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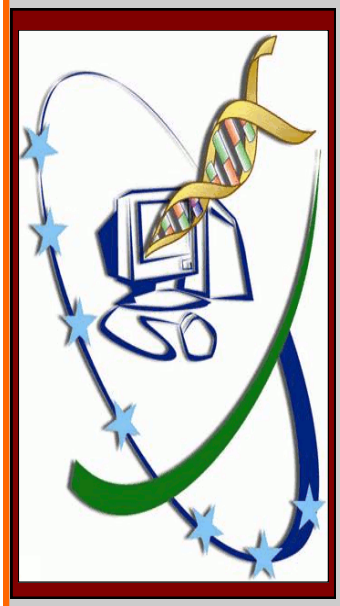
Bioinformatics up to Date

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

Inside…..

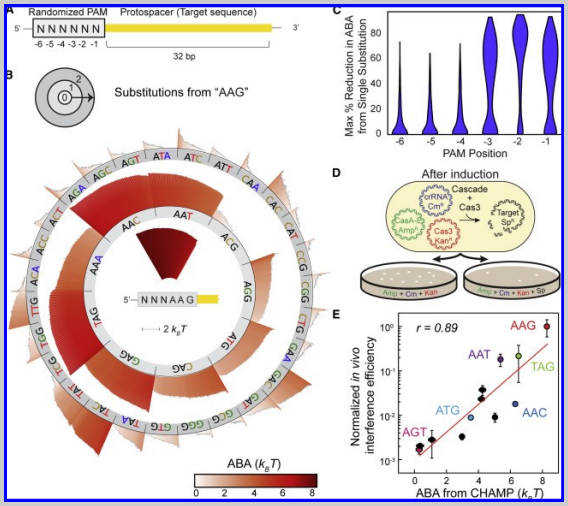


About us

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.

Massively Parallel Biophysical Analysis of CRISPR-Cas Complexes on Next Generation Sequencing Chips

CRISPR-Cas nucleoproteins target foreign DNA via base pairing with a crRNA. However, a quantitative description of protein binding and nuclease activation at off-target DNA sequences remains elusive. A chip-hybridized association-mapping platform (CHAMP) that repurposes next-generation sequencing chips to simultaneously measure the interactions between proteins and ~10^7 unique DNA sequences. Analysis of mutated target sequences and human genomic DNA reveal that Cascade recognizes an extended protospacer adjacent motif (PAM). Cascade recognizes DNA with a surprising 3-nt periodicity. The identity of the PAM and the PAM-proximal nucleotides control Cas3 recruitment by releasing the Cse1 subunit. These findings are used to develop a model for the biophysical constraints governing off-target DNA binding. CHAMP provides a framework for high-throughput, quantitative analysis of protein-DNA interactions on synthetic and genomic DNA.



[Source: Massively Parallel Biophysical Analysis of CRISPR Cas Complexes on Next Generation Sequencing Chips Cheulhee jung et al. Cell, June 2017]

ProtDec-LTR2.0: An improved method for protein remote homology detection by combining pseudo protein and supervised Learning to Rank

As one of the most important tasks in protein sequence analysis, protein remote homology detection is critical for both basic research and practical applications. ProtDec-LTR2.0 is an effective web server for protein remote homology detection.Experimental results showed that the detection performance is obviously improved

The web server is free and open to all users with no login requirement at http://bioinformatics.hitsz.edu.cn/ProtDec-LTR2.0

The web server provides a user-friendly interface to explore the sequence and structure information of candidate proteins and find their conserved domains by launching a multiple sequence alignment tool. The web server is also developed, by which users can detect the homologous proteins onlybased on the protein sequences, and the predicted results will be returned in a user-friendly manner. The improvement and friendly web service have led ProtDec-LTR 2.0 to be a more efficient and powerful tool. It is the first web server incorporating the profile-based pseudo proteins into the framework of LTR algorithm. Various results visualization and functions interpretation are provided, such as homologous protein 3D structure visualization and multiple sequence alignment interpretation. According to the experimental results, ProtDec-LTR 2.0 is one of the most accurate web servers for protein remote homology.

[***Source:*** *https://doi.org/10.1093/bioinformatics/btx429 Junjie Chen et al. Bioinformatics oxford (june 2017)*

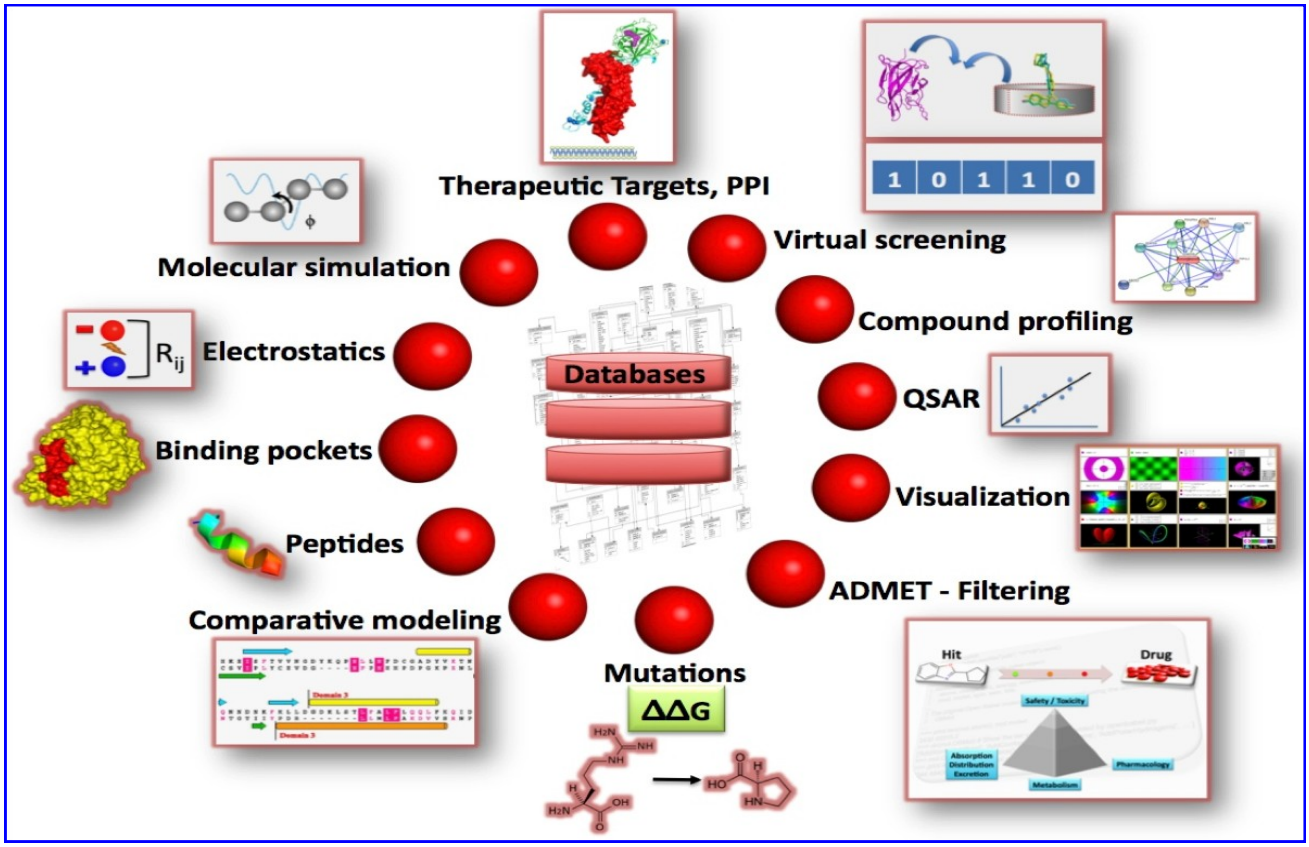
HEROD: a human ethnic and regional specific omics database

Genetic and gene expression variations within and between populations and across geographical regions have substantial effects on the biological phenotypes, diseases, and therapeutic response. The development of precision medicines can be facilitated by the OMICS studies of the patients of specific ethnicity and geographic region. However, there is an inadequate facility for broadly and conveniently accessing the ethnic and regional specific OMICS data.

HEROD is a new free database and it is a human ethnic and regional specific OMICS database. The database and web interface are implemented in MySQL, PHP and HTML with all major browsers supported. Its first version contains the gene expression data of 53 070 patients of 169 diseases in 7 ethnic populations from 193 cities/regions in 49 nations curated from the Gene Expression Omnibus (GEO), the ArrayExpress Archive of Functional Genomics Data (ArrayExpress), the Cancer Genome Atlas (TCGA), and the International Cancer Genome Consortium (ICGC). Geographic region information of curated patients was mainly manually extracted from referenced publications of each original study. These data can be accessed and downloaded via keyword search, World map search, and menu-bar search of disease name, the international classification of disease code, geographical region, location of sample collection, ethnic population, gender, age, sample source organ, patient type (patient or healthy), sample type (disease or normal tissue), and assay type on the web interface.

[***Source:*** *https://doi.org/10.1093/bioinformatics/btx340 Xian Zeng et al. Bioinformatics oxford (26 may 2017)*

Bioinfo. Animation

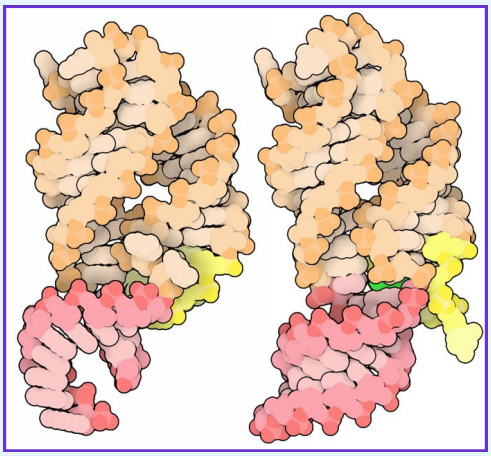


Bioinformatics drug discovery

Molecule of the month

Adenine Riboswitch in Action

Riboswitches are structurally dynamic RNA molecules, undergoing changes in shape as they perform their regulatory functions. Riboswitches typically have two domains: a ligand-binding "aptamer" domain that changes conformation when it binds to a specific ligand, which then sends a signal to an "expression platform" domain that regulates use of the RNA. Thus far, structures have been obtained for the aptamer domains, but the motions caused by ligand binding have been tricky to observe by crystallography: crystals typically freeze molecules in one shape, so crystallographic structures of unbound aptamers typically look very similar to the ligand-bound form. Researchers are using XFEL radiation sources in a clever way to help surmount this limitation and observe directly what happens when a ligand binds. In XFEL experiments, a stream of very tiny crystals is flowed past the beam, and each time a crystal is caught in one of the pulses, it creates an instantaneous diffraction pattern that captures the molecules in the crystal at a defined moment of time. By collecting similar diffraction patterns from many crystals caught in random orientations by the X-ray beam, researchers build up a full diffraction data set.



[*Source:http://http://pdb101.rcsb.org/motm/210]*

Patents

Bioinformatics, systems, apparatus, and methods executed on an integrated circuit processing platform

US 20170161213 A1

Inventors : Pieter Van Rooyen

ABSTRACT

A system, method and apparatus for executing a sequence analysis pipeline on genetic sequence data includes an integrated circuit formed of a set of hardwired digital logic circuits that are interconnected by physical electrical interconnects. One of the physical electrical interconnects forms an input to the integrated circuit connected with an electronic data source for receiving reads of genomic data. The hardwired digital logic circuits are arranged as a set of processing engines, each processing engine being formed of a subset of the hardwired digital logic circuits to perform one or more steps in the sequence analysis pipeline on the reads of genomic data. Each subset of the hardwired digital logic circuits is formed in a wired configuration to perform the one or more steps in the sequence analysis pipeline.

Kindly send us your feedback to

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