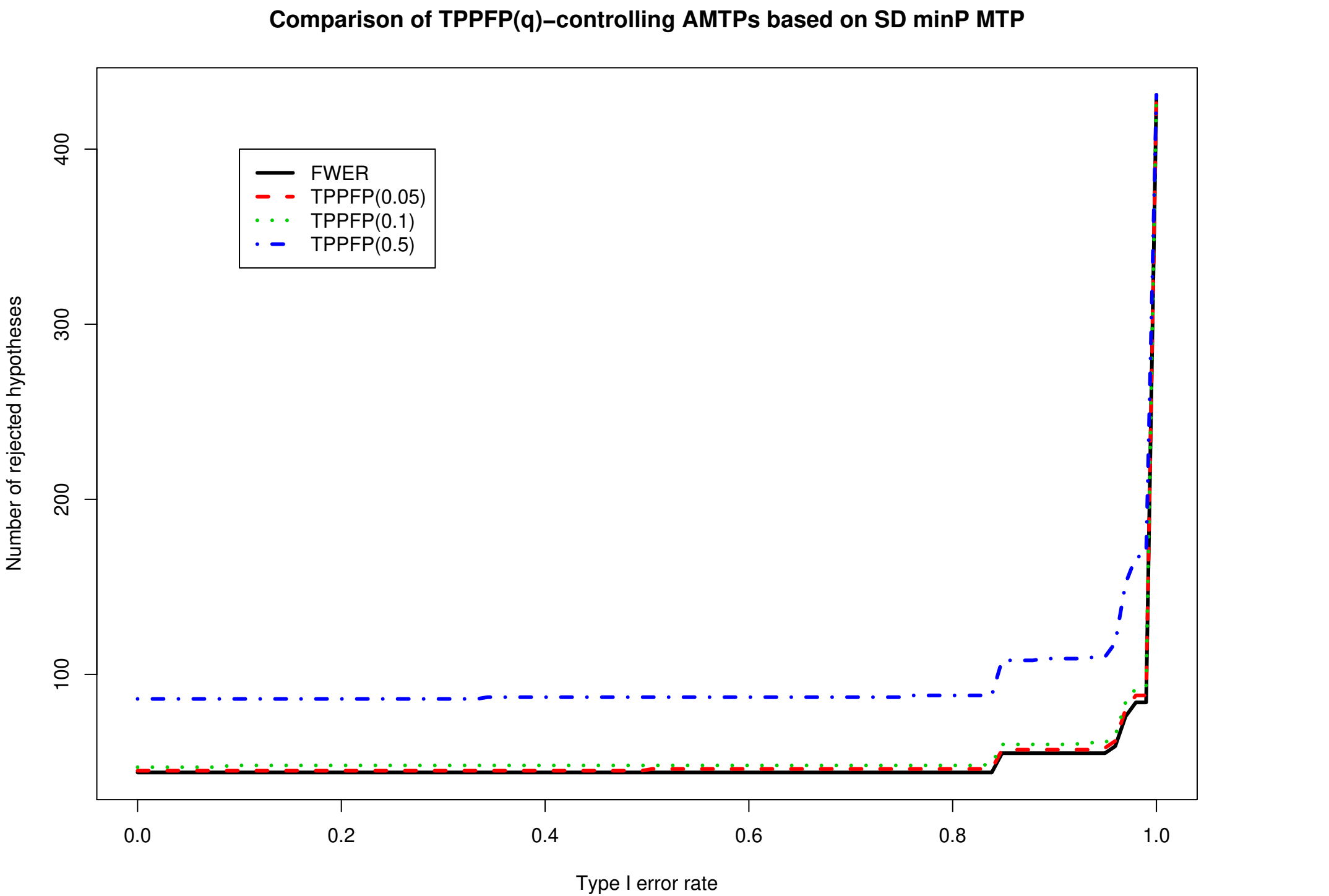

Ordered Adjusted p−values
Sorted Adjusted p−values
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400
Number of rejected hypotheses

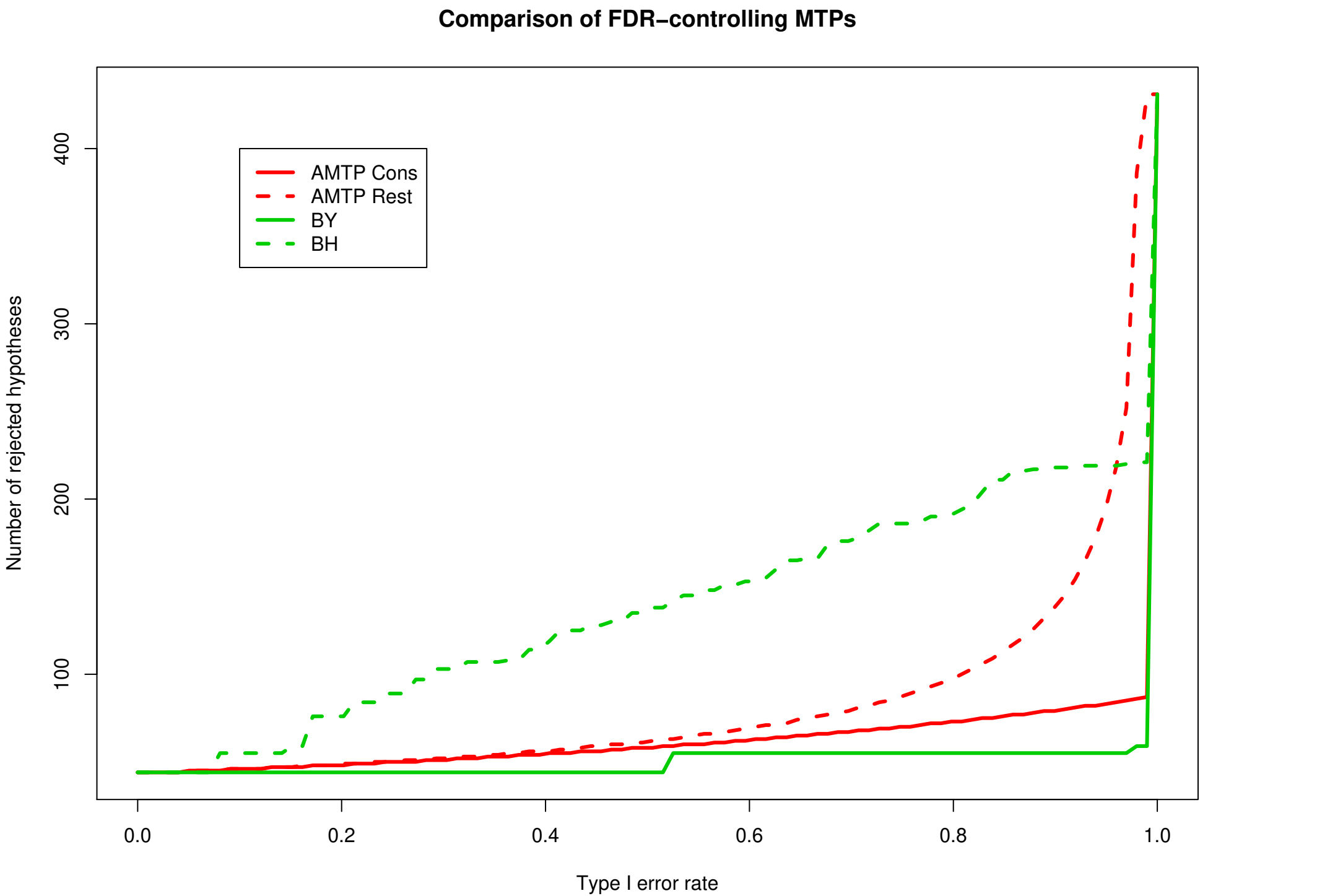

Adjusted p−values vs. Statistics
Adjusted p−values
0.0
0.2
0.4
0.6
0.8
1.0
−3
−2
−1
0
1
2
Test statistics

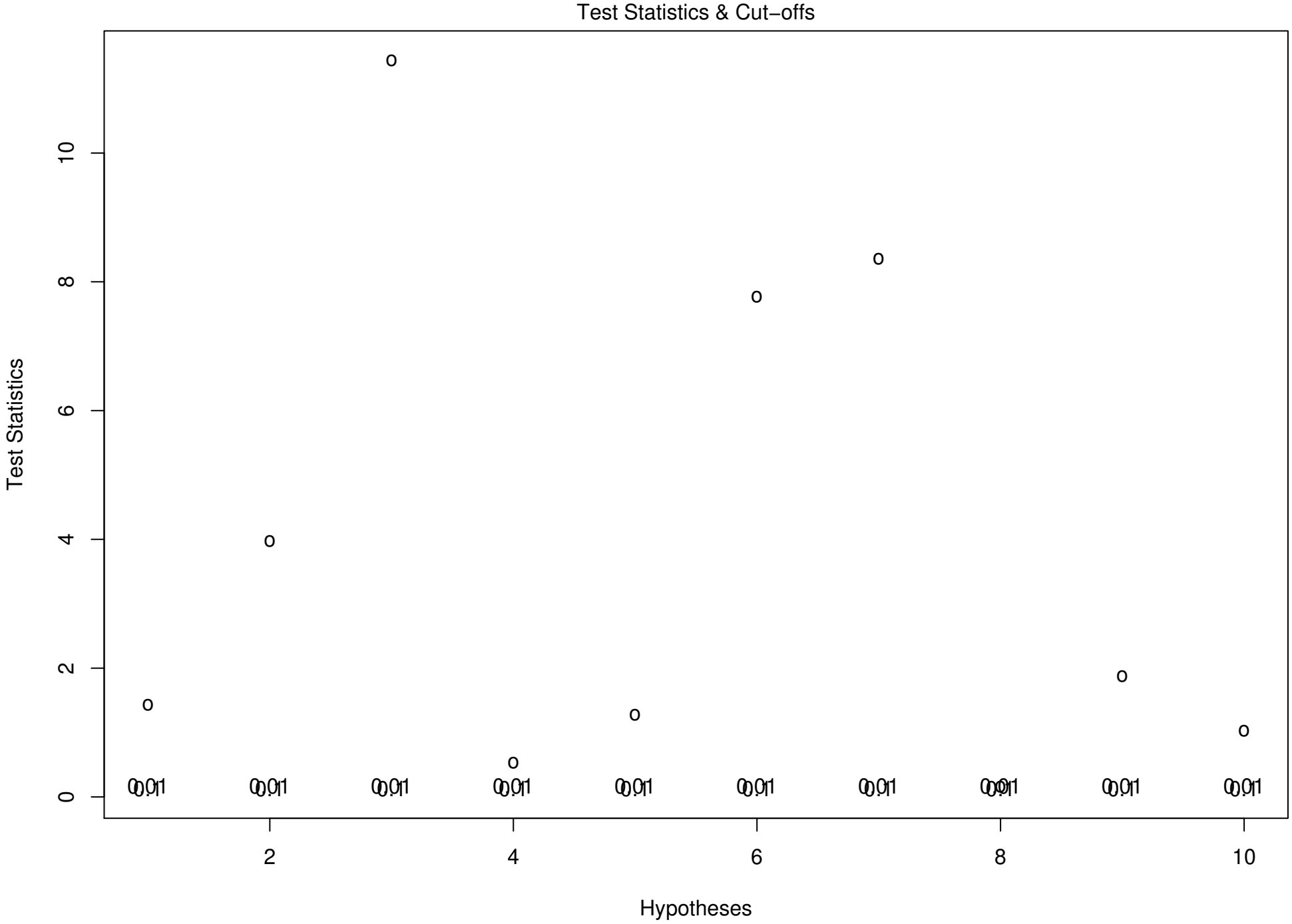

Unordered Adjusted p−values
Adjusted p−values
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400
Index

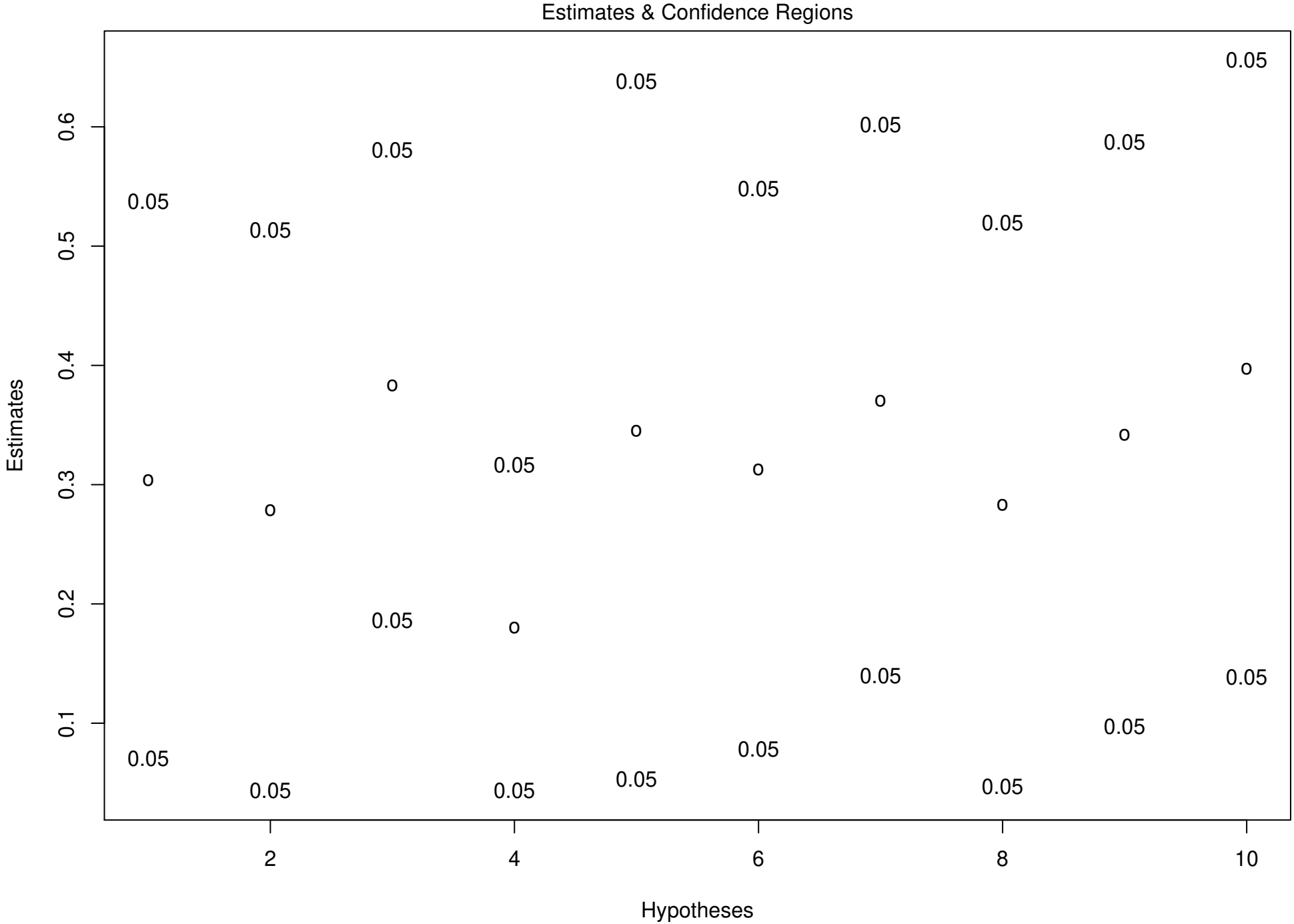

Comparison of marginal and step−down minP FWER−controlling MTPs
SD minP
Bonferroni
Holm
Hochberg
SidakSS
SidakSD
Number of rejected hypotheses
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0
Type I error rate


Comparison of gFWER(k)−controlling AMTPs based on SD minP MTP
gFWER(0)
gFWER(5)
gFWER(10)
gFWER(50)
gFWER(100)
Number of rejected hypotheses
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0
Type I error rate


Comparison of TPPFP(q)−controlling AMTPs based on SD minP MTP
FWER
TPPFP(0.05)
TPPFP(0.1)
TPPFP(0.5)
Number of rejected hypotheses
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0
Type I error rate


Comparison of FDR−controlling MTPs
AMTP Cons
AMTP Rest
BY
BH
Number of rejected hypotheses
100
200
300
400
0.0
0.2
0.4
0.6
0.8
1.0
Type I error rate


Top 10 Hypotheses
Test Statistics & Cut−offs
Test Statistics
0
2
4
6
8
10
Hypotheses
2
4
6
8
10
MTP(X = filtX, Y = mb, test = "f", alpha = c(0.01, 0.1), B = 100, get.cutoff = TRUE, seed = seed)


Top 10 Hypotheses
Estimates & Confidence Regions
Estimates
0.1
0.2
0.3
0.4
0.5
0.6
2
4
6
8
10
Hypotheses
MTP(X = relX, Y = rel.times, Z = relZ, Z.incl = "sex", Z.test = NULL, test = "coxph.YvsXZ", B = 100, get.cr = TRUE, seed = seed)