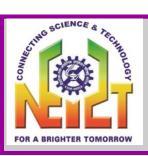
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Bioinformatics up to Date

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



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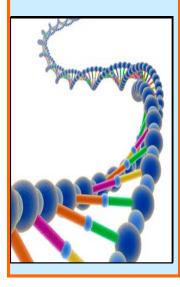
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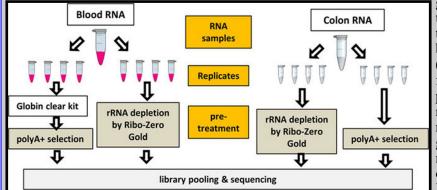


About us The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Minis-

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.

Evaluation of two main RNA-seq approaches for gene quantification in clinical RNA sequencing: polyA+ selection versus rRNA depletion

RNA sequencing (RNA-seq) has revolutionized the way biologists examine transcriptomes and has been successfully applied in biological research, drug discovery, and clinical development .To allow efficient transcript/gene detection, highly abundant ribosomal RNAs (rRNA) are



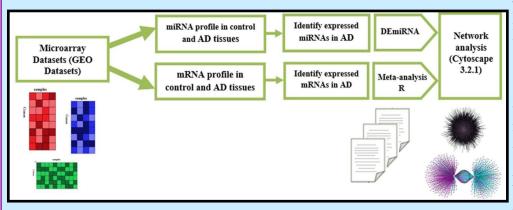
generally removed from total RNA either by positive polyA+ selection or rRNA depletion by (negative selection) before sequencing. Comparisons between the two methods have been carried out by various groups, but the assessments have relied largely on non-clinical samples. In this study, they evalu-

ated these two RNA sequencing approaches using human blood and colon tissue samples. The analyses showed that rRNA depletion captured more unique transcriptome features, whereas polyA+ selection outperformed rRNA depletion with higher exonic coverage and better accuracy of gene quantification. For blood- and colon-derived RNAs, we found that 220% and 50% more reads, respectively, would have to be sequenced to achieve the same level of exonic coverage in the rRNA depletion method compared with the polyA+ selection method. Therefore, in most cases they strongly recommend polyA+ selection over rRNA depletion for gene quantification in clinical RNA sequencing. There evaluation revealed that a small number of lncRNAs and small RNAs made up a large fraction of the reads in the rRNA depletion RNA sequencing data. Thus, they recommend that these RNAs are specifically depleted to improve the sequencing depth of the remaining RNAs.

Source: Shanrong Zhao et al. J Scientific Reports

Analysis of microRNA and Gene Expression Profiles in Alzheimer's Disease: A Meta-Analysis Approach

The molecular mechanisms underlying Alzheimer's disease (AD) is necessary for the diagnosis and treatment of this neurodegenerative disorder. It is therefore important to detect the most important genes and miR-



NAs, which are associated with molecular events, and studying their interactions for recognition of AD mechanisms. Here researchers focus on the genes and miRNAs expression profile, which they have detected the miRNA target genes involved in AD. These are the most quintessential to find the most important miRNA, to target genes and their important pathways. A total of 179 differentially ex-

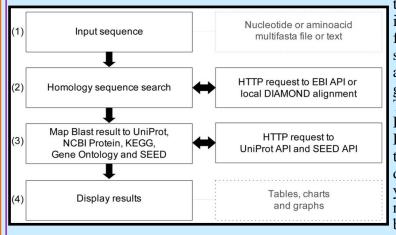
pressed miRNAs (DEmiRs) and 1404 differentially expressed genes (DEGs) were obtained from a comprehensive meta-analysis.

Also, regions specific genes with their molecular function in AD have been demonstrated. Then they focused on miRNAs which regulated most genes in AD, alongside we analyzed their pathways. The miRNA-30a-5p and miRNA-335 elicited a major function in AD after analyzing the regulatory network, they showed they were the most regulatory miRNAs in the AD. In conclusion, the most important genes, miRNAs, miRNAmRNA interactions and their related pathways in AD using Bioinformatics methods. Accordingly, their defined genes and miRNAs could be used for future molecular studies in the context of AD.

Source :Shirin Moradifard et al. J Scientific Reports(2018)

GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data.

Downstream analysis of genomic and transcriptomic sequence data is often executed by functional annota-



tion that can be performed by various bioinformatics tools and biological databases. However, a full fast integrated tool is not available for such analysis. Besides, the current available software is not able to produce analytic lists of annotations and graphs to help users in evaluating the output results. Therefore, researchers present the Gene Ontology Functional Enrichment Annotation Tool (GO FEAT), a free web platform for functional annotation and enrichment of genomic and transcriptomic data based on sequence homology search. The analvsis can be customized and visualized as per users' needs and specifications. GO FEAT is freely availahttp://computationalbiology.ufpa.br/ ble at

gofeat/ and its source code is hosted at https://github.com/fabriciopa/gofeat.

Source: Fabricio Almeida Araujo et al. J Sc. Reports,(2018)

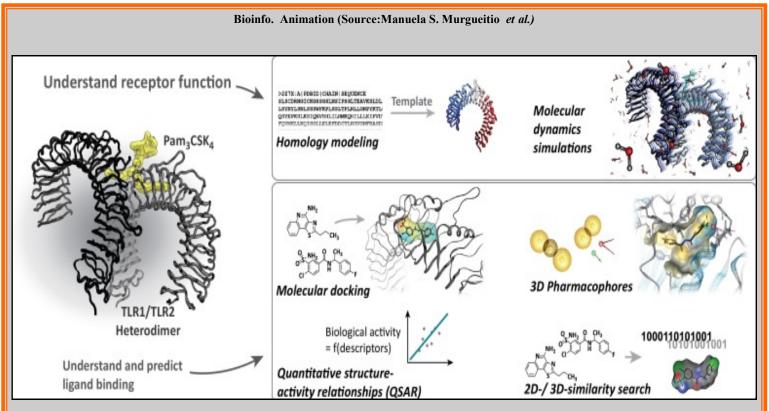
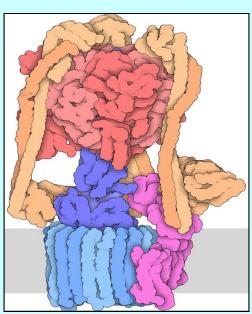


Fig:Overview on Aims and Methods in Computer -Aided Drug Design

An overview on the key methods used to understand protein function (top) and to elucidate and predict ligand binding (bottom) in computer-aided drug design is given. Molecular dynamics simulations and homology modeling are often utilized to unravel structure and function of the receptors. Molecular docking, QSAR, similarity searches and 3D pharmacophores are used to identify novel receptor ligands and understand their binding modes.

Vacuolar ATPase

The vacuolar ATPase (V-ATPase) is an ATP-powered proton pump composed of two rotary motors, as



shown here from PDB entry 5vox. The portion at the top (shown in pink) is an ATP-driven motor that turns an axle (shown in dark blue). This then turns a second motor (light blue and magenta) that pumps protons across the membrane. The remaining protein chains (shown in orange) hold the whole complex together and make sure that the rotation of one motor is used to power the rotation of the other. V-ATPase is regulated by breaking the complex in half when it is not needed.

The ATP-powered motor separates from the proton pumping motor, stopping the process. Then, when they are needed again, they are reconnected and pumping restarts. V-ATPases are made by eukaryotic cells and are used to control acidity .V-ATPases are complex molecular machines with many moving parts, so they have proven difficult to study. Currently, the most complete structures have been obtained by cryoelectron microscopy.

V/A-ATPases (PDB entry 5gar) have a variety of functions, as proton pumps or ATP generators. As an additional twist, some of these ro-

tary pumps use sodium ions instead of protons.

Source : http://pdb101.rcsb.org/motm/219



Patents

Intelligent data integration system

Taylor et al.

Data objects stored in a data store include data attribute(s) and associated value(s) for the attributes. Data analysis tools (DATs) stored in a data store are associated with reference data attribute(s). The data objects are identified by one or more DATs based on each reference data attribute(s) of a corresponding DAT matching one of the data attribute(s) of the corresponding data object(s) and independent of the value for the data attribute(s). The DATs generate an additional data object as a function of the identified data object, and the additional data object is stored in the data store.

Kindly send us your feedback to

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