



Bioinformatics up to Date

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



Inside.....

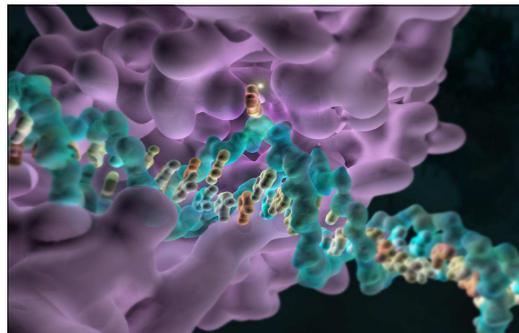
Cover story	1
Genomics	2
Proteomics	2
Bioserver	3
Computers for Biologists	3
Bioinfo.	
Animation	4
Bioinfo. Patent	4
Molecule of the month	5
Upcoming Events	5
Contact Us	5

Advisor:
Dr. D. Ramaiah

Editors:
Mr Robin Das
Dr R.L. Bezbaruah

Epigenetic signatures that differentiate triple-negative breast cancers

The new study, published in *Nature Communications*, compares the breast cancer DNA



'methylome' with that of healthy individuals. The methylome provides a new picture of the genome and shows how it is epigenetically 'decorated' with methyl groups, a process known as DNA 'methylation'.

Triple-negative breast cancers, which make up 15-20% of all breast cancers, lack any of the three receptors (oestrogen, progesterone or HER2) that would make them responsive to targeted drugs. Overall, patients have a higher risk of disease recurrence and shorter survival than those with other breast cancers.

Professor Susan Clark, Dr Clare Stirzaker and Dr Elena Zotenko from Sydney's Garvan Institute of Medical Research, performed whole genome methylation capture sequencing on archival tissue samples from triple negative breast cancer patients and matched normal samples, followed by next generation sequencing to determine cancer-specific changes in DNA methylation.

Sea slug has taken genes from algae it eats, allowing it to photosynthesize like a plant



"This is the first study to investigate the methylome of triple negative breast cancer - and its association with disease outcome," said project leader Professor Susan Clark.

How a brilliant-green sea slug manages to live for months at a time "feeding" on sunlight, like a plant, is clarified in a recent study published in *The Biological Bulletin*.

The authors present the first direct evidence that the emerald green sea slug's chromosomes have some genes that come from the algae it eats. These genes help sustain photosynthetic processes inside the slug that provide it with all the food it needs. Importantly, this is one of the only known examples of functional gene transfer from one multicellular species to another, which is the goal of gene therapy to correct genetically based diseases in humans.

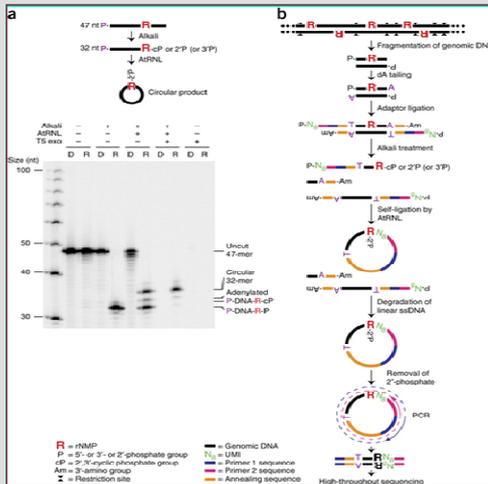
"Is a sea slug a good [biological model] for a human therapy? Probably not. But figuring out the mechanism of this naturally occurring gene transfer could be extremely instructive for future medical applications," says study co-author Sidney K. Pierce, an emeritus professor at University of South Florida and at University of Maryland, College Park.



Ribose-seq: global mapping of ribonucleotides embedded in genomic DNA

Genomic DNA contains embedded ribonucleotides (rNMPs) that are incorporated during DNA replication and repair or formed during DNA damage. Abundant ribonucleotide incorporation in DNA during replication and repair has profound consequences for genome stability, but the global distribution of ribonucleotide incorporation is unknown.

Ribose-seq, a new method developed for capturing unique products generated by alkaline cleavage of DNA at embedded ribonucleotides. High-throughput sequencing of these fragments in DNA from the yeast *Saccharomyces cerevisiae* revealed widespread ribonucleotide distribution, with a strong preference for cytosine and guanosine, and identified hotspots of ribonucleotide incorporation in nuclear and mitochondrial DNA. Ribonucleotides were primarily incorporated on the newly synthesized leading strand of nuclear DNA and were present upstream of (G+C)-rich tracts in the mitochondrial genome. Ribose-seq is a powerful tool for the systematic profiling of ribonucleotide incorporation in genomic DNA.

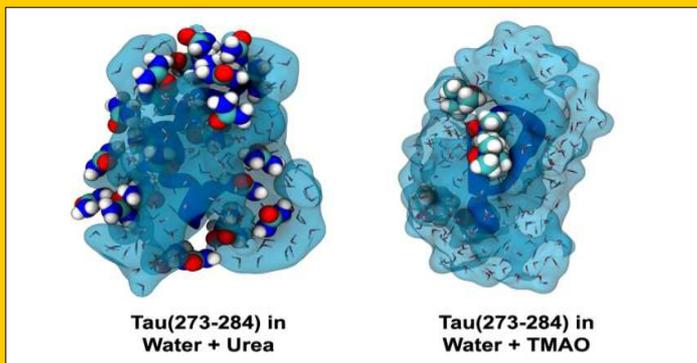


[<http://www.nature.com/nmeth/journal/v12/n3/full/nmeth.3259.html>]

Intrinsically disordered proteins (IDPs)

Like the shape-shifting robots of "Transformers" fame, a unique class of proteins in the human body also has the ability to alter their configuration.

These so-named intrinsically disordered proteins (IDPs) lack a fixed or ordered three-dimensional structure, which can be influenced by exposure to various chemicals and cellular modifications.



A new study by a team of UC Santa Barbara scientists looked at a particular IDP called tau, which plays a critical role in human physiology. Abundant in neurons located in the nervous system, tau stabilizes microtubules, the cytoskeletal elements essential for neuronal functions such as intracellular transport. Lacking a fixed 3-D structure, tau can change shape so that it forms clumps or aggregates, which are associated with Alzheimer's disease and related dementias. The researchers' findings appear online in the Proceedings of the National Academy of Sciences.

The researchers' findings appear online in the Proceedings of the National Academy of Sciences.

[<http://scicasts.com/proteomics/2035-structural-genomics/9030-the-body-s-transformers-some-proteins-can-alter-their-configuration/>]



BioRxiv (pronounced "bio-archive") is a free online archive and distribution service for unpublished preprints in the life sciences. It is operated by Cold Spring Harbor Laboratory, a not-for-profit research and educational institution. By posting preprints on bioRxiv, authors are able to make their findings immediately available to the scientific community and receive feedback on draft manuscripts before they are submitted to journals.

Articles are not peer-reviewed, edited, or typeset before being posted online. However, all articles undergo a basic screening process for offensive and/or non-scientific content. No endorsement of an article's methods, assumptions, conclusions, or scientific quality by Cold Spring Harbor Laboratory is implied by its appearance in bioRxiv. An article may be posted prior to, or concurrently with, submission to a journal but should not be posted if it has already been published.

Authors may submit a revised version of an article to bioRxiv at any time. Once posted on bioRxiv, articles are citable and therefore cannot be removed.

MetaBase

MetaBase is a user-contributed list of all the biological databases available on the internet. Currently there are 1,802 entries, each describing a different database. The databases are described in a semi-structured way by using templates and entries can carry various user comments and annotations (see a random entry). Entries can be searched, listed or browsed by category.

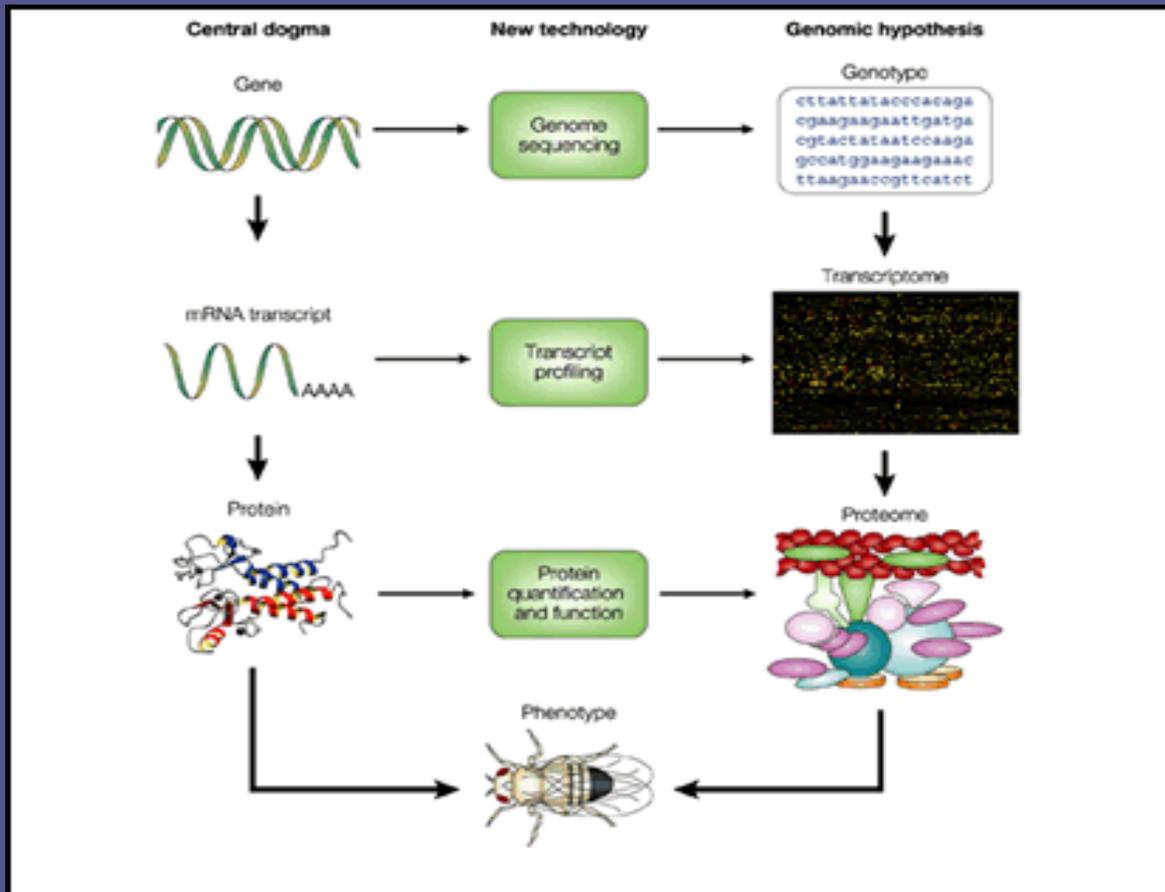
The site uses the same MediaWiki technology that powers Wikipedia, probably the best known user-contributed resource on the internet. The Mediawiki system allows users to participate on many different levels, ranging from authors and editors to curators and designers.

MetaBase aims to be a flexible, user-driven (user-created) resource for the biological database community.

The main focus of MetaBase is summarized below:

- As a basic requirement, MB contains a list of databases, URLs and descriptions of the most commonly used biological databases currently available on the internet.
- The system should be **flexible**, allowing users to contribute, update and maintain the data in different ways.

In the future we aim to generate **more communication** between the database developer and user communities.



Genetic fingerprinting and identification method

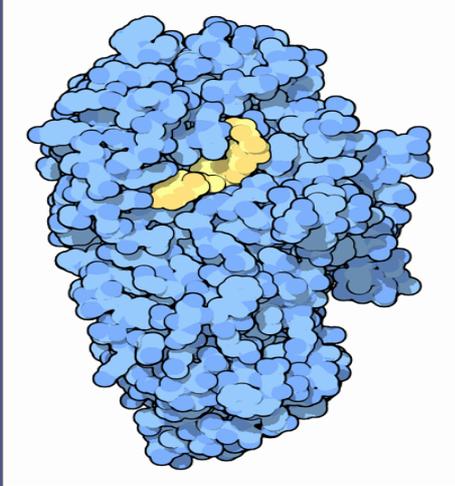
Inventors: Burns; Frank R. (Philadelphia, PA),
Peng; Xuan (Hockessin, DE)

Abstract

The present disclosure provides methods for molecular fingerprinting for the characterization and identification of organisms. More specifically, in one aspect the present invention provides a method of identifying an organism in a sample by embedding fingerprint bands from any amplification based fingerprinting method within a DNA sequence so that small differences in size are resolvable. Fingerprint output is provided in a text file format that can then be analyzed by bioinformatics tools.

Alpha-amylase

Alpha-amylase begins the process of starch digestion. It takes starch chains and breaks them into smaller pieces with two or three glucose units.



Two similar types of amylase are made in our body--one is secreted in saliva, where it starts to break down starch grains, and the other is secreted by the pancreas, where it finishes its job. Then, these little pieces are broken into individual glucose units by a collection of enzymes that are tethered to the walls of the intestine.

Since amylase needs to perform its job in the unpleasant environment of the intestine, it is a small, stable enzyme resistant to unfavorable conditions. The amylase shown here is made by the pancreas in pigs. A small chain of five sugars (colored yellow) is bound in the active site, which is found in a large cleft on the enzyme.

Alpha-amylase is used in large quantities in the production of high fructose corn syrup, a mixture of sugars created from corn that is similar in taste and sweetness to the sucrose obtained from sugar beets and sugar cane.

National Conference on Approaches towards Protection of Biological Resources

May 8th -9th 2015

Organized By

Department of Biotechnology

Faculty of Biological Engineering

Shobhit University, Meerut

International Congress on Friedreich 's Ataxia and International conference on "DNA Structure in Health & Disease "

11-13 April, 2015

Organized By

Department of Biochemistry

All India Institute of Medical Sciences

Kindly send us your feedback to

Robin Das
Project Fellow; BIF, Biotech Division.
CSIR-North East Institute of Science and Technology, Jorhat, Assam
E-mail: robindas460@gmail.com
Ph No-07399923578