**DATE** : 30 June 2022

**PROJECT NAME** : Bioinformatics

**GROUP** : D

**GROUP MEMBERS** : Aachal Tiwari, Shraddha Mishra, Chinmayee Shinde, Niranjan Kathavate, Shraddha Dubey, Akshita Poojary, Sancia Fernandes, Sanika Naik.

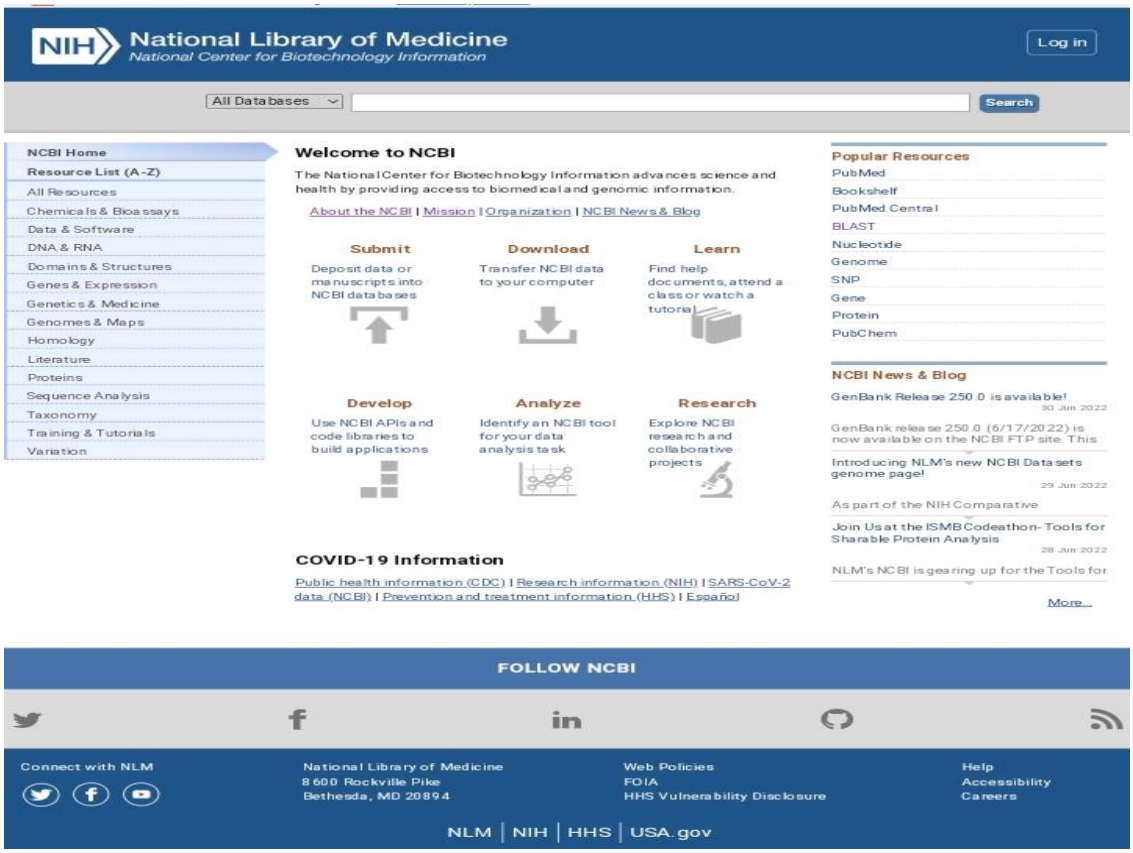
**30 June,2022**

**Bhavans College, Mumbai :**

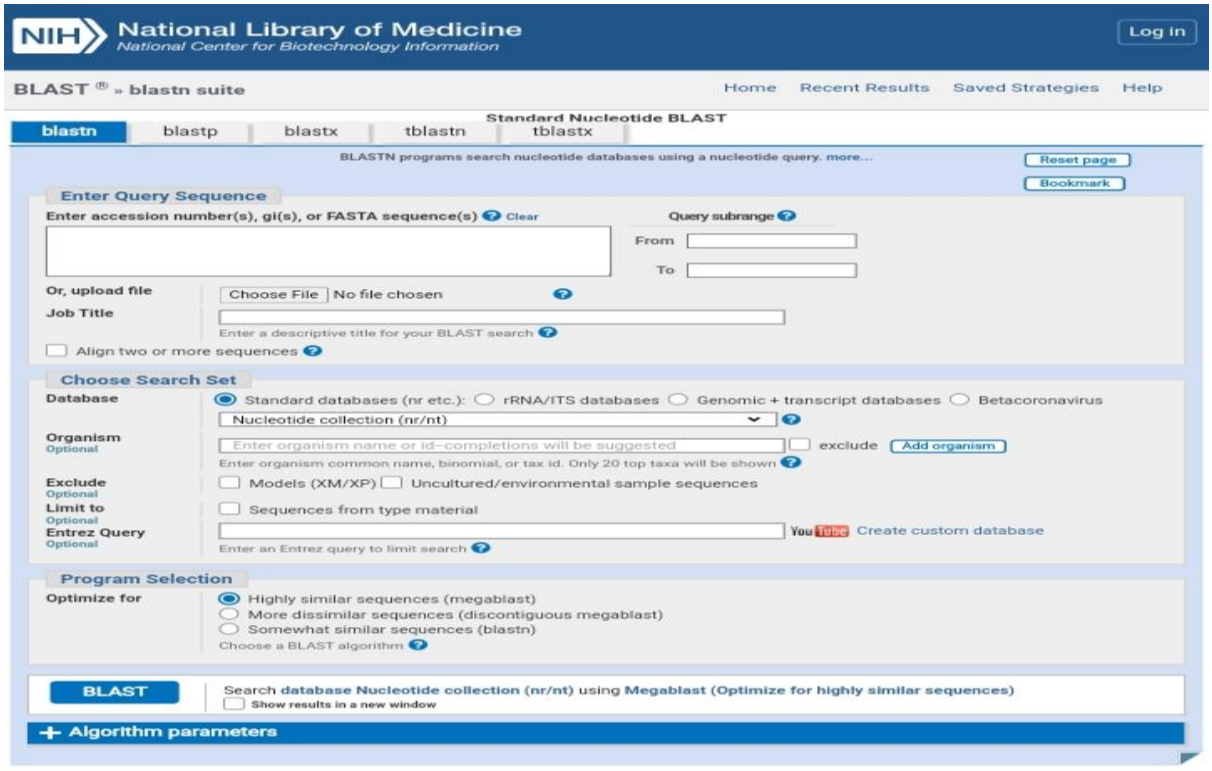
Bioinformatics was one among the three projects that were assigned to the interns. Bioinformatics, as related to genetics and genomics, is a scientific subdiscipline that involves using computer technology to collect, store, analyze and disseminate biological data and information, such as DNA and amino acid sequences or annotations about those sequences. Respected Sir Anubrata Das conducted online sessions giving us a vast insight on the topic of bioinformatics and gave us hands on experience increasing our practical skills.

During the tenure of the project we go an overview about systems biology, various databases (FungiDB, NCBI etc), Polymerase Chain Reaction, PCR Primer Design Guidelines, real time PCR machine, sanger sequencing, data flow in software, scoring matrix, number of possible alignments, BLAST, FASTA and multiple sequence alignment.

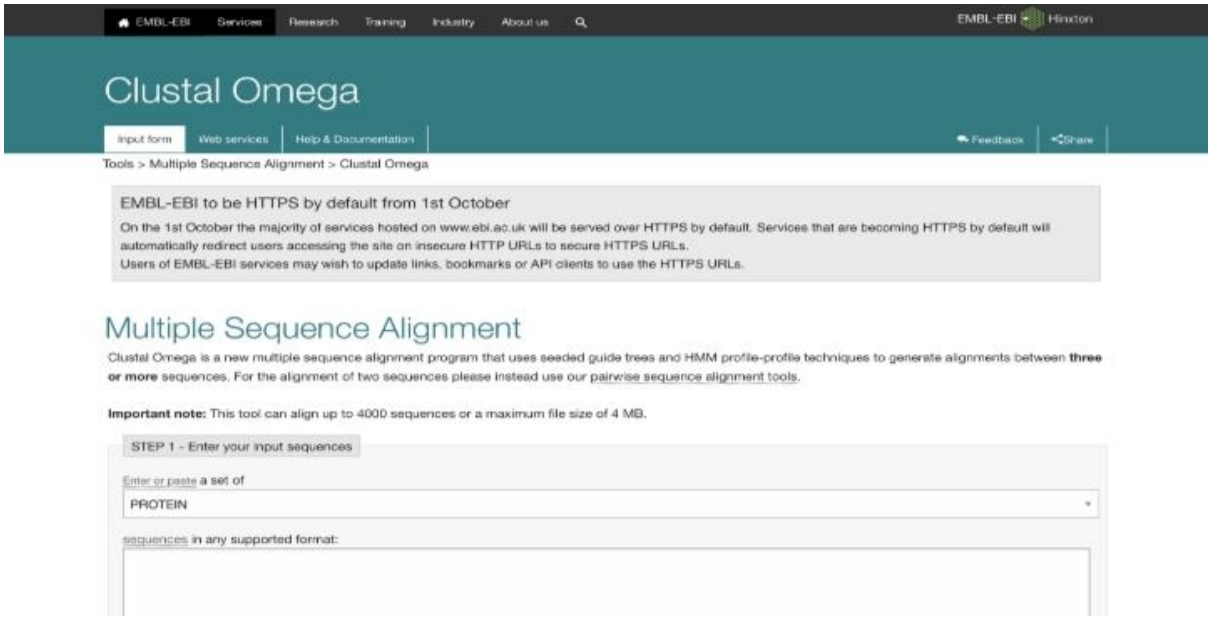
Inorder to gain practical experience we were assigned with various assignments that involved preparing a group presentation on primary data bases (NCBI/EBI/DDBJ) and databases on fungi ,also each group had to select a genus and each student from the group a particular genera and download one sequence of 18S rDNA each from NCBI –our group selected *penicillium* as the genus and *penicillium samsonianum, penicillium hennebertii, penicillium chrysogenum, penicillium citrinum, penicillium expansum, penicillium viticola* as the genera after which each group members downloaded one sequence from NCBI, we then ran the sequences through BLASTn and downloaded any five 18S rDNA sequences, further in Clustal Omega we pasted the five sequences and downloaded the alignment file and opened it in jalview software. As our final assignment we compiled the five 18S rDNA sequences of each genera downloaded by each intern, got a single alignment sequence after running it through Clustal Omega , downloaded it and ran it through jalview software creating a Multiple Alignment Sequence for our group.



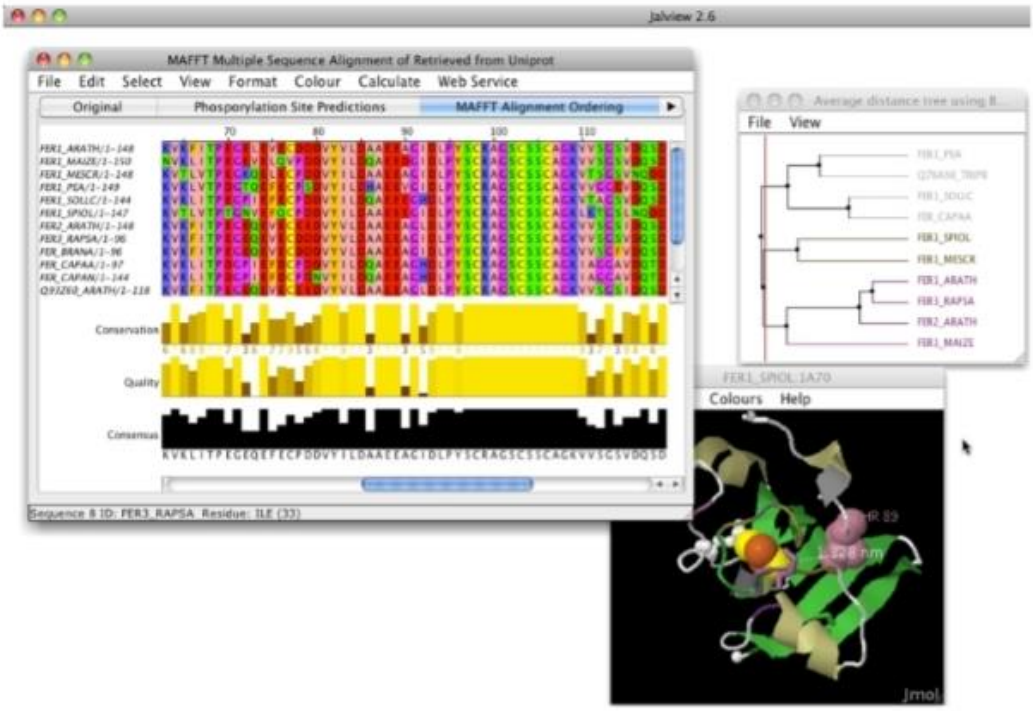

NCBI DATABASE




blastn




CLUSTAL OMEGA




JALVIEW SOFTWARE