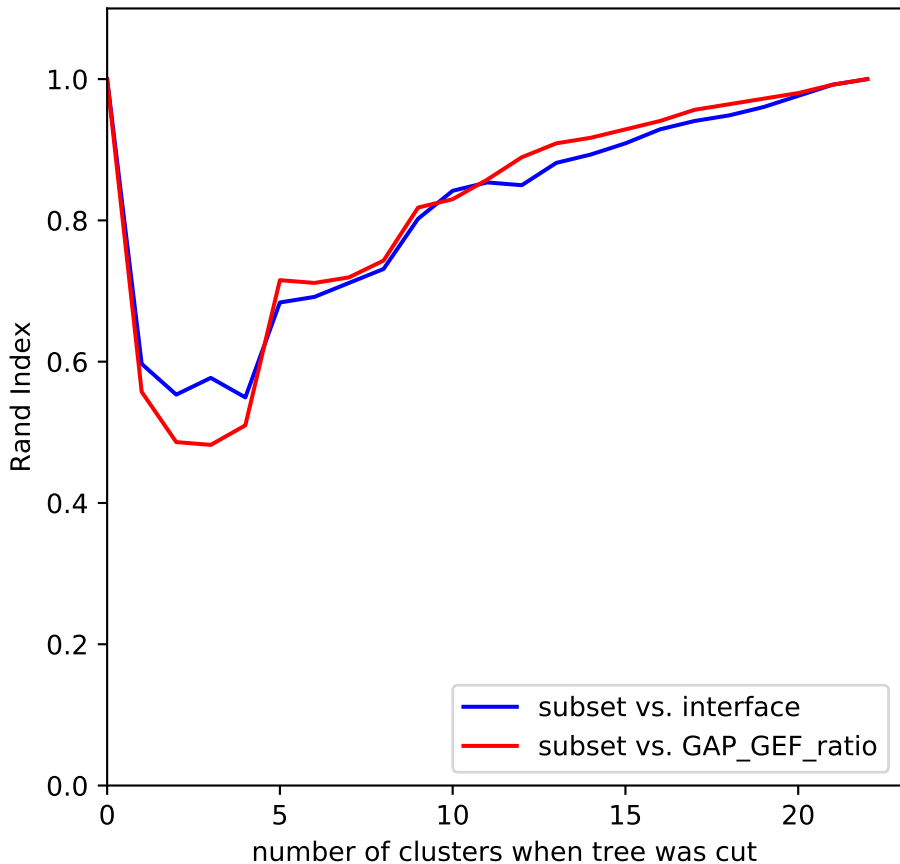
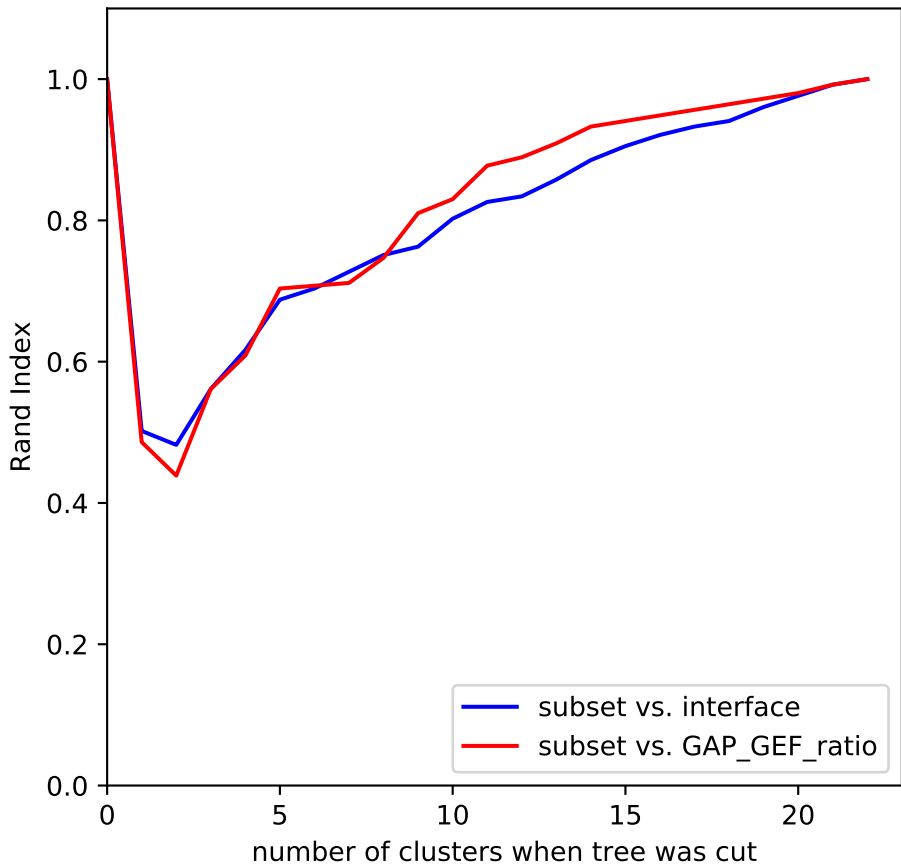


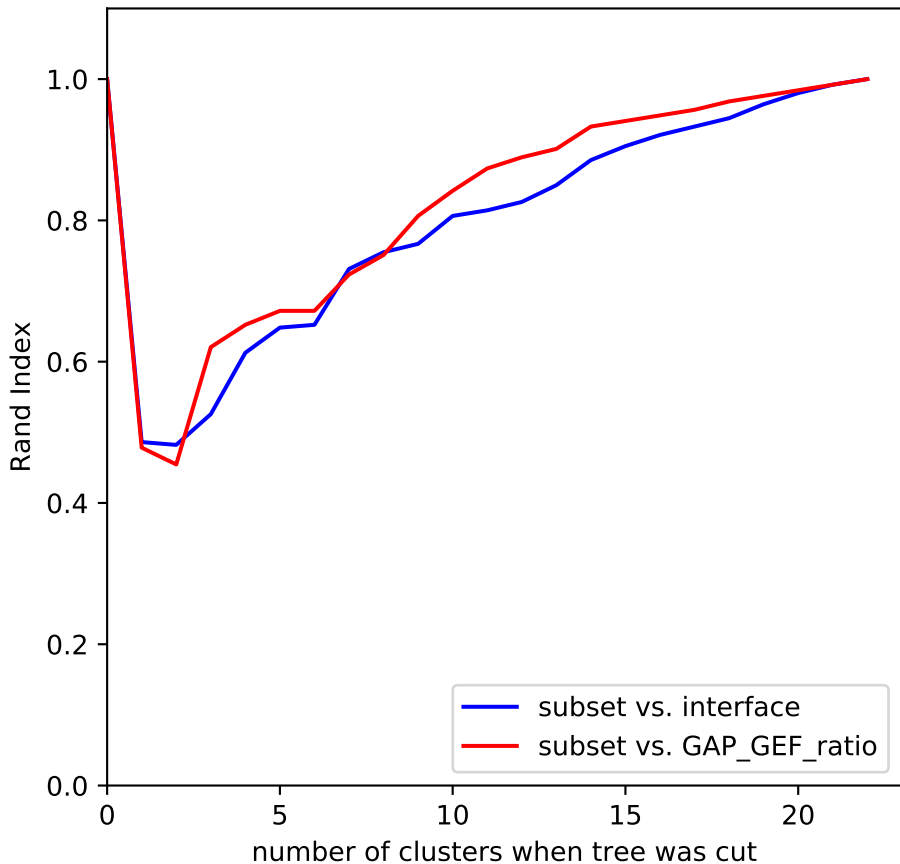
dataset = full_emap



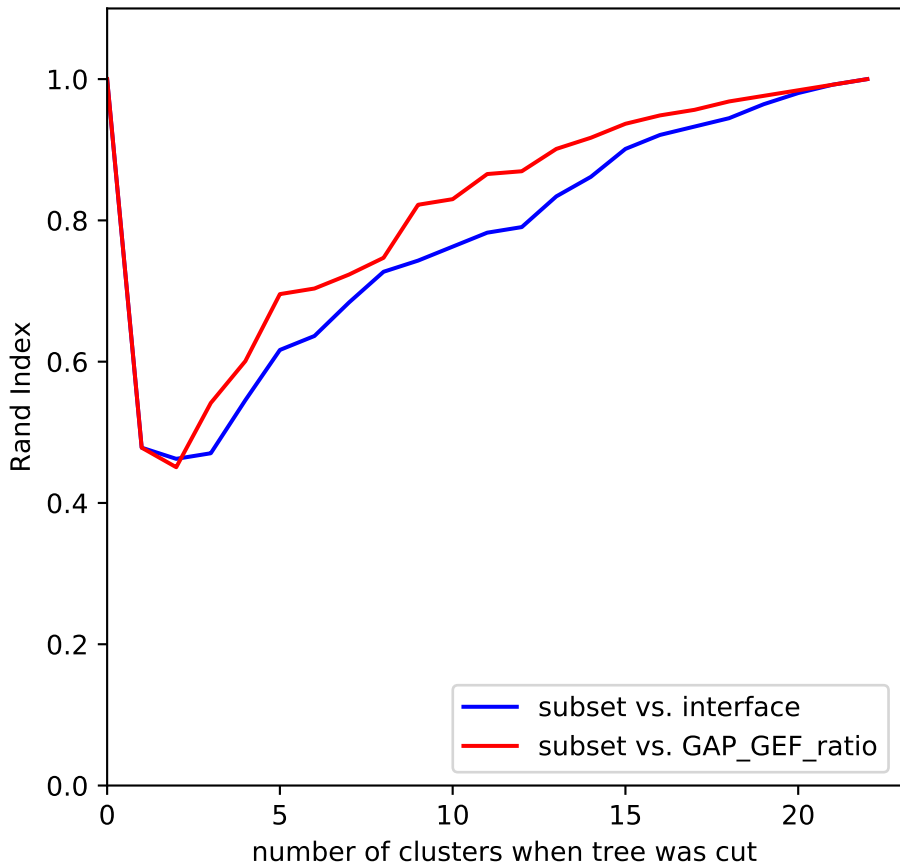
dataset = SET3



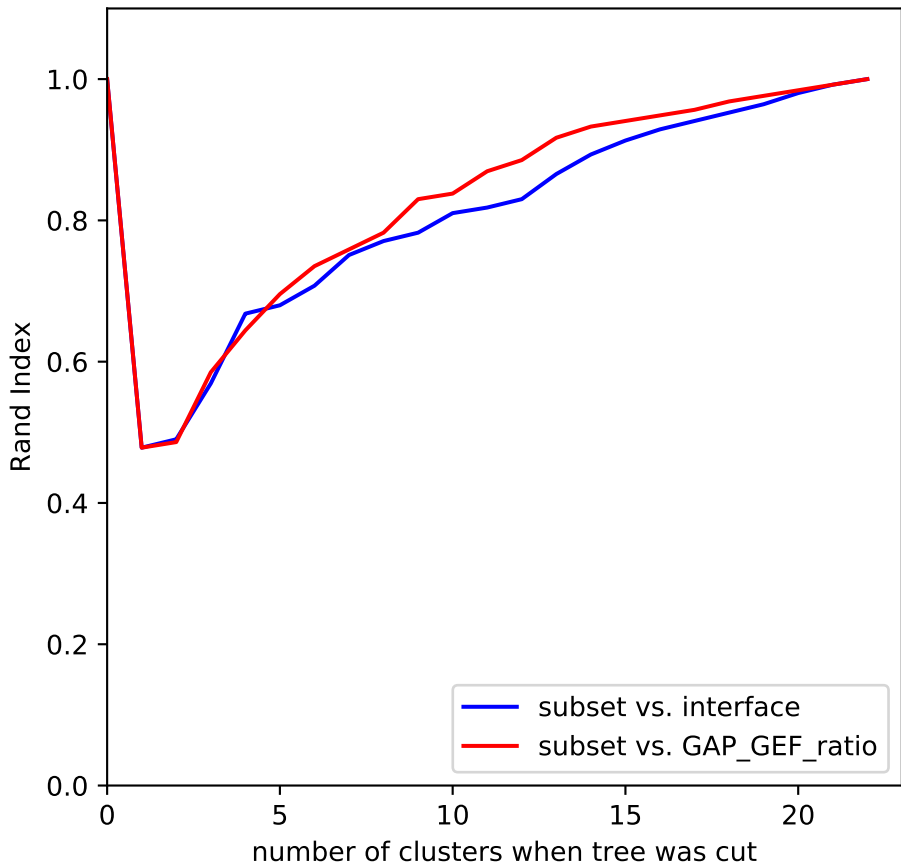
dataset = Arl GTPases



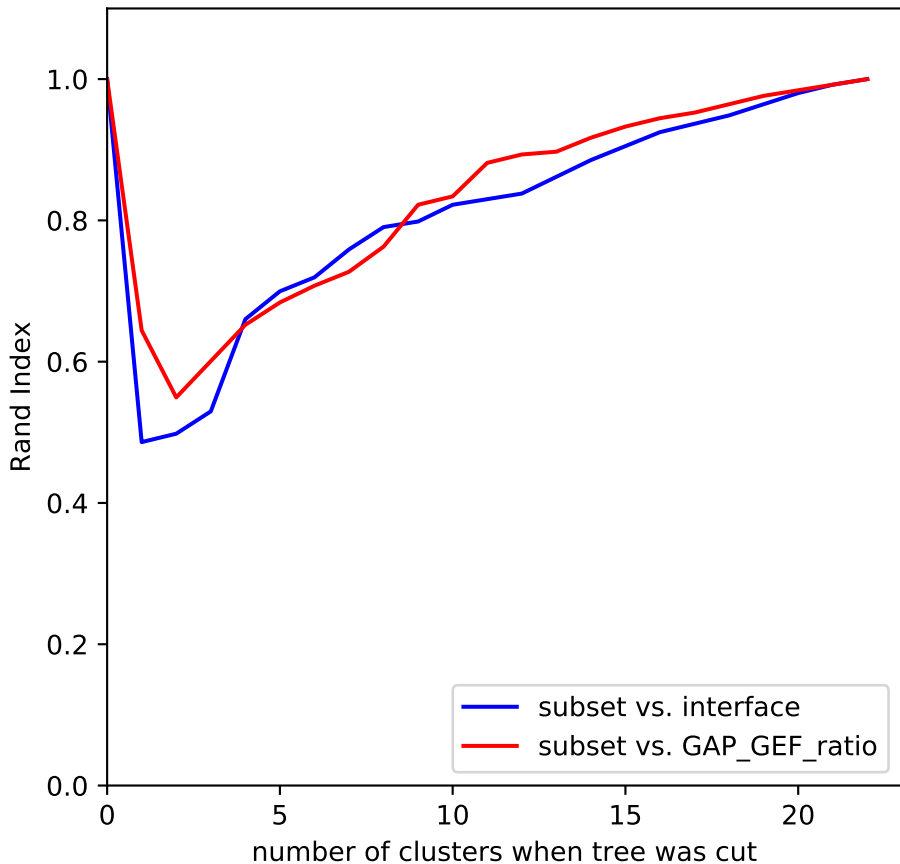
dataset = ADA



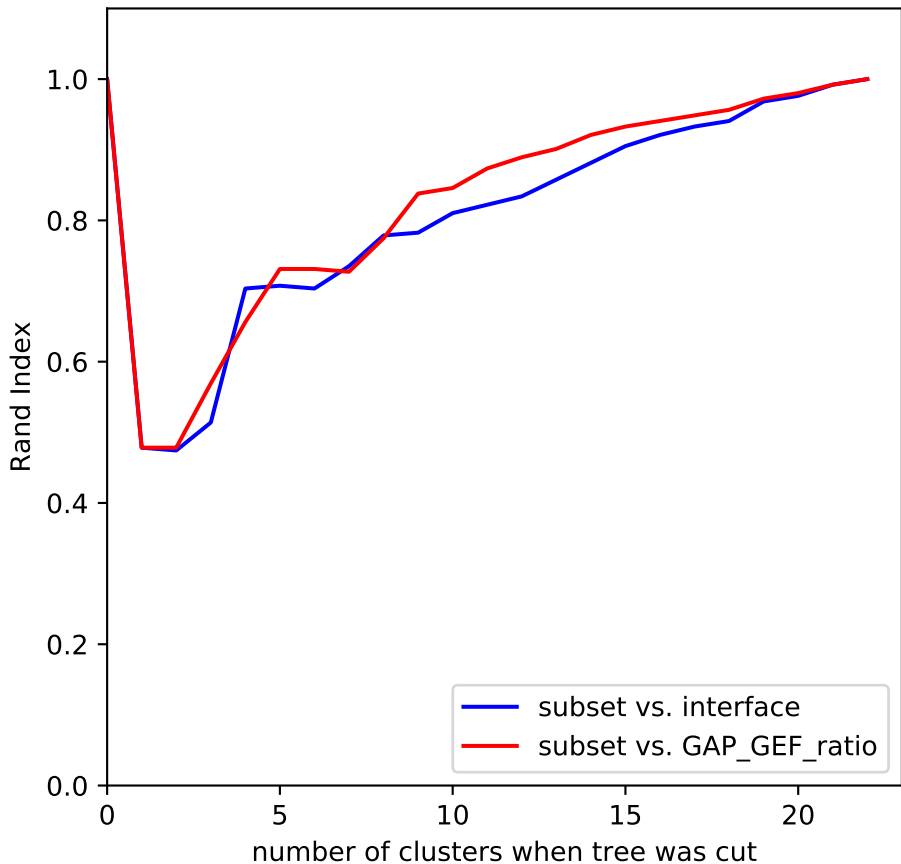
dataset = mitochondrial



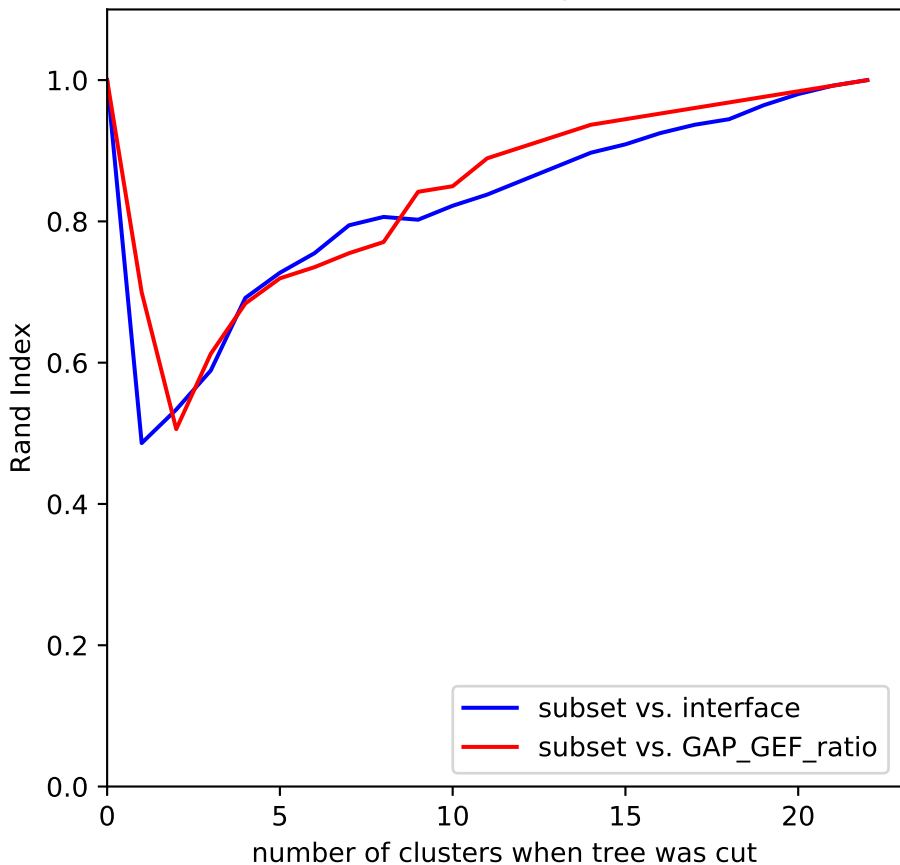
dataset = RIM101



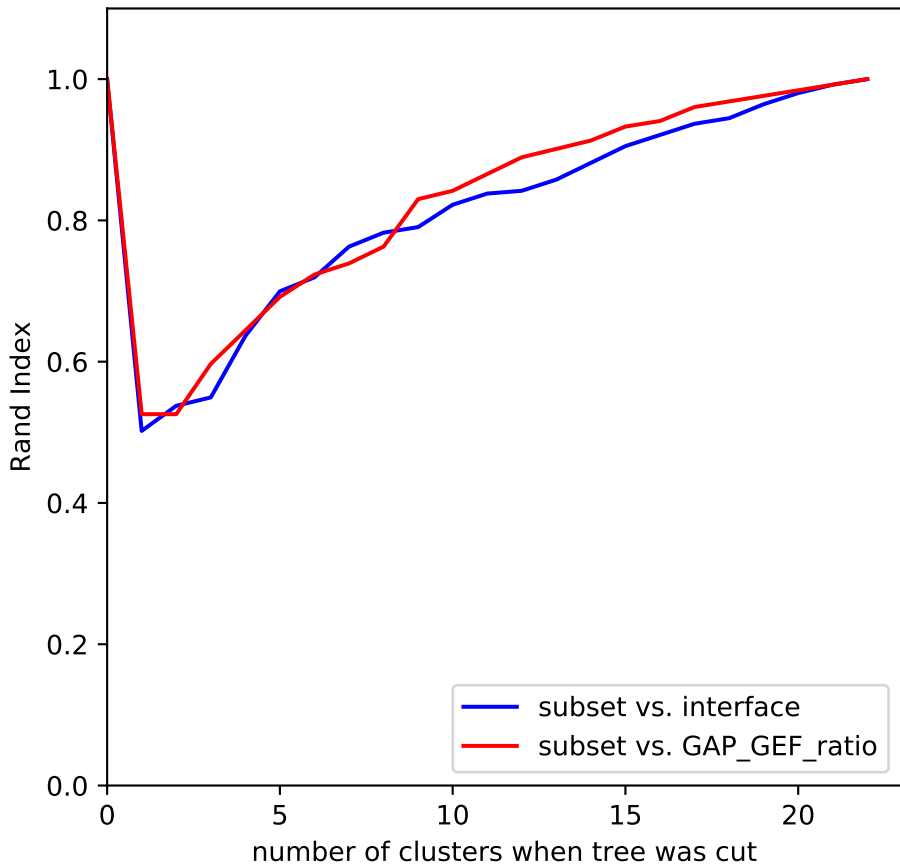
dataset = Elongator



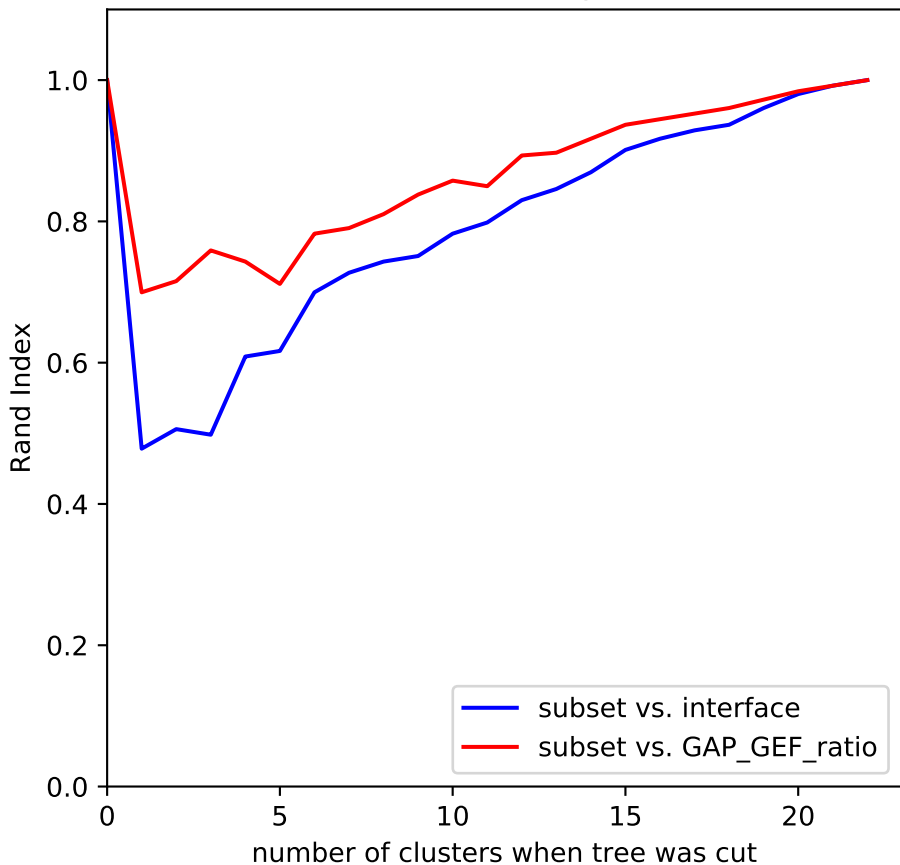
dataset = Rpd3L



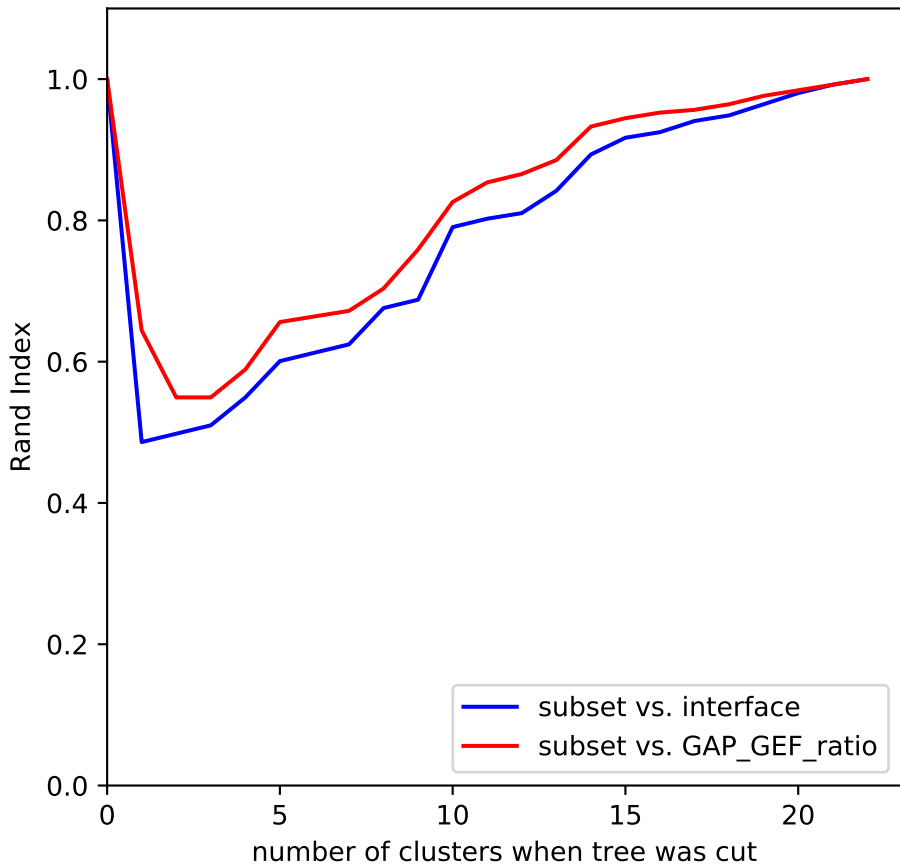
dataset = HOG1



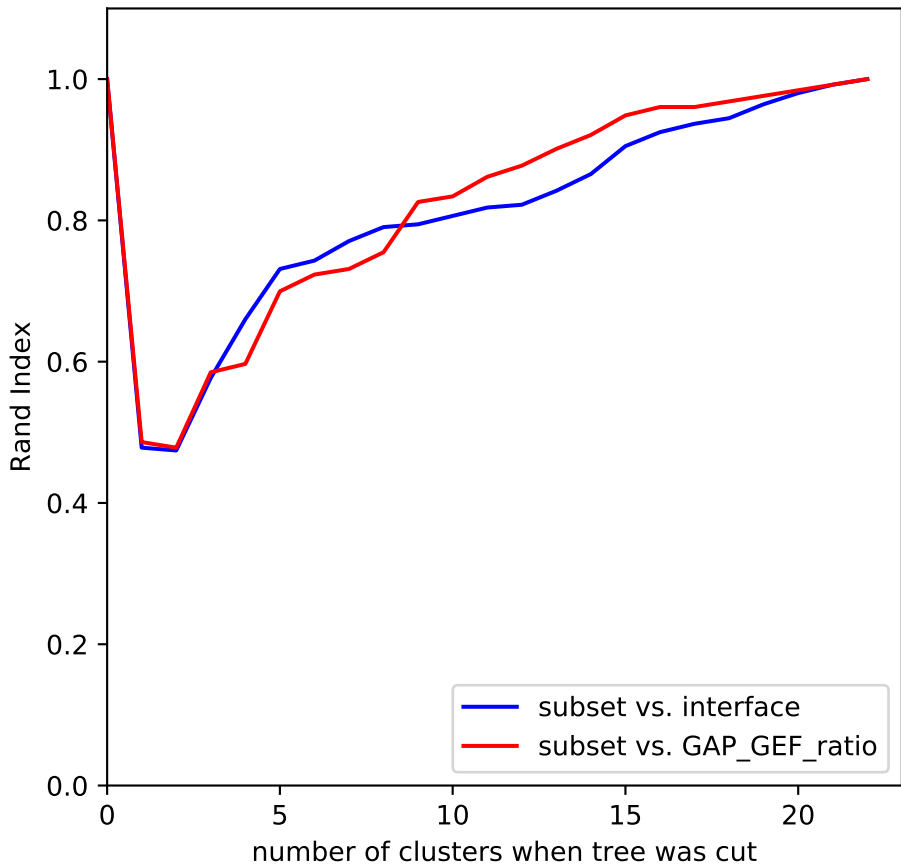
dataset = DNA Replication



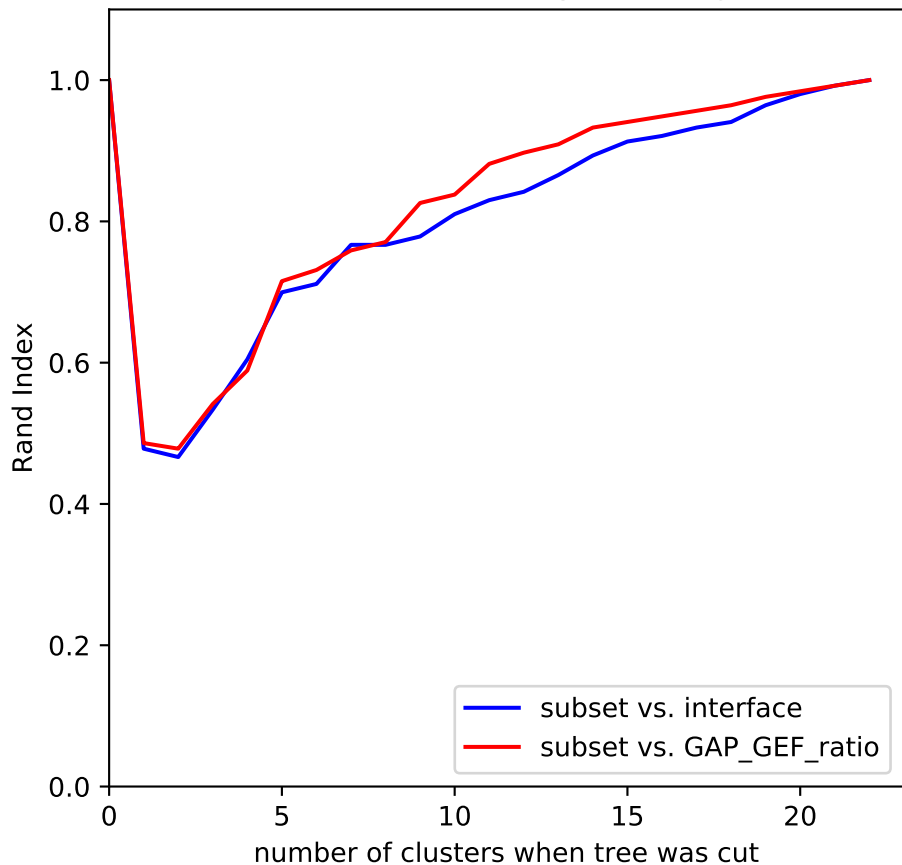
dataset = Peroxins



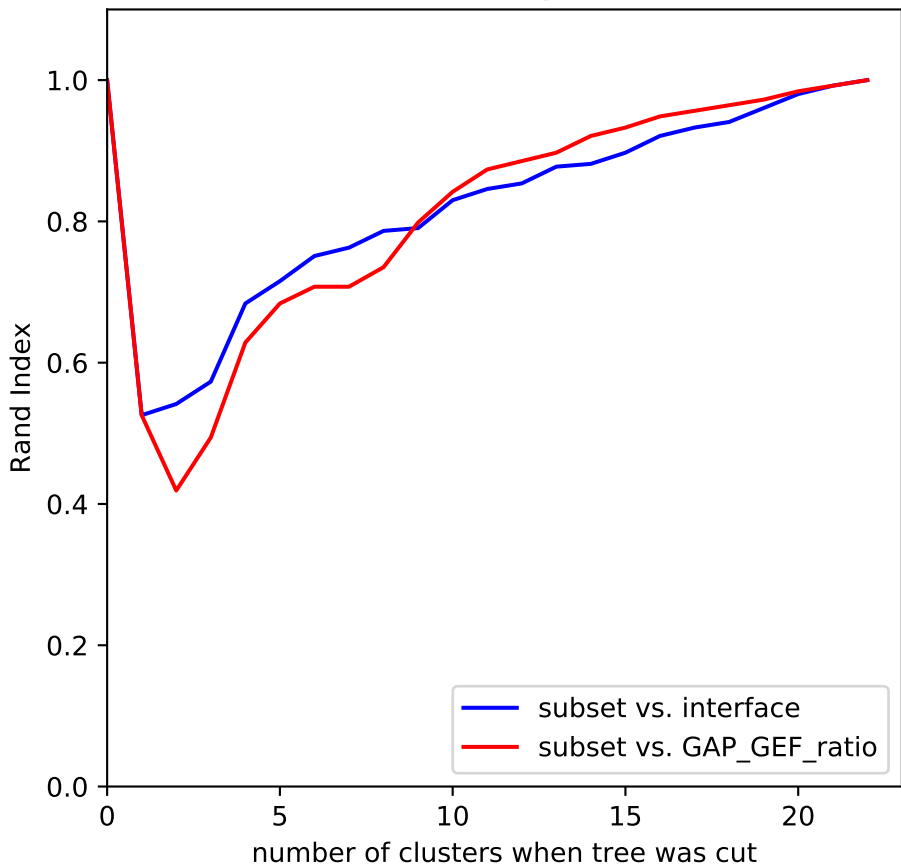
dataset = SWR1



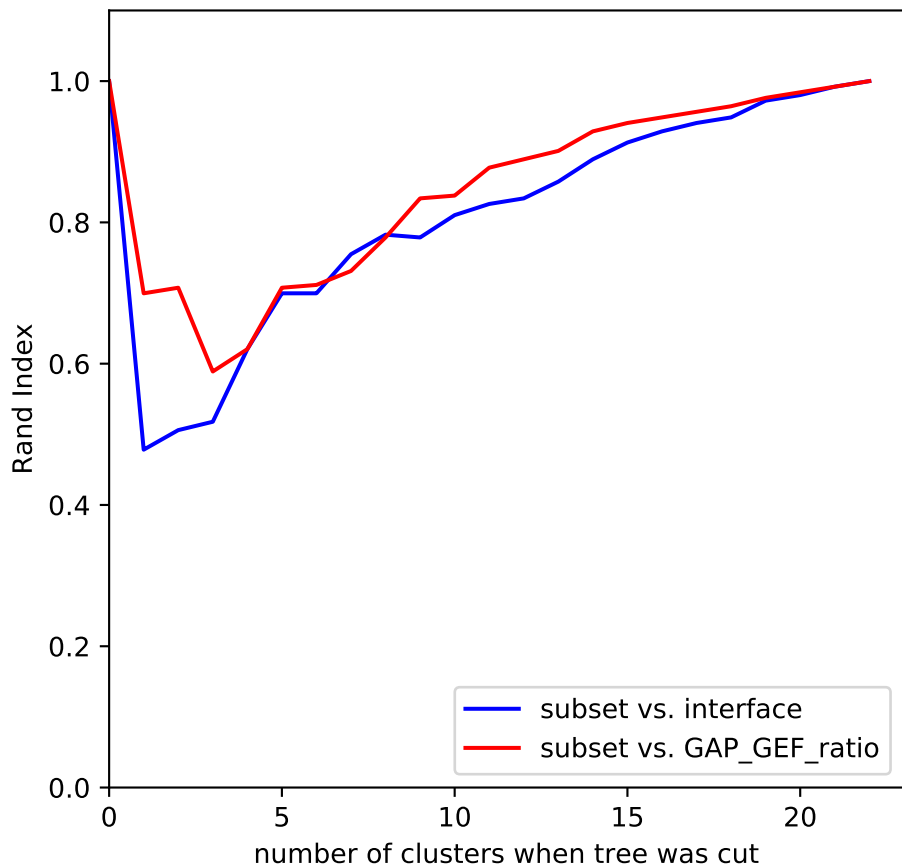
dataset = mRNA processing



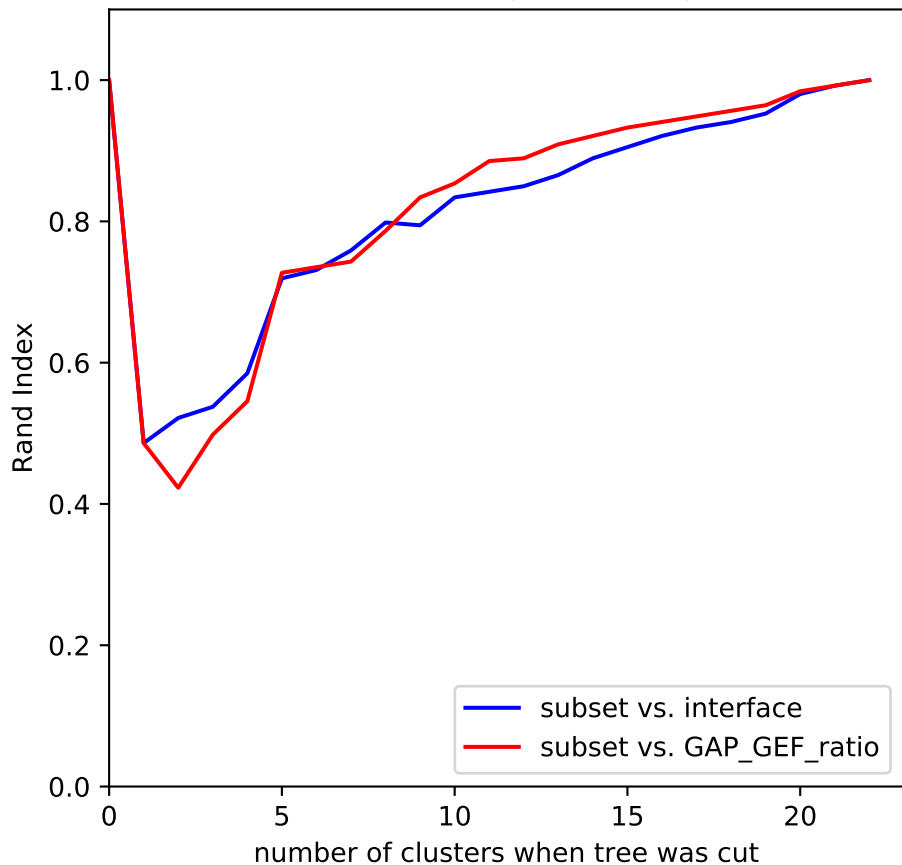
dataset = Dynactin



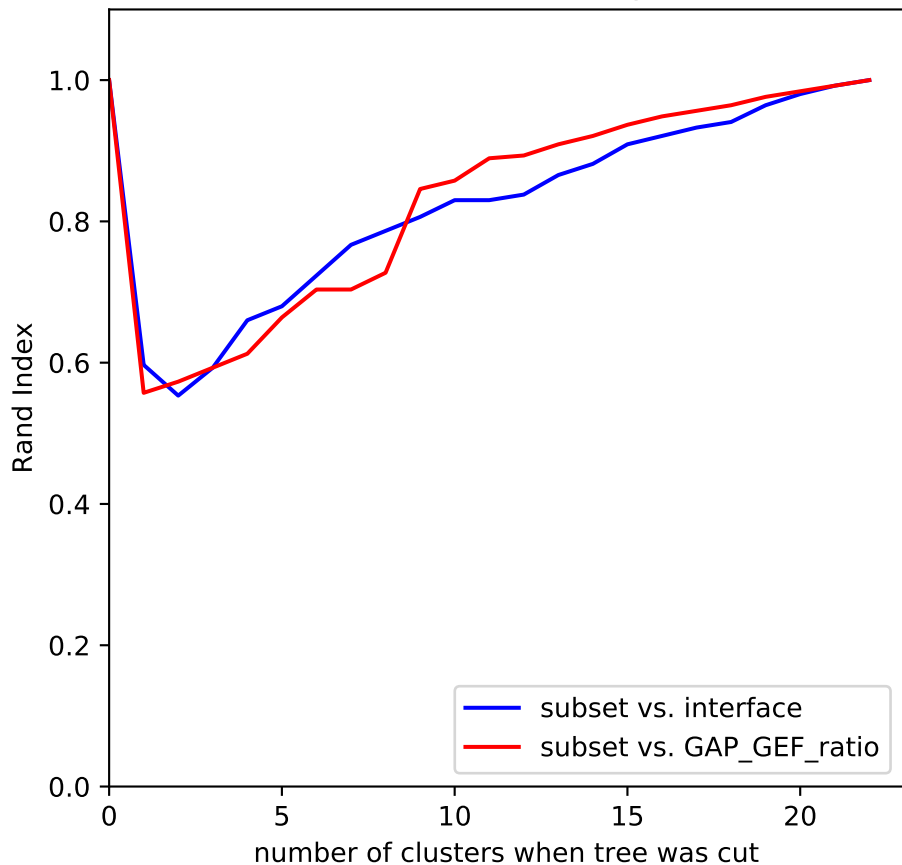
dataset = ERMES



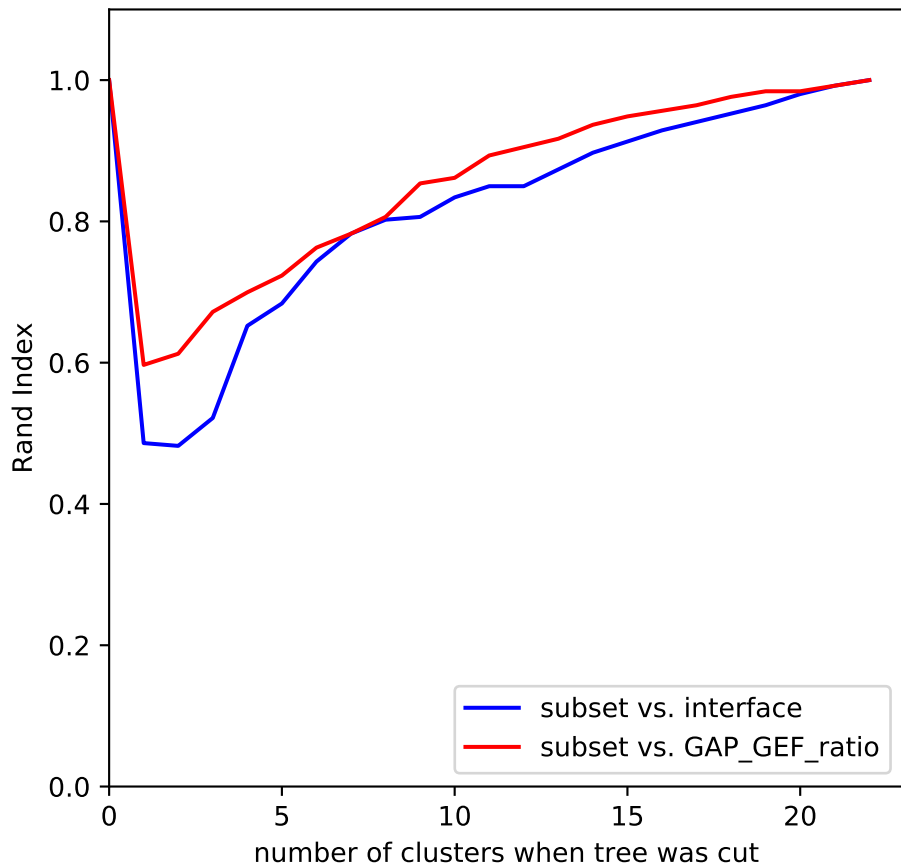
dataset = Cell Cycle Checkpoint



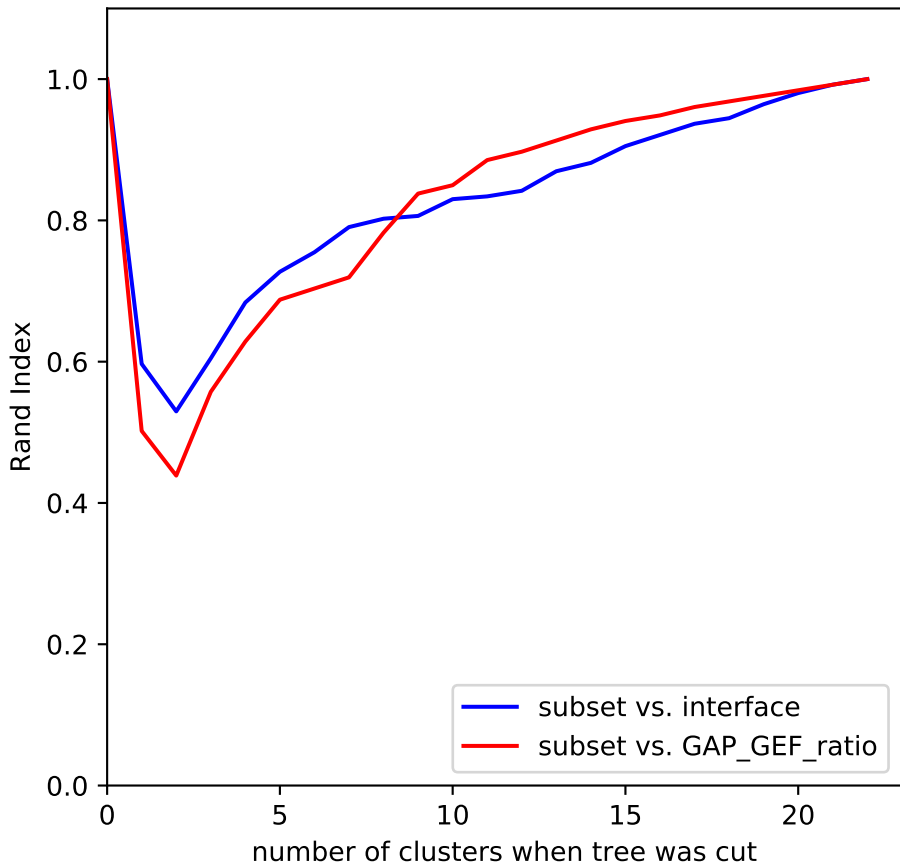
dataset = mRNA export



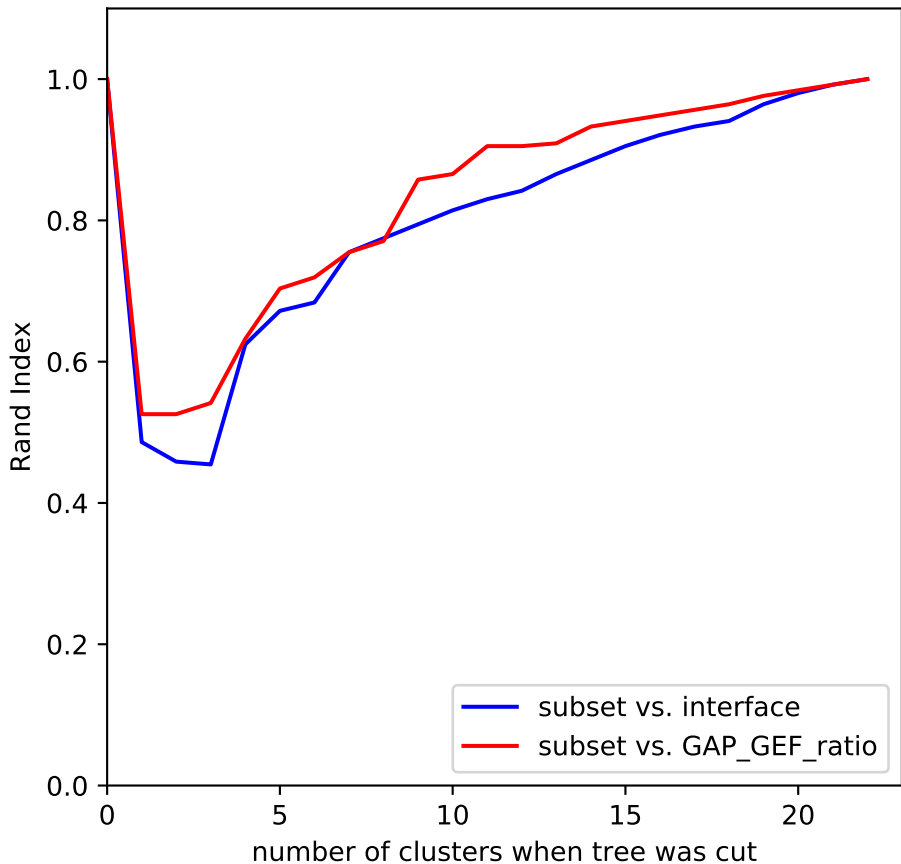
dataset = SAGA



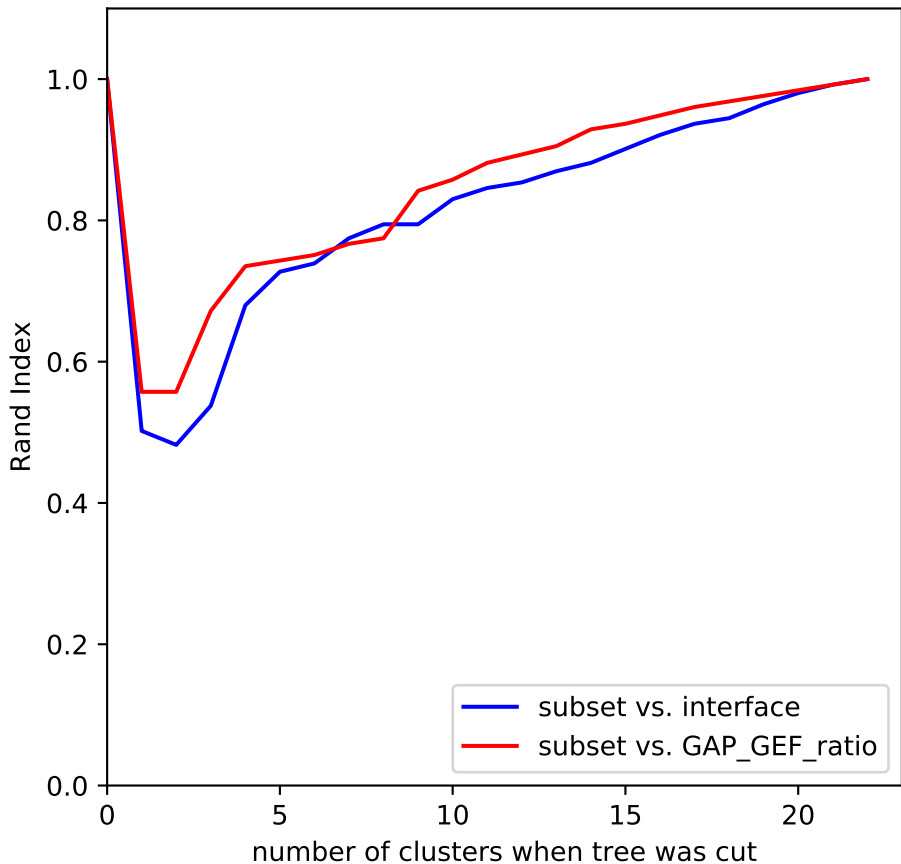
dataset = Inner NPC



dataset = SIT4



dataset = APC



dataset = Urmylation

