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Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat - 785 006, Assam

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.

Workshop cum Training on Biological Data Analysis Using R–Package

With the support of DBT Govt of India, a 2 day workshop on Biological data analysis Using R–Package had successfully organized at BIF Center, CSIR-NEIST. The program was held on January 5-6, 2017 under the successful coordination of Dr Ratul Saikia, Senior Scientist, Biotechnology, CSIR-NEIST and other members of Biotechnology group. There are total of 35 Nos participants joined coming from different regions of North East India. Most of the participants are PhD scholars and others are post graduate student and faculty members. The main objectives of the workshop were to generate knowledge on applications and using of R language on analysis of genome sequence data. The statistical concepts of data analysis on biological fields and implementation of R-packages makes the participants in depth understanding about data analysis.

Uncover New pathway to regulates spread of prostate cancer

A research team from University of Adelaide have recently uncovered a new pathway which regulates the spread of prostate cancer around the body. The work published in the journal *Cancer Research* January, 2017. The discovery has potential to lead to the development of a blood test that could predict whether cancer will spread from the prostate tumour to other parts of the body. The research also reveals potential new targets for drugs that may inhibit the spread of cancer.

The international research team - led by the University of Adelaide and including members from the University of Michigan, Vancouver Prostate Centre, the Mayo Clinic and Johns Hopkins University - showed that a specific microRNA (a type of molecule involved in regulating the level and activity of genes) called miR-194 promotes cancer metastasis by inhibiting a key protein called SOCS2.

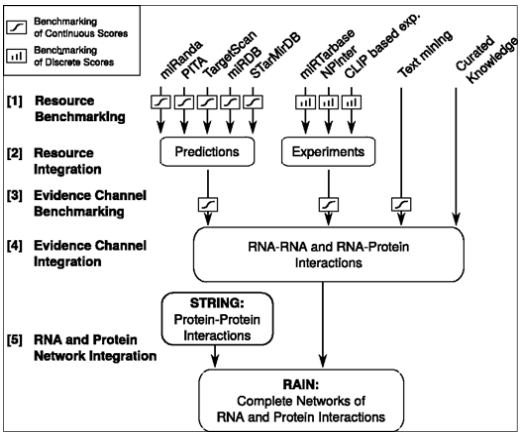
"In previous work, we had found that a high level of miR-194 in a patient's blood was associated with rapid relapse of prostate cancer following surgical removal of the tumour," says Dr. Selth. "This new work explains why miR-194 is associated with a poor outcome, and in the process reveals a completely novel pathway regulating prostate cancer metastasis.

Dr. Selth says miR-194 also represents a potential therapeutic target. "There are currently no drugs that effectively inhibit the spread of prostate cancer," he says. "We propose that inhibiting miR-194 could reduce rates of metastasis in patients with aggressive disease, but the development of a drug to achieve this goal is still a long way off."

[*MicroRNA-194 promotes prostate cancer metastasis by inhibiting SOCS2. Rajdeep Das et al. Cancer Research (December 23, 2016)*]

RAIN: RNA–protein Association and Interaction Networks

Protein association networks can be inferred from a range of resources including experimental data, literature mining and computational predictions. These types of evidence are emerging for non-coding RNAs (ncRNAs) as well. However, integration of ncRNAs into protein association networks is challenging due to data heterogeneity. Here, we present a database of ncRNA–RNA and ncRNA–protein interactions and its integration with the STRING database of protein–protein interactions. These ncRNA associations cover four organisms and have been established from curated examples, experimental data, interaction predictions and automatic literature mining. RAIN uses an integrative scoring scheme to assign a confidence score to each interaction. RAIN can be operated through an easily accessible web interface and all interaction data can be downloaded. The URL for RAIN is http://rth.dk/resources/rain.



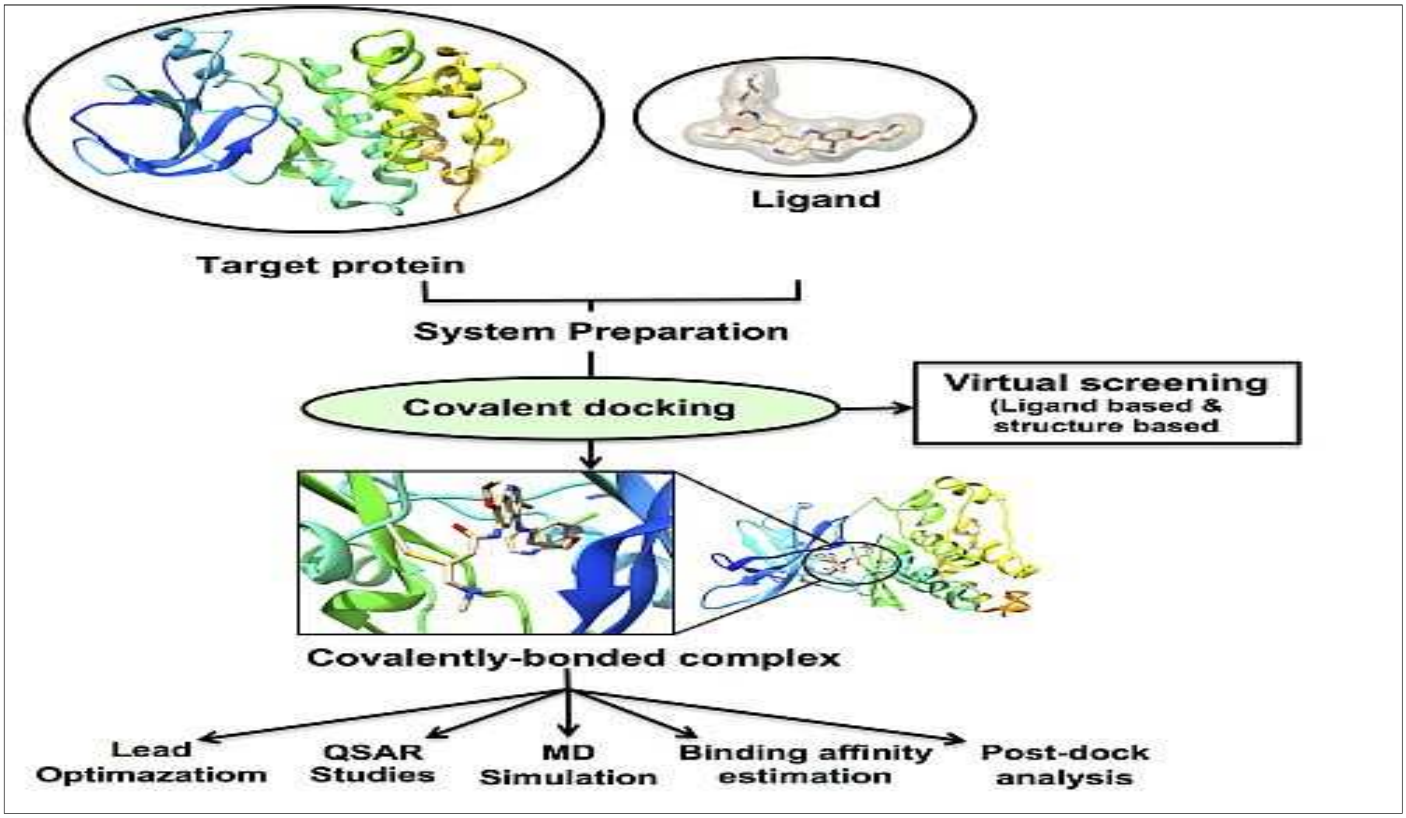
[Alexander Junge et al., RAIN: RNA–protein Association and Interaction Networks. Database (Oxford) 2017; 2017 (1): baw167]

HEDD: the human epigenetic drug database

A research team from Jilin Normal University, China developed a relatively comprehensive database for human epigenetic drugs. Epigenetic drugs are chemical compounds that target disordered post-translational modification of histone proteins and DNA through enzymes, and the recognition of these changes by adaptor proteins.

The research output published in journal *Database (Oxford)* Dec 2016. Epigenetic drug-related experimental data such as gene expression probed by high-throughput sequencing, co-crystal structure probed by X-RAY diffraction and binding constants probed by bio-assay have become widely available. The mining and integration of multiple kinds of data can be beneficial to drug discovery and drug repurposing. The human epigenetic drug database (HEDD) focuses on the storage and integration of epigenetic drug datasets obtained from laboratory experiments and manually curated information. The latest release of HEDD incorporates five kinds of datasets: (i) drug, (ii) target, (iii) disease, (vi) high-throughput and (v) complex. In order to facilitate data extraction, flexible search options were built in HEDD, which allowed an unlimited condition query for specific kinds of datasets using drug names, diseases and experiment types.

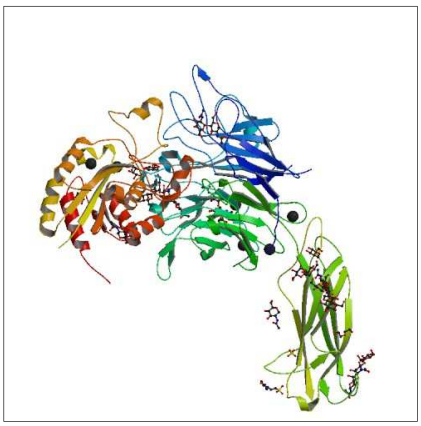
[Yunfeng Qi *et al.*,HEDD: the human epigenetic drug database. *Database (Oxford)* 2016]



Bioinformatics drug discovery

Crystal structure of integrin alpha V beta 6 head

Integrins are adhesion receptors that transmit force across the plasma membrane between extracellular ligands and the actin cytoskeleton. In activation of the transforming growth factor-β1 precursor (pro-TGF-β1), integrins bind to the prodomain, apply force, and release the TGF-β growth factor. However, we know little about how integrins bind macromolecular ligands in the extracellular matrix or transmit force to them. Herein it shows how integrin $\alpha_V\beta_6$ binds pro-TGF-β1 in an orientation biologically relevant for force-dependent release of TGF-β from latency. The conformation of the prodomain integrin-binding motif differs in the presence and absence of integrin binding; differences extend well outside the interface and illustrate how integrins can re-model extracellular matrix.



Remodelled residues outside the interface stabilize the integrin-bound conformation, adopt a conformation similar Method: X-RAY DIFFRACTION to earlier-evolving family members, and show how macromolecular components outside the binding motif contribute to integrin recognition. Regions in and outside the highly interdigitated interface stabilize a specific integrin/pro-TGF-β orientation that defines the pathway through these macromolecules which actin-cytoskeleton-generated tensile force takes when applied through the integrin β-subunit. Simulations of force-dependent activation of TGF-β demonstrate evolutionary specializations for force application through the TGF-β prodomain and through the β- and not α-subunit of the integrin.

Classification: CELL ADHESION
Deposited: 2015-12-18
Released: 2017-01-25
Resolution: 2.25 Å
R-Value Free: 0.246

[source: Force interacts with macromolecular structure in activation of TGF-β, Xianchi Dong et al. NATURE, 542, 55–59]

Upcoming events

International Conference on Advances in Biotechnology and Biotherapeutics (ICABBS-2017)

Advances in Drug Discovery

6-7 March 2017
Wellcome Genome Campus Conference Centre
Cambridge, UK

Patents

Bioinformatics based system for assessing a condition of a performance animal by analysing nucleic acid expression

US20040236516A1

Inventor: Richard Brandon

Abstract

A condition and ability of an animal to perform to its best ability may be determined by correlating gene expression with clinical and other data. The invention provides methods for assessing a performance animal's condition including the steps of collecting biological samples and clinical history, generating digital results on relative or absolute gene expression levels in the samples, transmitting the digital results via a communications network to a remote diagnostic server and associated database, comparing the results with information stored in the remote database and returning a report of the condition of the animal. A diagnostic system comprising a microarray, a microarray reader, a remote database for storing information from the reader, and a remote server receiving digital signals from the reader is also disclosed.

Kindly send us your feedback to

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