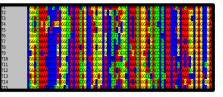
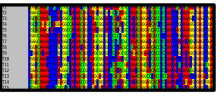
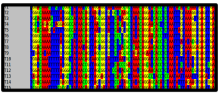
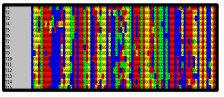


IN

MSA Infiles (FASTA, CLUSTAL, PHYLIP)



FASconCAT-G

SEQ RENAMING

SEQ TRANSLATION

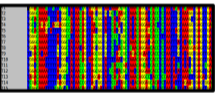
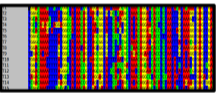
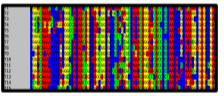
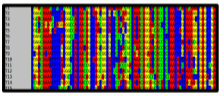
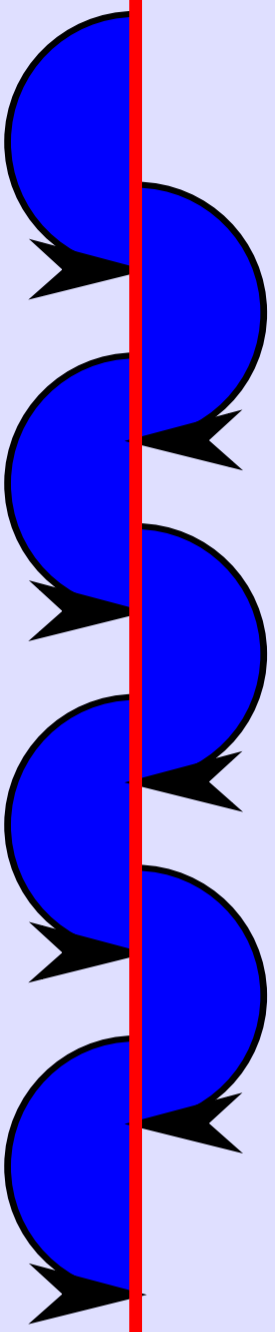
CONSENSUS SEQ

SEQ RECODING

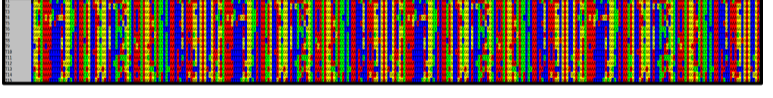
SITE EXCLUSION

SEQ CONCATENATION

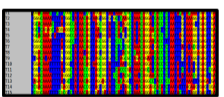
SITE EXTRACTION



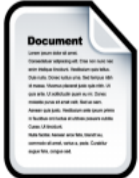
Converted Outfiles (FASTA, CLUSTAL, PHYLIP, NEXUS)



Supermatrix (FASTA, CLUSTAL, PHYLIP, NEXUS)



Parsimony Informative Sites (FASTA, CLUSTAL, PHYLIP, NEXUS)



Base Composition / Supermatrix Information



Secondary Structure Information



Gene Partition Outfiles (RaxML / Mr.BAYES)

OUT