⇒ Sequence Alignment
　↳ Lab sequence (LS) → fand sequence
　↳ Reference Sequence (RS)
　　　　　↳ original sequn

Sequence Alignment is the process of comparing and detecting similarities between biological sequences.

We have two types of sequence:

~~Lab sequence~~ the reference/sequence you can get from a lab during experiment.

~~Reference Sequence~~ - a standard original sequence that you want to match/compare with (LS)

Sequence Alignment
　　　　SR

↓ Pairwise Alignment
- used to Identify regions of similarity that may include functional, structure and/or evolutionary relationship between two biological sequences.

↓ Multiple Alignment
- is the alignment of three or more biological sequence of similar length.

Alignment Score

└➤ highest number of sequence between two.

Alignment score: the value that measures the degree of sequence similarity is called alignment sequence.

Pairwise: two types:
→ Local Alignment

Local Alignment	Global Alignment
• find local regions with the highest number of similarity and align them.	The process that is used to find the matching of whole/entire sequence is called global alignment.
- Algorithm: Smith - waterman Algorithm	- Algorithm: Needleman - wansch algorithm.

Example:

LS= - - - A C G T - - - - -
RS= AACACGTGTCT

LS= A - C - - G T - - - -
RS= AACAGGTGTCT
                  CG

②

LS= A C G T
RS= AACACGTGTCT

Parameter

$$match = \to 1$$
$$misMatch = 0$$
$$gap \quad - \quad 0 \ 1$$

Dynamic Algorithm

$\ominus$ Gap

(1) match

Edit Distance.

nucleotides

$$identity(LS, RS) = \frac{numbers \ of \ match \ identical}{min(length(LS), \ Length(RS))} \times 100\%$$

$$identity(LS, RS) = \frac{9}{min(9, 11)} \times 100\%$$

$$= \frac{9}{9} \times 100$$

$$= 100\%$$