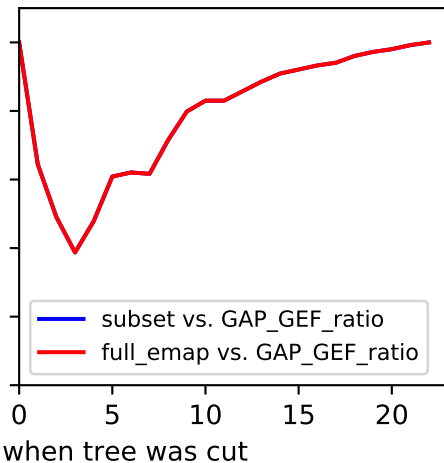
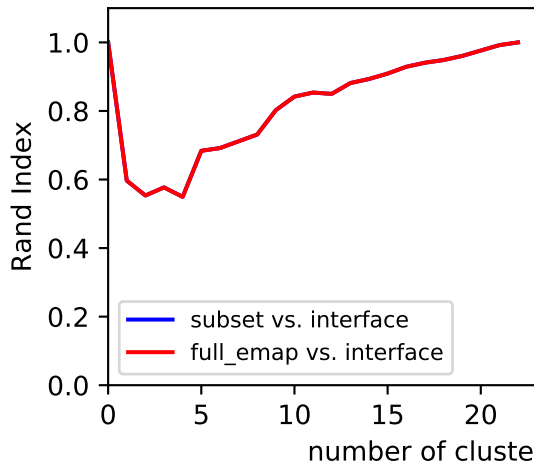


dataset = full_emap

Interface
 Δ to full_emap: 0.0

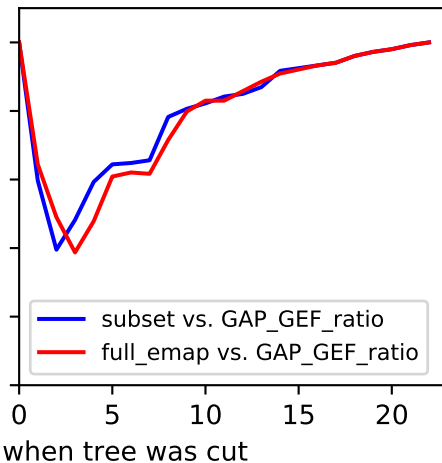
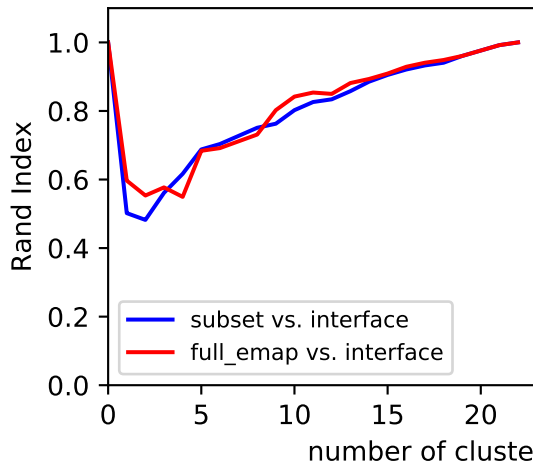
GAP/GEF ratio
 Δ to full_emap: 0.0



dataset = SET3

Interface
 Δ to full_emap: -0.011

GAP/GEF ratio
 Δ to full_emap: 0.01



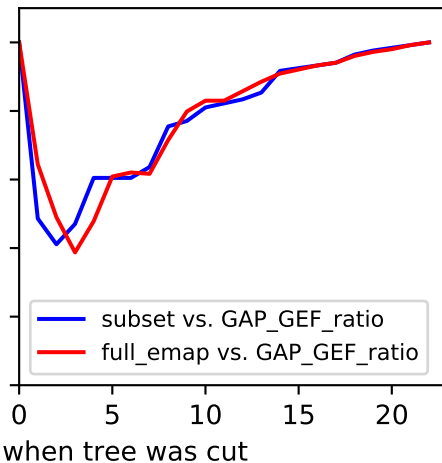
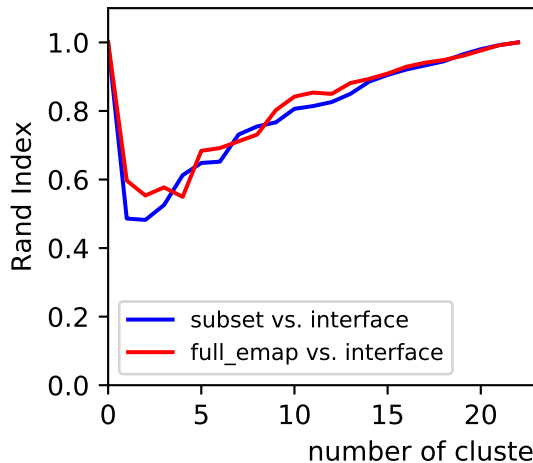
dataset = Arl GTPases

Interface

Δ to full_emap: -0.017

GAP/GEF ratio

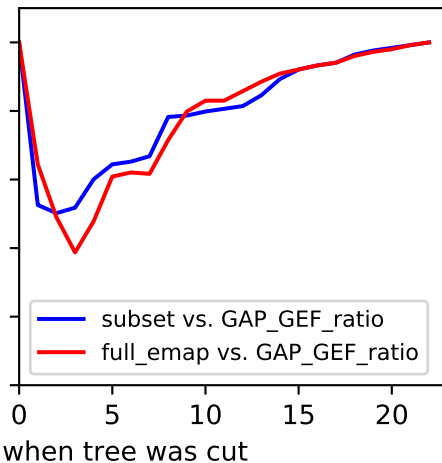
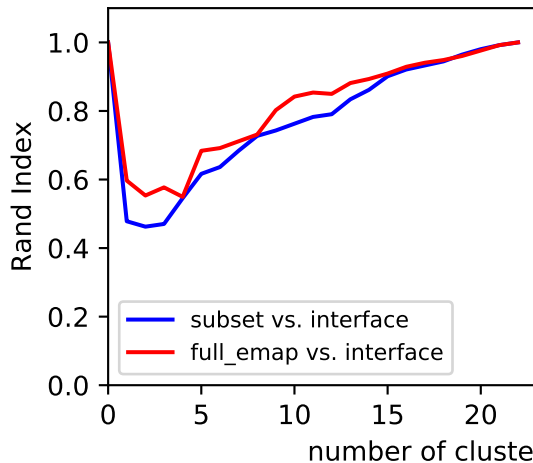
Δ to full_emap: -0.003



dataset = ADA

Interface
 Δ to full_emap: -0.037

GAP/GEF ratio
 Δ to full_emap: 0.008



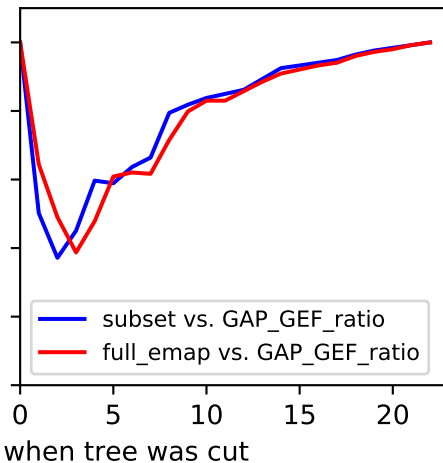
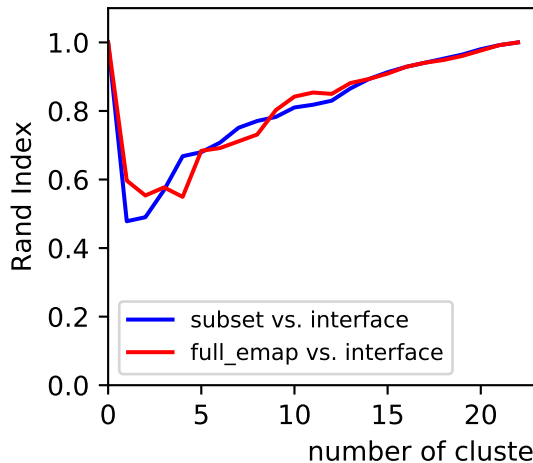
dataset = mitochondrial

Interface

Δ to full_emap: -0.004

GAP/GEF ratio

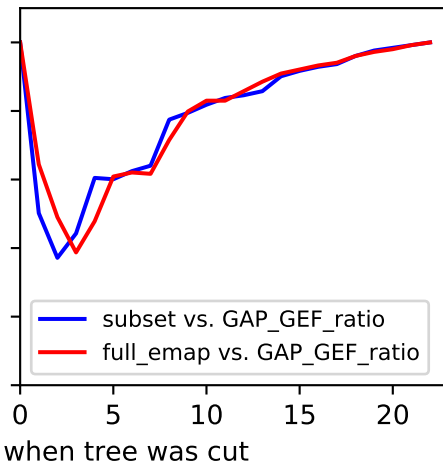
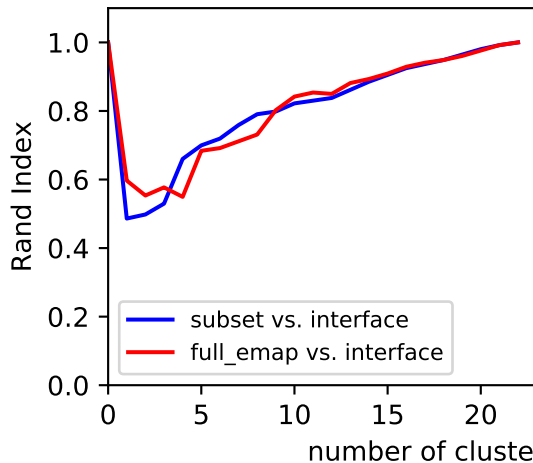
Δ to full_emap: 0.007



dataset = RIM101

Interface
 Δ to full_emap: -0.002

GAP/GEF ratio
 Δ to full_emap: -0.003



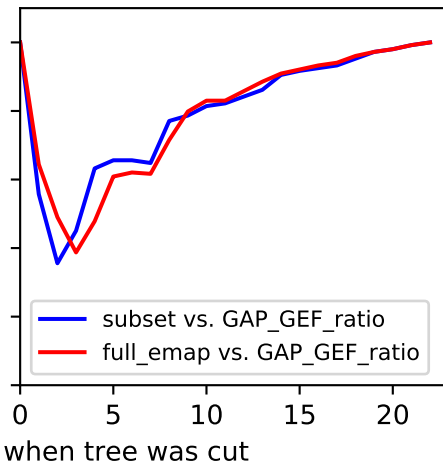
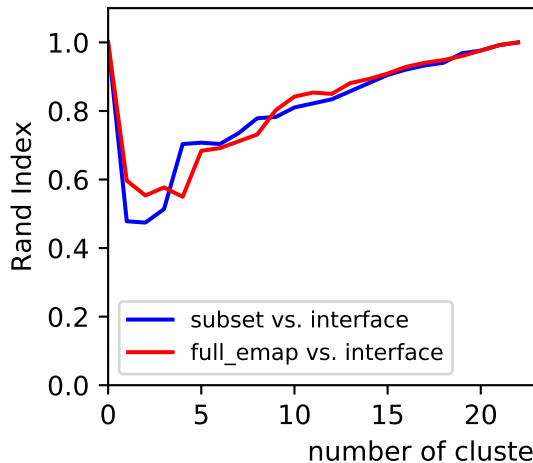
dataset = Elongator

Interface

Δ to full_emap: -0.007

GAP/GEF ratio

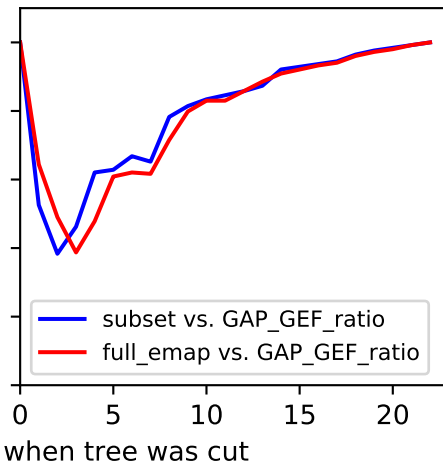
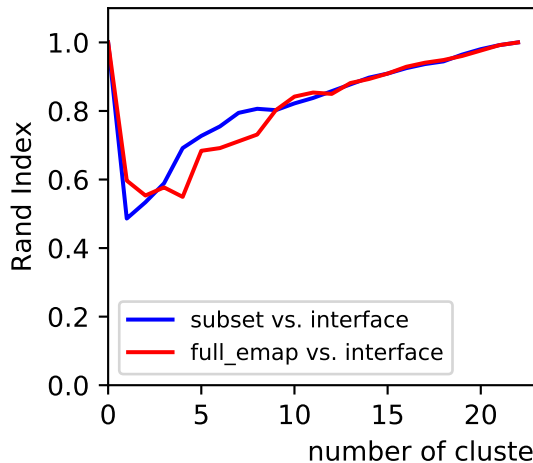
Δ to full_emap: 0.003



dataset = Rpd3L

Interface
 Δ to full_emap: 0.011

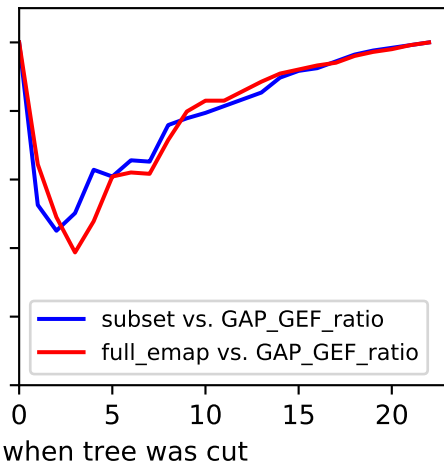
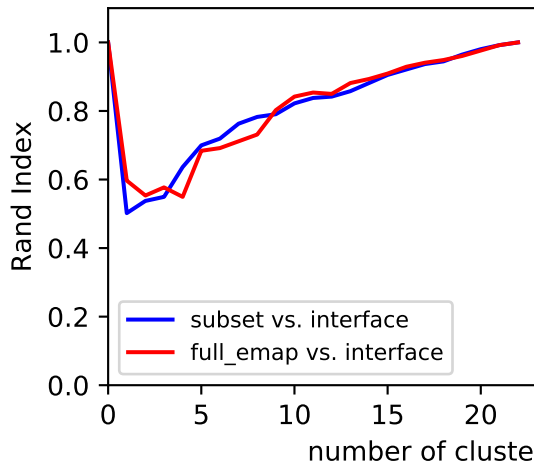
GAP/GEF ratio
 Δ to full_emap: 0.01



dataset = HOG1

Interface
 Δ to full_emap: -0.0

GAP/GEF ratio
 Δ to full_emap: 0.004



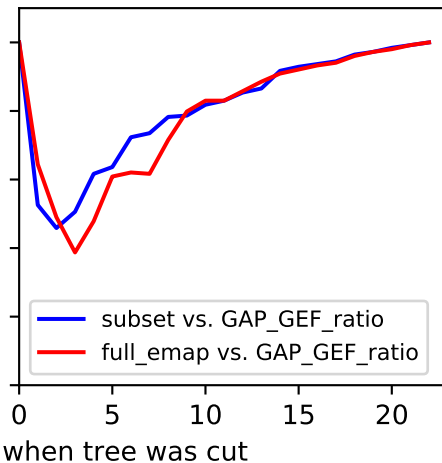
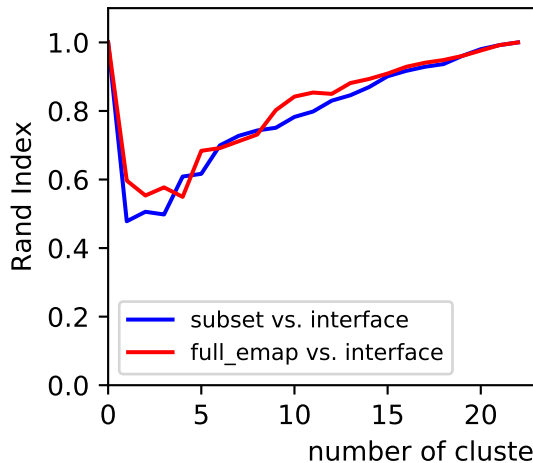
dataset = DNA Replication

Interface

Δ to full_emap: -0.022

GAP/GEF ratio

Δ to full_emap: 0.018



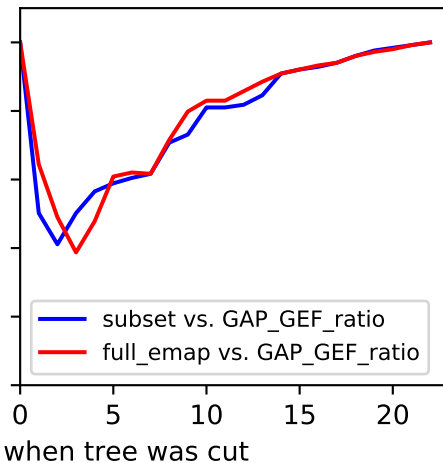
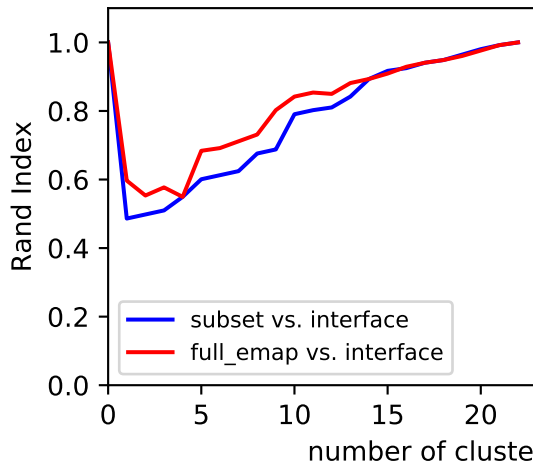
dataset = Peroxins

Interface

Δ to full_emap: -0.036

GAP/GEF ratio

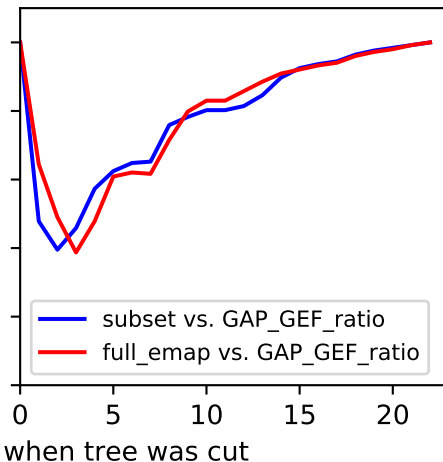
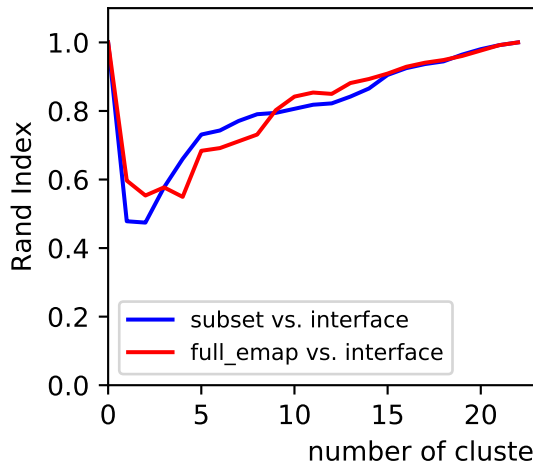
Δ to full_emap: -0.011



dataset = SWR1

Interface
 Δ to full_emap: -0.002

GAP/GEF ratio
 Δ to full_emap: -0.005



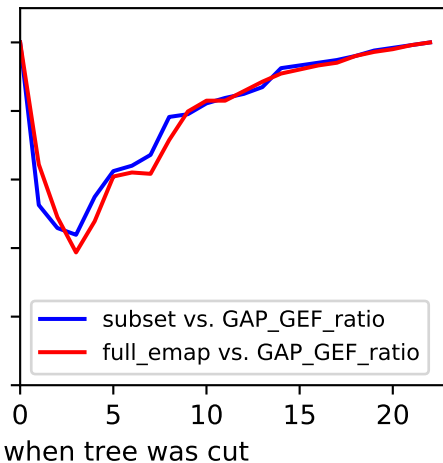
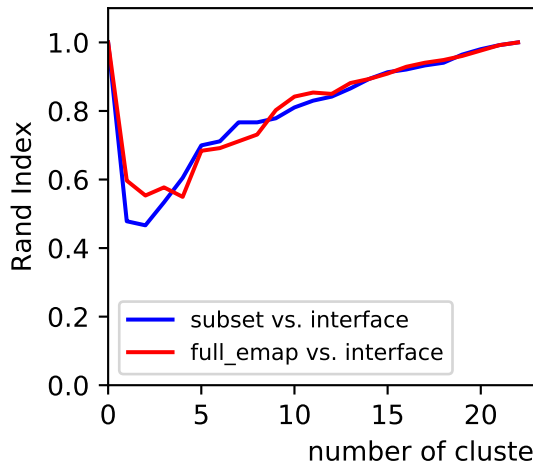
dataset = mRNA processing

Interface

Δ to full_emap: -0.008

GAP/GEF ratio

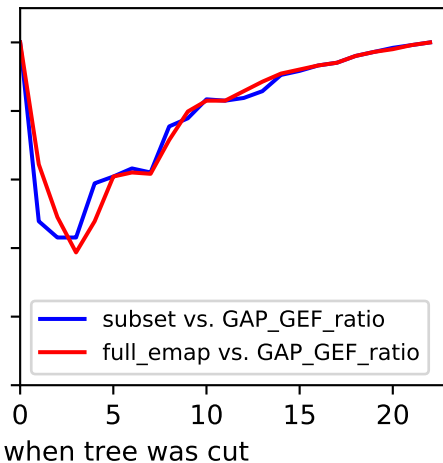
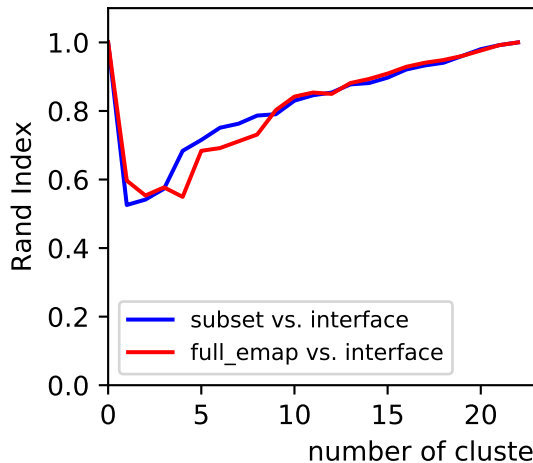
Δ to full_emap: 0.007



dataset = Dynactin

Interface
 Δ to full_emap: 0.007

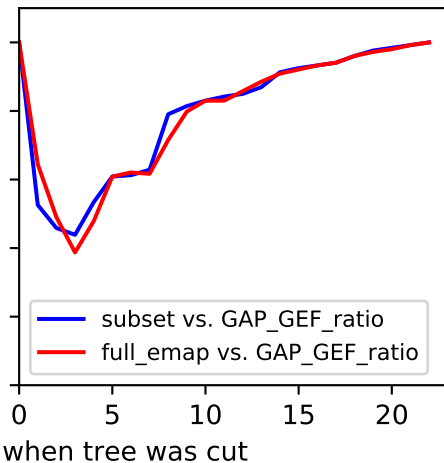
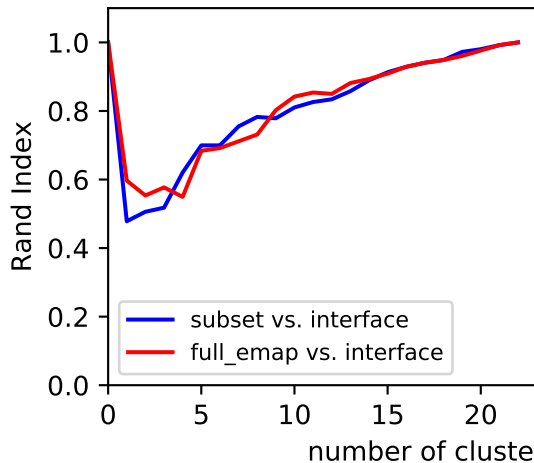
GAP/GEF ratio
 Δ to full_emap: -0.004



dataset = ERMES

Interface
 Δ to full_emap: -0.006

GAP/GEF ratio
 Δ to full_emap: 0.002



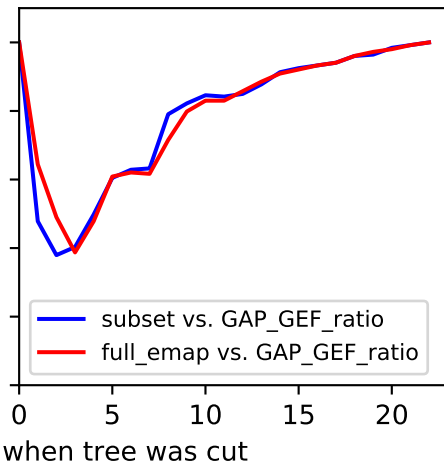
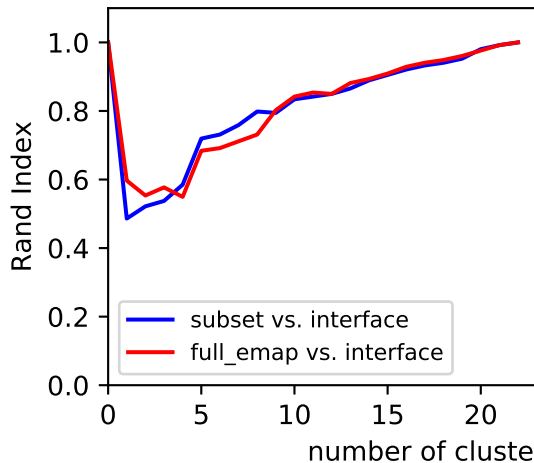
dataset = Cell Cycle Checkpoint

Interface

Δ to full_emap: -0.002

GAP/GEF ratio

Δ to full_emap: -0.005



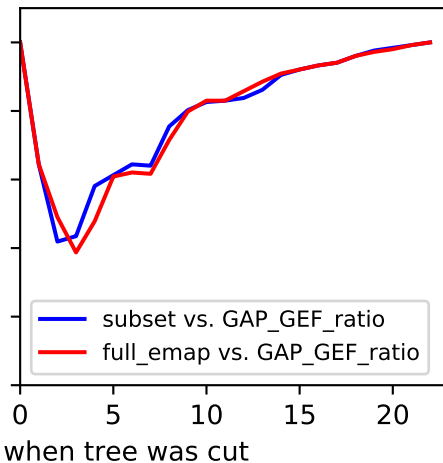
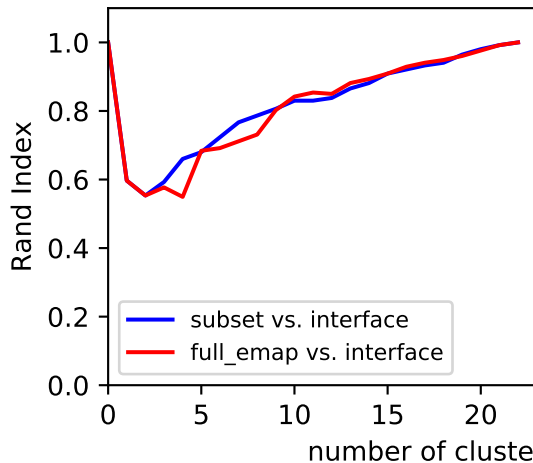
dataset = mRNA export

Interface

Δ to full_emap: 0.008

GAP/GEF ratio

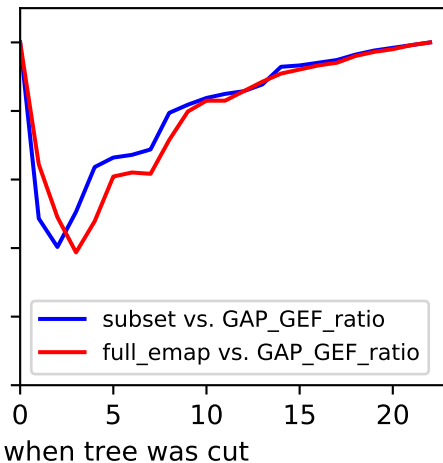
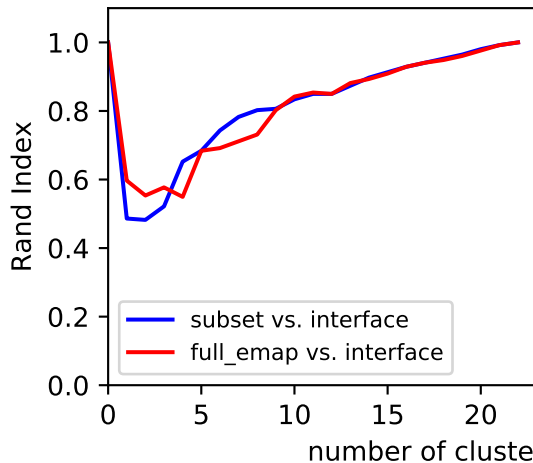
Δ to full_emap: 0.006



dataset = SAGA

Interface
 Δ to full_emap: 0.003

GAP/GEF ratio
 Δ to full_emap: 0.017



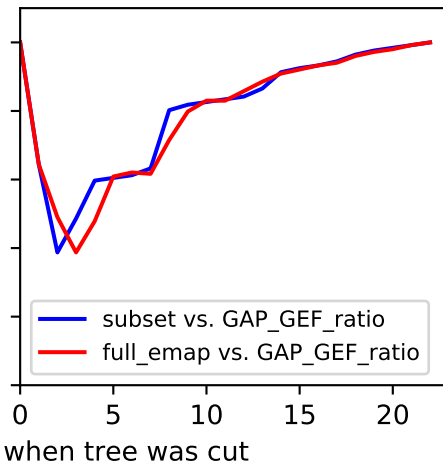
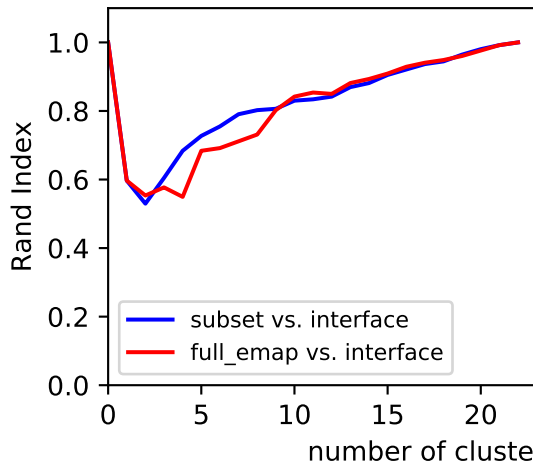
dataset = Inner NPC

Interface

Δ to full_emap: 0.014

GAP/GEF ratio

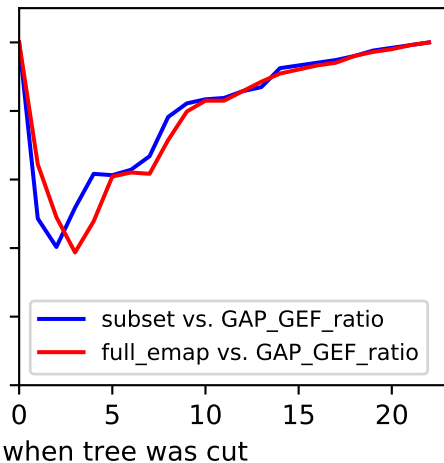
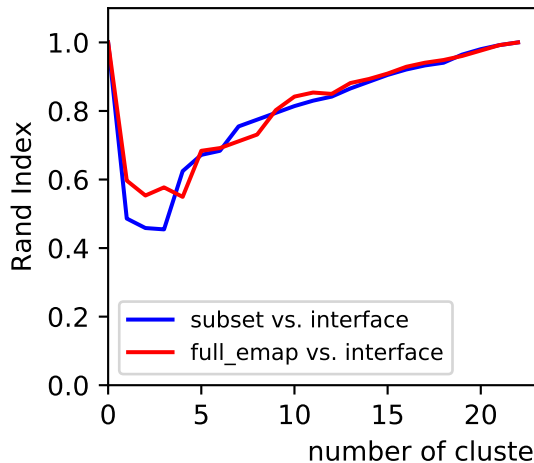
Δ to full_emap: 0.009



dataset = SIT4

Interface
 Δ to full_emap: -0.013

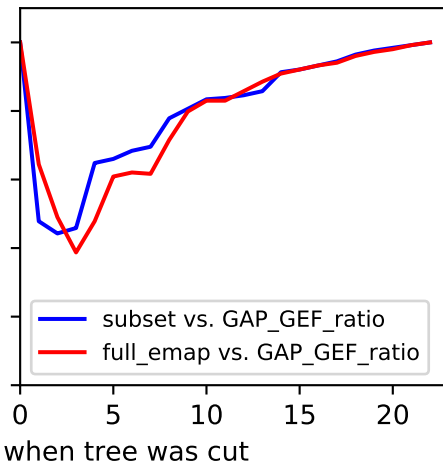
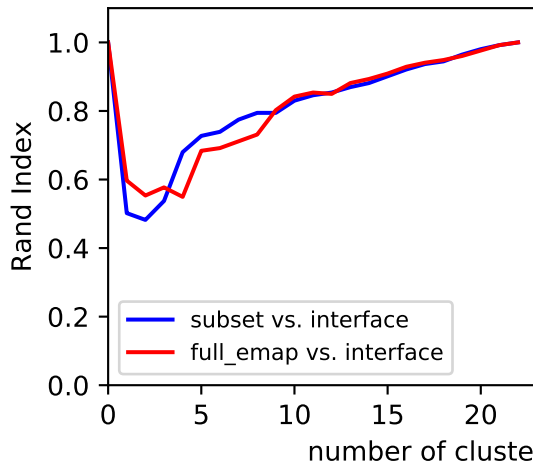
GAP/GEF ratio
 Δ to full_emap: 0.01



dataset = APC

Interface
 Δ to full_emap: 0.003

GAP/GEF ratio
 Δ to full_emap: 0.012



dataset = Urmylation

Interface
 Δ to full_emap: 0.02

GAP/GEF ratio
 Δ to full_emap: -0.0

