

[VI.6.3 in silico Biology]
31st march to 14th April, 2020 class

Dear Students,

Hope, all of you are keeping well and staying safe.

As per our earlier discussion, study materials and weblinks are/ will be shared with all the students on our google group for understanding/ revising all the topics of this paper. Also, the following needs to be done for the class during 31st march-14th April, 2020. Rest, we can keep discussing, as we are already doing on our whatsapp group. I am always available for any subject related query/ difficulty faced by any of you during this time.

Presentation Topics

All students are required to make a presentation on the following topics elaborating specifically upon various applications of these softwares/ programs/ online websites (henceforth will be called as module) etc. Presentation should specifically have the following:

1. Basic description of the module
 2. Detailed Procedure/ protocol to use the module by showing proper snapshots
 3. Applications, which are targeted by these modules by giving various examples
 4. Weblinks of research papers, which have utilized this module
 5. References should be mentioned with hyperlinks
 6. Also, at least 5 recent most research papers mentioning about the modules have to be enclosed with ppt mail.
-
1. Motif and Promoter searches (e.g. CD-Search, SMART, SignalP); linkage of promoters with various diseases and SNP search in the promoter regions; CpG islands and DNA methylation: Hardik
 2. Phylogenetic analysis (PHYLIP, MEGA): elaborate with examples of at least two organism's data: Rajkumar
 3. Protein interaction (STRING, BioGRID), Analysis of protein-ligand interactions and gene-gene interactions for deciphering answers to unsolved questions related to biology: Devansh
 4. Protein structure, Function (PROSITE programs, Chimera); Visualization of protein ligand interaction data showing binding sites & positions of amino acids etc.: Manas

5. Gene expression, function (GEA, Gene card, OMIM), Analysis of Chip-seq data and its integration with gene expression; Microarray (types, principle, procedure: Yatharth
6. Binding sites and pockets prediction using autodock, metapocket or any other program for protein-Ligand and DNA-ligand interaction: Prakhar
7. Discovery studio and RasMol for visualization of proteins and nucleic acids; DNA, RNA secondary structure prediction and 3 D modelling (Web 3DNA 2.0, HNADOCK0, Kegg database: Ravikesh
8. Sequence analysis (BLAST, FASTA) and Database (NCBI, DDBJ, EMBL); To be explained with examples: Nitesh

Note: All these ppts/ assignments will be used for internal assessments/ Project marks. Also, we will keep doing some additional learning activities, as we are already doing, not only during the class timings, but otherwise also.

Best wishes to all of you.

Stay safe, happy and healthy.

Mahima Kaushik