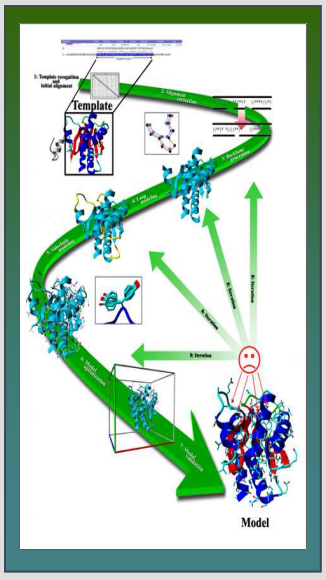
Bioinformatics up to Date

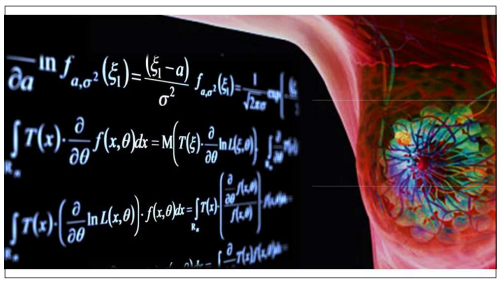
(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat - 785 006, Assam

Inside…..



New Possibilities for the Treatment of Breast Cancer Arise, with the Help of Mathematics

A means of reprogramming a flawed immune response into an efficient anti-tumoral one was brought to light by the results of a translational trial relating to breast cancer. Thanks to the innovative combination of mathematical modelization and experimentation, only 20 tests were necessary, whereas traditional experimentation would have required 596 tests to obtain the same results.



The study was jointly conducted by Doctor Marie-Agnès Doucey (Experimental oncology, Centre Ludwig de l'UNIL pour la recherche sur le cancer), Professor Ioannis Xenarios (UNIL, SIB, Vital-IT) and Professor Jean-François Delaloye (Breast care center-CHUV, UNIL). Beyond demonstrating the continued collaboration between three of Switzerland's leading scientific institutions, the trial is noteworthy for its combination of experimental oncology and modelization. Indeed, it is the first such trial to exploit modelization to identify efficient therapeutic approaches to be used on cells of breast cancer patients. The funding awarded by the Fond National Suisse pour la Recherche Scientifique and the publication of its results in the scientific review PLOS Computational Biology further give weight to both the validity and to the potential of its findings.

The shortest DNA sequences reveal insights into the world's tallest trees

Researchers from the University of California, Berkeley, are uncovering important information about patterns of coast redwood clones with a new DNA analysis method that could help forest management and preservation efforts.

The new method, described in a recent issue of *Applications of Plant Sciences*, will enable scientists to identify clonal lineages and study how clonal diversity varies throughout the geographic range of this species.

They designed the new protocol to overcome challenges associated with mutations and with the high genetic copy number in redwood DNA. Narayan and her colleagues tested the clonal identification protocol by collecting DNA samples from 770 redwoods and successfully identified 449 distinct clones.

A key aspect of the new method is the use of short repeating DNA sequences from different coast redwood tissue types. The short DNA sequences, known as microsatellites, are present in all living organisms and widely used to distinguish individuals from one another. The researchers analyzed microsatellite data from coast redwood cambium, leaf, and sprout tissue.

Novel Platform for Treatment of Breast, Pancreatic Cancer

Scientists from the Florida campus of The Scripps Research Institute（TSRI） have identified a novel synthetic compound that sharply inhibits the activity of a protein that plays an important role in in the progression of breast and pancreatic cancers.

In the new study, published in the February 2015 print edition of the journal Molecular Pharmacology, the scientists showed that the compound, known as SR1848, reduces the activity and expression of the cancer-related protein called "liver receptor homolog-1" or LRH-1.

"Our study shows that SR1848 removes LRH1 from DNA, shutting down expression of LRH-1 target genes, and halts cell proliferation," said Patrick Griffin, chair of the TSRI Department of Molecular Therapeutics and director of the Translational Research Institute at Scripps Florida. "It's a compound that appears to be a promising chemical scaffold for fighting tumours that are non-responsive to standard therapies."

LRH1 plays a crucial role in breast cancer through its regulation of genes involved in hormone synthesis and cholesterol metabolism—also key risk factors in cardiovascular disease. LRH-1 has also been implicated as a tumour promoter in intestinal and pancreatic cancer. Overexpression of LRH-1 has been shown to promote invasiveness and m tastasis, the usually lethal spread of the disease.

New Sequencing Technique Reveals Genetic Clues to Rare Breast Tumours

A new study from researchers at the University of Michigan Comprehensive Cancer Center characterizes the genetic underpinnings of a rare type of breast tumour called phyllodes tumours, offering the first comprehensive analysis of the molecular alterations at work in these tumours.

The analysis uses next-generation sequencing techniques that allow researchers to identify alterations in more than 100 genes from archived tissue samples.

"We know little about the biology of phyllodes tumours. In part, they have not been studied much because it's difficult to accumulate a large number of samples. Using these new sequencing techniques, we were able to study archived tissue samples, which allowed us to identify enough samples to perform a meaningful analysis," says study author Dr. Scott A. Tomlins, assistant professor of pathology and urology at the University of Michigan Medical School.

Researchers looked at 15 samples of phyllodes tumours . They found two genes, EGFR and IGF1R, that were amplified in multiple malignant phyllodes tumours. Therapies have already been developed against EGFR and IGF1R proteins and tested in other cancers. Results from this study support evaluating these therapies in phyllodes tumours as well.

Building a genomic GPS

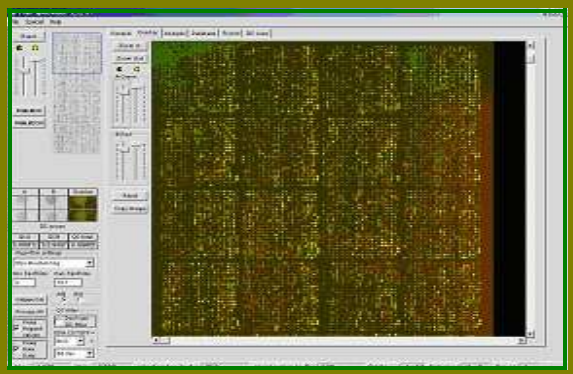
A new "app" for finding and mapping chromosomal loci using multicolored versions of CRISPR/Cas9, one of the hottest tools in biomedical research today, has been developed by scientists at the University of Massachusetts Medical School. This labeling system, details of which were published in *PNAS* and first presented at the American Society for Cell Biology/International Federation for Cell Biology annual meeting in Philadelphia in December, could be a key to understanding the spatial and temporal regulation of gene expression by allowing researchers to measure the precise linear distance between two known points on different chromosomes or two locations on the same chromosome in live human cells.

For a gene to be transcribed and expressed, it must be accessible on the chromosome. Knowing the location and the intra-nuclear conformation of chromosomes is critical to understanding how genes actually work because the human cell nucleus is a very crowded place, according to study authors Thoru Pederson, PhD, professor of biochemistry and molecular pharmacology, and research specialist Hanhui Ma, PhD, at UMass Medical School.

By deploying pairs of fluorescent tags from their three-color system, Pederson and colleagues showed that it's possible to plot where a chromosome is inside the cell nucleus and where it is in relation to other chromosomes. Their CRISPR app can also measure the distance between two points on the same chromosome, giving a read-out of chromosome compaction, which is a key factor in gene expression.

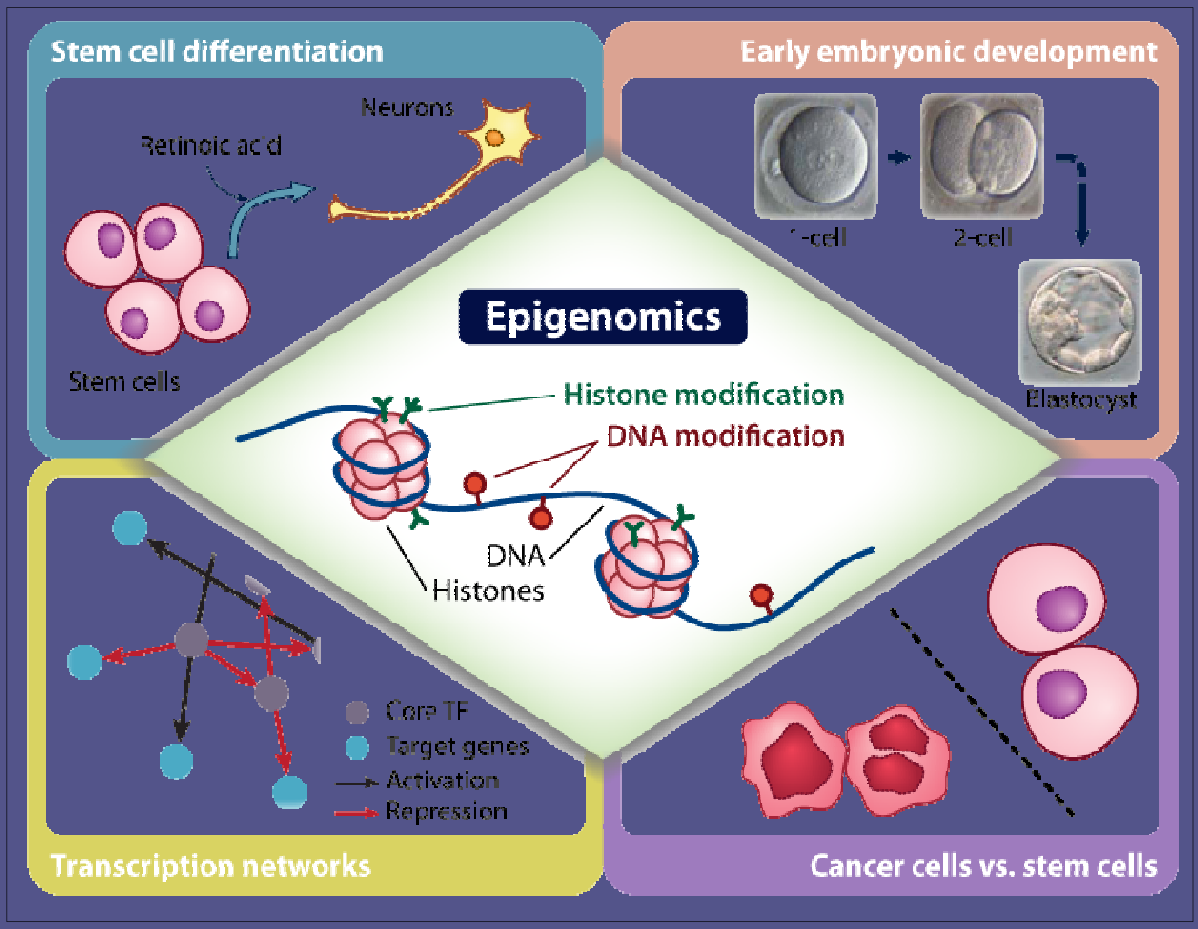
Spotfinder

Image analysis is a crucial step in the microarray process. TIGR Spotfinder was designed for the rapid, reproducible and computer-aided analysis of microarray images and the quantification of gene expression. TIGR Spotfinder reads paired



16-bit or 8-bit TIFF image files generated by most microarray scanners. Semi-automatic grid construction defines the areas of the slide where spots are expected. Automatic and manual grid adjustments help to ensure that each rectangular grid cell is centered on a spot. Two available segmentation methods (histogram and Otsu) define the boundaries between each spot and the surrounding local background. Spot intensities are calculated as an integral of non-saturated pixels, although other options including spot median and mean values are available. Local background subtraction for each reported value is applied by default but can be disabled. The calculated intensities, medians, and means along with each spot position on the array, spot area, background values, and quality control flags are written to a MEV file or the database. Reusable grid geometry files and automatic grid adjustment allow user to analyze large quantities of images in a consistent and efficient manner. To complement the automated methods, particularly in noisy areas of the slide, the user may manually identify or discard spots. Quality control views allow the user to assess systematic biases in the data. TIGR Spotfinder was written in C++.

Bioinfo. Animation



Bioinfo. Patent

Bs and rrbs sequencing-based bioinformaticsanalysis method and device

WO 2013097061 A1

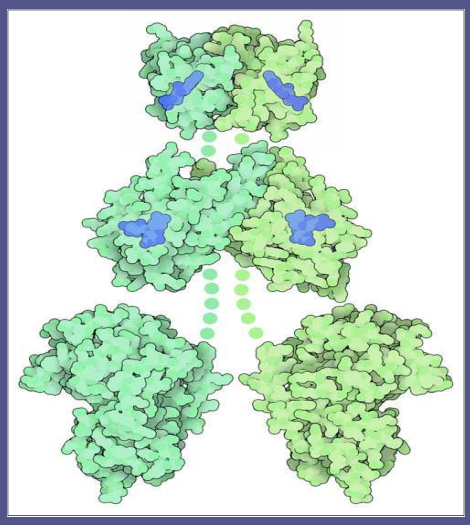
Inventors: Honglong WU et al.

ABSTRACT

Provided in the present invention are a method and a device for analyzing methylation in a genome by bisulfite sequencing or reduced representation bisulfite sequencing. Also provided in the present invention is a bioinformaticsanalysis method based on bisulfite sequencing or reduced representation bisulfite sequencing. The method comprises: detecting DNA methylation, then performing the bioinformatics analysis, wherein the analysis is an analysis for one or more items selected from the following : data output, sequencing fragments alignment, the coverage situation of methylation sites, the methylation level of the methylation sites, the distribution trend of the whole genome methylation data, the whole genome DNA methylation map, the differentially methylated regions, the statistic for the length of insert fragments, and the coverage of CpG sites.

Phototropin

The light-sensing protein shown here is phototropin, found in many types of plants. It is important for responses that maximize the efficiency of photosynthesis, such as relocation of chloroplasts to optimal positions and expansion of leaves. Phototropin is composed of several domains. Two of these domains, termed "LOV" domains (short for "light, oxygen, or voltage"), hold flavin chromophores (shown in blue) that absorb blue light. These domains are connected to a serine-threonine kinase, which propagates the signal when the LOV domains are activated.



When the flavin chromophore absorbs light, the surrounding protein passes the signal along, ultimately changing how the plant will respond. For phototropin, the signal is passed to the kinase domain, which modifies other signaling proteins in the cell. Scientists have solved structures of the phototropin LOV domains, as well as other blue-light sensing proteins, in both the dark and after they absorb light. In phototropin, the photo-activated flavin reacts with a nearby cysteine amino acid, forming a covalent bond. This distorts the flavin ring, and also distorts the surrounding protein.

International Conference on Civil, Mechanical, Biological and Medical Engineering (ICMBME - 2015)

VENUE: Chennai , Tamil Nadu , India
WEBSITE: http://www.iraj.in/Conference/2015/Chennai/ICMBME7/

International Conference on Advances in Biomedical Engineering, Cancer Biology, Bioinformatics and Applied Biotechnology (ABECBAB-2015)

23rd to 24th May 2015
New Delhi, Delhi, India

Website: http://krishisanskriti.org/abecbab.html

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