

RETRIEVAL

OF

DATA

PRACTICAL: 2

RETRIVAL OF SEQUENCES OF DATABASE

→ Single Entry Retrieval (Flow chart):-

Go to Website:-
NCBI:- National centre
for Biotechnology centre

click on All Databases
Select :- Nucleotide

Go to Search Bar:-
Type :- 16S rRNA

Enter

Select:- 1 Gene Database
Beet leafhopper transmitted viresence
phytoplasma 16S ribosomal RNA (16S rRNA)
gene complete sequence.

Send to

Select the format
FILE:- FASTA

Click on :-
CREATE FILE

complete sequence
displayed

→ Batch Retrieval (Flow chart) :-

Go to website :-
NCBI :- National centre for
Biotechnology Information

click on all Database :-
Select :- NUCLEOTIDE

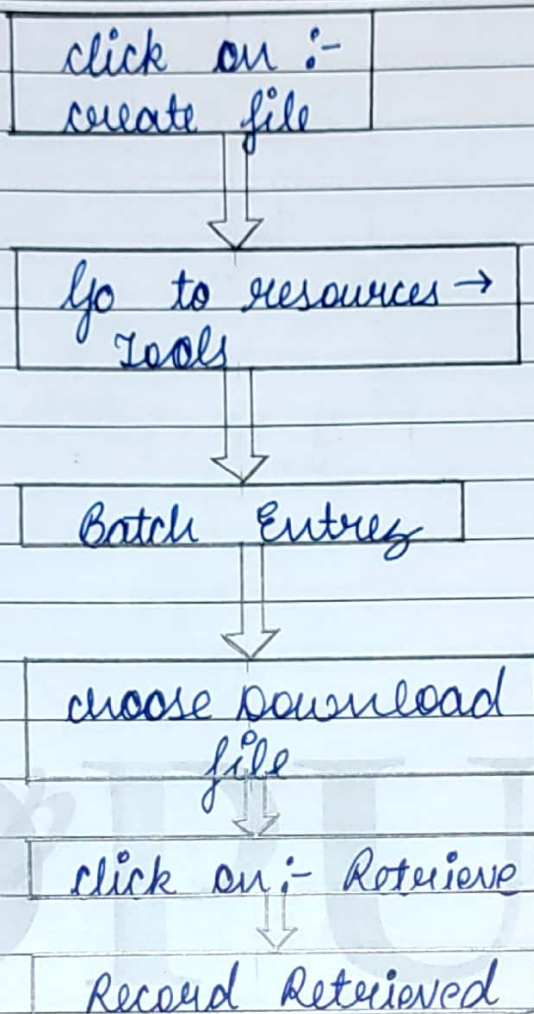
Go to Search Bar :-
Type :- 16S rRNA and
Escherichia

Enter

Select multiple files (5)

Send to

Select the format :-
FILES :- ACCESSION LIST



TOOLS

To

DYPU
ANALYZER

DATA

PRACTICAL :- 3

* BLAST :-

(Basic local Alignment search tool)

In Bioinformatics, Blast is an algorithm and program for comparing primary biological sequences information, such as the amino acid sequence of proteins or the nucleotides of DNA and / or RNA sequences. A BLAST search enables a researcher to compare a subject protein or nucleotide sequence with a library or database of sequences and identify database sequences that resemble the query sequence a certain threshold.

* TYPES OF BLAST :-

1. Nucleotide Blast :- (blastn)

→ Refers to the use of a member of the BLAST suite of programs such as "Blastn" to search with a nucleotide "query" against a database of nucleotide "subject" sequences.

2. Protein Blast :- (blastp)

→ Refers to when BLAST finds regions of local similarity between proteins sequences. This program searches protein databases using a protein

3. BLAST X :-

→ It searches protein databases using translated nucleotide query.

4. tblastn :-

→ For identifying database sequences encoding proteins similar to the query.

→ BLASTN FLOW CHART :-

