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Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
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Inside…..

Bioinformatics Centre, CSIR– NEIST wishing you all ……..

Happy New Year

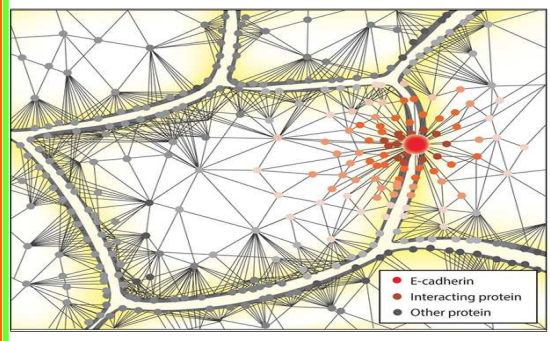
2015

Mapping the Interactome: Proteomics Reveals the E-cadherin Interaction Network Methicillin

Researchers at the Mechanobiology Institute at the National University of Singapore have comprehensively described the network of proteins involved in cell-cell adhesions, or the cadherin interactome. This work was published in Science Signaling.

Unlocking the complexity of cell adhesion

Many biological processes depend on the ability of cells to stick to one another. Defects in the ability of cells to adhere to one another have been found in many diseases, such as cancer, Alzheimer's disease and cardiovascular disease. In the case of cancer, ineffective cell adhesion allows tumour cells to detach and invade other tissues, thereby spreading cancer throughout the body.



Cell-cell adhesion is made possible through various cellular structures that are collectively known as cell-cell adhesion complexes. The most prominent cell-cell adhesion complex is the Adherens Junction. Central to adherens junctions is a protein known as E-cadherin, or epithelial cadherin. E-cadherin spans the cell membrane, providing a link between the interior, and exterior of the cell. Outside the cell, E-cadherin binds to other E-cadherins from neighbouring cells in a mechanism that can be described as a 'cellular handshake'. On the inside of the cell, E-cadherin binds to linker proteins known as catenins, which attach to a structural scaffold that lies adjacent to the adhesion site, the actin cytoskeleton. This physical link between the cytoskeletons of neighbouring cells allows for the generation and transduction of mechanical signals.

To better identify the components of this wider network in maintaining and regulating adhesion, researchers at the Mechanobiology Institute, National University of Singapore, applied a combination of experimental and computational techniques to reveal and dissect the complex network of proteins that interact with E-cadherin. To achieve this, E-cadherin was labelled with an enzyme that, when activated, releases a small cloud of a tagging molecule to flag all other proteins in the immediate vicinity. When coupled with quantitative proteomics, this provides a list of proteins interacting with E-cadherin, thus capturing many of the proteins that influence the adhesive properties of the cell.

[http://esciencenews.com/sources/newswise.scinews/2014/12/03/mapping.interactome]

Scientists identify rare cancer's genetic pathway

An international research team, including four Simon Fraser University scientists, has identified the "mutational landscape" of intrahepatic cholangiocarcinoma (ICC), a rare, highly fatal form of liver cancer that disproportionately affects people in Asian countries.

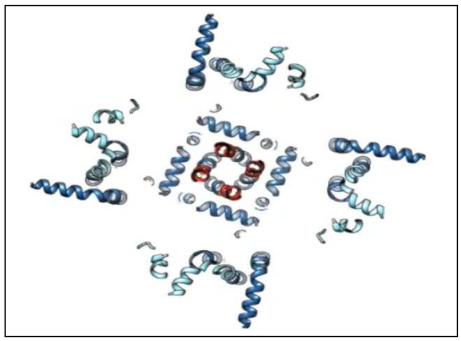
SIMON FRASER UNIVERSITY (SFU) molecular biology and biochemistry professor Jack (Nansheng) Chen and three of his lab members collaborated with Chinese researchers to identify how these mutations affect genes and signalling pathways that might drive the formation of tumours in ICC. The researchers' findings, published Dec. 15 in the journal Nature Communications, could potentially lead to earlier and more accurate diagnosis and increased survival rates for patients with the disease, also known as intra-hepatic bile duct cancer.

"Our research is by far the most comprehensive sequencing effort to identify mutations associated with ICC and will be an important resource for scientists working to improve understanding and therapy for the disease," says Chen, who specializes in genomics and bioinformatics. The study is also the first and only large-scale effort to target ICC patients in China and the largest of all such projects worldwide. It revealed that Chinese ICC patients show substantial important differences in mutation profile when compared with patients from other countries, which could have important implications for Chinese Canadians with the disease.

"Results from this study could help us understand the driver mutations in Chinese Canadians with intrahepatic bile duct cancer. And our work illustrates that this is a real opportunity and sets up a model for working on rare disease conditions."

The Ryanodine Receptor: Calcium Channel in Muscle Cells

Whenever muscles contract, so-called ryanodine receptors come into play. Calcium ions, which are ultimately responsible for the contraction of muscle cells, are released from storage organs and flow through these ion channels.

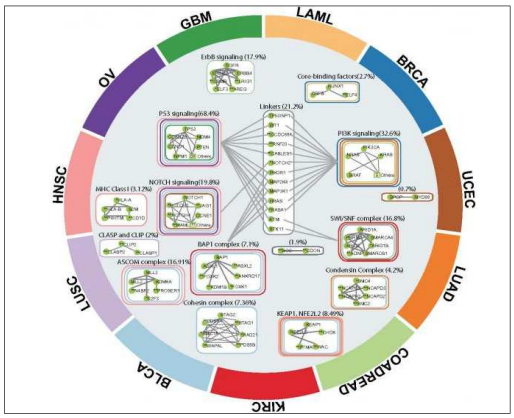


Defective ryanodine receptors can lead, for example, to cardiac arrhythmias or sudden heart failure. Researchers at the Max Planck Institute of Molecular Physiology in Dortmund have now analyzed the three-dimensional structure of the ryanodine receptor. The researchers inserted the receptors into tiny nano-membranes in order to study the proteins in a milieu similar to their natural environment in cells. With the help of electron cryo-microscopy and a new technique for detecting electrons, they were able to elucidate the structure of the receptor with high accuracy. The animation shows how the protein changes its structure when calcium ions bind to it. Armed with this knowledge, scientists may be able to develop new materials in future to repair malfunctioning ryanodine receptors.

The ryanodine receptor forms a channel that is permeable for calcium ions. The animation illustrates how the protein changes its structure upon the binding of calcium. Four helical domains in the center form an ion gate, which allows solely calcium to pass. The so-called EF-hand is the sensor that recognizes the ions. The domain is also known from other calcium-sensing proteins. It consists of charged amino acids and opens the gate region when calcium is bound.

Algorithm Identifies Networks of Genetic Changes Across Cancers

Using a computer algorithm that can sift through mounds of genetic data, researchers from Brown University have identified several networks of genes that, when hit by a mutation, could play a role in the development of multiple types of cancer.



The algorithm, called Hotnet2, was used to analyze genetic data from 12 different types of cancer assembled as part of the pan-cancer project of The Cancer Genome Atlas (TCGA). The research looked at somatic mutations — those that occur in cells during one's lifetime — and not genetic variants inherited from parents. The study identified 16 subnetworks of genes — several of which have not previously received much attention for their potential role in cancer — that are mutated with surprising frequency in the 3,281 samples in the dataset.

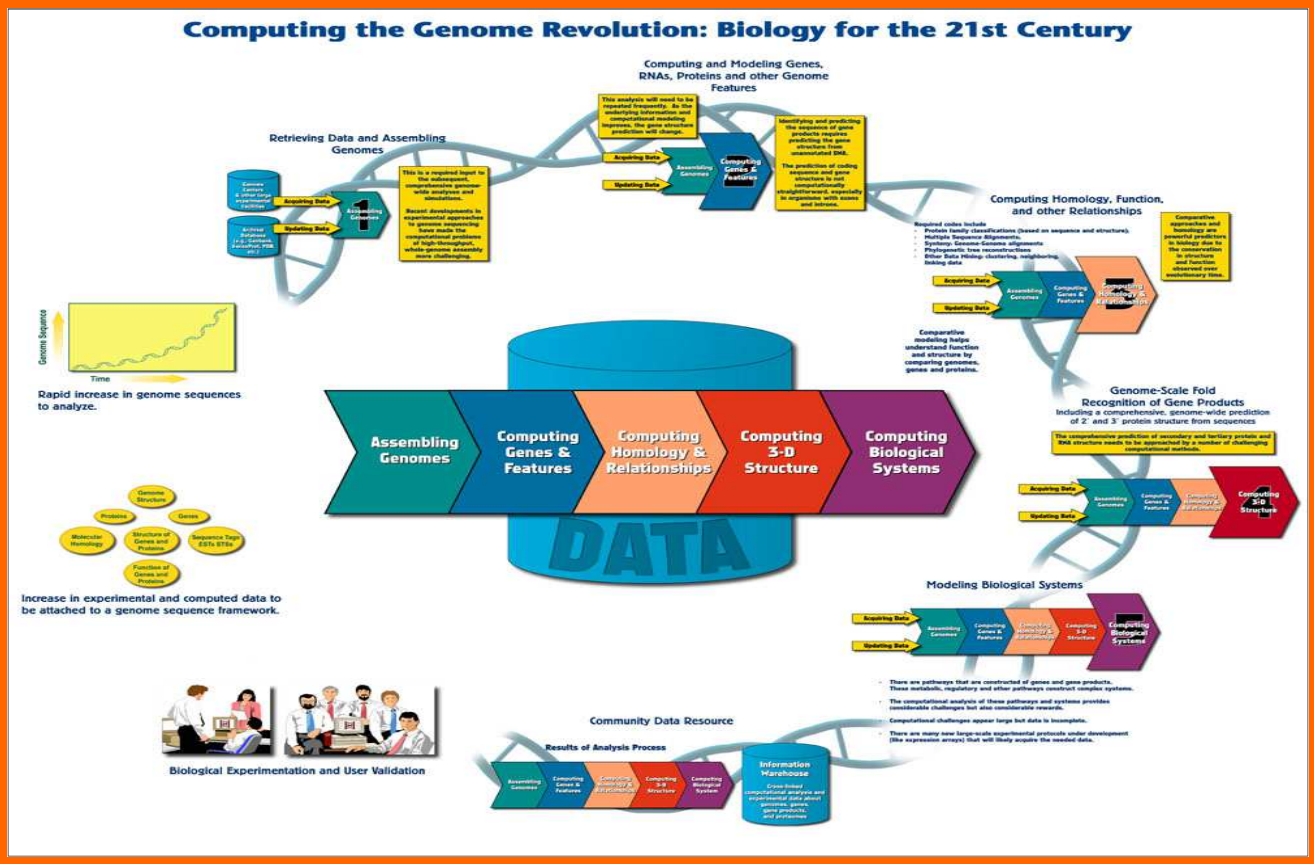
The researchers hope the new findings, published in Nature Genetics, will provide scientists with new leads in the search for somatic mutations that drive cancer. Additional data from the project, along with a downloadable version of the Hotnet2 software, is also available online.

Biological General Repository for Interaction Datasets (BioGRID)

The Biological General Repository for Interaction Datasets (BioGRID) is a curated biological database of protein-protein and genetic interactions created in 2003 by Mike Tyers, Bobby-Joe Breitkreutz, and Chris Stark at the Samuel Lunenfeld Research Institute at Mount Sinai Hospital. It strives to provide a comprehensive resource of protein–protein and genetic interactions for all major model organism species while attempting to remove redundancy to create a single mapping of interactions. Users of The BioGRID can search for their protein of interest and retrieve annotation, as well as physical and genetic interaction data as reported, by the primary literature and compiled by in house large-scale curation efforts. The BioGRID is hosted in Toronto, Ontario, Canada and is partnered with the Saccharomyces Genome Database. The BioGRID is funded by the BBSRC, NIH, and CIHR. BioGRID is a member of the International Molecular Exchange Consortium

As of 1 August 2013, BioGRID contains 703,150 interactions from 32 different species, as derived from 41,099 high-throughput and conventional focused studies. Through comprehensive curation efforts, BioGRID now includes a virtually complete set of interactions reported to date in the primary literature for budding yeast (Saccharomyces cerevisiae), thale cress (Arabidopsis thaliana), and fission yeast (Schizosaccharomyces pombe). A number of new features have been added to the BioGRID including an improved user interface to display interactions based on different attributes, a mirror site and a dedicated interaction management system to coordinate curation across different locations. The BioGRID provides interaction data with monthly updates to Saccharomyces Genome Database, Flybase, GeneDB, TAIR, and Entrez Gene.

Bioinfo. Animation



Patent News

Method and apparatus for predictive cellular bioinformatics

WO 2000070528 A9

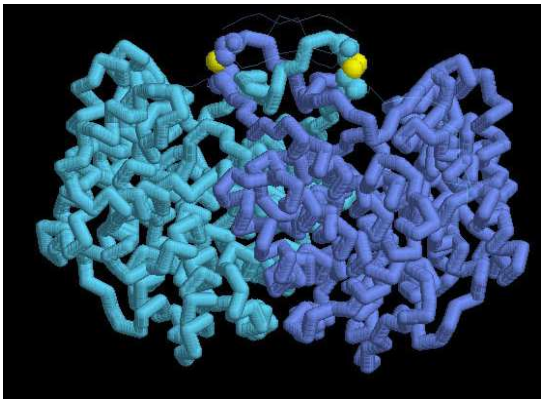
Inventors Cynthia L Adams,
Publication date 29 Nov 2001

ABSTRACT

Techniques for using information technology in therapeutics or drug discovery. In an exemplary embodiment, techniques for determining information about the properties of substances based upon information about structure of living or non-living cells exposed to substances are provided. A method according to the present invention enables researchers and/or scientists to identify promising candidates in the search for new and better medicines or treatments using, for example, a cellular informatics database. The present invention further teaches a system for acquiring knowledge from cellular information. The system has a database 1012 comprising a database management module ('DBMS'). The system also has a variety of modules, including a population module coupled to the DBMS for categorizing and storing a plurality of features (e.g., cell size, distance between cells, cell population, cell type) from an image acquisition device into the database. The system has a translation module coupled to the DBMS for defining a descriptor from a set of selected features from the plurality of features. In a specific embodiment, the descriptor is for a known or unknown compound, e.g., drug. A prediction module is coupled to the DBMS for selecting one of a plurality of descriptors from known and unknown compounds from the database based upon a selected descriptor from a selected compound. The selected compound may be one that is useful for treatment of human beings or the like.

Citrate synthase

Citrate synthase is a central enzyme in this process of sugar oxidation. It is the first step of the citric acid cycle, also known as the Krebs cycle. Glucose has previously been broken into several pieces by glycolysis, releasing two carbon atoms as carbon dioxide and leaving the rest as two molecules of acetate, carried in an activated form on special cofactor molecules. In the citric acid cycle, these remaining carbon atoms are fully oxidized to form carbon dioxide. Citrate synthase starts this process by taking the molecules of acetate and attaching them to oxaloacetate, which acts as a convenient handle as the carbon atoms are passed from enzyme to enzyme in the citric acid cycle.



Citrate synthase is found in all living cells, so it has been a useful enzyme for comparing differences from organism to organism. In particular, it has been used to study the unusual adaptations in cells that live in extreme environments. Structures have been obtained from organisms that live in very cold environments (see, for instance, PDB entry 1a59, not shown here) and others that live in hot environments. The enzyme shown here, from PDB entry 2ibp, has an interesting structural feature that allows it to resist high temperatures. Each chain has a disulfide linkage that closes the chain into a loop. Looking at the whole structure, we see that these two loops are linked, so even if the structure melts now and then, the two chains stay linked together.

Upcoming Events

5th International Conference on Biological and Medical Sciences (ICBMS'15)

Centro Capital Centre Hotel,

Al Khaleej Al Arabi St - Abu Dhabi - United Arab Emirates

http://www.isaet.org/listing.php?subcid=607&mode=detail#607

2nd International Conference on Biotechnology and Bioinformatics (ICBB-2015)

6th to 8th February 2015

Pune, Maharashtra, India

Website: http://www.icbb.in

VIth Workshop on

"**Bioinformatics for gene discovery**" **Feb 16-20, 2015**.

DBT-AAU Centre for Agricultural Biotechnology

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