



Genomics and bioinformatics analysis – NCBI BLAST

● Aim

Basic Local Alignment Search Tool (BLAST) is a computer algorithm that is available for use online at the National Center for Biotechnology Information (NCBI) website and many other sites. We use BLAST to find regions of local similarity between sequences. The program compares protein sequences to sequence databases and calculates the statistical significance of matches. A significant match should have at least 25% of the same sequence and more than 80 amino acid segments.

● Procedure

1. Open the BLAST homepage at <http://blast.ncbi.nlm.nih.gov/Blast.cgi>.

Blast realized blastn and other five ways of sequence alignment by calling different alignment modules. Click Protein BLAST to enter the interface of Protein sequence and Protein library alignment.

2. Parameter setting. In the sequence input window, paste our target sequence in FASTA format. Select the search set option and set the search database as non-redundant protein sequences (nr), which can improve the comparison accuracy. The alignment algorithm is set to PSI-Blast. Click BLAST to start the first round of alignment. (The main idea of the psi-blast program is to reconstruct the site-specific scoring matrix for the next iteration to find the



best result through multiple iterations, using the most similar sequence from each iteration. Eventually, highly conserved regions get higher scores, making it easier to find homologous sequences that are more distant.)

3. Select the sequence of alignment results whose e-value meets the preset threshold, click RUN for the next iteration and repeat several times.

