Bioinformatics up to Date

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Inside…..

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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 model for universal Histocompatibility Complex (MHC) binding prediction

Immunotherapy is a promising advance approach in cancer treatment that helps our immune system fight against cancer disease. Immune system helps our body to fight against infections and other disease. Immunotherapy activates the host immune system to destroy cancer cells expressing unique peptide signatures (neoepitopes). The cancer-specific neoepitopes in the form of synthetic peptide vaccine have been proven effective in both mouse models and human patients. This approach for immunogenicity prediction is based on the effective neoepitope should bind with the MHC with high affinity.
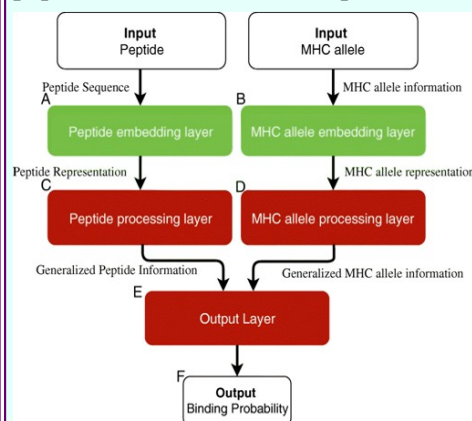
In this present study, the researchers developed MHCSeqNet, an open-source deep learning system model, which can used as a predictors on both MHC binding affinity and MHC ligand peptidome datasets. This model also reveal promising overview to evident MHC class I alleles. MHCSeqNet work in neural network architectures developed for natural language processing (NLP) to construct model amino acid sequence representations of MHC allele and epitope peptide as sentences with amino acids as individual words. Artificial Neural network algorithm is a network like human brain neurons. In modern sense, Aritificial Neural network composed of artificial neurons or nodes. This concern allows this model to accept new MHC alleles as well as peptides of any length. Figure 1 shows the Workflow of MHCSeqNet architecture.

Figure 1:Workflow of MHCSeqNet architecture

MHCSeqNet should make it a valuable tool for screening effective neoepitopes in cancer vaccine development for their improved appearance and the flexibility over existing tools for predicting binding energy and peptidome datasets of MHC class I ligands. MHCSeqNet using Python 3 ,various packages such as numpy version 1.14.3, Keras version 2.2.0, tensowflow version 1.6.0, scipy version 1.1.0, and scikit-learn version 0.19.1.

Source: Poomarin Phloyphisut,2019,J BMC Bioinformatics

News articles with support vector machine for predicting weekly ILI (Influenza Like Illness)

Influenza a viral infection that attacks the respiratory system still continues to be a serious threat to human health all over the world. Due to this, detecting influenza infection patterns is a challenge which must be addressed urgently. However, as the epidemic spread of influenza occurs occasionally and rapidly, it is not easy to estimate the future variance of influenza virus infection. In addition, accumulating influenza related data is not easy so building a prediction model with these data are necessary steps t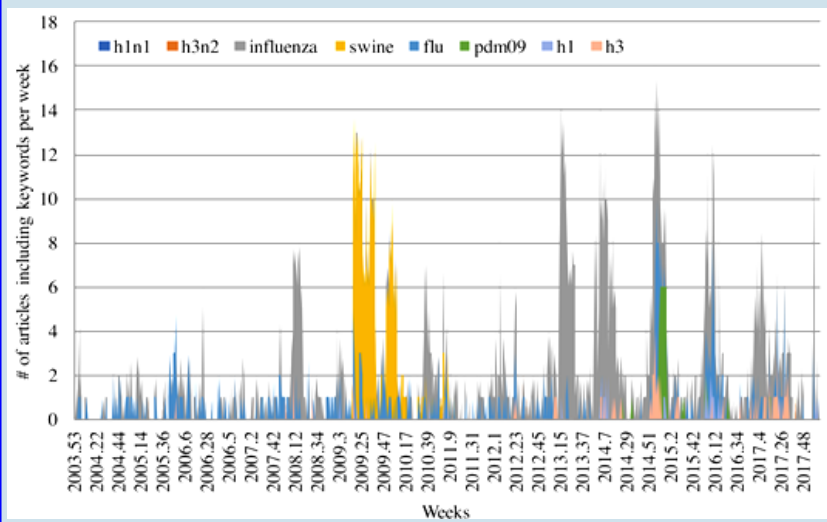oward predicting if the number of patients will increase or decrease. This can be achieved by collecting the database of numerous press releases which are published every day that reflect currently pending issues.

Figure: Representation of total weekly counts of news articles including the keywords of 'influenza', 'h1n1', 'h3n2', 'swine', 'flu', 'pdm09', 'h1', and 'h3' from 2004.01–2018.02 . Image source :Juhyeon Kim and Insung Ahn1,2019

In this mentioned work, Internet articles related to infectious diseases were collected from the Centre for Health Protection (CHP), which is maintained by Hong Kong Department of Health. In total, 7769 articles related to infectious diseases published from 2004 January to 2018 January were collected and evaluated. The support vector machine (SVM) model was used for prediction and detecting the pattern of influenza spread variance. The prediction result using news text data with SVM exhibited a mean accuracy of 86.7 % on predicting whether weekly ILI (Influenza Like Illness) patient ratio would increase or decrease, and a root mean square error of 0.611 on estimating the weekly ILI patient ratio.

In order to solve the problems of conventional data, using news articles can be a suitable choice, as they can help estimate if ILI patient ratio will increase or decrease as well as how many patients will be affected. Thus, advancements in research on using news articles for influenza prediction should continue as the result showed acceptable performance as compared to existing influenza prediction researches and can be beneficial for understanding the disease.

Bioinformatics Animation

Fig: AI in drug discovery
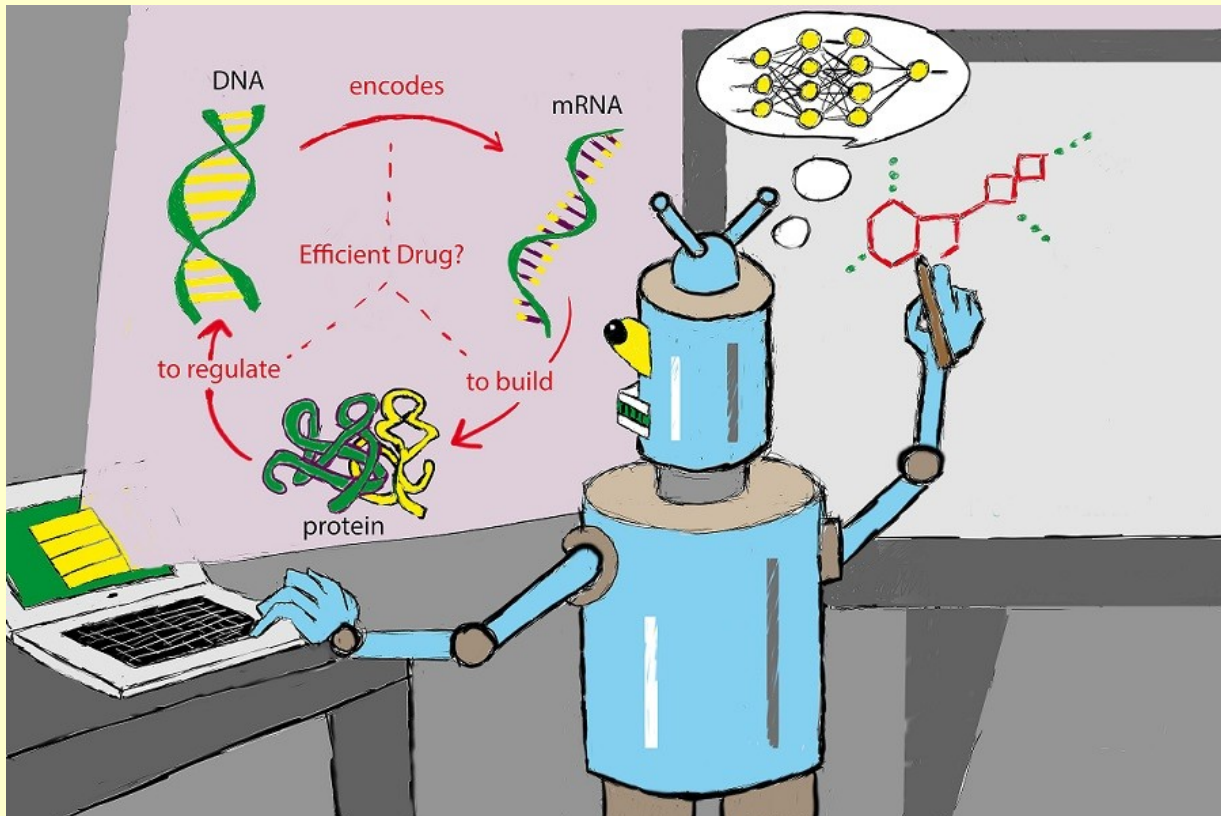
Source:Andrii Buvailo , 2019

Upcoming Events

1. https://www.townscript.com/e/international-conference-on-artificial-intelligence-and-robotics-icair19-330301
2 . https://ijcai19.org/

Molecule of the month

S-Nitrosylated Haemoglobin

Haemoglobin in our blood has been designed through evolution to deliver oxygen efficiently throughout our body. It binds to large quantities of oxygen in the lungs and transports it to every part of our body system through blood vessels. The control of blood flow in the blood vessels can be controlled. Blood vessels can be dilated to increase the transportation of oxygen to the tissues which demand more oxygen.

NO is a signalling molecule synthesized by nitric oxide synthase. NO preferentially forms complexes with the conserved cysteine present in the beta chains of oxygenated haemoglobin . The conformational change of haemoglobin from oxygenated to de-oxygenated form after releasing oxygen in the tissues also causes the released of NO from it. The released of NO from red blood cells then causes induction of surrounding blood vessels to dilate and increase blood flow through the tissue. Hemoglobin as an oxygen sensor as well as oxygen transporter release NO the regions where oxygen is more demanded.
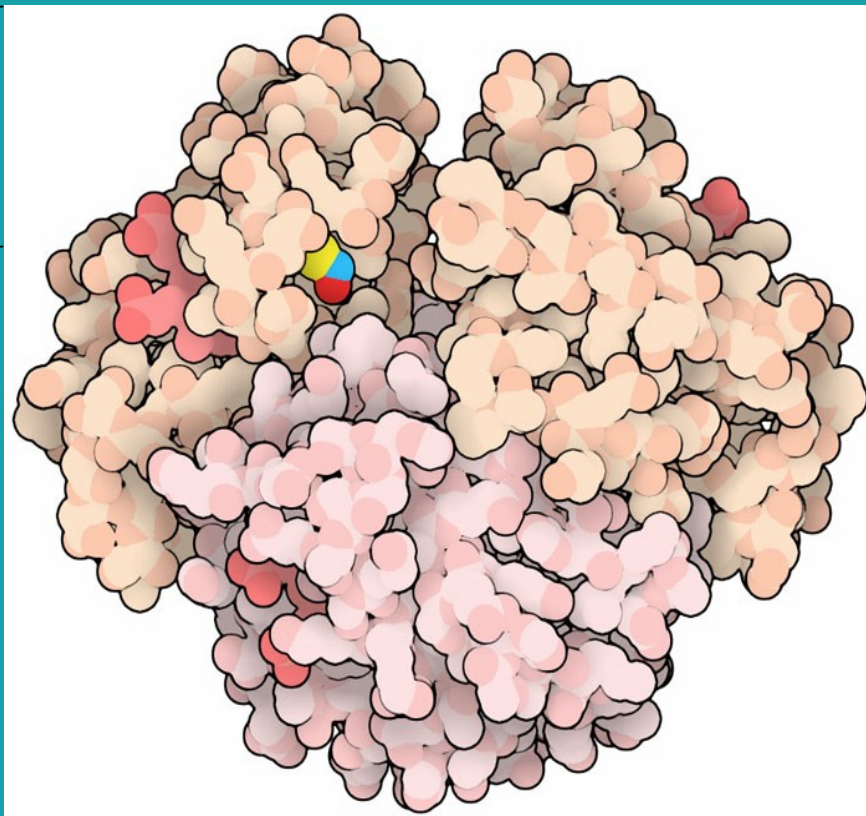

Fig: NO (blue and red) forming complex with the cysteine sulphur atom (yellow) present in beta chains of haemoglobin.

Source: http://pdb101.rcsb.org/motm/233

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