

Prerequisites:

In order for you to understand the main topic in hand; you should first go through these concepts given ahead:

- Multiple Sequence Alignment (MSA)
- ≻ EMBOSS
- > Pairwise Sequence Alignment.
- Clustal Omega
 [Kindly watch our video on Clustal Omega]

Introduction:

Needle is an alignment tool used by Bioinformaticians. It is a pairwise alignment tool; design to write the optimal global alignment. It's one of the sub-software/tool which is available in EMBOSS.

★ Pairwise Sequence Alignment

It is the process of finding similar regions between two biological sequences, which could point towards evolutionary, functional and structural relationships between those sequences.

★ Needleman-Wunsch Algorithm

This algorithm was developed by Saul B. Needleman and Christian D. It is an optimal matching algorithm used in bioinformatics, for the comparison of biological sequences. What it actually does is that it breaks a larger problem into smaller problems and find the solutions for the smaller problems so an optimal solution can be found out for the larger problem.

★ Global Alignment Vs Local Alignment

There is a very general difference between global and local alignment.

Global Alignment	Local Alignment
 In Global Alignment, end to end sequence alignment take place. 	 In Local Alignment, your query is matched with the portion of your reference sequence.
2. The length of both sequences is about the same.	The length of both sequences varies greatly.
3. Gaps are in higher quantity if the query and the reference sequences are quite dissimilar.	3. Gaps can be introduced in local alignment.

→ Global Alignment Example

→ Local Alignment Example

Steps: