Volume 7, Issue 6 June 2014

Bioinformatics up to Date

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

Inside…..

Protein Data Bank

As of Tuesday Jun 06, 2014 at 5 PM PDT there are 101040 Structures

Sequencing Electric Eel Genome unlocks shocking secrets

For the first time, the genome of the electric eel has been sequenced. This discovery has revealed the secret of how fishes with electric organs have evolved six times in the history of life to produce electricity outside of their bodies. The research, published in the current issue of Science, sheds light on the genetic blueprint used to evolve these complex, novel organs. It was co-led by Michigan State University, University of Wisconsin-Madison, University of Texas-Austin and the Systemix Institute.

"It's truly exciting to find that complex structures like the electric organ, which evolved completely independently in six groups of fish, seem to share the same genetic toolkit," said Jason Gallant, MSU zoologist and co-lead author of the paper. "Biologists are starting to learn, using genomics, that evolution makes similar structures from the same starting materials, even if the organisms aren't even that closely related."

"Evolution has removed the ability of muscle cells to contract and changed the distribution of proteins in the cell membrane; now all electrocytes do is push ions across a membrane to create a massive flow of positive charge," said Lindsay Traeger, U-W graduate student and co-author of the study.

The new work provides the world's first electric fish genome sequence assembly. It also identifies the genetic factors and developmental pathways the animals use to grow an organ that, in the case of the electric eel, can deliver a jolt several times more powerful than the current from a standard household electrical outlet. Other electric fishes use electricity for defense, predation, navigation and communication.

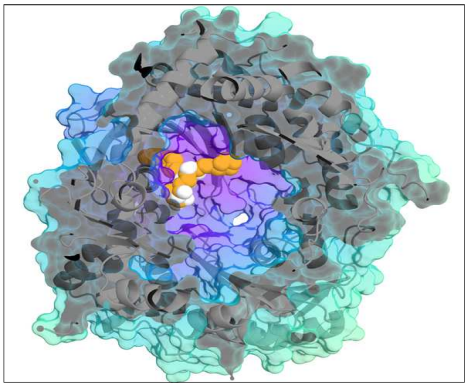
[http://www.biologynews.net/archives/bioinformatics/index.html]

Bioinfo. Carrier

1. **3-yearPhD Studentship in the Department of Bioengineering : IMPERIAL COLLEGE LONDON, United Kingdom on "Mathematical modelling of multi-scale control mechanisms for skin barrier homeostasis"; [http://www.bg.ic.ac.uk/research/r.tanaka]**
2. **Bioinformatics Scientist - NGS : Chennai, India; Genome Life Sciences Private Limited [http://www.nature.com/naturejobs/science/employer-directory/56325]**
3. **PhD Fellowship in the Field of Natural Products-based Drug Discovery and Medicinal Chemistry : Odense, Denmark [http://sdu.dk/en/]**

Discovery of Compound May Open New Road to Diabetes Treatment

The discovery of an inhibitor of the Insulin Degrading Enzyme (IDE), a protein responsible for the susceptibility of diabetes because it destroys insulin in the body, may lead to new treatment approaches for diabetes.



In collaboration with the discoverers of the inhibitor, David Liu and Alan Saghatelian, Stony Brook Medicine scientist Dr. Markus Seeliger, and colleagues nationally, demonstrated the efficacy of the compound in a research paper in the early online edition of Nature. (http://www.nature.com/nature/journal/vaop/ncurrent/full/nature13297.html)

More than 20 million people live with type II diabetes in the United States, a disease in which the body cannot make sufficient amounts of the hormone insulin. IDE removes insulin from the blood. To date, diabetes treatment strategies are based on patients either injecting insulin, taking medicine to make their body more sensitive to insulin, or taking other drugs to stimulate insulin secretion. In the paper, “Anti-diabetic action of insulin-degrading enzyme inhibitors mediated by multiple hormones,” the authors reveal results that point to a potential new approach – regulating the degradation of insulin in the blood.

[http://scicasts.com/proteomics/2043-protein-functions/7949-discovery-of-compound-may-open-new-road-to-diabetes-treatment/]

GeneMANIA

GeneMANIA finds other genes that are related to a set of input genes, using a very large set of functional association data. Association data include protein and genetic interactions, pathways, co-expression, co-localization and protein domain similarity. One can use GeneMANIA to find new members of a pathway or complex, find additional genes that may have missed in screen or find new genes with a specific function, such as protein kinases.

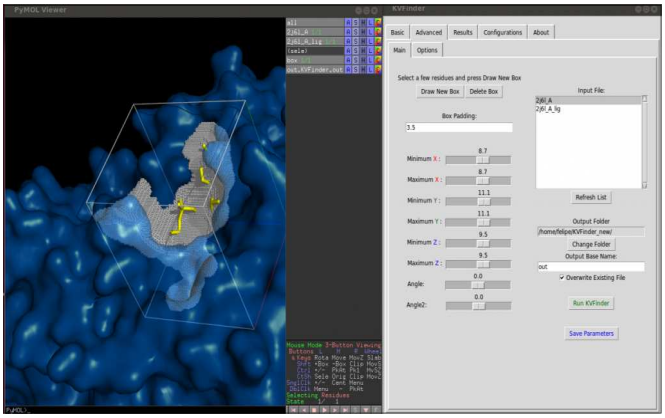
If members of your gene list make up a protein complex, GeneMANIA will return more potential members of the protein complex. If one enter a gene list, GeneMANIA will return connections between your genes, within the selected datasets.

GeneMANIA is also accessible via a Cytoscape plugin, designed for power users. GeneMANIA is actively developed at the University of Toronto, in the Donnelly Centre for Cellular and Biomolecular Research, in the labs of Gary Bader and Quaid Morris. GeneMANIA development was originally funded by Genome Canada, through the Ontario Genomics Institute (2007-OGI-TD-05) and is now funded by the Ontario Ministry of Research and Innovation.

GeneMANIA searches many large, publicly available biological datasets to find related genes. These include protein-protein, protein-DNA and genetic interactions, pathways, reactions, gene and protein expression data, protein domains and phenotypic screening profiles.

[http://www.genemania.org/]

KVFinder: Steered identification of protein cavities as a PyMOL plugin



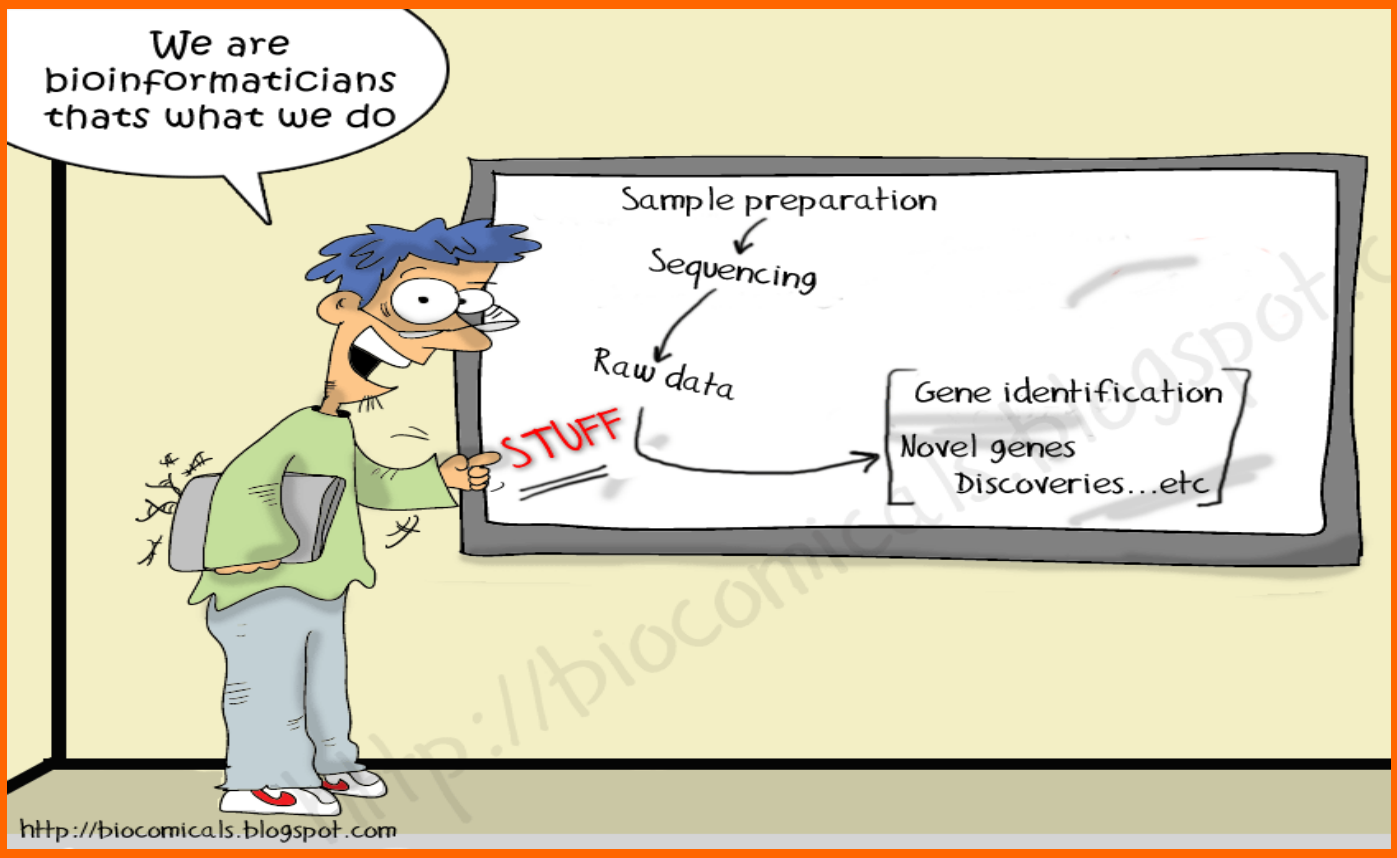
KVFinder a highly versatile and easy-to-use tool for cavity prospection and spatial characterization developed by a research team from National Laboratory of Biosciences, Brazil; University of São Paulo, Brazil and University of Oxford, UK. KVFinder is a geometry-based method that has an innovative customization of the search space. The characterization of protein binding sites is a major challenge in computational biology. Proteins interact with a wide variety of molecules and understanding of such complex interactions is essential to gain deeper knowledge of protein function. Furthermore, these protein structural features have been shown to be useful in assisting medicinal chemists during lead discovery and optimization. This feature provides the possibility of cavity segmentation, which alongside with the large set of customizable parameters, allows detailed cavity analyses. Although the main focus of KVFinder is the steered prospection of cavities, they tested it against a benchmark dataset of 198 known drug targets in order to validate our software and compare it with some of the largely accepted methods. KVFinder is also user friendly, as it is available as a PyMOL plugin, or command-line version. KVFinder presents novel usability features, granting full customizable and highly detailed cavity prospection on proteins, alongside with a friendly graphical interface. KVFinder is freely available on http://lnbio.cnpem.br/bioinformatics/main/software/ website.

Babelomics

Babelomics is an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Babelomics is a suite of web tools for the functional annotation and analysis of groups of genes in high throughput experiments. Tools include: FatiGO, FatiGOplus, Fatiscan, Gene Set Enrichment Analysis (GSEA), Marmite, and the Tissues Mining Tool (TMT). Other tools include Biocarta pathways, Transfac and a tool de novo functional annotation of sequences. This new version of Babelomics integrates primary (normalization, calls, etc.) and secondary (signatures, predictors, associations, TDTs, clustering, etc.) analysis tools within an environment that allows relating genomic data and/or interpreting them by means of different functional enrichment or gene set methods. Such interpretation is made not only using functional definitions (GO, KEGG, Biocarta, etc.) but also regulatory information (from Transfac, Jaspar, etc.) and other levels of regulation such as miRNA-mediated interference, protein-protein interactions, text-mining module definitions and the possibility of producing de novo annotations through the Blast2GO system .

Babelomics has been extensively re-engineered and now it includes the use of web services and Web 2.0 technology features, a new user interface with persistent sessions and a new extended database of gene identifiers. Babelomics is available at http://babelomics.bioinfo.cipf.es

Bioinfo. Animation



Patent News

Systems and Methods for Inferring biological Networks

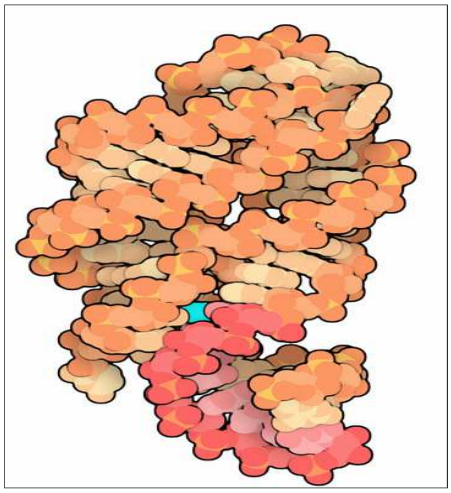
US Patent No. 7,512,497

March 31, 2009

Abstract

Described herein is a system for inferring one or a population of biochemical interaction networks, including topology and chemical reaction rates and parameters, from dynamical or statical experimental data, with or without spatial localization information, and a database of possible interactions. Accordingly, the systems and methods described herein may be employed to infer the biochemical interaction networks that exist in a cell. To this end, the systems and methods described herein generate a plurality of possible candidate networks and then apply to these networks a forward simulation process to infer a network. Inferred networks may be analyzed via data fitting and other fitting criteria, to determine the likelihood that the network is correct. In this way, new and more complete models of cellular dynamics may be created.

Riboswitches



Riboswitches are regulatory elements built directly into a messenger RNA. For instance, the riboswitch shown here (PDB entry 1u8d) senses the level of purine bases, binding tightly to guanine, hypoxanthine and xanthine. This riboswitch is part of the messenger RNA that encodes enzymes that transport and metabolize purines. So, when purine bases are prevalent, they bind to the riboswitch and slow down the production of the proteins when they're not needed.

Riboswitches use several tricks to perform their function. First, the folded riboswitch is stabilized by the ligand molecule, so the cell can sense the level of this ligand by seeing if the riboswitch is folded around it. Second, part of the riboswitch is used to control the expression of the messenger RNA. When the small molecule is bound, this "switching" sequence (shown here in pink) is locked in the folded riboswitch. But when the ligand is not available, the switching sequence is released. This switching sequence then typically forms part of an alternative riboswitch conformation that regulates transcription or protein synthesis, enhancing the production of proteins in some cases, and inhibiting it in others.

Upcoming Events

31st August to 2nd September 2014
Malang, East Java, Indonesia

Website: http://matematika.ub.ac.id/symomath/

Organized by: The Indonesian Biomathematical Society

Drug Discovery India 2014
2nd Annual International Conference and Exhibition
11th to 12th September 2014
Mumbai, India, India

Website: http://selectbiosciences.com/conferences/index.aspx?conf=DDI14

Kindly send us your feedback to

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