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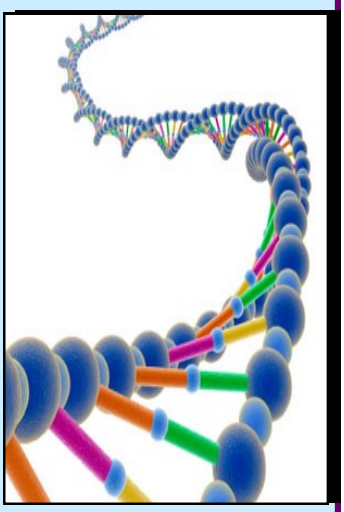
Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat -785006, Assam
(http://www.rrljorhat.res.in/biotechnology.html)

Inside…..



About us

The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was established on 2nd February, 2008 to promote innovation in Biological research and education through Bioinformatics accomplishment. The main goal is to facilitate and expose students and researchers from different academic institutions of North East India in Bioinformatics. The center conduct training and workshops for enlightening the use of bioinformatics applications in biological research and development. The Centre has access to global information through 24 hour high speed internet facility, and also e-journal facilities with DeLCON, Science Direct etc. To date the Centre has profoundly extended support in R & D work with a great intensity to different biological discipline including medicinal chemistry, computer aided drug design, genomics and proteomic data analysis etc.

A comprehensive bioinformatics analysis on multiple Gene Expression Omnibus datasets of nonalcoholic fatty liver disease and nonalcoholic steatohepatitis

Fatty liver disease is one of the leading causes of chronic damage in western countries. Nonalcoholic fatty liver disease (NAFLD) and its subtype nonalcoholic steatohepatitis (NASH) have become an increasingly important clinical and economic burden for public health. In this study, the researchers used the Gene-Cloud of Biotechnology Information bioinformatics platform to carry out a comprehensive bioinformatics analysis identifying differentially expressed genes (DEGs), key biological processes and intersecting pathways. They imported 3 Gene Expression Omnibus datasets (GSE31803,GSE49541,GSE63067).Then, they assessed the expression of the DEGs in clinical samples. They found that CD24 was the only gene co-expressed in all 3 datasets. Glycolysis,p53 signaling pathway and glycine, serine and threonine metabolism were 3 common pathways related to the fatty liver process. In NAFLD tissues,CD24,COL1A1, LUM, THBS2 and EPHA3 were upregulated, and PZP was downregulated. In this study, Co-expressed genes, common biological processes and intersecting pathways identified may play an important role in NAFLD progression.

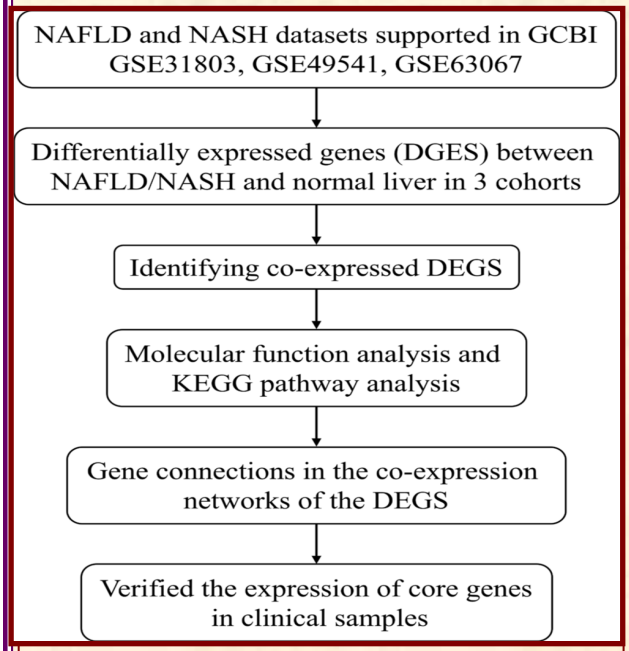


Fig:Flow diagram of the study design. NAFLD, nonalcoholic fatty liver disease; NASH, nonalcoholic steatohepatitis; DEGs, differentially expressed genes; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Source: **Shanzhou Huang *et al. 2018,J Scientific Reports***

LOLAweb: a containerized web server for interactive genomic locus overlap enrichment analysis

The past few years have seen an explosion of interest in understanding the role of regulatory DNA. This interest has driven large-scale production of functional genomics data and analytical methods. One popular analysis is to test for enrichment of overlaps between a query set of genomic regions and a database of region sets. In this way, new genomic data can be easily connected to annotations from external data sources. Here, they present an interactive interface for enrichment analysis of genomic locus overlaps using a web server called LOLAweb. LOLAweb accepts a set of genomic ranges from the user and tests it for enrichment against a database of region sets. LOLAweb renders results in an R Shiny application to provide interactive visualization features, enabling users to filter, sort, and explore enrichment results dynamically. LOLAweb is built and deployed in a Linux container, making it scalable to many concurrent users on our servers and also enabling users to download and run LOLAweb locally.

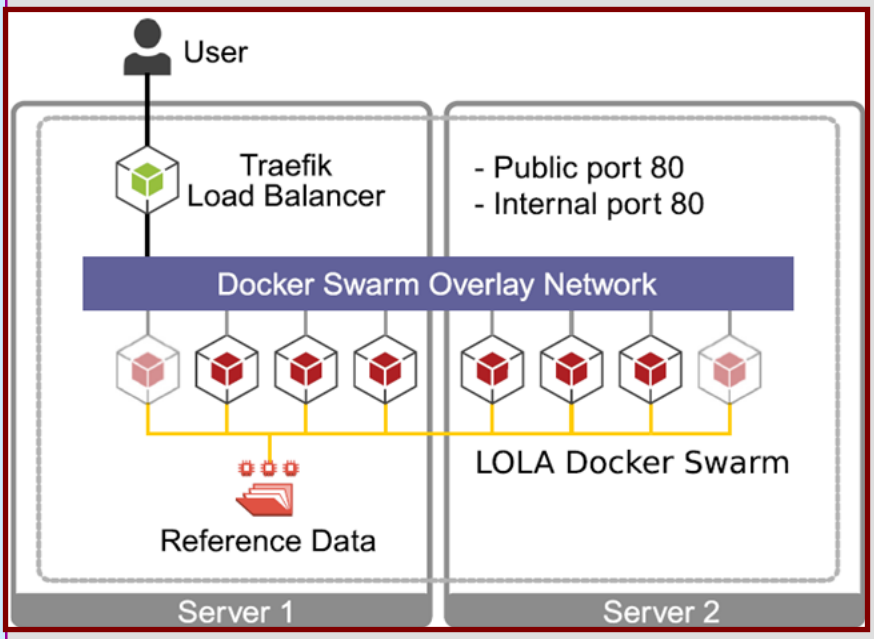
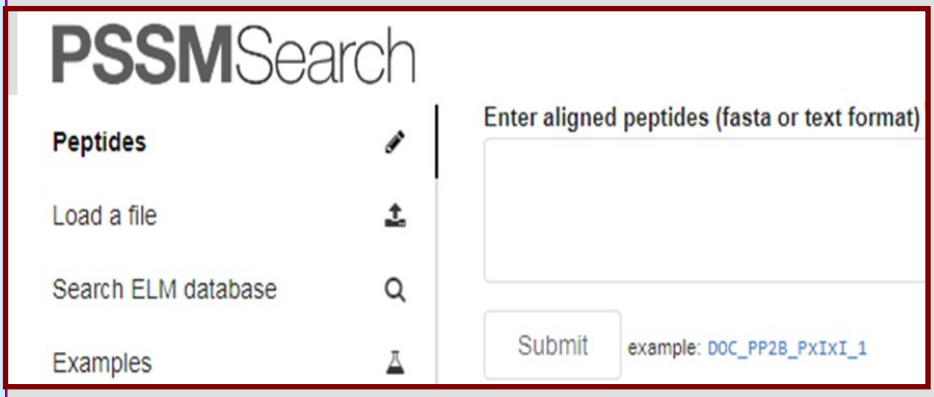


Fig: Overviewof the LOLAweb architecture.

Source: V. P. Nagraj *et al. (2018).J Nucleic Acids Research*

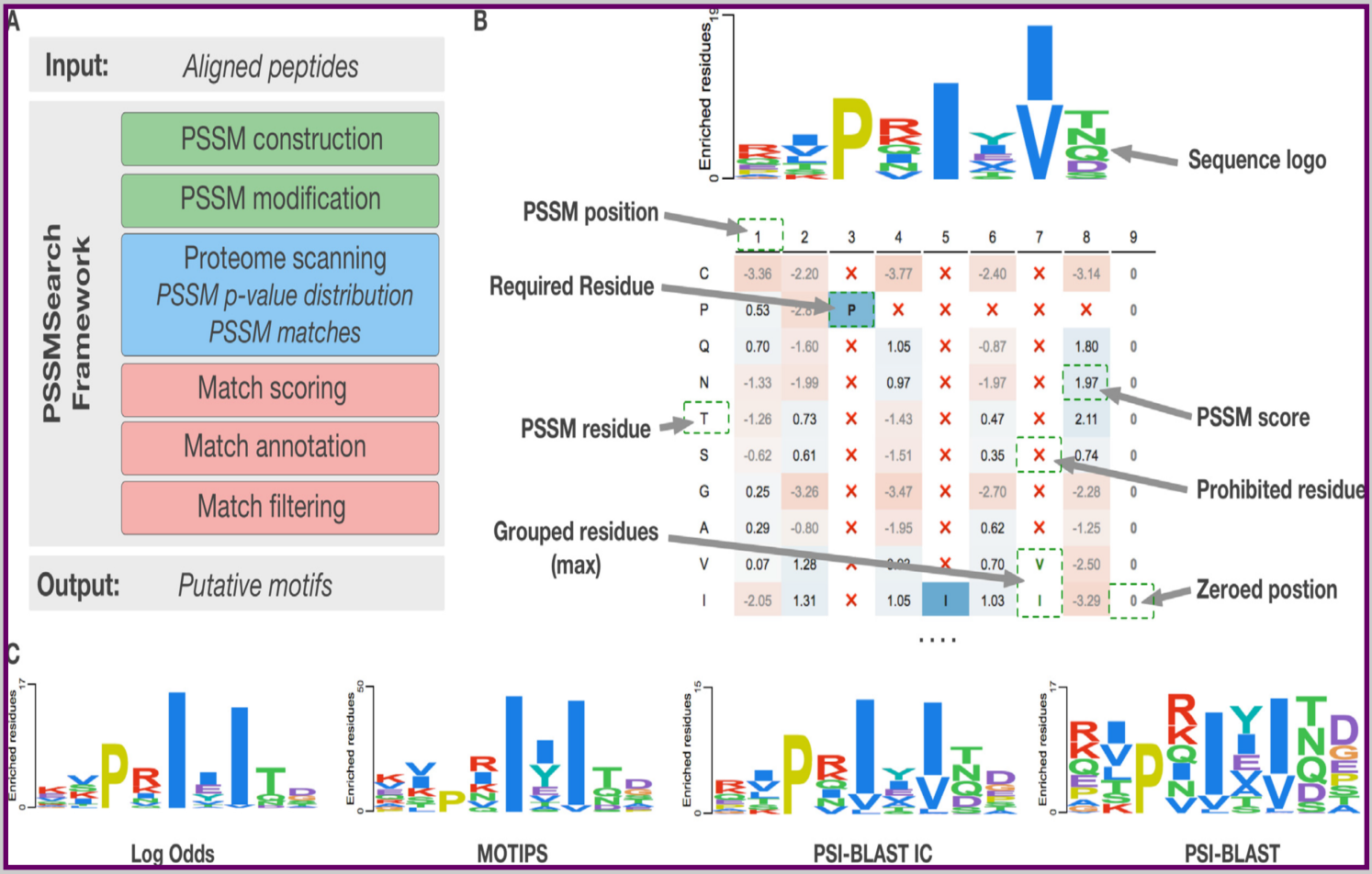
PSSMSearch: a server for modeling, visualization, proteome-wide discovery and annotation of protein motif specificity determinants

There is a pressing need for in silico tools that can aid in the identification of the complete repertoire of proteinbinding (SLiMs, MoRFs, miniMotifs) and modification (moiety attachment/removal, isomerization, cleavage motifs. They have created PSSMSearch, an interactive web-based tool for rapid statistical modeling, visualization, discovery and annotation of protein motif specificity determinants to discover novel motifs in a proteome-wide manner. PSSMSearch analyses proteomes for regions with significant similarity to a motif specificity determinant model built from a set of aligned motifcontaining peptides. Multiple scoring methods are available to build a position-specific scoring matrix (PSSM) describing the motif specificity determinant model. This model can then be modified by a user to add prior knowledge of specificity determinants through an interactive PSSM heatmap. PSSMSearch includes a statistical framework to calculate the significance of specificity determinant model matches against a proteome of interest. PSSMSearch also includes the SLiMSearch framework's annotation, motif functional analysis and filtering tools to highlight relevant discriminatory information. Additional tools to annotate statistically significant shared keywords and GO terms, or experimental evidence of interaction with a motif-recognizing protein have been added. Finally, PSSM-based conservation metrics have been created for taxonomic range analyses. The PSSMSearch web server is available at http://slim.ucd.ie/pssmsearch/.

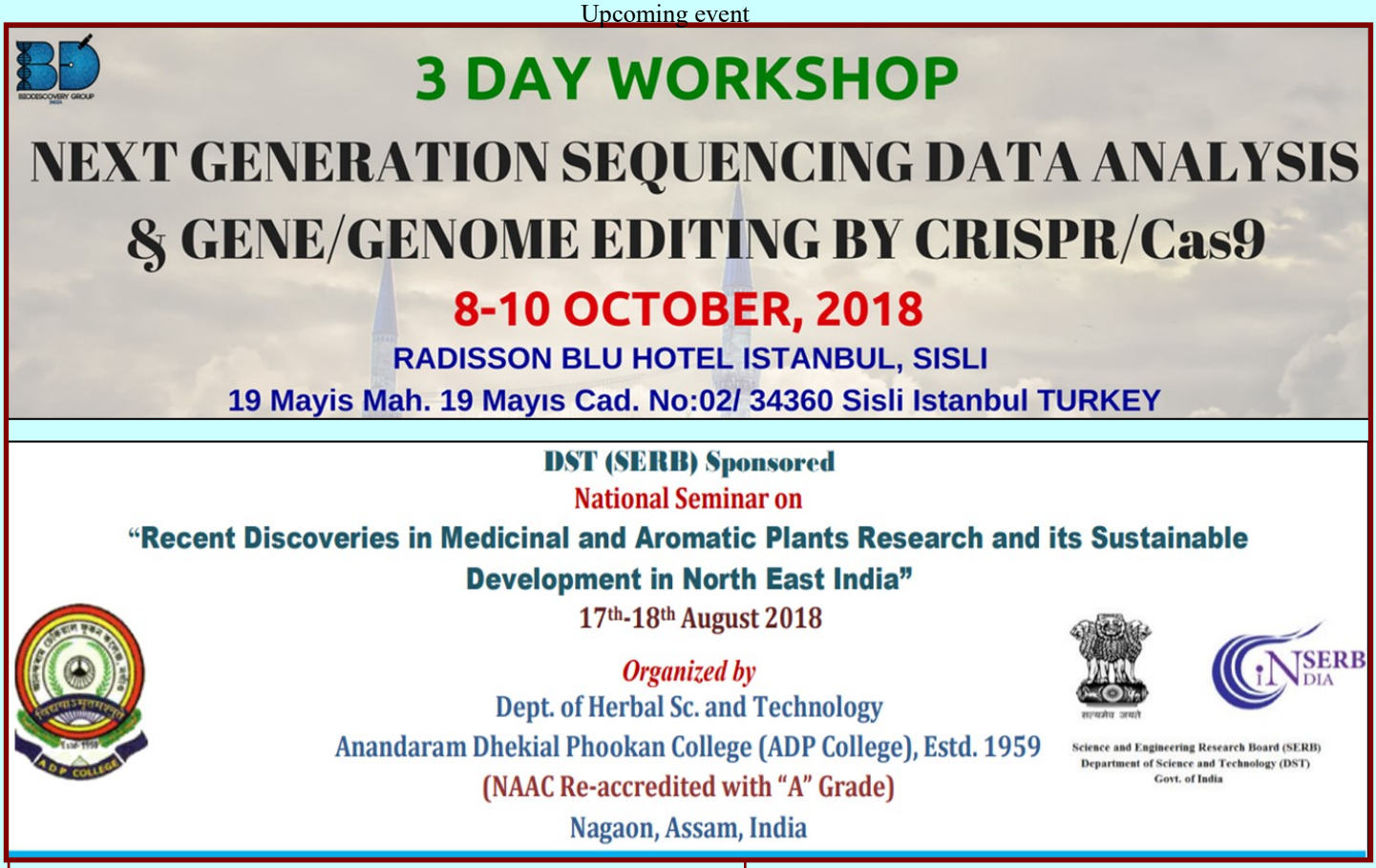


Source: Izabella Krystkowiak *et al. 2018,J Nucleic Acids Research*

Bioinfo. Animation (Source : Izabella Krystkowiak *et al. 2018, J Nucleic Acids Research)*



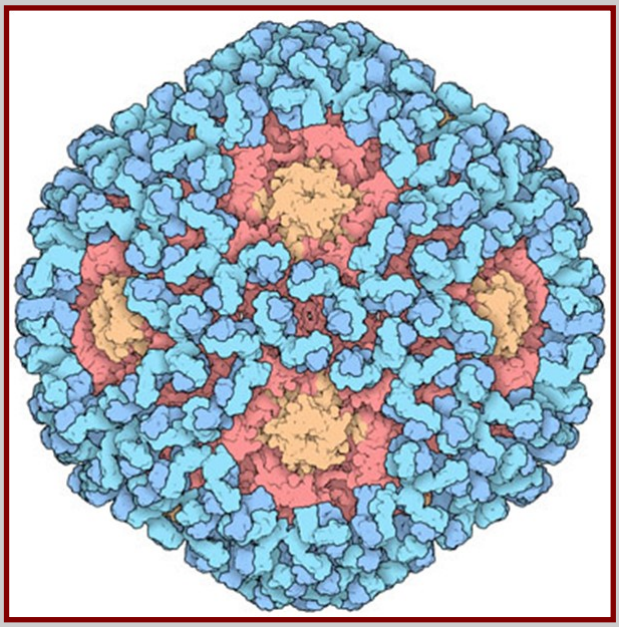
Upcoming event



1. http://events.biodiscoverygroup.com/NGS Turkey/ngsturkey.html
2. www.adpcollege.ac.in

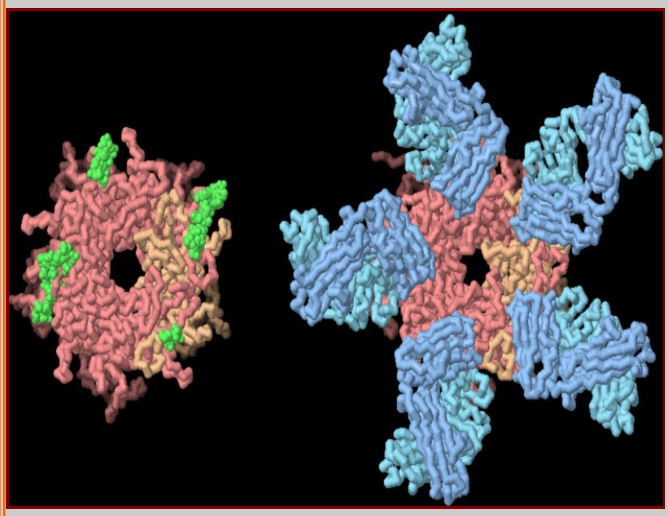
Human Papillomavirus

Papillomaviruses are annoying pests that occasionally turn into deadly dangers. They attack cells in our skin and mucous membranes. When they infect cells, they ramp up the normal growth functions, often forming warts. Usually our defenses are able to get the infection under control, but in some exceptional cases, the virus persists and the unwanted growth can turn into cancer. Alarmingly, infection by a few particularly-virulent types of papillomavirus is the leading cause of cervical cancer. Fortunately, by studying these viruses, scientists have discovered highly effective ways to fight them.



Papillomavirus is a small virus, with a simple capsid surrounding a circular DNA genome. The capsid (PDB entry 3j6r) includes 360 copies of the major capsid chain, called L1. A second capsid chain, called L2, is found on the inside and may help with packaging the genome. The capsid structure, however, is not a typical quasisymmetrical virus. Instead, like simian virus 40, the L1 chains form 72 pentameric "capsomeres", which then interact with one another through long flexible tails.

Human Papillomavirus



Papillomavirus binds to heparin molecules on the surface of the cells that it infects. Crystallographic structures of isolated L1 capsomeres have revealed that the heparin chains (on the left in green) are recognized by lysine-lined grooves on the surface of the virus (PDB entry 5w1o). Similar L1 capsomere structures with antibodies (on the right in blue) show that they can block this recognition, thus blocking attachment to the cell (PDB entry 5y9f). To compare these two structures, click on the image for an interactive JSmol.

Source:http://pdb101.rcsb.org/motm/221

Kindly send us your feedback to

Dr Ratul Saikia
BIF Center, Biotechnology Group, BSTD
CSIR-North East Institute of Science and Technology, Jorhat, Assam
E-mail: rsaikia19@gmail.com

Dr Yumnam Silla Devi
BIF Center, Biotechnology Group, BSTD
CSIR-North East Institute of Science and Technology, Jorhat, Assam
E-mail: **bio.sillayumnam@gmail.com**
Mobile:**+91-9599149208**