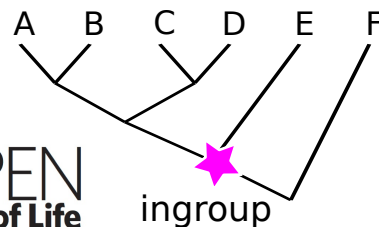
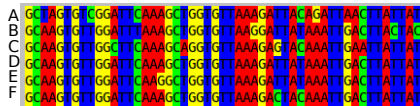
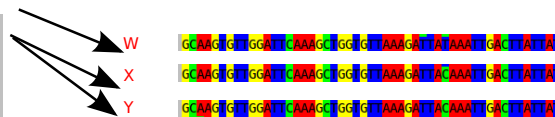





Starting alignment  
and phylogeny

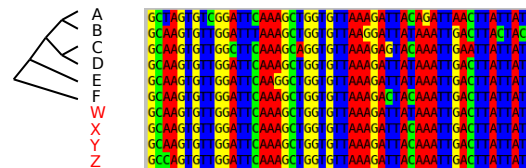


Database search  
(e.g. GenBank)

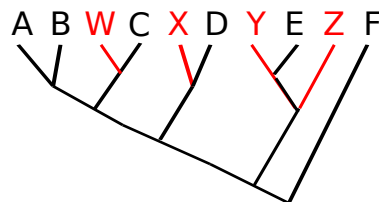


Limit to taxa in search taxon  
(defaults to ingroup  of input tree )

Extended multiple  
sequence alignment



Updated Phylogenetic inference  
with tips mapped to unified taxonomy



Repeat search on added taxa  
until no new sequences are found