**Course: Advanced Bioinformatics**

**Module title: Types of Sequence Alignment**

**Module no. : 28**

There are two types of Sequence Alignment methods.

* Global Alignment
* Local Alignment

**Global Alignment:** In global alignment, an attempt is made to align the entire sequence

Find best match of both sequences in their entirety.

Input: treat the two sequences as potentially equivalent.

Goal: identify conserved regions and differences.

Useful when sequences are similar or roughly same length

Applications: Comparing two genes with same function (in human vs. mouse). Comparison of two proteins with similar functionality.

**Local Alignment:** Find the best subsequence match from two sequences.

Input: The two sequences may/may not be related.

Goal: see whether a substring in one sequence aligns well with a substring in the other.

Applications: Dissimilar sequences which are suspected to have similar portion. Useful for comparing DNA sequences that share a similar motif.

Useful for comparing protein sequences that share a common motif.

**Why Local Alignment?**

More meaningful: finds conserved regions between two sequences

Aligns two sequences of different lengths to be matched

Aligns two partially overlapping sequences

Aligns two sequences where one is a subsequence of another

Global alignments, which attempt to align every residue in every sequence, are most useful when the sequences in the query set are similar and of roughly equal size. (This does not mean global alignments cannot end in gaps.) A general global alignment technique is the Needleman–Wunsch algorithm, which is based on dynamic programming. Local alignments are more useful for dissimilar sequences that are suspected to contain regions of similarity or similar sequence motifs within their larger sequence context. The Smith–Waterman algorithm is a general local alignment method also based on dynamic programming.

Hybrid methods, known as semi-global or "glocal" (short for global-local) methods, attempt to find the best possible alignment that includes the start and end of one or the other sequence. This can be especially useful when the downstream part of one sequence overlaps with the upstream part of the other sequence. In this case, neither global nor local alignment is entirely appropriate: a global alignment would attempt to force the alignment to extend beyond the region of overlap, while a local alignment might not fully cover the region of overlap.[[6]](https://en.wikipedia.org/wiki/Sequence_alignment#cite_note-brudno-6) Another case where semi-global alignment is useful is when one sequence is short (for example a gene sequence) and the other is very long (for example a chromosome sequence). In that case, the short sequence should be globally aligned but only a local alignment is desired for the long sequence.

