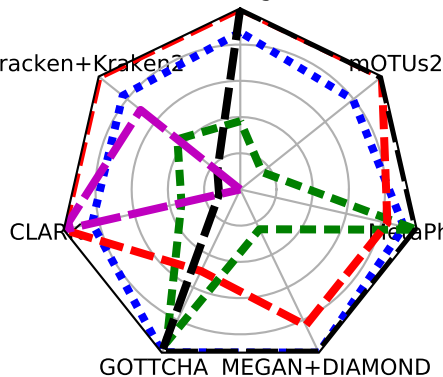


--- Weighted UniFrac error    
 --- L1 norm error    
 --- Completeness (recall)    
 --- Purity (precision)    
 --- False positives

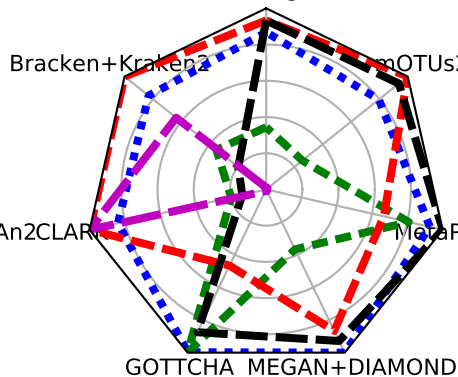
### phylum

Metalign



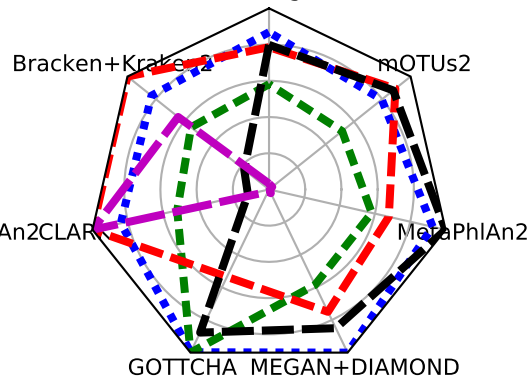
### class

Metalign



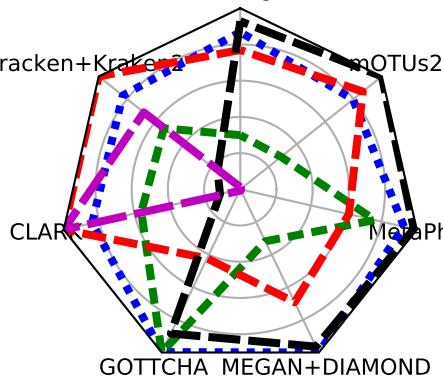
### order

Metalign



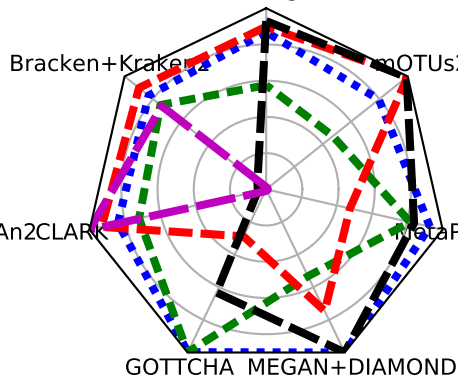
### family

Metalign



### genus

Metalign



### species

Metalign

