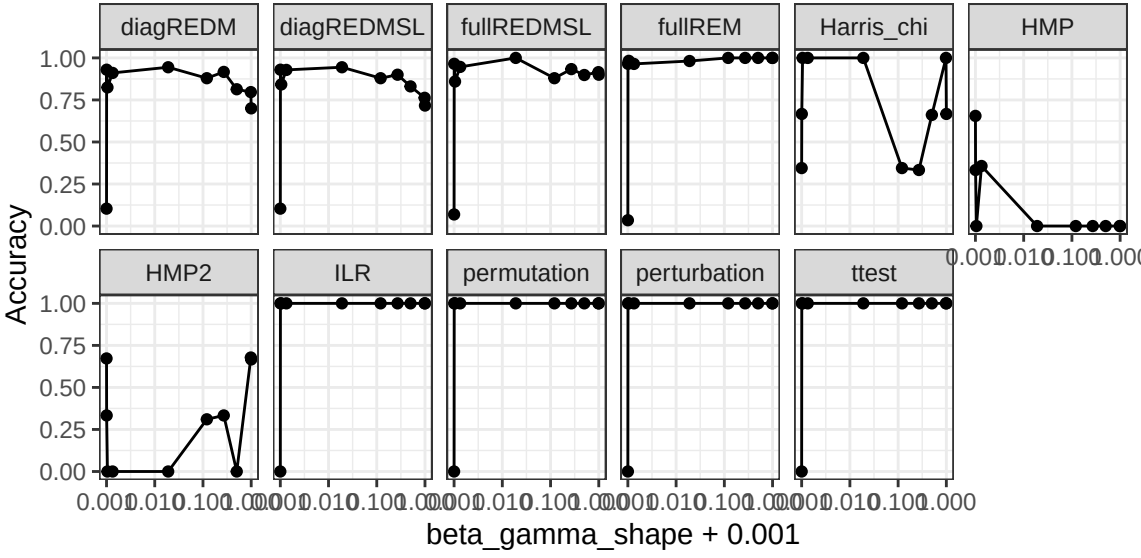
diagREDM
diagREDMSL
fullREDMSL
fullREM
Harris_chi
HMP
HMP2
ILR
permutation
perturbation
ttest
Accuracy
1.00
0.75
0.50
0.25
0.00
0.001
0.010
0.100
1.000
beta_gamma_shape + 0.001