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Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
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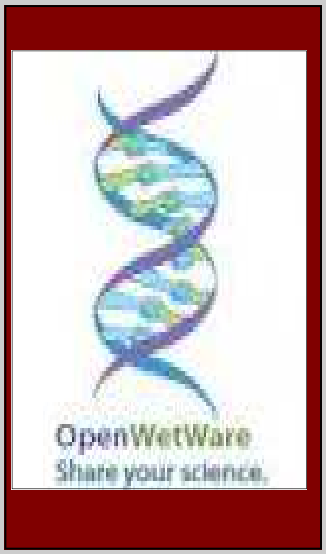
Jorhat - 785 006, Assam

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.

Researchers Use DNA to Create World's Smallest Thermometer

A team of scientists at the University of Montreal, Canada, has created a DNA-based nanothermometer that is 20,000 times smaller than a human hair. In recent years, researchers discovered

that biomolecules such as proteins or RNA are employed as nanothermometers in living organisms and report temperature variation by folding or unfolding. "Inspired by those natural nanothermometers, which are typically 20,000 times smaller than a human hair, the teamhave created various DNA structures that can fold and unfold at specifically defined temperatures," said lead author Prof. Alexis Vallée-Bélisle, from the Laboratory of Biosensors and Nanomachines and the Department of Biochemistry and Molecular Medicine at the University of Montreal.

This research was published online April 8, 2016 in the journal *Nano Letters*.

By adding optical reporters to DNA structures, they create 5 nm-wide thermometers that produce an easily detectable signal as a function of temperature," said co-author Dr. Arnaud Desrosiers.

These nanothermometers open many avenues in the emerging field of nanotechnology, and may even help researchers to better understand molecular biology.

LIGR-Seq: A New Tool to Understand the Role of Non-Coding RNAs

A team of researchers at the University of Toronto's Donnelly Centre have developed a new method that enables scientists to explore in depth what non-coding RNAs (ncRNAs) do in human cells. Professor Benjamin Blencowe the team leader at the University, including lead authors Eesha Sharma and Tim Sterne-Weiler, have developed a method, described in May 19, 2016 issue of *Molecular Cell*, that enables scientists to explore in depth what ncRNAs do in human cells . The study was published along with two other papers in Molecular Cell and Cell, respectively, from Dr. Yue Wan's group at the Genome Institute of Singapore and Dr. Howard Chang's group at Stanford University in California, who developed similar methods to study RNAs in different organisms.

The new tool, called 'LIGR-Seq', captures interactions between different RNA molecules. The method enabling the global-scale mapping of RNA-RNA duplexes cross-linked in vivo, 'LIGation of interacting RNA followed by high-throughput Sequencing' (LIGR-Seq). Applying this method in human cells reveals a remarkable landscape of new RNA-RNA interactions involving all major classes of ncRNA, and mRNA. LIGR-Seq data reveal unexpected interactions between small nucleolar (sno)RNAs and mRNAs, including interactions involving the orphan C/D box snoRNA, SNORD83B, that control steady-state levels of its target mRNAs. LIGR-Seq thus represents a powerful approach for illuminating the functions of the myriad of uncharacterized RNAs that act via base-pairing interactions.

*[**Global Mapping of Human RNA-RNA Interactions.** Sharma, E et al. Molecular Cell (May 19, 2016)]*

Mathematical model for Cancer Metastasis

Researchers from the University of Iceland, have built a model to investigate the metastasis of cancer by examining the metabolism of breast epithelial cells and look at the role of signaling. The research works published in PLOS Computational Biology, that may contribute to the development of cell specific anti-cancer interventions.

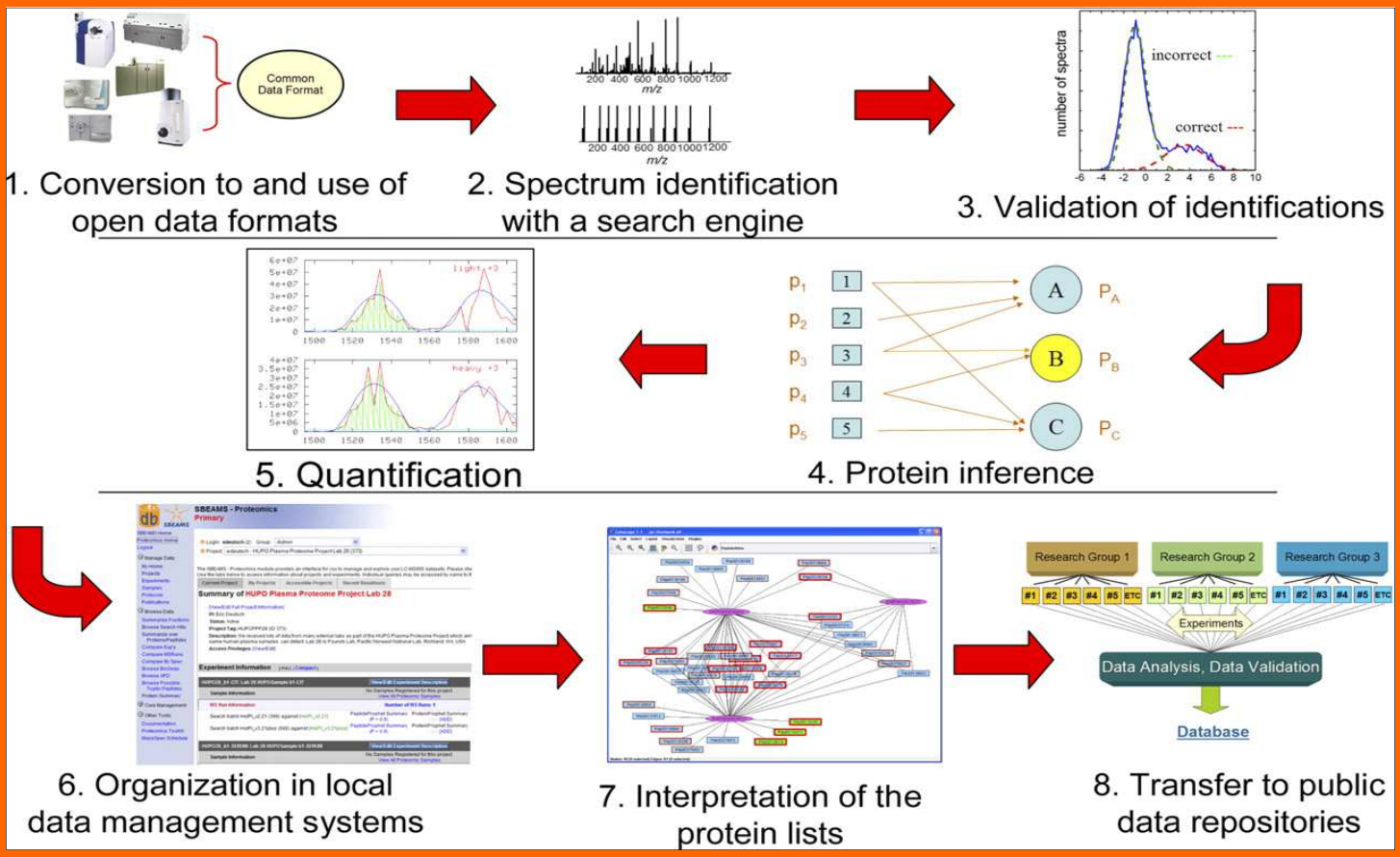
The built mathematical model examines the metabolism of breast epithelium as the majority of breast cancers originate from these cells. The model specifically looks at the process of epithelial to mesenchymal transition (EMT) which is an important event during development and cancer metastasis.

One of the key metabolic alterations that takes place during EMT is that of the epidermal growth factor receptor (EGFR) which is a pathway that regulates growth, survival, proliferation, and differentiation in mammalian cells. EFGR signalling often affects metabolic rate in tumour cells and controls their progression the dysregulation of signalling pathways during this process is therefore a hallmark of metastasis.

The scientists' model looks at the EGFR signalling cascade to investigate crosstalk between EFGR signalling and EMT in cell culture models of human breast epithelium. The model was then used to obtain a list of potential signalling and metabolic targets of EMT. These targets may aid in the understanding of the molecular mechanisms that underlie EMT and cancer metastasis. The results also show how the metabolic signposts of cancer cell growth and EMT can be predicted based on the transcriptome analysis of EGFR signalling genes alone (where current methods are inconsistent) thus supporting the idea of cell specific anti-cancer interventions.

[*EGFR Signal-Network Reconstruction Demonstrates Metabolic Crosstalk in EMT. Kumari Sonal Choudhary et al. PLOS Computational Biology (2016)*]

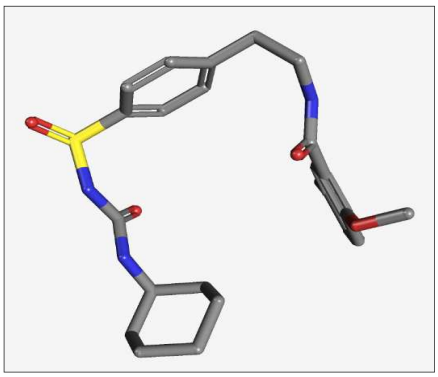
Bioinfo. Animation



Molecule of the month

Glyburide

Glyburide is a sulfonamide urea derivative with anti hyperglycemic activity that can potentially be used to decrease cerebral edema. Upon administration, glyburide binds to and blocks the sulfonylurea receptor type 1 (SUR1) subunit of the ATP-sensitive inwardly-rectifying potassium (K(ATP)) channels on the membranes of pancreatic beta cells. This prevents the inward current flow of positively charged potassium (K+) ions into the cell, and induces a calcium ion (Ca2+) influx through voltage-sensitive calcium channels, which triggers exocytosis of insulin-containing granules. In addition, glyburide also inhibits the SUR1-regulated nonselective cation (NC) Ca-ATP channel, melastatin 4 (transient receptor potential cation channel subfamily M member 4; (TRPM4)), thereby preventing capillary failure and brain swelling. SUR1-TRPM4 channels are formed by co-assembly of SUR1 with TRPM4 in neurons, astrocytes, and capillary endothelium during cerebral ischemia. Upon ischemia-induced ATP depletion, channels open which results in sodium influx, cytotoxic edema formation, capillary fragmentation and necrotic cell death. SUR1-TRPM4 is not expressed in normal, uninjured tissues.



PubChem CID:	**3488**
Chemical Names:	**Glyburide; Glibenclamide;**
Molecular Formula:	**C23H28ClN3O5S**
Molecular Weight:	**494.00352 g/mol**
InChI Key:	**ZNNLBTZKUZBEKO-UHFFFAOYSA-N**

Upcoming events

Patents

Genomic pipeline editor with tool localization

US 20150066381 A1

Inventors: Deniz Kural

ABSTRACT

The invention provides systems and methods for creating and using genomic analysis pipelines in which each analytical step within the pipeline can be independently set to run in a particular location. Steps that involve patient-identifying information or other sensitive research results can be restricted to running on a computer that is under the user's control, while steps that require a vast amount of processing power to sift through large amounts of raw data can be set to run on a powerful computer system such as a multi-processor server or cloud computer. The system provides a genomic pipeline editor with a plurality of genomic tools that can be arranging into pipelines. For one or more of the tools, the system receives a selection indicating execution by a particular computer. The system will cause genomic data to be analyzed according to the pipeline and the location selection.

Kindly send us your feedback to

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