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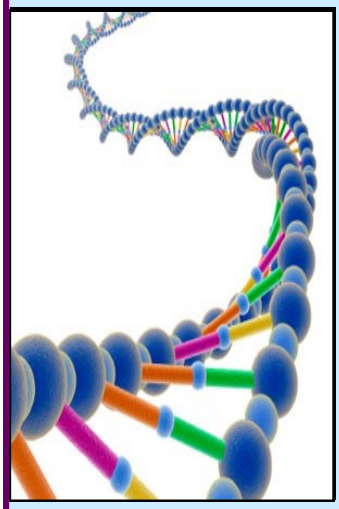
Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat -785006, 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.

Computational repositioning and preclinical validation of mifepristone for human vestibular schwannoma

The computational repositioning of existing drugs represents an appealing avenue for identifying efective compounds to treat diseases with no FDA-approved pharmacotherapies. In this study, researchers introduced the largest meta-analysis to date of diferential gene expression in human vestibular schwannoma (VS), a debilitating intracranial tumor, and use these data to inform the first application of algorithm-based drug repositioning for this tumor class. They applied an open-source computational drug repositioning platform to gene expression data from 80 patient tumors and identified eight auspicious FDA-approved drugs with potential for repurposing in VS. These eight, mifepristone, a progesterone and glucocorticoid receptor antagonist, consistently and adversely afects the morphology, metabolic activity, and proliferation of primary human VS cells and HEI-193 human schwannoma cells. Here, they reported that Mifepristone treatment reduces VS cell viability more signifcantly than cells derived from patient meningiomas, while healthy human Schwann cells remain unaffected.

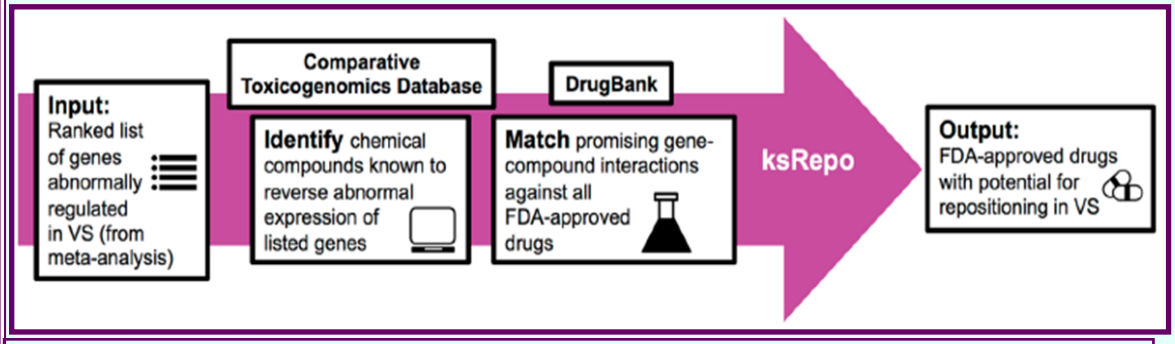
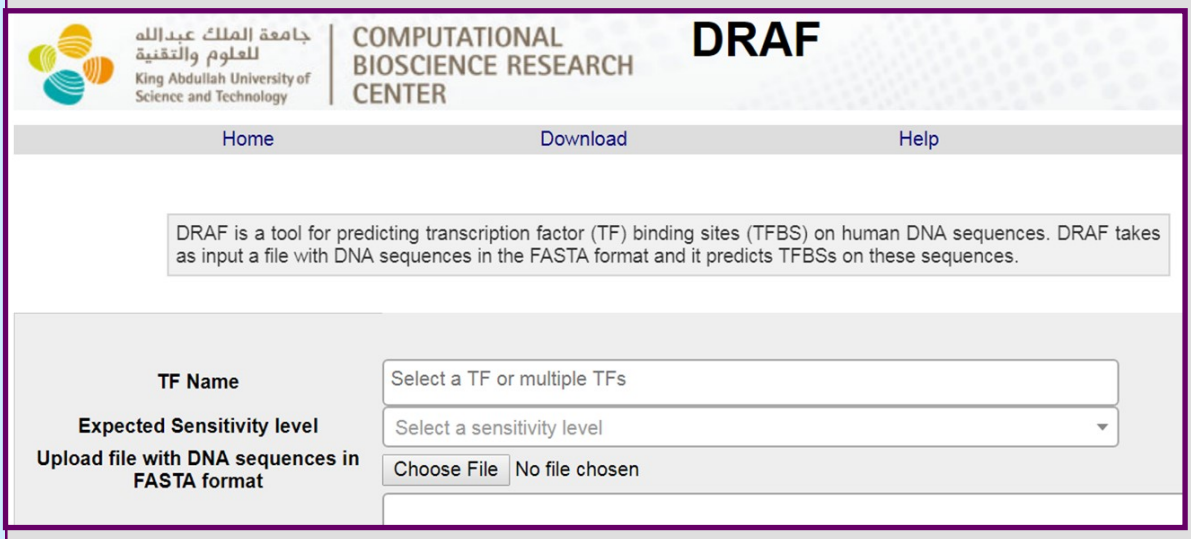


Fig: Computational repositioning of FDA-approved drugs using ksRepo.ksRepo workflow schematic.

Source: **Jessica E. Sagers *et al. 2018 J Scientific Reports***

A novel method for improved accuracy of transcription factor binding site prediction



Identifying transcription factor (TF) binding sites (TFBSs) is important in the computational inference of gene regulation. Widely used computational methods of TFBS prediction based on position weight matrices (PWMs) usually have high false positive rates. Moreover, computational studies of transcription regulation in eukaryotes frequently require numerous PWM models of TFBSs due to a large number of TFs involved. To overcome these problems in this report researchers developed DRAF, a novel method for TFBS prediction that requires only 14 prediction models for 232 human TFs, while at the same time significantly improves prediction accuracy. DRAF models use more features than PWM models, as they combine information from TFBS sequences and physicochemical properties of TF DNA-binding domains into machine learning models. Evaluation of DRAF on 98 human ChIP-seq datasets shows on average 1.54-, 1.96- and 5.19-fold reduction of false positives at the same sensitivities compared to models from HOCOMOCO, TRANSFAC and DeepBind, respectively. This observation suggests that one can efficiently replace the PWM models for TFBS prediction by a small number of DRAF models that significantly improve prediction accuracy. The DRAF method is implemented in a web tool and in a stand-alone software freely available at http://cbrc.kaust.edu.sa/DRAF.

Source: Khamis AM *et al. 2018, J Nucleic Acids Research*

DynaMut: predicting the impact of mutations on protein conformation, flexibility and stability

Proteins are highly dynamic molecules, whose function is intrinsically linked to their molecular motions. Despite the pivotal role of protein dynamics, their computational simulation cost has led to most structure-based approaches for assessing the impact of mutations on protein structure and function relying upon static structures. Here the scientists introduced DynaMut, a web server implementing two distinct, well established normal mode approaches, which can be used to analyse and visualise protein dynamics by sampling conformations and assess the impact of mutations on protein dynamics and stability resulting from vibrational entropy changes. DynaMut integrates our graph-based signatures along with normal mode dynamics to generate a consensus prediction of the impact of a mutation on protein stability. They demonstrated their approach outperforms alternative approaches to predict the effects of mutations on protein stability and flexibility (p-value < 0.001), achieving a correlation of up to 0.70 on blind tests. DynaMut also provides a comprehensive suite for protein motion and flexibility analysis and visualisation via a freely available.It is a user friendly web server.

Source: Carlos HM Rodrigues *et al. 2018,J Nucleic Acids Research*

Bioinfo. Animation (Source:Liang-Chin Huang *et al. 2018,J scientific reports)*

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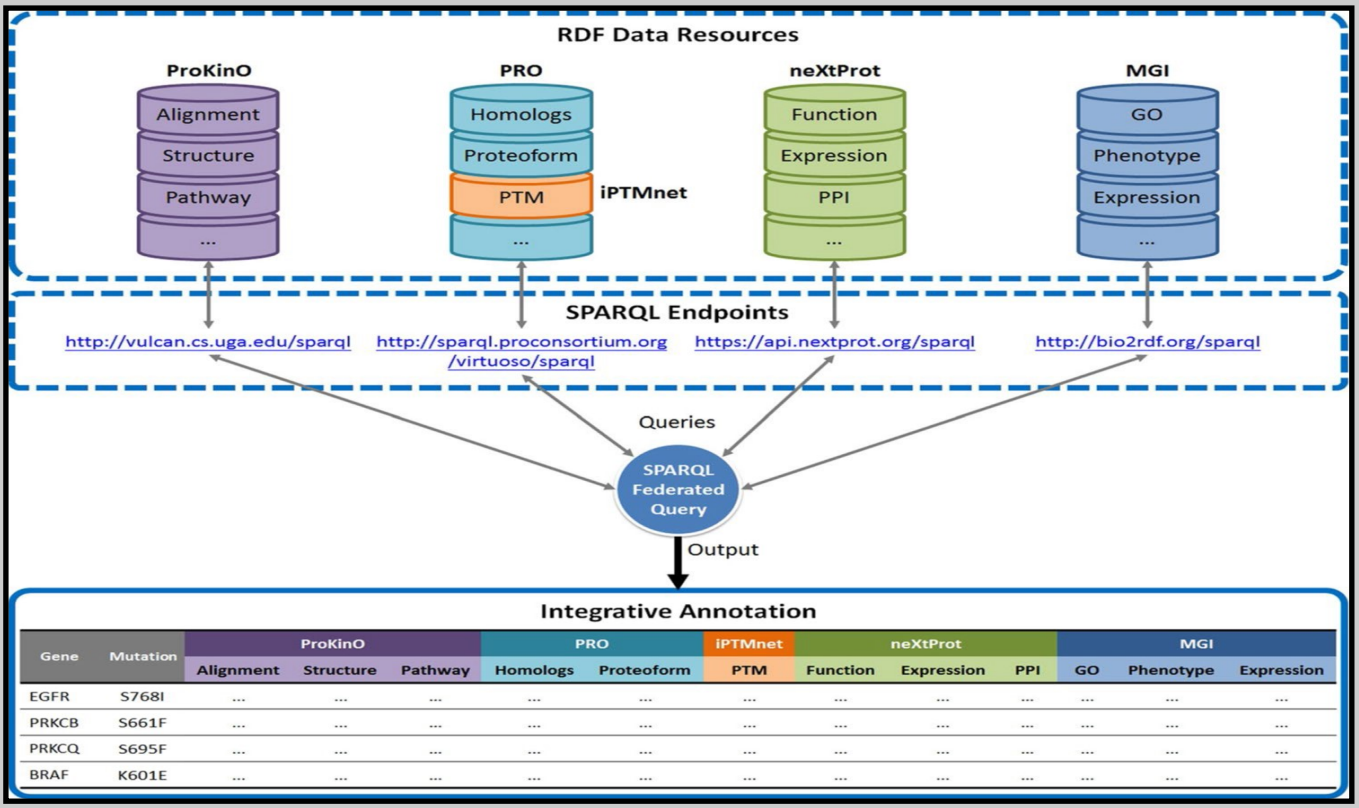


Gene	Mutation	ProKinO			PRO		iPTMnet	neXtProt			MGI		
		Alignment	Structure	Pathway	Homologs	Proteoform	PTM	Function	Expression	PPI	GO	Phenotype	Expression
EGFR	S768I	...	...	...	...	...	...	...	...	...	...	...	...
PRKCB	S661F	...	...	...	...	...	...	...	...	...	...	...	...
PRKCQ	S695F	...	...	...	...	...	...	...	...	...	...	...	...
BRAF	K601E	...	...	...	...	...	...	...	...	...	...	...	...

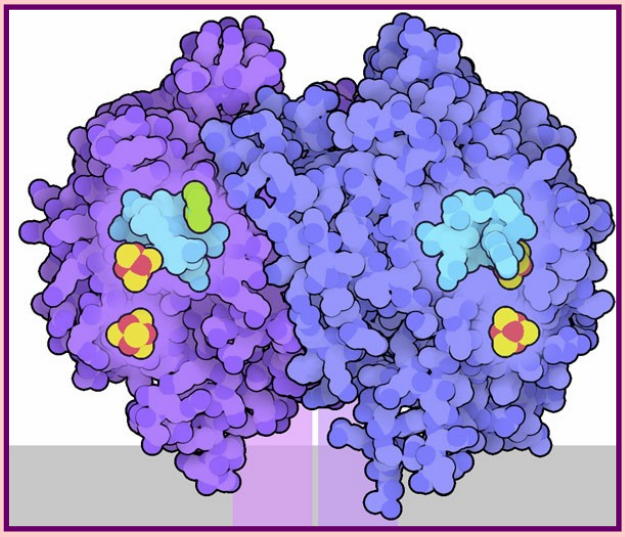
Fig:A framework for aggregate queries and integrative annotation. Integrative annotation across five resources, including ProKinO, PRO, iPTMnet, neXtProt, and MGI, is built using SPARQL federated query against four SPARQL endpoints; iPTM-net data is available via querying through PRO. Types of information are shown in each RDF data resource. PTM: post-translational modification; PPI: protein-protein interaction; GO:Gene Ontology.

Upcoming event

1. https://recombcg2018.usherbrooke.ca
2. http://www.incob2018.org/

Dehalogenases

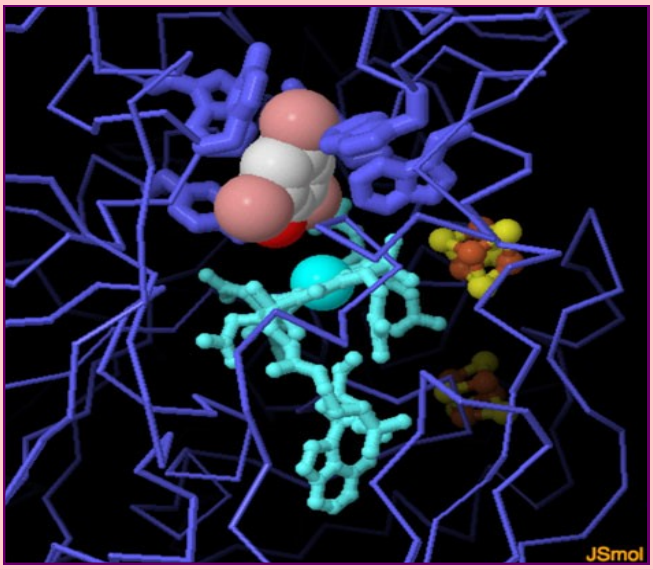
Halogens (fluorine, chlorine, bromine, and iodine) play essential roles in our lives. Several thyroid hormones must include iodine atoms for proper function. Chloride ions, which are obtained from the salt we eat, play diverse roles in basic cellular function and nerve transmission, and are shuttled from place to place by specialized chloride channels. However, halogens are highly reactive, so they often pose grave dangers. Industrial halogenated compounds are commonly used as solvents (for example in dry cleaning) and as pesticides (such as DDT). Unfortunately, many are toxic or carcinogenic, and cause problems when they escape and pollute the environment.



This dehalogenase uses several molecular tools in its reaction. During the reduction reaction, it needs to feed two electrons into the halogenated molecule. These are delivered by two iron-sulfur clusters. The reductive reaction also requires a cofactor similar to vitamin B12, which has a cobalt atom in the center. Together, the enzyme and these cofactors position the halogenated compound, add electrons, and replace the halogen atom with a hydrogen atom.

Reductive Dehalogenase

Three structures of a reductive dehalogenase (PDB entries 5m2g, 5m92, 5m8u) capture the enzyme as it successively removes bromine atoms from a brominated compound. The cobamide cofactor (light blue) helps position the molecule by interacting with a hydroxyl group, and six tryptophan and tyrosine amino acids (dark blue) make a cage around the active site to interact with the halogen atoms. The structure with tribromophenol (carbon in white, bromine in pink, and oxygen in red) is shown here. Click on the image to explore this and the other structures in more detail.



Source:http://pdb101.rcsb.org/motm/220

Kindly send us your feedback to

Dr Ratul Saikia
BIF Center, Biotechnology Group, BSTD
CSIR-North East Institute of Science and Technology, Jorhat, Assam
E-mail: rsaikia19@gmail.com

Dr Yumnam Silla Devi
BIF Center, Biotechnology Group, BSTD
CSIR-North East Institute of Science and Technology, Jorhat, Assam
E-mail: **bio.sillayumnam@gmail.com**