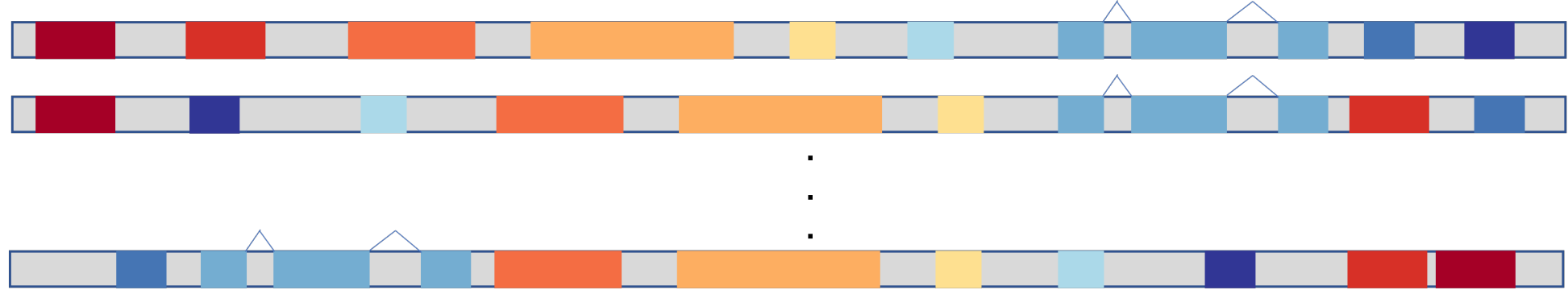


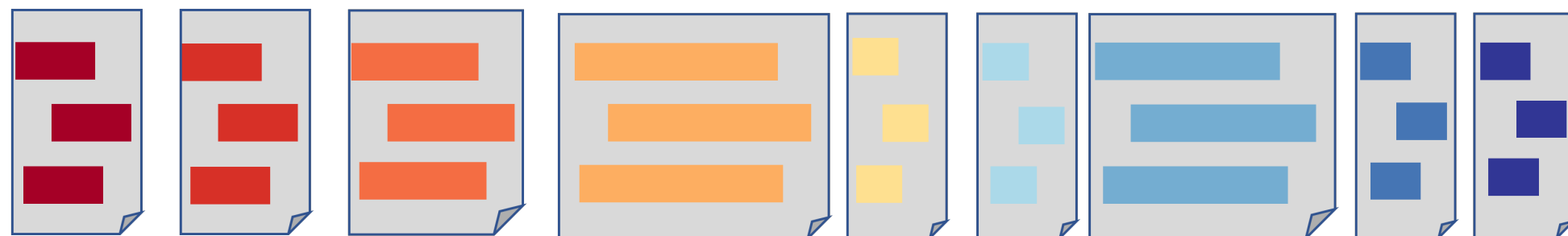
n
organism
s with g
genes
each



(A)

SPLIT

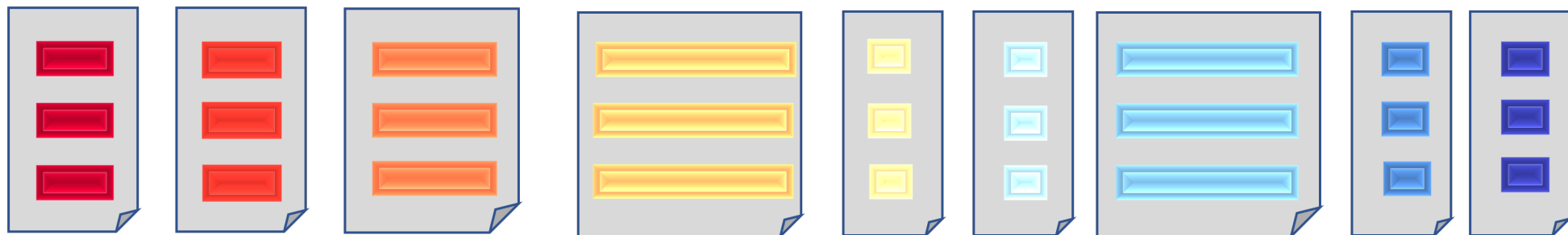
g FASTA
files



(B)

Sequence
Alignment

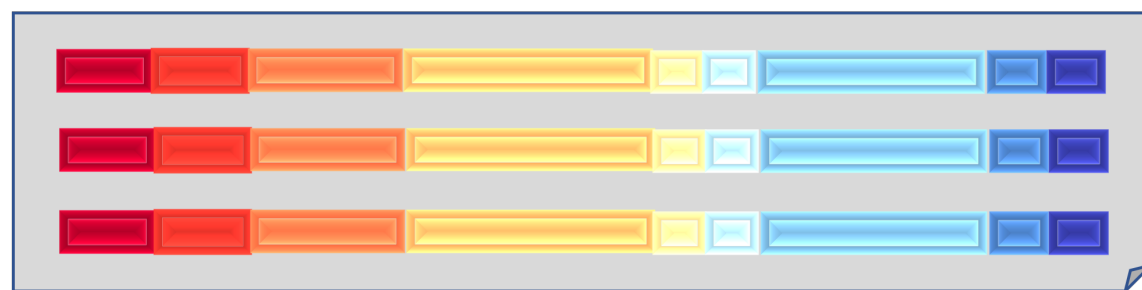
g' aligned
FASTA
files



(C)

Concatenation

A single
FASTA
file with n
aligned
sequence
s



(D)

Phylogenetic
Tools



(E)