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Bioinformatics up to Date

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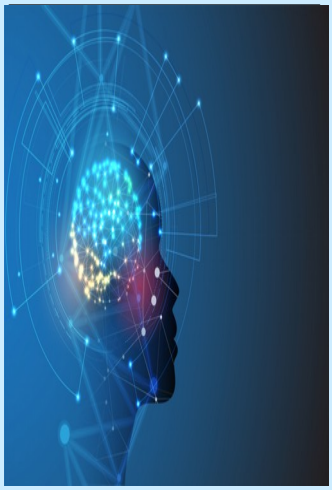
Inside…..



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.

SCGid, a consensus approach to contig filtering and genome prediction from single cell sequencing libraries of uncultured eukaryotes:

The Whole genome sequencing of uncultured eukaryotic genomes isvery difficult for acquiring sufficient amounts of tissue. Single cell genomics (SCG) by multiple displacement amplification (MDA) is a technical workaround, yielding whole genome libraries that can be assembled. Downsides of MDA also having coverage biases and exacerbation of contamination.These factors also affect assembly continuity and fidelity, thus complicating discrimination of genomes from contamination and noise generated by currently available tools. Uncultured eukaryotes and their relatives are sometimes underrepresented in large sequence data repositories, and further impairing identification and separation.

Here they compare the ability of filtering approaches to remove contamination and resolve eukaryotic draft genomes from SCG metagenomes, thus finding significant variation in results. To address these problem, they introduce a consensus approach that is codified in the SCGid software package. SCGid parallelly filters assemblies by using different approaches, yielding three intermediate drafts from which consensus is extracted. Using genuine and mock SCG metagenomes, they show that their approach is corrects for variation among draft genomes predicted by individual approaches and outperforms them in recapitulating published drafts in a fast and repeatable way, thus providing a useful alternative to available methods.

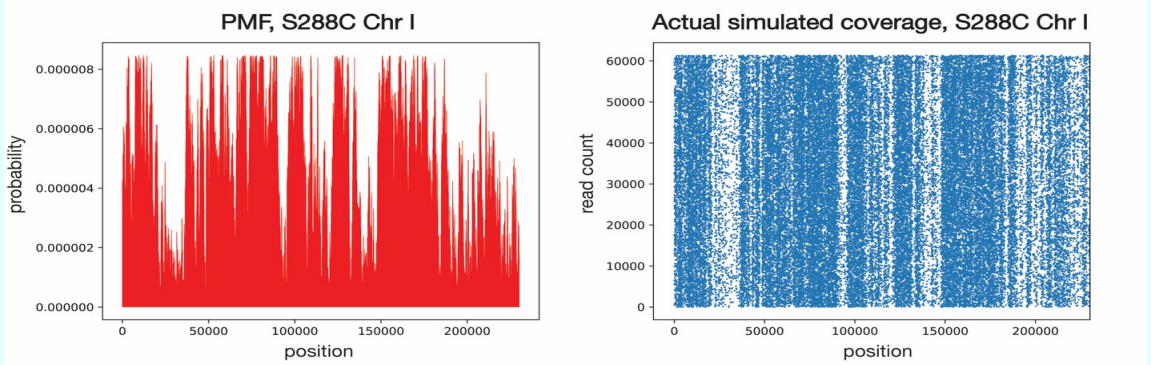


Figure: Plots showing exemplar probability mass functions (left) and scatter plot showing draws from that PMF (right)

Source: Kevin R Amses., *et al,* Bioinformatics, (OXFORD ACADEMIC), 2019.

TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology:

The Gene Ontology (GO) information is the world's most important source of information on the functions of genes. Since the beginning of GO project, various tools and software have been developed for performing various GO enrichment analysis experiments. GO enrichment analysis has been a commonly used method of various gene function analysis. All the existing GO enrichment analysis tools did not have consider tissue-specific information, although this information is very important and valuable for various research activities.

In this paper, they developed an easy-to-use web tool called TS−GOEA that allows users to easily access and perform experiments based on tissue-specific GO enrichment analysis. TS−GOEA uses strict threshold statistical method for performing various GO enrichment analysis, and provides various statistical tests to improve the reliability and quality of the analysis results. Meanwhile, TS−GOEA provides various tools for compare different experimental results or data, which is helpful for users to compare the experimental results. To evaluate its performance, they tested various genes associated with platelet disease with TS−GOEA.

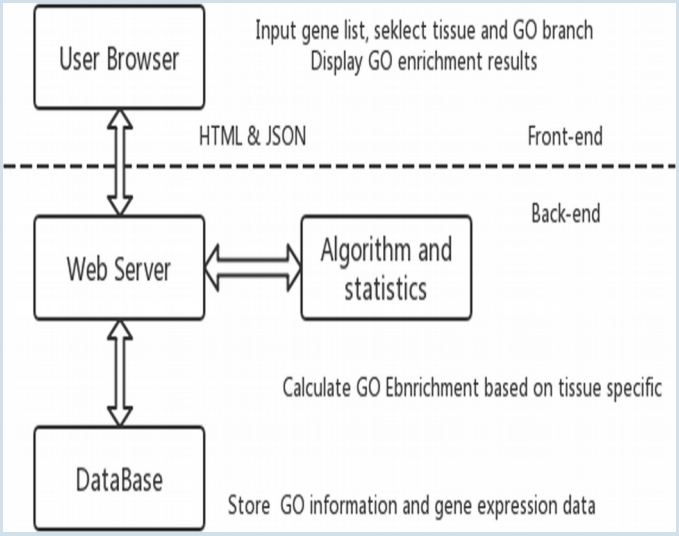


Figure: The whole framework of TS-GOEA. The front-end provides a user browser which inputs gene list and displays.

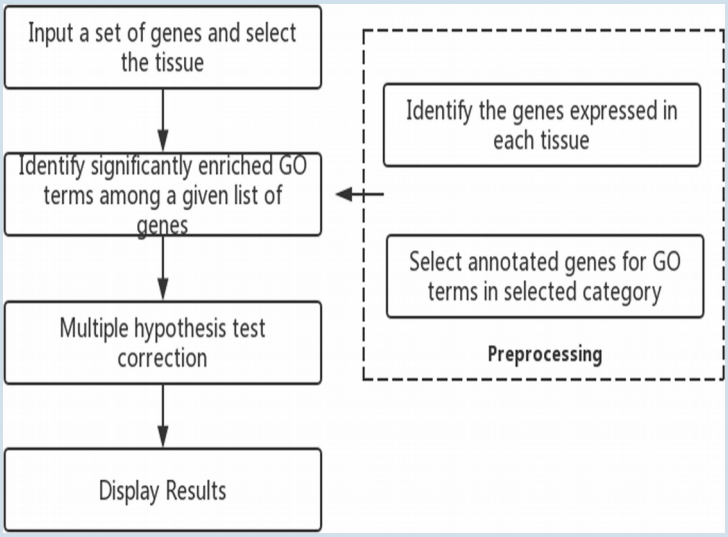


Figure: Workflow of tissue-specific GO enrichment analysis

The Gene Ontology (GO) information is the world's biggest source of information on the functions of genes. This information is both human-readable and machine-readable, and is a foundation for various computational analysis for various large-scale molecular biology and genetics experiments in biomedical research. The main objective of the Gene Ontology Consortium is to introduced a dynamic, structured, controlled vocabulary that can cover several domains related to molecular and cellular biology. GO and GO annotations provide a convenient way for researchers to explore the function of several gene sets in biological experiments. In detail, GO terms represent a kind of biological information which describes the various functions of genes and its corresponding gene products. As a unified information source, GO provides three accessible and independent ontology, namely biological processes(BP), cellular components(CC) and molecular functions(MF). GO has been widely used in molecular biology and genomics research to describe gene products. In addition to it, GO also provides an ontology annotation system that associates genes or gene products with GO terminology to form a "snapshot" of current biological information. Biologists can now also design experiments based on GO to verify their biological hypothesis.

In addition, existing tools only show the results of enrichment analysis, but they did not show users the relationship between those GO Terms in the results of enrichment analysis. they believe that visualizing the important relationship between the GO terms can help us for a better understand the experimental results. In order to improve these shortcomings, based on Homo sapiens' GO Annotated data and the Genotype-Tissue Expression data, They constructed an easy-to-use web tool called TS−GOEA, that allows users to easily conduct experiments based on organization-specific Go enrichment analysis. The tool uses appropriate statistical methods to determine whether the Go term significantly enriches specific organizations based on a given gene list. Compared it with various existing tools.

TS−GOEA is an effective GO analysis tool with various unique features. The experimental results show that their method has better performance and provides a useful example for the existing GO enrichment analysis tools. TS−GOEA is available at http://120.77.47.2:5678.

Source: Peng, J,et al. BMC Bioinformatics (2019)

Bioinformatics Animation

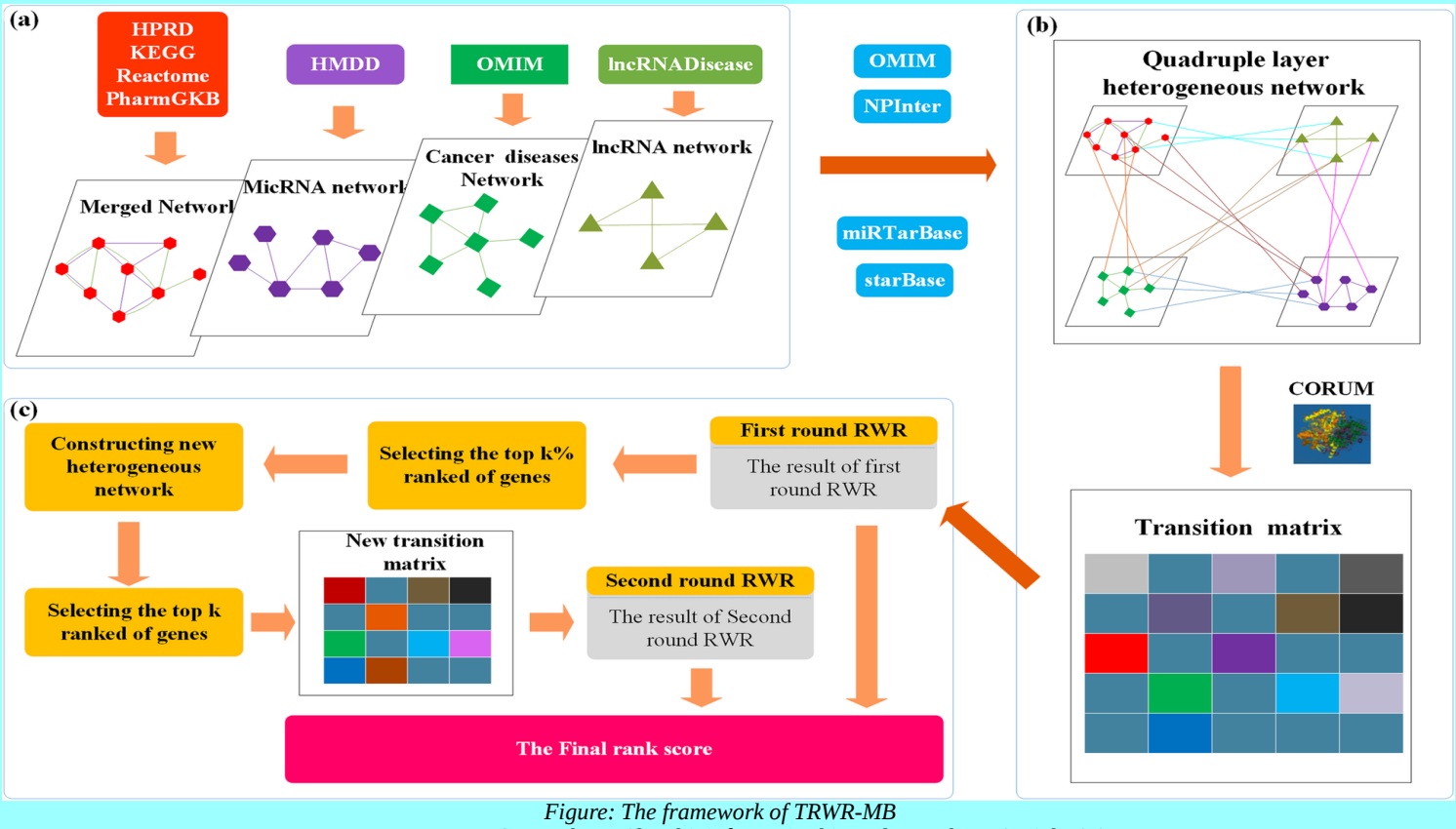


Figure: The framework of TRWR-MB
Source:https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-019-3123-8/figures/1

Upcoming Events

EMBO Workshop — Intrinsically Disordered Proteins: From Molecules to Systems

08 Dec 2019 - 13 Dec 2019 • Bangaluru, India

Topics: Proteins & Biochemistry | Systems Biology

Event listing ID: 1141917

Related subject(s): Molecular Biology, Biochemistry and Medicinal Chemistry, Toxicology

Event website: http://www.embo.org/events/events-calendar

CSEDU 2020 : 12th International Conference on Computer Supported Education

Conference Series : International Conference on Computer Supported Education

Link: http://www.csedu.org

When	May 2, 2020 - May 4, 2020
Where	Prague, Czech Republic
Submission Deadline	Jan 29, 2020
Notification Due	Mar 5, 2020
Final Version Due	Mar 18, 2020

Categories engineering education higher education computer science

Call For Papers

https://conference-service.com/conferences/in/mathematical-biology.html
http://www.wikicfp.com/cfp/servlet/event.showcfp?eventid=93845&copyownerid=45217

Molecule of the month

Phospholipase A2

Phospholipase A2 breaks membrane lipids for forming molecules that causes various inflammation and pain signaling. Over 100 years ago, scientists discovered that an enzyme present in snake venom breaks the lipid molecules in several cellular membranes. Since then, scientists have discovered many similar enzymes. Some types of phospholipase A2 are secreted, such as the phospholipases made by the pancreas use in digestion. Many others are made inside cells, where they participate with creation of signaling molecules.

Snake venom phospholipases and pancreatic phospholipases are small enzymes that can survive the harsh unfriendly environment when they are secreted (or injected) outside of the cells. They are bind together by a specific collection of disulfide linkages that helps to stabilize the folded structure. The one shown here, from cow pancreas (PDB entry 1bp2), has seven crosslinks. The active site is a pocket on one side of the protein, with a calcium ion that assists the cleavage reaction.

Many of the lipid tails that are released by phospholipase A2 helps to build signaling molecules involved in inflammation and pain. Because of such action, disorders in phospholipase action can contribute to many important diseases such as atherosclerosis and Crohn's disease. The research community is currently using the structures of phospholipases to discover new drugs to fight these diseases by blocking the action of the enzyme.

Several different forms of phospholipase A2 were made for different functions. Secreted phospholipase A2 is small, on the other hand cytoplasmic enzymes are larger, with separate domains that are associated with interaction with membranes and catalyzing the cleavage reaction (shown here from PDB entry 1cjy). These enzymes have regions on their surface that can interact with the face of a membrane, permitting the enzyme to extract lipids for cleavage.

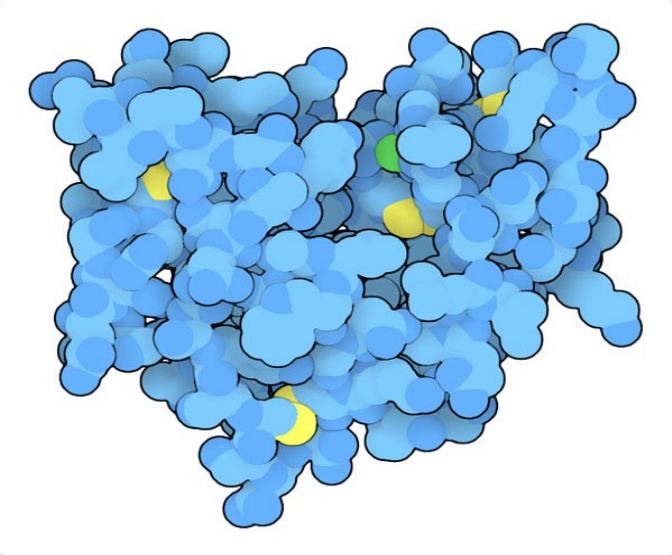


Figure 1:Pancreatic phospholipase A2, with calcium in green and cysteine sulfur atoms in yellow.

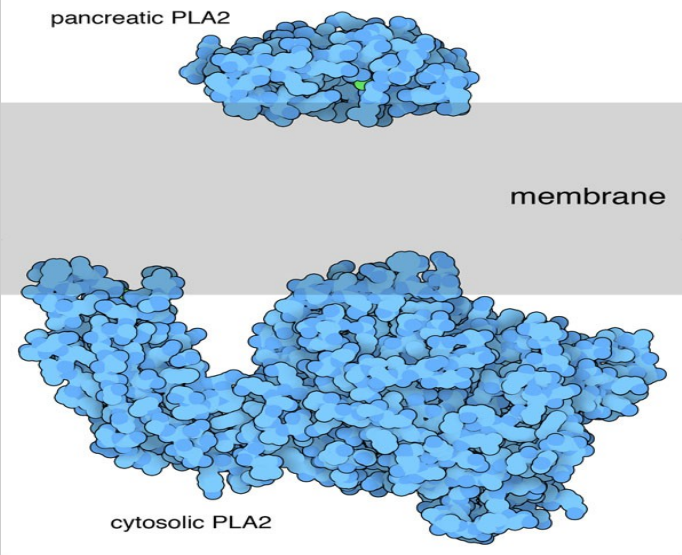


Figure 2: Pancreatic and cytosolic phospholipase A2. A membrane is shown schematically in gray.

Source: http://pdb101.rcsb.org/motm/239

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