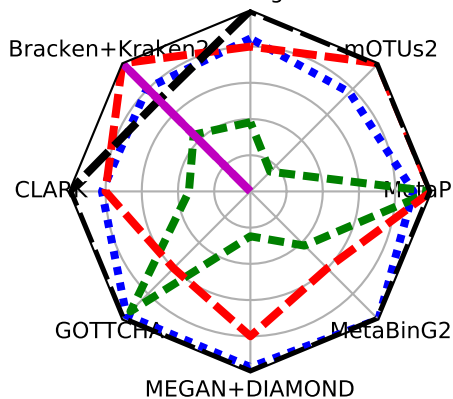


--●-- Weighted UniFrac error    
 --■-- L1 norm error    
 --■-- Completeness (recall)    
 --■-- Purity (precision)    
 --■-- False positives

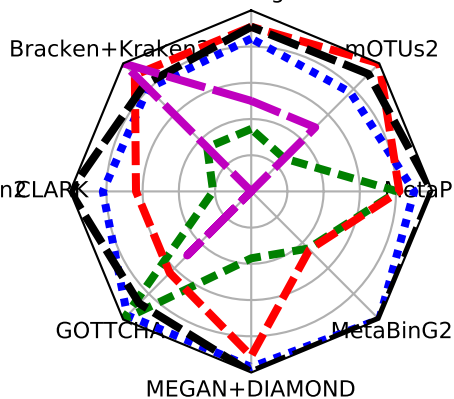
### phylum

Metalign



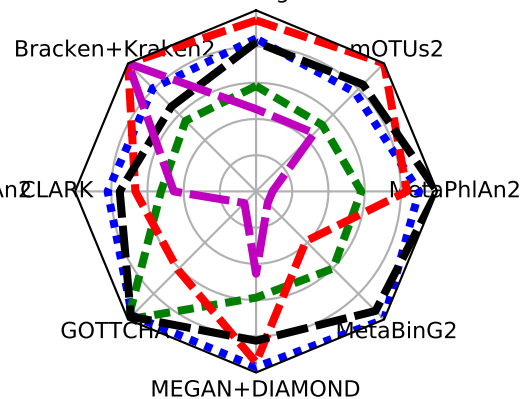
### class

Metalign



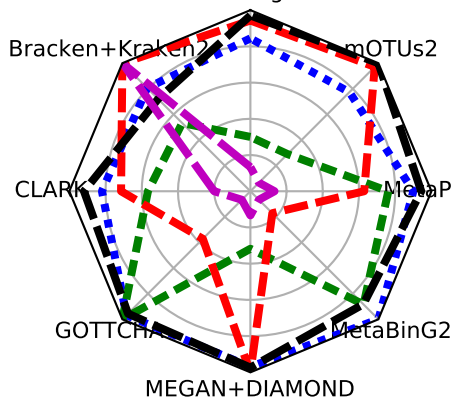
### order

Metalign



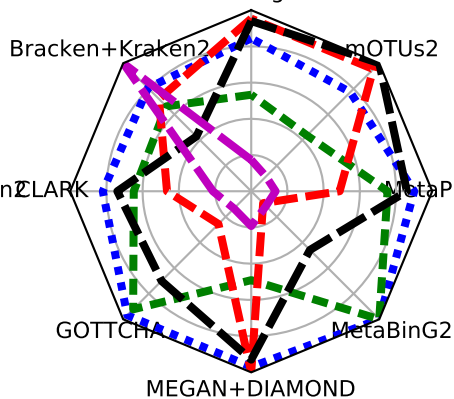
### family

Metalign



### genus

Metalign



### species

Metalign

