**Course: Advanced Bioinformatics**

**Module title: Introduction- Sequence Alignment**

**Module no. : 26**

**Sequence Alignment:** It is a way of arranging the sequences of DNA, RNA, or protein to identify regions of similarity that may be consequence of functional, structural, or evolutionary relationships between sequences.

Procedure of comparing two (pair-wise alignment) or more sequences by searching for a series of individual characters or patterns that are in the same order in the sequences.

**Why Alignment?**

1. To discover structural, functional and evolutionary information.

2. If two sequences are similar, they might share the same ancestor (Homology).

3. If two sequences are similar, they may share the same structure, therefore similar function

**Homologs:** Similar sequences in two different organisms that have been derived from a common ancestor sequence.

**Orthologs**: Similar sequences in two different organisms that have arisen due to a speciation event retain their functionality throughout evolution.

Paralogs: Similar sequences within a single organism that have arisen due to a gene duplication event.

**Xenologs:** Similar sequences that do not share the same evolutionary origin, but rather have arisen out of horizontal transfer events through

symbiosis, viruses, etc.