



# LEARN PYTHON & R FOR BIOINFORMATICS

## Introduction:

In bioinformatics, Basic Local Alignment Search Tool (BLAST) is an algorithm and program for comparing primary biological sequence information, such as the amino-acid sequences of proteins or the nucleotides of DNA and/or RNA sequences. Query is searched against the entire database of GenBank or the entire datasets which have been incorporated in NCBI.

## Steps:

- You can access BLAST whether from web-browser, or through installing the command line BLAST to your computer or through programming languages such as Python and R.
- Go to the BLAST [web-browser](#).

- Here you will see four kind of Blast which you can use.

<b>BLAST Type</b>	<b>Query Type</b>	<b>Database type</b>
Nucleotide BLAST	Nucleotide	Nucleotide
Protein BLAST	Protein	Protein
BLASTX	Translated Nucleotide	Protein
TBLASTN	Protein	Translated Nucleotide

### **Nucleotide BLAST**

- A page will be opened, where you can customize your search according to your analysis.
- In the **'Enter Query Search'** box, you can put *accession number* or copy the *FASTA* sequence of your nucleotide query.
- Beside this box, you can see **'Query subrange'** box, from where you can subset your query and tell from what nucleotide to what nucleotide you want to search.
- You can also upload the sequence file from your computer.
- In **'Job Title'**, you can give a descriptive title for your BLAST search.
- In **'Database'**, you can select any kind of database you want to search against; For nucleotide sequences, non-redundant (nr/nt) database is a good option.
- In **'Organism'** (which is optional), you can select the organism or organisms you want to search against or you can exclude those organisms from your search.
- All of the next parameters are optional, which won't matter until you want to include them according to your own analysis.
- In **'Program Selection'** section, you can select the option which is better for your own analysis.
- Click on the **'BLAST'**.
- The BLAST analysis will be opened, where you can analyze your query with many other aligned nucleotide sequences.

### **TBLASTN**

- From Blast [web-browser](#), go to **'tblastn'**.
- Put in the *accession number* or *FASTA* sequence in the query box.
- Select nucleotide non-redundant(nr/nt) database from the **'Database'**.
- BLAST it.
- The analysis page is same as any other kind of BLAST (for example Nucleotide Blast).
- You can analyze your query with aligned mRNA sequences.
- You can see that **'Percentage Identity'** is lower as compared to Nucleotide BLAST, it's because of Codon Degeneracy.
- You can also visualize your sequences in many kinds of alignments.

### **Summary:**

In this video, we learnt about BLAST and how we can use it to compare different biological sequences to different databases.