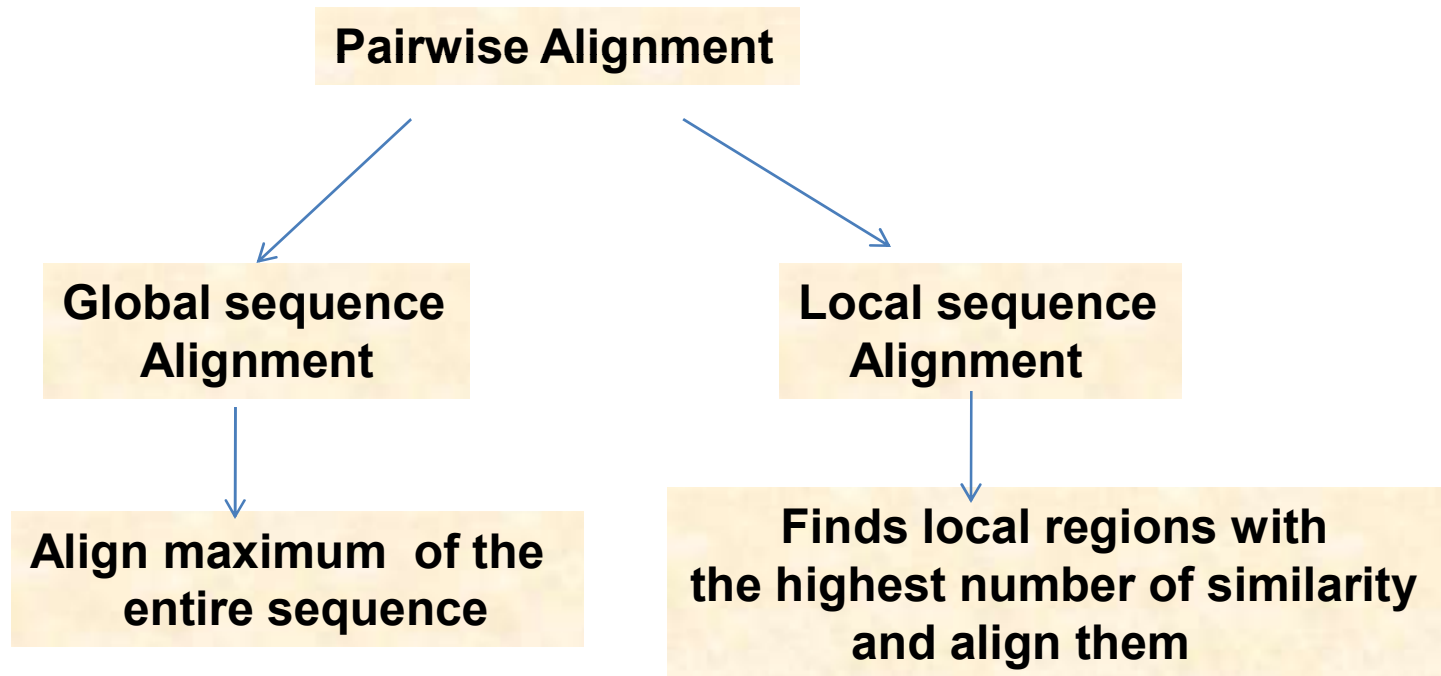
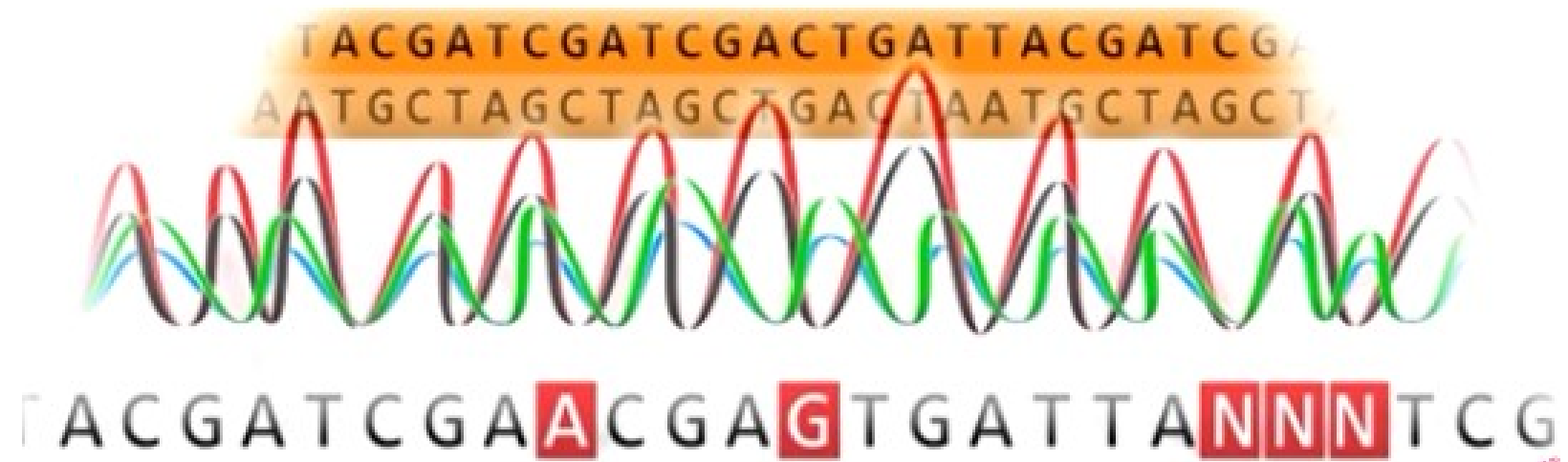


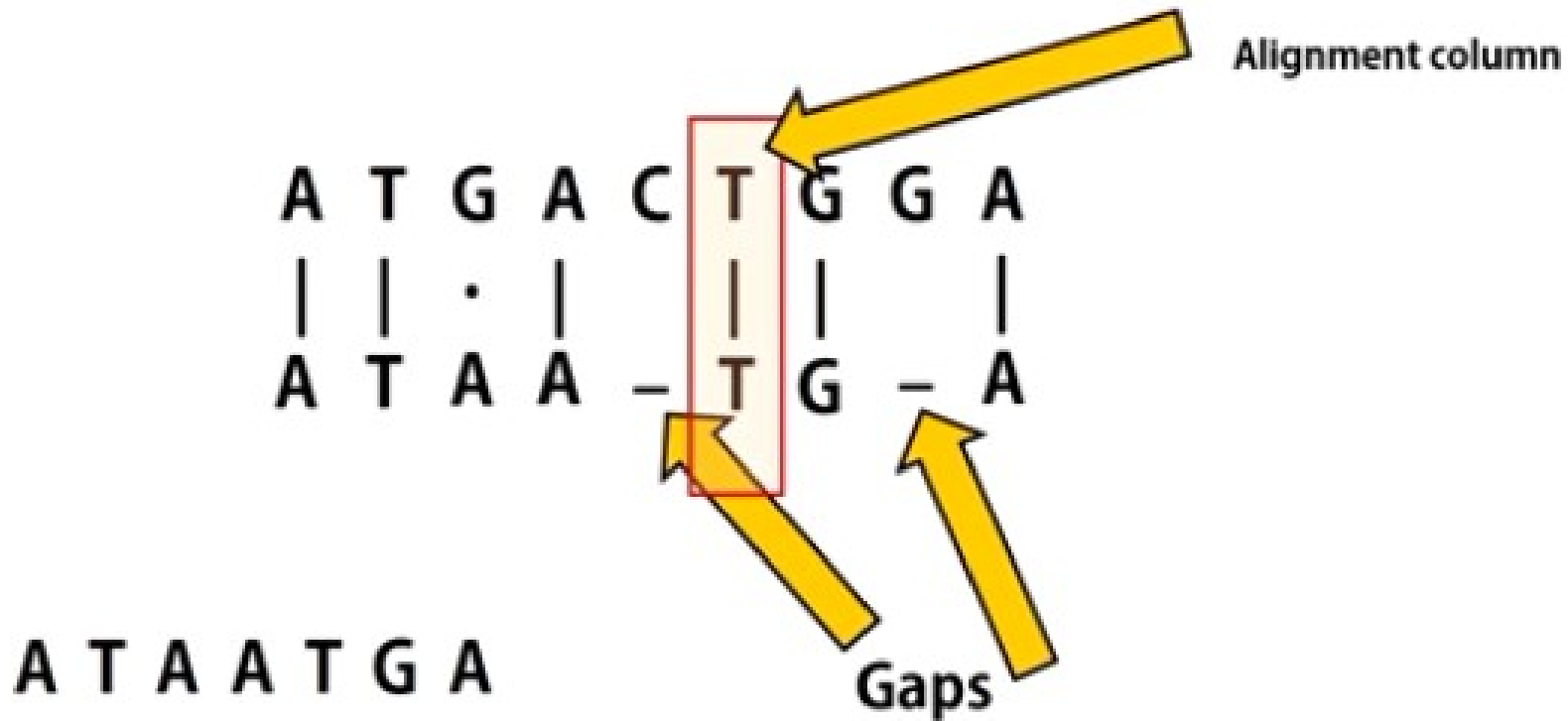
Pairwise Alignment

Pairwise Sequence Alignment is used to identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid).



Local and Global Alignment of Sequences





Gaps in a DNA sequence alignment represent evolutionary deletions and insertions



MNPYIYLG GAILAEVIGTTLMKFSEGF
TRLWPSVGTIICYCASFWLLAQTLAYIP
TGIAYAIW SGGVIVLISLLSWGFFGQRL
DLP AIIGMMLICAGVLIINLLSRSTPH



MSEALKILNNIRTLRAQARECTLELEEMI
KLEVVVNERREEESAAAAEVEERTRKLC
REMLIADGIDPNELLNSLAAVKSGTKAKR
QRPAKYSYVDENGETKTWTGQGRTPAVI



To align two sequences of 300 aa/nt lengths,
approximately 10^{88} comparisons are to be made

