

21 Days Workshop

on

“BIOLOGICAL DATA ANALYSIS AND BIOINFORMATICS”

(Virtual Mode)

(10th April – 30th April, 2024)

Organized By:

GROWING SEED

Dharmanagar, North Tripura

Training Partner ID: TP155604 (Govt. of India)

In Collaboration with:

INDIAN SCIENCE CONGRESS ASSOCIATION

(Dharmanagar Chapter)

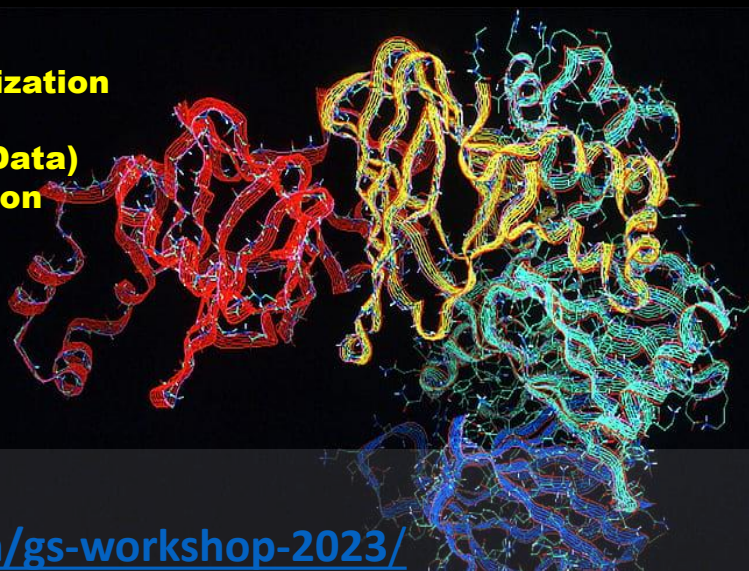
Eligibility:

Student of B.Sc/ M.Sc/Ph.D in Life Science or any Branches of Biological Sciences (Agriculture/Biotechnology/ Veterinary/Pharma/Medical Etc.), JRF-SRF, Researcher, Faculty, and Corporate. Candidates will be selected based on first cum first serve basis.

(Participants must be Indian National)

Topic Highlights:

- **Genomic Databases & Visualization**
- **Statistical Data Analysis (Molecular and Quantitative Data)**
- **Gene Prediction and Annotation**
- **Sequence Alignment**
- **Protein Structure Modelling**
- **Molecular Docking**
- **Drug Discovery**



Registration link:

<https://www.growingseed.in/gs-workshop-2023/>

Time: The program will start from 6 PM to 9 PM during training days

About Host Organization

Growing Seed, a social welfare organization established in 2011 with the aspiration to influence society in a positive manner. Growing Seed Organization has been working continuously for the betterment of the environment as well as for the people. We believe in dynamic and youthful work culture, and our working field is diverse, ranging from medical awareness to agriculture and farmer's development, from conciliation of scientific temper to nurturing of local culture, tradition, and literature. Growing Seed, as an organization, believe in selfless contributions and consider sky as the only limit.

About ISCA- Dharmanagar Chapter

The Dharmanagar Chapter of ISCA, the state chapter for Tripura is housed in the GDC-DMR and has started functioning from June 2017. With guidance from ISCA H.Q. and well wishers across the state the chapter is working to fulfil the aims of ISCA.

Background

Biological data analysis and bioinformatics are two interconnected fields that have revolutionized the study of life sciences. With the rapid advancement of technology and the availability of massive amounts of biological data, the need for sophisticated analytical methods and tools has become crucial. Biological data analysis involves the extraction of valuable information from biological datasets, ranging from genomic sequences and gene expression profiles to protein structures and metabolic pathways. This information provides insights into the fundamental principles of life, disease mechanisms, and potential targets for therapeutic interventions. Bioinformatics, on the other hand, encompasses the development and application of computational algorithms, statistical models, and databases to organize, analyze, and interpret biological data. It combines biology, computer science, and statistics to tackle the challenges posed by the vast and complex nature of biological information. In recent years, the integration of high-throughput technologies, such as next-generation sequencing and mass spectrometry, has led to an explosive growth in biological data generation. This surge in data volume has spurred the development of innovative computational approaches and bioinformatics tools for data storage, retrieval, analysis, and visualization. In biological data analysis, researchers employ various techniques, including sequence alignment, gene expression profiling, network analysis, and machine learning, to unravel the intricate relationships between genes, proteins, and biological processes. These analyses provide crucial insights into genetic variations, gene function, molecular interactions, and regulatory mechanisms. Moreover, bioinformatics plays a pivotal role in the annotation and interpretation of genomic sequences, identification of disease-associated genes, prediction of protein structure and function, drug discovery, and personalized medicine. The integration of diverse data types, such as genomics, transcriptomics, proteomics, and metabolomics, enables researchers to comprehensively study biological systems and unravel complex biological phenomena. Additionally, biological data analysis and bioinformatics contribute significantly to advancements in fields like evolutionary biology, population genetics, comparative genomics, and synthetic biology. They enable researchers to explore the evolutionary history of species, identify genetic variations associated with adaptation, and design novel genetic circuits and synthetic organisms. Overall, biological data analysis and bioinformatics have emerged as indispensable tools for deciphering the mysteries of life. The combination of computational methods and biological expertise has paved the way for groundbreaking discoveries and has the potential to revolutionize healthcare and biotechnology. As biological data continues to grow in volume and complexity, the importance of robust analytical techniques and computational infrastructure will only continue to increase, further driving innovation in these fields.

Patron

Dr. Pradip Bhaumik

**Sectional President of The Indian Science Congress Association (ISCA)
Medical Science (Including Physiology)**

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Organizing Secretary

Dr. Sahanob Nath, Growing Seed, Dharmanagar, India

Joint Organizing Secretary

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Organizing Convener

Mr. Punam Bhattacharjee, Growing Seed, Dharmanagar, India

Joint Organizing Convener

Dr. Subhradip Bhattacharjee, GS Research, Growing Seed, Dharmanagar,
India

Registration link: <https://www.growingseed.in/gs-workshop-2023/>

Bank Details for Online Payment

Bank- UCO Bank

Branch- Chandrapur, Dharmanagar

A/C Name- Growing Seed

A/C No - 25200210001516

IFSC- UCBA0002520

MICR CODE- 799028102

Important Dates

Last date for receipt of application form : 04th April 2024

Confirmation about participation : 7th April 2024

Commencement of program : 10th April 2024

Contact us : training23growingseed@gmail.com

The Organizing Secretary, Growing Seed City Office (admin)

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Contact no: +91 9402595841/ +91 9862636233

Venue: The training and practical programme (Biological Data Analysis And Bioinformatics) will be organized through a virtual lecture/class (Online Mode).

Time: The program will start from 6 PM to 9 PM during training days, Consisting around 1 hour of theory and 2 hours of practical session.

Requirement for Training:

The aspirants should be proficient in the following:

- Basic computer skills.
- Sending/receiving email.
- Sending and receiving attachments via email.
- Using a web browser.
- Finding web resources through search engines.
- Downloading and installing software and/or viewing electronic files.
- Familiarity with using browser plug-ins (e.g., PDF reader, video, audio).
- Using word processing, presentation software, or other productivity applications.
- Experience/familiarity with a variety of file formats such as: .rtf "Rich Text Format", .doc or .docx "Microsoft Word Document", and .txt "Text document".
- The ability to be self-directed in learning new technology skills (for example, following a handout, a step-by-step tutorial, online video help, or access to support to learn necessary skills).

Highlights

The programme will be organized in 6 quadrants i.e.,

1. Lecture through an online platform (Zoom platform or Google Meet).
2. Preparing delivered material that can be downloaded /printed.
3. Self-assessment tests through google classroom assignments/tests/quizzes.
4. An online discussion forum for clearing doubts.
5. The hard copy of the certificate will be provided through India Post.
6. Recorded lectures may be provided on-demand basis.

The above-cited steps have to be taken to enrich the learning experience by using audio-video and multi-media state of art pedagogy/technology. In order to ensure that best quality content lecture is delivered, the course director and his coordinators will monitor the whole technology programme.

Registration Fee Details

Category	Member (Growing Seed)	Non Members
Scientists & Faculty	4000.00	5000.00
Research Scholars, JRF, SRF, RA	2500.00	3000.00
Students	1700.00	2100.00
Corporate	5000.00	7000.00

MAJOR THEMES/SUBTHEMES AND TRACKES OF THE TRAINING PROGRAMME

- 1. Gene Prediction and Annotation:** Gene prediction involves identifying the location and structure of genes within a genome. This is accomplished using computational algorithms that analyze DNA sequences and identify patterns indicative of genes, such as start and stop codons. Gene annotation involves assigning biological functions and characteristics to predicted genes, often by comparing them to known genes or utilizing functional databases.
- 2. Data analysis:** Data analysis in biology involves R software for quantitative & molecular data and specialized software like TASSEL, Structure, and GenAlEx for molecular data. R offers statistical and graphical techniques. TASSEL is used for genetic association and GWAS. Structure infers population genetic structure. GenAlEx assesses genetic diversity and differentiation among populations. These tools empower researchers to make discoveries and support evidence-based decisions.
Data analysis using R software involves performing various quantitative techniques like PCA, correlation analysis, ANOVA (Analysis of Variance) for different models, and more. R's robust libraries and functions make it a powerful tool for analyzing and interpreting data efficiently and effectively.
- 3. Genome Visualization:** Genome visualization tools enable researchers to visualize and explore genomic data in a graphical format. These tools allow for the examination of gene locations, structural variations, epigenetic modifications, and other genomic features. Popular genome visualization tools include the UCSC Genome Browser and the Integrated Genome Viewer (IGV).
- 4. Sequence Alignment and Phylogeny:** Sequence alignment is crucial for phylogenetic analysis, which aims to reconstruct evolutionary relationships between organisms based on their genetic sequences. By aligning sequences from different species or individuals, researchers can identify similarities and differences. These aligned sequences can then be used to construct phylogenetic trees, illustrating the evolutionary history and relatedness of different organisms.
- 5. Protein Structure Databases and Modeling:** Protein structure databases, such as the Protein Data Bank (PDB), store experimentally determined 3D structures of proteins. These databases serve as valuable resources for understanding protein function and drug discovery. Protein modeling techniques, such as homology modeling and ab initio methods, are used to predict protein structures when experimental data is unavailable.
- 6. Protein 3D Structure Prediction and Validation:** Protein 3D structure prediction involves computational methods to predict the 3D structure of a protein based on its amino acid sequence. These methods include template-based modeling, which relies on known structures, and de novo methods, which predict structures from first principles. Validation techniques, such as Ramachandran plots and energy-based scoring functions, are employed to assess the quality and reliability of predicted structures.
- 7. Basics of Molecular Docking of DNA and Protein:** Molecular docking is a computational technique that predicts the binding orientation and affinity between a protein and a ligand, such as a drug molecule or DNA segment. Docking algorithms explore the conformational space of the ligand and receptor to identify optimal binding configurations. It plays a crucial role in drug discovery, allowing researchers to study interactions and design molecules that target specific proteins.
- 8. Concepts of Drug Discovery:** Drug discovery encompasses the identification and development of new therapeutic compounds. It involves various stages, including target identification, lead discovery, lead optimization, preclinical testing, and clinical trials. Genomics data, along with other omics data, plays a significant role in target identification, understanding disease mechanisms, and optimizing drug design.

In summary, genomics databases and tools enable gene prediction, annotation, and visualization, while sequence alignment techniques provide insights into evolutionary relationships. Protein structure databases and modeling aid in understanding protein function, while molecular docking facilitates the design of potential drugs. These concepts form the foundation of genomic research, molecular biology, and drug discovery.

Organizing Coordinator

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