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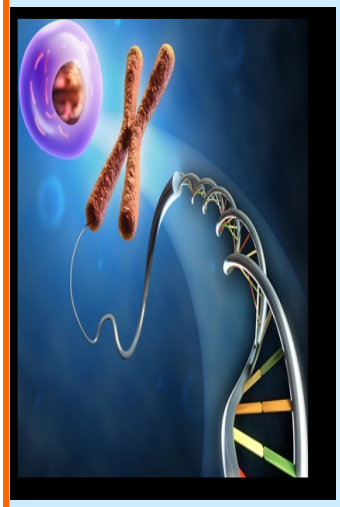
Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat - 785 006, Assam
(http://www.rrljorhat.res.in/biotechnology.html)

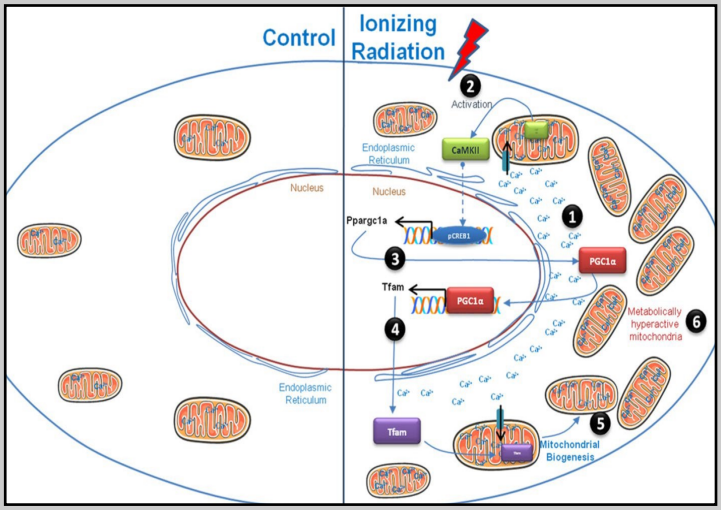
Inside…..



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.

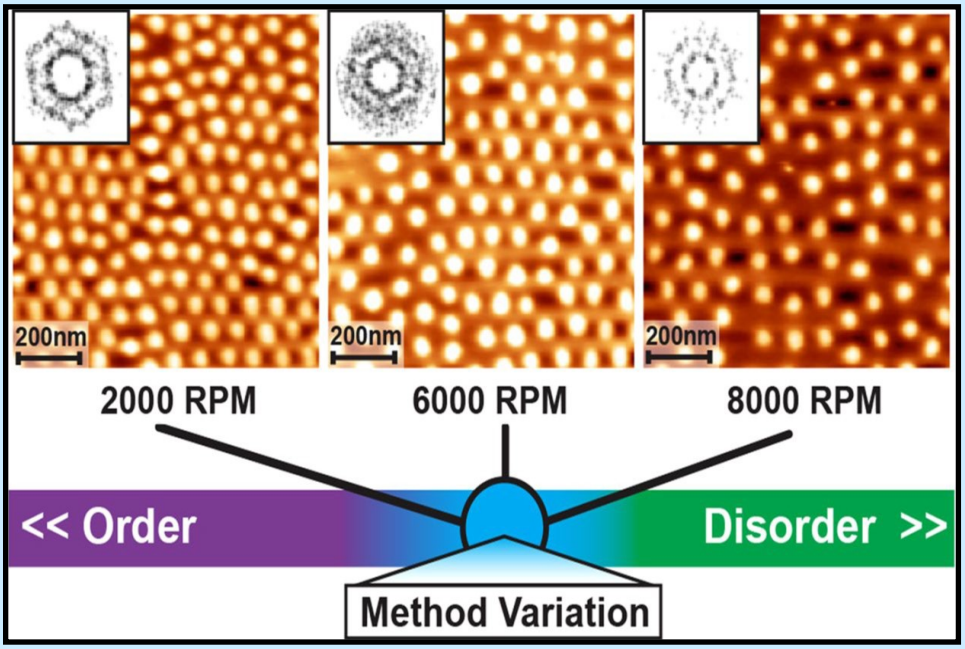
Mitochondrial biogenesis and metabolic hyperactivation limits the application of MTT assay in the estimation of radiation induced growth inhibition.



Metabolic viability based high throughput assays like MTT and MTS are widely used in assessing the cell viability. However, alteration in both mitochondrial content and metabolism can influence the metabolic viability of cells and radiation is a potential mitochondrial biogenesis inducer. Therefore, the researchers tested if MTT assay is a true measure of radiation induced cell death in widely used cell lines. Radiation induced cellular growth inhibition was performed by enumerating cell numbers and metabolic viability using MTT assay at 24 and 48 hours (hrs) after exposure. The extent of radiation induced reduction in cell number was found to be larger than the decrease in MTT reduction in all the cell lines tested. They demonstrated that radiation induces PGC-1α and TFAM to stimulate mitochondrial biogenesis leading to increased levels of SDH-A and enhanced metabolic viability. Radiation induced disturbance in calcium (Ca2+) homeostasis also plays a crucial role by making the mitochondria hyperactive. These findings suggest that radiation induces mitochondrial biogenesis and hyperactivation leading to increased metabolic viability and MTT reduction. survival.

Source:Keiko Shinoda *et al.* *J* Scientific Reports

disLocate: tools to rapidly quantify local intermolecular structure to assess two-dimensional order in self-assembled systems.



Order classification is particularly important in photonics, optoelectronics, nanotechnology, biology, and biomedicine, as self-assembled and living systems tend to be ordered well but not perfectly. Engineering sets of experimental protocols that can accurately reproduce specific desired patterns can be a challenge when (dis)ordered outcomes look visually similar. Robust comparisons between similar samples, especially with limited data sets, need a finely tuned ensemble of accurate analysis tools.

Numerical Mathematical package disLocate, a suite of tools to rapidly quantify the spatial structure of a two-dimensional dispersion of objects. The full range of tools available in dislocate give different insights into the quality and type of order present in a given dispersion, accessing the translational, orientational and entropic order. The utility of this package allows for researchers to extract the variation and confidence range within finite sets of data using different structure metrics to quantify local variation in disorder. Containing all metrics within one package allows for researchers to easily and rapidly extract many different parameters simultaneously, allowing robust conclusions to be drawn on the order of a given system. Quantifying the experimental trends which produce desired morphologies enables engineering of novel methods to direct self-assembly.

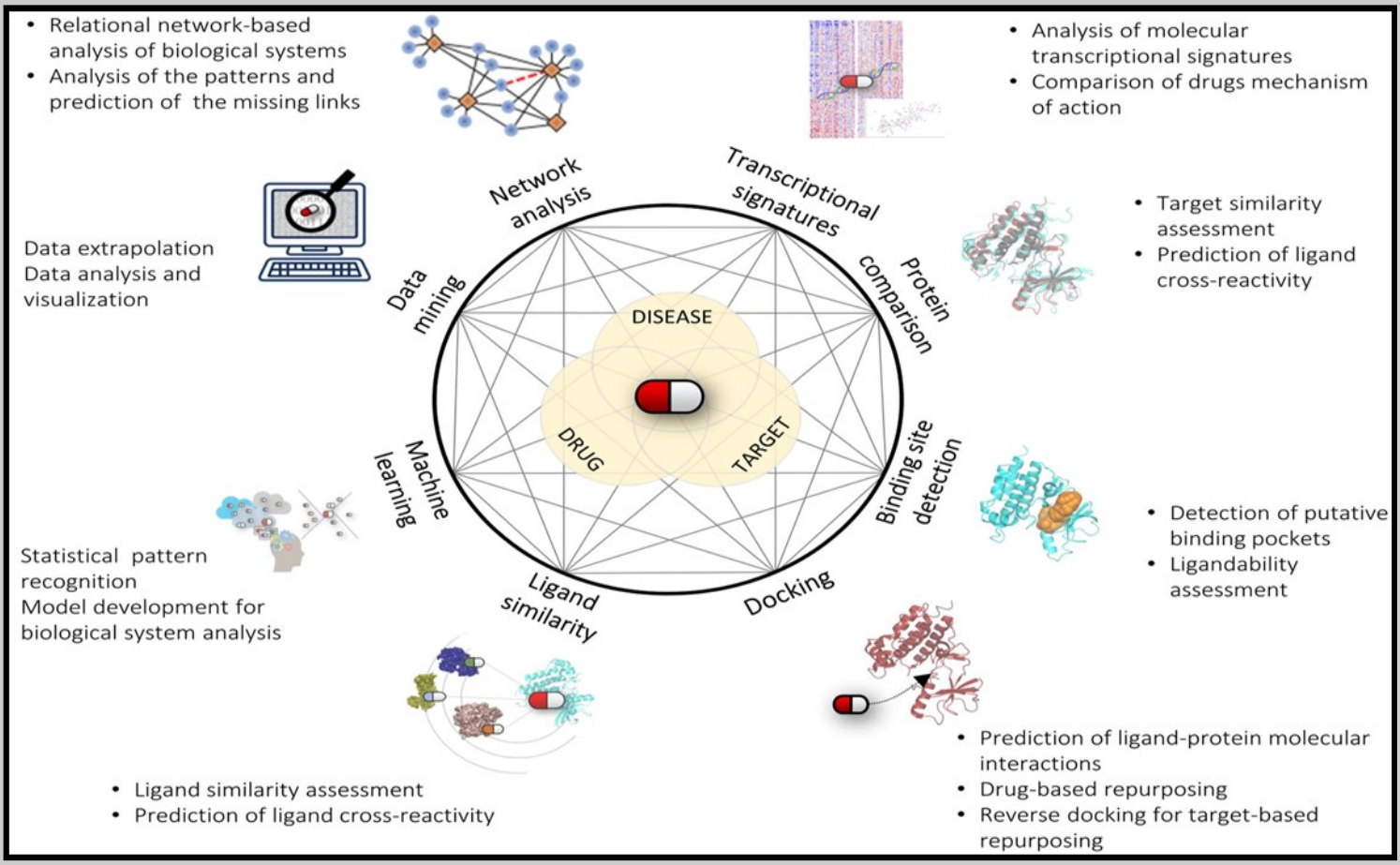
Source: **Matt Bumstead *et al.* J Sci Reports(2018)**

ADEPTUS: a discovery tool for disease prediction, enrichment and network analysis based on profiles from many diseases.

ADEPTUS is a web-tool that enables various functional genomics analyses based on a high-quality curated database spanning >38, 000 gene expression profiles and >100 diseases. It offers four types of analysis: (i) For a gene list provided by the user it computes disease ontology (DO), pathway, and gene ontology (GO) enrichment and displays the genes as a network.
(ii) For a given disease, it enables exploration of drug repurposing by creating a gene network summarizing the genomic events in it.
(iii) For a gene of interest, it generates a report summarizing its behavior across several studies.
(iv) It can predict the tissue of origin and the disease of a sample based on its gene expression or its somatic mutation profile. Such analyses open novel ways to understand new datasets and to predict primary site of cancer.
This database contains more than 38000 gene expression profiles and more than 100 diseases.

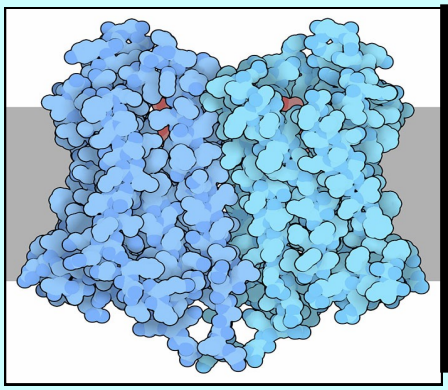
Source: David Amar *et al* .J Oxford Bioinformatics(2018)

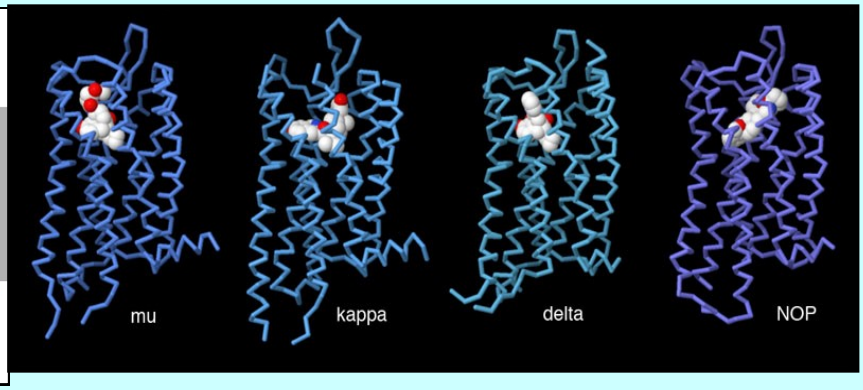
Bioinfo. Animation (Source: Eric March-Vila *et al*)



Opioid Receptors

Small peptide neurotransmitters, called enkephalins and endorphins, are the natural inhibitors of pain signals. They bind to opioid receptors in pain-signalling cells of the nervous system. Opioids mimic this action, also causing opioid receptors to slow down the pain response. Opioid receptors are typical G-protein coupled receptors (GPCR) that bind to neurotransmitters or opioids on the outside of the cell, and launch a response through G-proteins inside the cell. The structure shown here (PDB entry 4dkl) is one type of opioid receptor bound to an analog of morphine.





Several types of opioid receptors are made in our nervous system to manage the many shades of pain signaling. There are three general classes of opioid receptors, termed mu, kappa, delta, and a related nociceptin opioid (NOP) receptor. Atomic structures have been determined for examples from each of these classes, in PDB entries 4dkl, 4djh, 4ej4, and 4ea3).

Source : http://pdb101.rcsb.org/motm/217

Plant Genomics and Gene Editing Congress: Europe

WHEN

14th-15th May 2018

Biotech Bioinfo Workshop

5-Days Hands-on Workshop on Molecular Biotechnology and Bioinformatics, Pune, India

Venue: ICSCCB, R.H. 2, Ujwal Regalia, Near Prabhavee Tech Park Building, Baner Road, Pune – 411045, India

Patents

Apparatus and methods for training path navigation by robots
US 20170326726 A1
Grotmol *et al*.

An apparatus and methods for training and/or operating a robotic device to follow a trajectory. A robotic vehicle may utilize a camera and stores the sequence of images of a visual scene seen when following a trajectory during training in an ordered buffer. Motor commands associated with a given image may be stored. During autonomous operation, an acquired image may be compared with one or more images from the training buffer in order to determine the most likely match. An evaluation may be performed in order to determine if the image may correspond to a shifted (e.g., left/right) version of a stored image as previously observed. If the new image is shifted left, right turn command may be issued. If the new image is shifted right then left turn command may be issued.

Kindly send us your feedback to

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