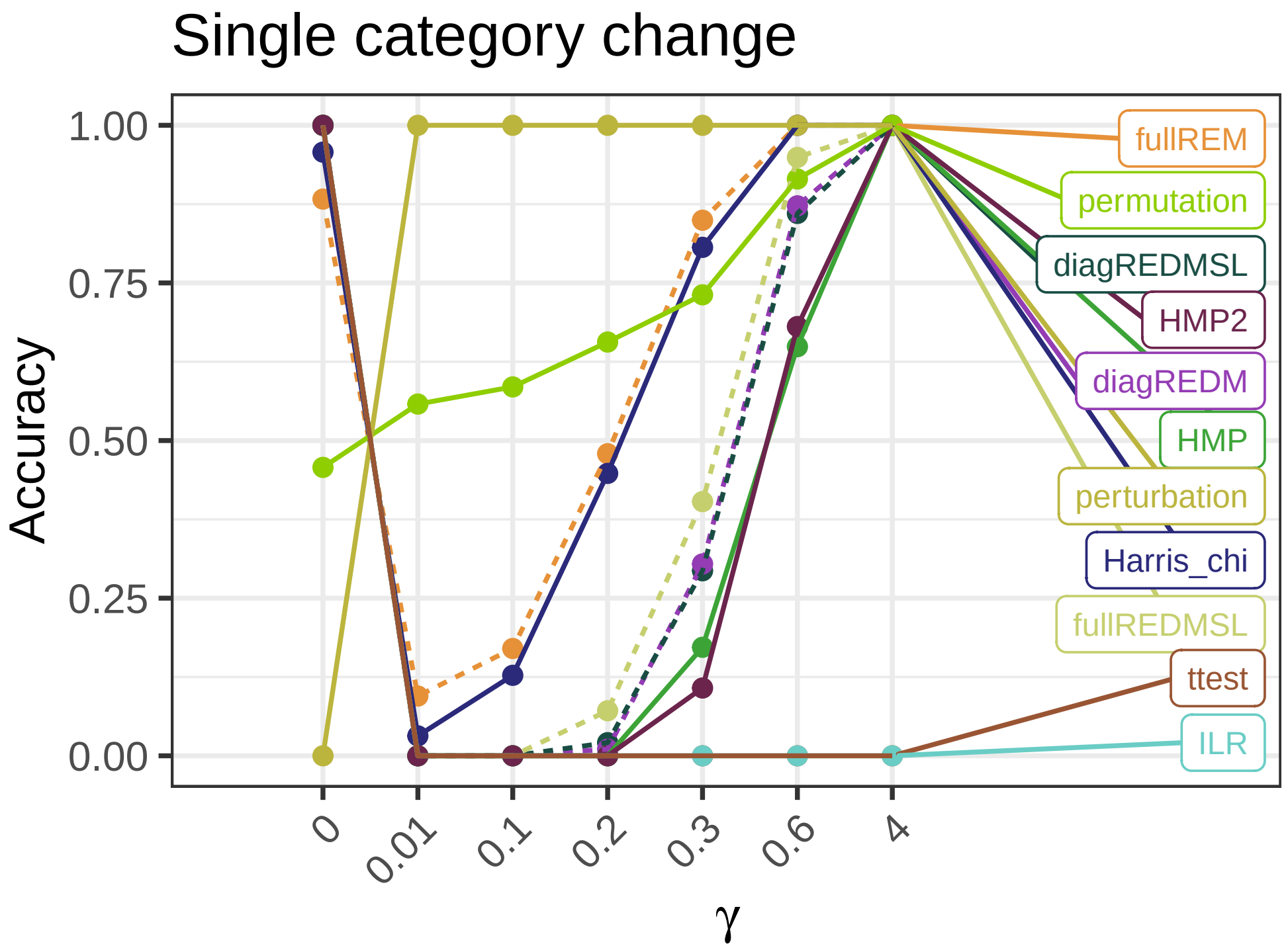
Single category change
Accuracy
1.00
0.75
0.50
0.25
0.00
0
0.01
0.1
0.2
0.3
0.6
4
γ
fullREM
permutation
diagREDMSL
HMP2
diagREDM
HMP
perturbation
Harris_chi
fullREDMSL
ttest
ILR