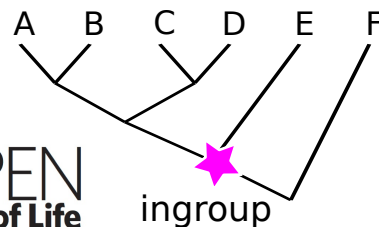
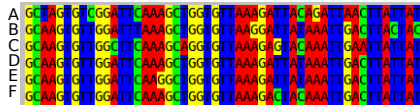
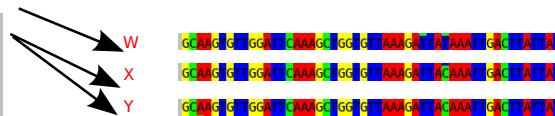





Starting alignment
and phylogeny

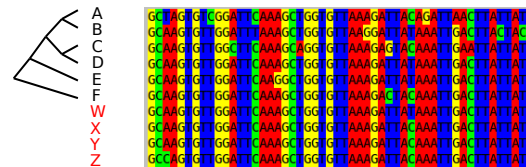


Database search
(e.g. GenBank)

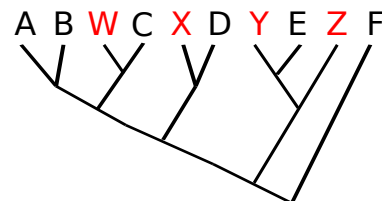


Limit to taxa in search taxon
(defaults to ingroup 
of input tree)

Extended multiple
sequence alignment



Updated Phylogenetic inference
with tips mapped to unified taxonomy



Repeat search on added taxa
until no new sequences are found