**Course: Advanced Bioinformatics**

**Module title: Blas Variants**

**Module no. : 36**

This module gives evidence about the different blast variants.

**BLASTP:** Compares an amino acid query sequence against a protein sequence database.

**BLASTN:** Compares a nucleotide query sequence against a nucleotide sequence database.

**BLASTX:** Compares a nucleotide query sequence translated in all reading frames against a protein sequence database. You could use this option to find potential translation products of an unknown nucleotide sequence

**TBLASTX:** Compares the six-frame translations of a nucleotide query sequence against six-frame translations of a nucleotide sequence database.

**TBLASTN:** Compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames.

**PHI-BLAST:** Pattern Hit Initiated Blast. PHI-Blast uses protein motifs to increase the chance of finding biologically significant matches.

**PHI-BLAST** (pattern hit initiated blast) functions in same manner as PSI-BLAST except that the query sequence is first searched for a complex pattern, or regular expression, provided by the user. The subsequent search for similar sequences is then focused on regions containing the pattern. One example of a regular expression that might be used is:

[LIVMF]-G-E-x-[GAS]-[LIVM]-x(5,11)-R-[STAQ]-A-x-[LIVMA]-x-[STACV]

**PSI-BLAST:** Position Specific Iterative Blast uses an iterative alignment procedure to develop position specific scoring matrices which increases its capability to detect weak pattern matches.

PSI-BLAST (position specific iterated blast) is a newer version of BLAST designed to take in an initial query sequence and find similar sequences to the query which can then be multiply aligned to create a scoring matrix that can be used to search the database for even more matches. At this point, even more sequences are potentially found, that can then be added onto the multiple alignment. This process of iteratively building the multiple alignment continues until the user is satisfied with the search results.

Of course, caution should be used with PSI-BLAST since a greedy algorithm is used in the sense that the most recently added sequences will now influence the next round of sequences that are to be found.