June '22

4th Edition

GEN(E)IUS

The Student-Run Bioinformatics Magazine

COMBIGS

www.sastra.edu/combigs

Foreword

COMBIGS, the student run committee by the department of Bioinformatics is delighted to launch the fourth edition of GEN(E)IUS, a student run magazine. COMBIGS was started in the year 2005, with the main aim of creating awareness and exposing the students to the latest developments in Bioinformatics. This is achieved by organizing symposiums, conferences, publishing a bi-semester magazine, a well-connected alumni network and several such works. In 2012, COMBIGS organized the first International Conference on Structural and Functional Genomics.

In 2016, COMBIGS was happy to release its first edition of the e-magazine at the 2nd International Conference on Structural and Functional Genomics. A subsidiary group of COMBIGS called the BIOIN-FORUM was created in the year 2018 and in 2022, on June 11, BIOIN-FORUM conducted ‘ALGO-AMIGOS’ and ‘SAY IT WITH SKETCHES’ events for all students and the students participated with much enthusiasm. The event day had a session where faculties had a good interaction with all the students.

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DNA pulled from thin air identifies nearby animals

Do you know that DNA can be discovered in the air?

Yes, DNA may be found in the air. DNA from a wide variety of species can be found in the atmosphere in detectable quantities. It is a significant advance to be able to identify so many species in air samples using DNA. The unexpected thing is that you can obtain mammals and birds by sampling air.

Animal eDNA in air has only received a small number of research to date. It's unclear how much tissue an animal sheds or how long its genetic material lingers in the air. In several earlier research, airborne bacteria and fungi were identified using metagenomic sequencing, a method for identifying DNA mixes. However, the idea of how terrestrial animals shed cells that float away is unclear when using this technique.

Recently, laboratory air samples were shown to contain eDNA from naked mole rats. Air samples were collected from the zoo solely to detect eDNA from the outdoors. The key justification for choosing a setting like a zoo was that these animals could identify the source of airborne eDNA and were separated from other animals outside of that area.

A total of 72 samples, both within and outside the zoo, were collected. The sparse genetic components were amplified into sufficient DNA for sequencing using the Polymerase Chain Reaction (PCR). Sequences in a database were compared to snippets discovered from the sequencing of the eDNA.

They discovered 17 species, both indoor and outdoor, that were housed at the zoo. And these DNA could only be located 300 metres away from the animal. It's interesting to note that they also found airborne DNA in the chicken, pig, cow, and horse meat supplied to indoor caged predators. 25 different bird and animal species were found in total. With eDNA experiments, contamination prevention is a constant concern.

In recent years, an XPRIZE Rainforest team has been formed to develop airborne DNA technology for monitoring biodiversity. Airborne DNA may help reveal the presence of otherwise hard to detect animals, such as those in dry environments, burrows, or caves, and those that fly out of sight of wildlife cameras, like some birds, Lockwood says.

In conclusion, it is intriguing to discover that extracting eDNA from air allows us to learn more about the local species.

T G Sai Sharadhaa

Bioinformatics’23

GAME THEORY IN BIOINFORMATICS

Love to play games? By the way, do you know about the game theory? GGGAAAMMMEEE TTTHHHEEEOOORRRYYY…

HAHA! Everyone for sure knew this but not the name of it. So here is the theory about Game theory. A player's strategy is one of the options, which they choose in the setting where the outcome depends not only on their own actions but on the action of others. Game theory is a framework for understanding and making optimal decision in situations among competing players in a strategic setting. In terms, Game Theory is a branch of applied mathematics that provides tools for analyzing situations in which players make decisions that are interdependent.

We are aware that the terms computational biology and bioinformatics are frequently used synonymously. However, the term "Bioinformatics" is more accurately used to describe the development of theory and algorithms to address both formal and practical issues brought about by the study of biological data. Bioinformatics employs mathematical methods to draw out relevant information from data generated by high-throughput biological processes like genome sequencing. Here, we review how game theory has been used to analyze biological data. Clearly, the goal of such applications is not to provide answers to normative questions. It is comparable to offering advice to a collection of variables such as genes, proteins, etc. on how they should act inside a biological cell.

This game theoretic approach was used, for instance, to cluster a family of multi-domain proteins. At the beginning of this section, for a certain set of taxa, a biological affinity graph was introduced. This biological affinity network was constructed using a game-theoretic approach to evolution. Evolution plays the function of conservation when an evolutionary event involves an accurate vertical transmission of genetic information, and else it plays the role of diversity. That is, the two sides of evolution that cannot be separated are conservation and diversification, and the methods of evolution as a process are its byproducts.

At the genome level, any increase in gene or gene composition affinity between two genomes is a play of diversification, whereas any increase in the difference between two genomes' gene or gene compositions is a play of conservation. At the protein level, any divergent domain differences are a result of the diversity play whereas the overall similarity between two proteins is a result of conservation. The reward at each stage is not a literal completion of the game or procedure but rather the evolutionary similarity or dissimilarity in their bioinformatics, which can be quantified in terms of different informational distances. The results showed that this game-theoretic technique offers a new paradigm in biological sequence analysis, especially in the study of gene-genome and other known protein subfamilies, as the protein clusters found were consistent with those of known protein subfamilies.

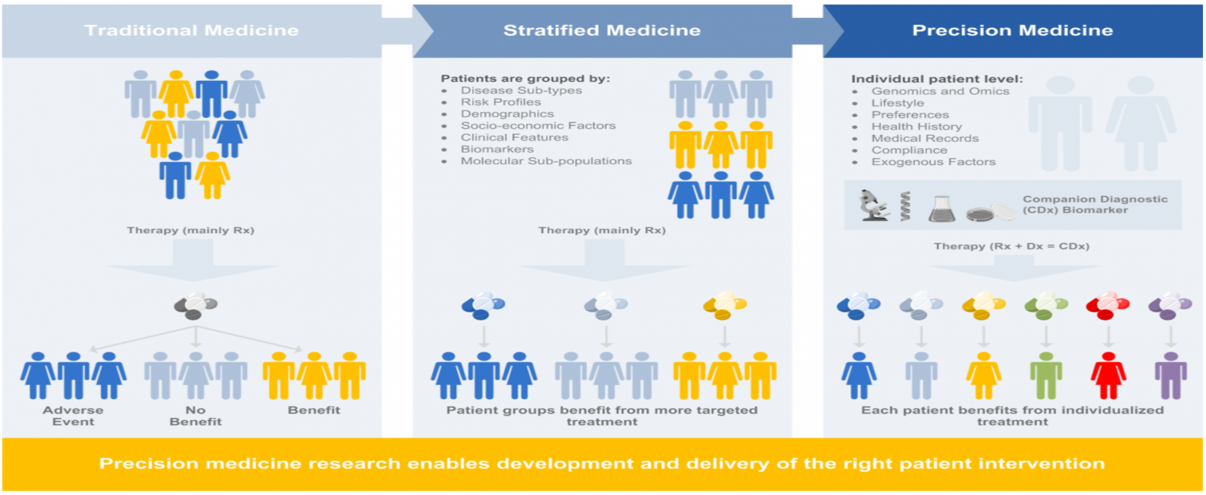
This is just one of the applications of Game theory towards Bioinformatics. Apart from this, Game theory is widely used in various forms in our real life. It is totally applied for determining different strategies as like we use in our games.

Subhiksha M

Bioinformatics'24

AI transforming tailored treatments to patients

Gone are the days when a single medicine is prescribed to a whole lot of people with the same disease. Nowadays, physicians are focused on providing the right drug to the right person at the right time. The specific term used to describe the personalized treatment curated according to an individual's genetics, lifestyle, and environment is precision medicine. When you go to a clothes store, you try on several clothes before you find the right one that fits you the best. Likewise, it is absurd to think that one medicine cures everyone. Each and every one of us has different genetic makeup and lifestyle. So, one medicine cannot have the same therapeutic effect with the same efficacy on every diseased individual. For example, breast cancer is caused due to many reasons such as the family history of breast cancer, genetic predisposition, radiation exposure, and obesity. So providing one specific pill or therapy for all breast cancer patients may not give desired results. Hence, it is necessary to curate the treatment and therapeutic strategies specific to an individual.

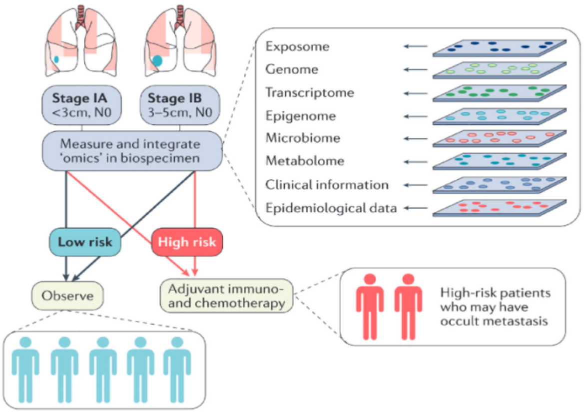


Source - Linguamatics

Artificial intelligence has gained more recognition in the past few years. Let it be the manufacturing, automobile, or healthcare industry, AI has played a crucial role in each of the sectors. The convergence of Artificial intelligence and precision medicine can revolutionize the healthcare industry. Data is the oil of the 21st century. The amount of patient data is increasing exponentially. Wearable devices like smartwatches collect health-related data like body temperature, heart rate, and quality of sleep. AI plays a crucial role in aggregating the patient data and deriving insights about the patient’s disease progression and recovery.

Digital biomarkers help to track behaviours specific to diseases. These biomarkers can be either audio or video-based like facial expressions, eye twitches, speeches, and movements. The digital biomarkers are monitored by AI-powered predictive analytics which helps in choosing the best treatment for the patient. These biomarkers are collected using digital devices that are wearable and portable. The identification and validation of biomarkers have gained importance in the field of precision medicine. For example, in cancer, biomarkers information is collected from the tumor that helps in planning treatment regimes and monitoring treatment provided to the patient.

Let’s consider an example where biomarkers are discovered for early-stage lung cancer. Biomarkers are crucial for drug development; it helps to assess the patient’s response to drugs. Precision medicine is used to classify lung cancer into further subtypes to provide appropriate treatment.



Radio-genomics is a novel field that associates cancer imaging features with gene expression to predict the patient’s risk of developing toxicity followed by radiotherapy. This technique has applications in breast cancer, lung cancer, and colorectal cancer.

Traditional medicine is solely based on trial-and-error methods.

The doctor prescribes medicines based on the patient's symptoms. But precision medicine is curated for a specific patient, hence, there is less chance of failure. Precision medicine is the future of healthcare. Let's embrace it and live in a disease-free world.

M.B.Sanju Vikasini

Bioinformatics'23

BIOINFORMATICS IN FOOD INDUSTRY

In recent days food industry have been revolutionized and bioinformatics playing a crucial role in it. food, health, nutrition on one hand and environment, population growth, demand and sustainability of nature on the other hand. The nutritional values from the biomolecules like proteins, carbohydrate and lipids that has to conserved and lay out it in a novel approaches and techniques. The large amount of biological data and resources that are crucial to the study of food and nutrition are stored, updated, and used thanks to bioinformatics in food. And make use of it for new inventions.

UNCOVER BIOACTIVE PEPTIDES:

The identification of bioactive peptides found in the proteins of food has been made possible through bioinformatics . Bioactive peptides are the peptide sequence in the protein which assists in preventing diseases and modulating the physiological function when it is absorbed by the human body along with its nutritional values. These peptides have anti thrombotic, antioxidants and hypotensive activities and so on. Simultaneous evaluation of these different food proteins and the enzymes which help in the digestion of proteins i.e., enzymatic proteolysis -cleaving of parent protein to obtain this bioactive protein in gastrointestinal tract by proteolytic enzymes and also by food processing i.e., cooking. The bioinformatics method makes use of information found in numerous databases, including BIOPEP. To ascertain the frequency of bioactive peptide crypts in the primary structures of dietary proteins, protein sequences from the UniProtKB, SwissProt, and TreMBL databases can be retrieved. To create profiles for in silico peptides produced by the stimulation of different enzymes' proteolytic specificities ,bioinformatics software has been developed. Various in silico tools for proteolysis are BIOPEP ExPASY and PoPS. Ideally, this method is thorough and cuts down on the time that was previously needed to screen for bioactive peptides that are present in various protein sources by using a few proteases, which can lead to the discovery of new and reliable precursors of known bioactive peptides from nature, such as antidiabetic, antihypertensive, cholesterol-lowering, and anticancer peptides.

BIOINFORMATICS APPROACH IN FOOD PROCESSING:

The novel food processes and food products are impacted by the structural characteristics of live organisms that are being investigated and researched with the help of bioinformatics. The knowledge based on bioinformatics demonstrates the distinctive characteristics of the complexity of biomolecules and their roles. This knowledge creates conditions that allow for a precise and appropriate evaluation of the biomaterial qualities of each of the molecules in complex mixtures.For example The unabridged protein-protein synergy map of yeast i.e., all. Using these milk proteins, which are "chemically identical" to those found in milk and dairy products produced by cows thanks to a yeast-based fermentation process. The finished product is identical to genuine milk in every way but is free of lactose, cholesterol, growth hormones, and antibiotics. It was discovered that the proteins are the primary component in milk production after mapping out the chemical makeup of milk and analysing the fat, lactose, and sugar content of the fluid. The outcome is then dried and ground into powder. Bioinformatics is used to create dairy products that are absolutely identical to those made from cow's milk, including their flavour, texture, stretchiness, meltiness, lack of lactose, and lack of cholesterol

J.Thahirunnisa

Bioinformatics'23

BIOINFORMATICS APPROACH-DISEASE PREVENTION AND TREATMENT

You guys believe that Bioinformatics tools helps in identifying the genes that is responsible for diseases??

Here is a case study that uncovers additional intriguing information about the drug design for hypertension patients and identifies the genes that are differentially expressed between patients with the condition and controls.

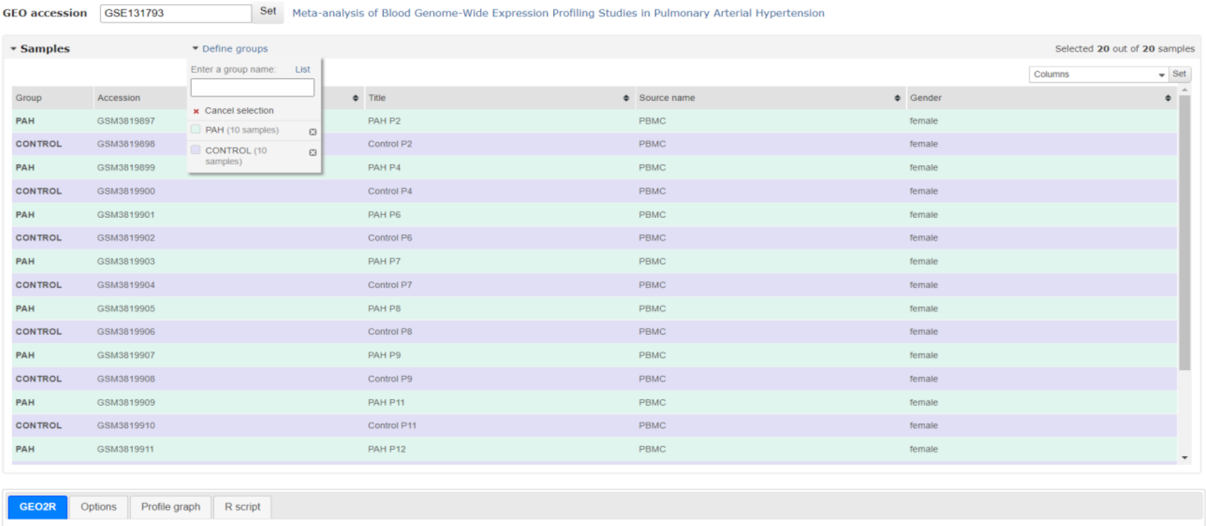
The condition known as pulmonary arterial hypertension (PAH), which is still frequently misdiagnosed, is nonetheless fatal. They used integrative bioinformatics approach to investigate the DEG's of PAH patients. Here, they gathered 10 PAH patients, 10 healthy control patients, and 13 female and 7 male subjects.

TOOLS USED FOR THE ANALYSIS:

GEO-gene expression omnibus-Gene Expression Omnibus (GEO) data were used to obtain expression information, and BD Vacutainer CPT cell preparation tubes were used to separate white blood cells (monocytes, lymphocytes, etc.) from whole blood of the patients. Here comes the big picture of Bioinformatics approach. They used GEO2R to identify the DEG's of PAH patients and control healthy patients.

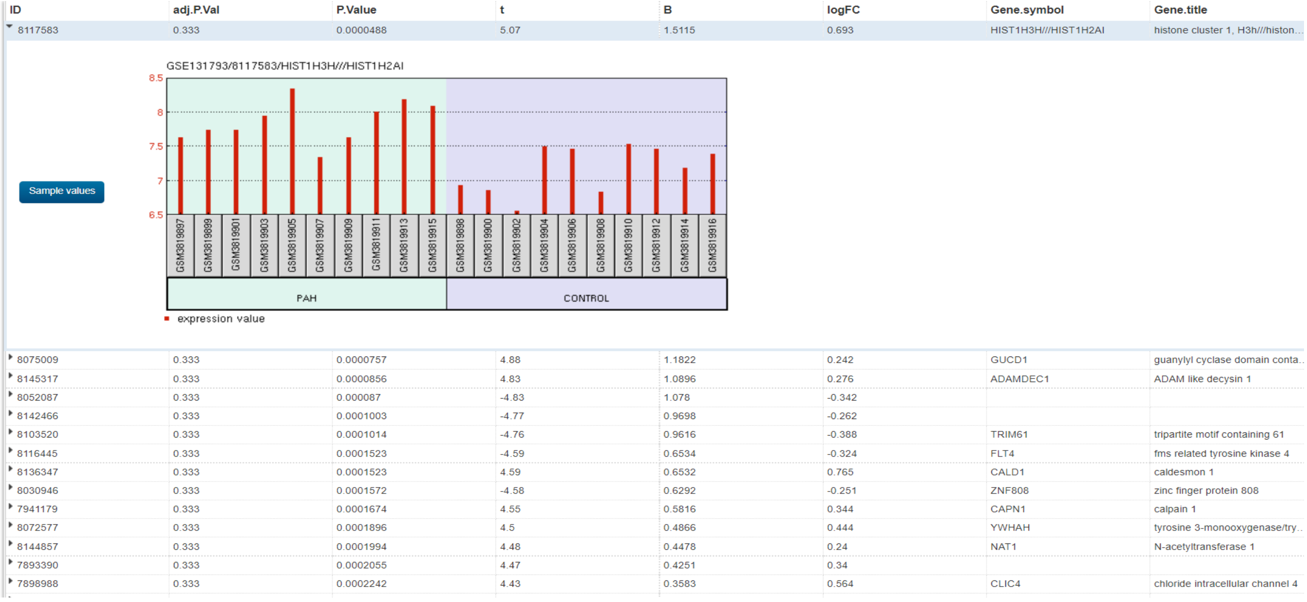
Gene Ontology: Through the use of the Gene Ontology technique, which is used to categorise the properties of gene expression, researchers were able to identify the cellular constituent, molecular function, and biological processes of the relevant genes.

PANTHER: : Protein Analysis through Evolutionary Relationships is a visualization tool helps in classifying the DEG's according to their biological processes, molecular functions of respective genes. So, I analysed using the GEO2R database and found those results.



Group	Accession	Title	Source name	Gender
PAH	GSM3819897	PAH P2	PBMC	female
CONTROL	GSM3819898	Control P2	PBMC	female
PAH	GSM3819899	PAH P4	PBMC	female
CONTROL	GSM3819900	Control P4	PBMC	female
PAH	GSM3819901	PAH P6	PBMC	female
CONTROL	GSM3819902	Control P6	PBMC	female
PAH	GSM3819903	PAH P7	PBMC	female
CONTROL	GSM3819904	Control P7	PBMC	female
PAH	GSM3819905	PAH P8	PBMC	female
CONTROL	GSM3819906	Control P8	PBMC	female
PAH	GSM3819907	PAH P9	PBMC	female
CONTROL	GSM3819908	Control P9	PBMC	female
PAH	GSM3819909	PAH P11	PBMC	female
CONTROL	GSM3819910	Control P11	PBMC	female
PAH	GSM3819911	PAH P12	PBMC	female

P-value at 0.05 and Log2 fold change (FC) > 1.0 was taken as the cut-off values in (GEO2R). The analysis was based on the top 250 genes being differentially expressed genes and found top 15 up-regulated and the top 15 down-regulated genes.



ID	adj.P.Val	P.Value	t	B	logFC	Gene.symbol	Gene.title
8117583	0.333	0.0000488	5.07	1.5115	0.693	HIST1H3H///HIST1H2AI	histone cluster 1, H3h///histon...
8075009	0.333	0.0000757	4.88	1.1822	0.242	GUCD1	guanylyl cyclase domain conta...
8145317	0.333	0.0000856	4.83	1.0896	0.276	ADAMDEC1	ADAM like decysin 1
8052087	0.333	0.000087	-4.83	1.078	-0.342		
8142466	0.333	0.0001003	-4.77	0.9698	-0.262		
8103520	0.333	0.0001014	-4.76	0.9616	-0.388	TRIM61	tripartite motif containing 61
8116445	0.333	0.0001523	-4.59	0.6534	-0.324	FLT4	fms related tyrosine kinase 4
8136347	0.333	0.0001523	4.59	0.6532	0.765	CALD1	caldesmon 1
8030946	0.333	0.0001572	-4.58	0.6292	-0.251	ZNF808	zinc finger protein 808
7941179	0.333	0.0001674	4.55	0.5816	0.344	CAPN1	calpain 1
8072577	0.333	0.0001896	4.5	0.4866	0.444	YWHAH	tyrosine 3-monooxygenase/try...
8144857	0.333	0.0001994	4.48	0.4478	0.24	NAT1	N-acetyltransferase 1
7893390	0.333	0.0002055	4.47	0.4251	0.34		
7898988	0.333	0.0002242	4.43	0.3583	0.564	CLIC4	chloride intracellular channel 4

RESULTS FROM GEO2R

They performed comparison study on both healthy and PAH patients differentiating them based on the biological process of the genes using PANTHER database-here the respective DEG's which was collected from GEO2R (top 20) is given as input. Based on this input we get the respective functions in which they involve. According to PANTHER database findings, upregulated genes are involved in a variety of biological processes, including biogenesis, cellular function, localization, and biological control.

This investigation revealed that PAH patients had elevated levels of the gene for ITGB3 (Integrin beta-3), a protein located on thrombocytes with high anti-oxidative properties, as well as haptoglobin (HP), a protein with these same properties. So they found certain genes that could be targeted for PAH prevention, management, and treatment using one of the bioinformatics methods.

Akshaya R

Bioinformatics'23

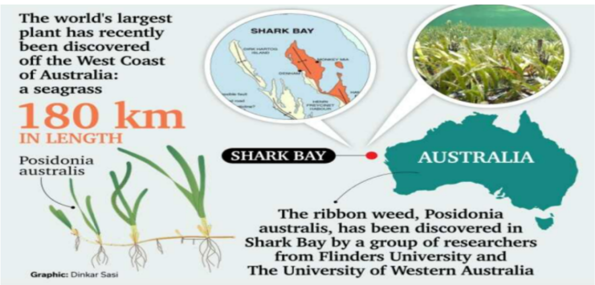
Kingdom plantae’s oldest champion of Solo gamy

Posidonia australis

Posidonia australis, additionally called **fiber-ball weed or ribbon weed**, is a species of seagrass that takes place inside the southern waters of Australia. The world's largest dwelling plant has been diagnosed in the shallow waters off the coast of Western Australia.

Distribution

The sprawling seagrass, a marine flowering plant called Posidonia australis, stretches for more than **112 miles** (a hundred eighty kilometers) in Shark Bay, a desolate tract region blanketed as a World Heritage internet page. That's more or less three instances the dimensions of Manhattan, off the coast of Australia.

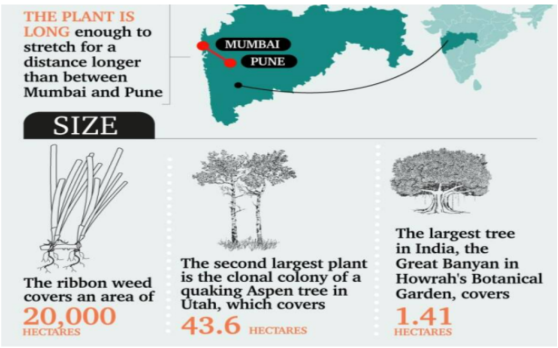

The world's largest plant has recently been discovered off the West Coast of Australia: a seagrass

180 km IN LENGTH

The ribbon weed, Posidonia australis, has been discovered in Shark Bay by a group of researchers from Flinders University and The University of Western Australia

Graphic: Dinkar Sasi

The plant is anticipated to have taken at least four,**500 years** to develop to this length via the use of rhizomes to colonize new components of the seafloor, assuming a rhizome boom rate of around **35 cm (14 in) a year.** This age puts it in a few of the oldest clonal vegetation too.


THE PLANT IS LONG enough to stretch for a distance longer than between Mumbai and Pune

SIZE

The ribbon weed covers an area of 20,000 HECTARES

The second largest plant is the clonal colony of a quaking Aspen tree in Utah, which covers 43.6 HECTARES

The largest tree in India, the Great Banyan in Howrah's Botanical Garden, covers 1.41 HECTARES

Taxonomy

This species is a family member of Posidoniaceae, considered certainly one of 8 occurring in Australia. Posidonia, is given for the god of the seas Poseidon, and australis refers back to the southern distribution.

The plant is so big as it clones itself, growing genetically identical offshoots. This device is a manner of duplication that is uncommon within the animal nation even though it takes location in sure environmental conditions and takes an area greater often amongst some flowers, fungi and microorganisms.

Mechanism

In the evolutionary history of flowering plants, whole-genome replication by polyploidy has been a remarkably frequent method of exceptional variation. According to recent phylogenomic studies, each angiosperm underwent at least one wave of polyploidization.

Materials and Methods

Aquatic plants are a polyphyletic group that emerged in the early Cretaceous as a result of at least three independent "go back to the water" occurrences. Although temperatures can surpass 30°C in the summer, seagrasses are subject to excessive slight concentrations (greater than 3000 mol m s1), have a wide average temperature difference of 17–26°C, as well as a saline variation of 35–64 psu.

Genetic sampling and laboratory protocols

Following, homogeneous across sites (within a 50 m in diameter location) were created using arbitrary shoot sampling. Prior to DNA isolation, shoot meristem (non-photosynthetic) tissue was treated and frozen, as stated in. At the sampling point, the in-situ measurements of the local ecosystem included depths (m), temperature of the water (°C), salinity (using realistic salinity devices, psu), and pH.

For 144 samples representing Ten examined grassland, genomic DNA was isolated from cryogenic shoots using a Qiagen DNeasy Plant Pro Toolkit (Qiagen, Germany) (12 to 14 in line with meadow).

Library preparations

Library instruction observed the protocol for **ddRAD-seq**. Pooled libraries had been utilizing a HighSeq sequencing platform gadget to be 2 × one hundred fifty bp paired-give up reads. Raw reads have been processed following the pipeline information.

Sampled seagrass shoots from for the duration of Shark Bay's variable environments and generated a 'fingerprint' the use of **18,000 genetic markers**.

In short, ddRAD loci assembled from scratch and identity abnormalities of single nucleotides (SNPs) became achieved the usage of the STACKS version 2.50's denovo map pipeline .The genome duration of the polyploids become a lot a little under twice (1.7) as much as the diploid individuals.

Guard of environment

Because seagrass performs a critical role within the environment, and if a number of it's far are hardy, it is right information for anybody in a world threatened by means of weather alternately.

In India, seagrass is determined in lots of coastal regions, maximum considerably inside the Gulf of Mannar and Palk Strait. Apart from being domestic to a spread of small organisms, seagrass traps sediments and prevent water from getting muddy, **absorb carbon** from the surroundings, and **prevent coastal erosion**.

The Shark Bay ribbon, for that reason, has served as sinkhole, hospitable metropolis, and firewall for centuries. They procreate sexually by producing flowers and seeds as well as phylogenetically through plant development caused by horizontal rhizome extension. And it has finished all this without mating, so possibly it has one extra difference – being one of **the oldest champions of sologamy**.

Sapthavahini G

Bioinformatics'23

Bioinformatics applications in the field of psychology

Psychology is a significant area which can give a good biological breakthrough.

As -omics and image processing technologies enable researchers to investigate the molecular and physiological underlying principles of numerous diseases, freedom to explore the biological basis for behavioural health and disease emerge.

Researchers in the field of mental health have generated wide - ranging data sets. Bioinformatics will contribute significantly in providing a basis for these datasets future use. In this article, we will take a glance at how bioinformatics can assist in organising these data sets

Mental Health disorders are associated with a multitude of symptoms that affect emotions, thoughts, and behaviour patterns. Furthermore, two people with no overlapping symptoms can be diagnosed with the same disorder, such as Schizophrenia. The National Institute of Mental Health (NIMH) RDoC initiative aims to develop new ways of classifying mental disorders based on dimensions of observable behaviour and neurobiological measures for research purposes. Rather than starting with a complex and heterogeneous illness definition and then searching for neurobiological underpinnings, the goal is to generate categories based on basic behavioural neuroscience.

Bioinformatics and other breakthroughs in high-throughput brain and behaviour evaluation have resulted in technologies that can quickly identify and characterise the function of biological systems in behavioural processes. As a result, new molecular targets for research, diagnostics, and therapies have been discovered. While much of this work is still in its early stages, significant progress is being made, and practice is already being implemented. The potential reconstruction of behaviour from its biological basis is a key prospect provided by the use of bioinformatics to behaviour. Ontology development establishes a framework and platform for data integration, allowing for the creation of a data-driven classification of behavioural processes from the bottom up.High-throughput biology generates data that can be quickly annotated to these ontologies, allowing for the discovery of relationships such as gene pleiotropy.

Researchers can make connections across disease-related phenotypes using strategies for aggregating single findings. These phenomena could be the endophenotypes that form the robustly measurable aspects of disorders rather than the currently named diseases themselves. The challenge is to move from identifying the disorder's substrate to defining the disorder based on its substrate.

The inputs and validating data are provided by real experimental data, which is frequently collected using high-throughput measurement systems. The idea is that "true" classifications can be found in the common biology of related disorders and compared to the distinct biology of distinct disorders.

Bioinformatics allows us to define, categorise, and structure our understanding of psychiatric disorders and their constituent processes and features. Furthermore, and crucial to any scientific endeavour, it presents a technology and framework that can be used to test these structures, allowing the classification scheme to be falsifiable.

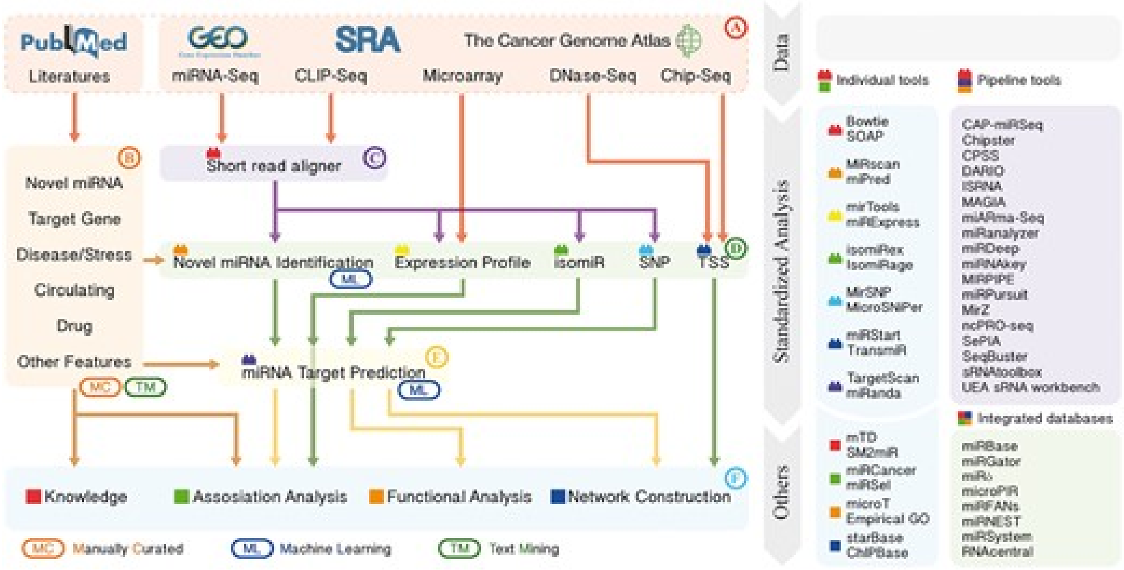
S.Helina Hilda

Bioinformatics'24

Bioinformatic analysis of extremely conserved, non-coding, miniature microRNA profiles

MiRNAs, the negative regulators of genetic expression, alter the production of mature B and T lymphocytes. Activation of cells produced by antibodies such as macrophages, dendritic cells, and natural killer cells are driven by miRNAs into the human genome and control at least 30% of the genes that make up proteins. MicroRNAs are synthesized by RNA polymerases II and III and undergo a series of breakdown events to produce precursors that form mature microRNAs. Bioinformatics analysis suggests that a single miRNA can actually compile up to 200 genetic targets. Combined miRNAs have the ability to regulate the expression of one third of all human genes.

Analysis of miRNA expression in a particular cell type can have a significant diagnostic value, and adjusting miRNA levels that have changed in clinical setting holds promising therapeutic prospects. Many bioinformatics tools are designed for each miRNA biosynthesis process. These tend to help biologists study biological questions on miRNA. Annotation tools such as miRBase, are the main site for storing miRNA and serve as a repository for collecting all known types of miRNA and annotations for all species. Rfam is an integrated system of RNA annotations that contain information about the miRNA family. MIRIAD data is designed to record information about intragenic miRNAs and binding genes, and mirtron Pred predicts mitrons from intron sequence. The secondary and tertiary structure of miRNAs is essential for the detection of certain binding proteins or interactions with other RNAs. Therefore, structural tools such as the Vienna RNA software package include many tools for predicting and comparing RNA structures. The identification of new miRNAs is a complex but important process, and various diagnostic tools are designed for this purpose. This includes MiRscan, the first and easiest tool to detect stored miRNAs in C. elegans, and miRNA Fold, a fast ab initio method for predicting large-scale miRNA predisposition within the genome.



This is a work in progress analysis of miRNA bioinformatics. MiRNA analysis data sets can be downloaded from the public website and books can be obtained from PubMed. Exposure data such as miRNA sequencing (miRNASeq) and miRNA microarrays are available in Gene Expression Omnibus (GEO), Sequence Read Archive (SRA), Cancer Genome Atlas (TCGA), and other data distribution centers biological. We can download it.

Several techniques have been developed that allows us to identify new animal miRNAs and their targets. Genetic mechanisms include Phenotypic Suppression screens. However, it is difficult to distinguish between direct and indirect targets of miRNAs so this process is replaced by computational methods such as miRbase that provide genomic information and sequence of mature miRNA and miRDB containing predictable miRNA targets that include five types of animals: humans, mouse, mouse, dog and chicken. Various Biochemical methods such as immune-purificationand quantitative PCR and western blotting are also used.

MiRNA identification and target predictions remain hot spots in the field of miRNA bioinformatics tools, while the latest advances in NGS technology provide improved targeted predictions based on assay validation. Since miRNAs have a variety of uses, identification of their targets is very important.

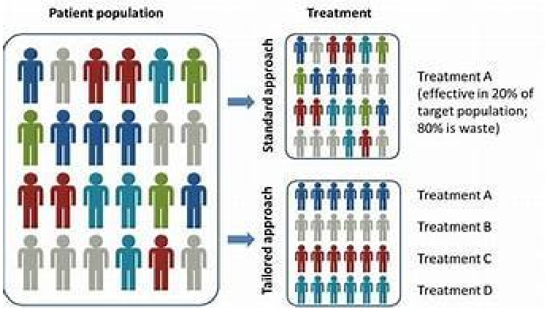
Krithika CK

Bioinformatics'24

The Role of Clinical Bioinformaticians in Precision Medicine

Patients…

No need to worry for handful of medicines for your chronic disorders! You can have medicines according to your genetic profile!



Interesting, isn't it!

In the 21st Century, we have many technologies that assist clinicians in the diagnosis and treatment of pathological conditions. One among them in the field of Bioinformatics is the **Precision Medicine**.

In the technique of precision medicine, treatment is customised for each patient based on the individual's genetic/molecular profile. Precision medicine trials depends on Bioinformatics.

Interested to know how Computational platforms are being used in Precision Medicine?

High-throughput screening (HTP) and Next-generation Sequencing methods are the key for the revolution in the big-data field in bioinformatics.

FARMAPRICE – An IT Based CDSS (Clinical Decision Support Systems)

This tool was developed in Italy and it is being used in Italian healthcare system.

Workflow of FARMAPRICE:

1. Physician is prescribing a medicine to a patient who is a poor metabolizer of some particular enzyme.
2. This in turn triggers a first level pop-up message
3. This in turn triggers pharmacogenomics recommendation of

dosage or drug selection based upon drug selection and dosage.

Bioinformaticians play a crucial role of presenting the information to decision-makers (mostly physicians).

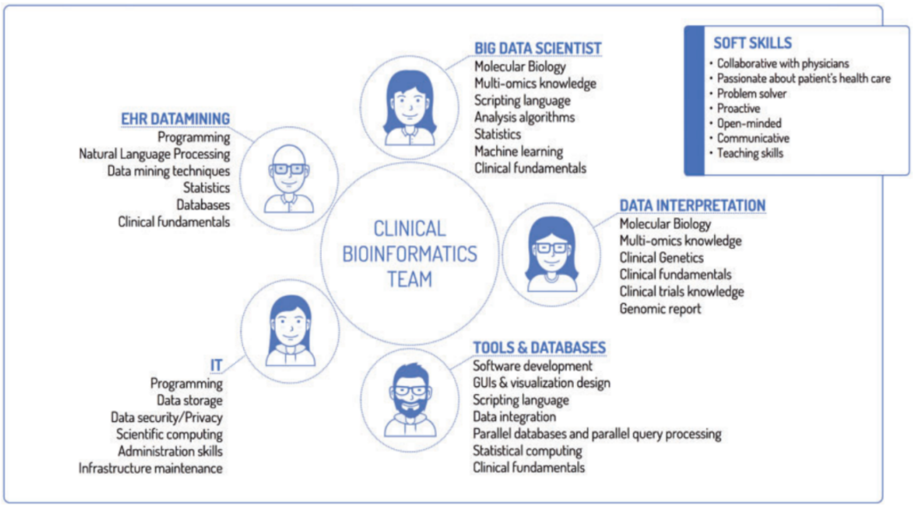


Fig. Laboratory profile of Clinical Bioinformaticians

Fundamental technical skills for Clinical Bioinformaticians

Computational skills:

Linux, Basics of python, R, Big data

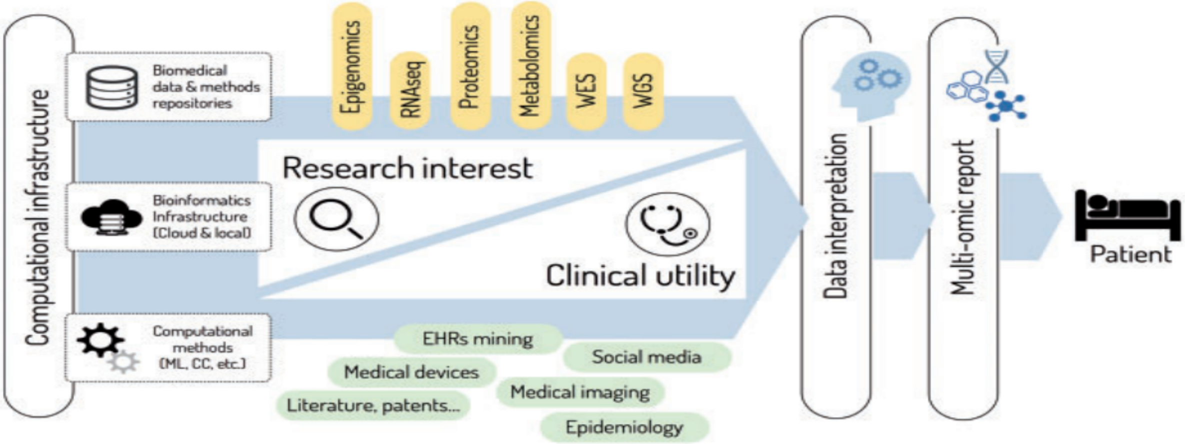
Life sciences:

Understanding Biological databases,

High-throughput data analysis, Multi-omics data

Clinical scenario:

Electronic Health Records (EHR), well skilled in clinical terminology, familiar with clinical trial procedures to improve quality tool for decision-making.



Workflow of precision medicine from patient to computational infrastructure :

Genomic information incorporation in healthcare is not yet achieved and needs to be achieved as it is crucial for many healthcare systems. Precision medicine has incorporated the human cancer with genome sequencing technologies. However, modern medicine in most countries aims at population scale sequencing and determines the prevention or treatment of the disease.

Precision medicine needs technologies for analyzing and processing the data for providing high-speed CDSS tools.

The current situation in the field

The application of systems to medicine is still relatively limited. Bioinformaticians collaborate closely with doctors in clinical decision-making, thereby becoming clinical bioinformaticians.

Statistical Multi-Omics Understanding Consortium (SOUND) develops statistical bioinformatics tools for multi-omics data mining. The clinical bioinformatician is a specialization that is highly demanded in the medical field. Precision medicine is an emerging field that can be expected in India soon by advancements in clinical and bioinformatics side (ie. By Clinical bioinformaticians).

Sruthisupraja G

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