



TWO-DAY DIAMOND JUBILEE
WORKSHOP ON

“TRANSCRIPTOMICS
DATA ANALYSIS:
BIOINFORMATICS
PERSPECTIVE”

MARCH 17-18, 2019

SPONSORED BY
DEPARTMENT OF BIOTECHNOLOGY
(GOVT. OF INDIA)

ORGANIZED BY
BIOINFORMATICS CENTER (SUB-DIC, DBT)
CSIR-CENTRAL INSTITUTE OF MEDICINAL
& AROMATIC PLANTS, LUCKNOW-226015

Workshop Contents:

Bioinformatics databases & data sources

Biological sequence analysis

Sequence families, alignment & phylogeny

Domain families & databases

Transcript profiling

Statistical issues in Transcriptomics analysis

Analyzing differential gene expression

Convener
Dr. Feroz Khan

Coordinator
Dr. A.K. Shasany

Chairman
Dr. Alok Kalra
Director, CSIR-CIMAP

About CSIR-CIMAP

CSIR-Central Institute of Medicinal & Aromatic Plants (CSIR-CIMAP) is a premier multidisciplinary research institute of Council of Scientific & Industrial Research (CSIR), New Delhi, India with its major focus on exploiting the potential of medicinal and aromatic plants (MAPs) by cultivation, bioprospection, chemical characterization, extraction, and formulation of bioactive phytochemicals. With a strength of 100 scientists, 162 technical officers, 129 support staff and nearly 300 doctoral and post-doc scholars at its head-quarter in Lucknow and research centers at Bengaluru, Hyderabad, Pantnagar, and Purara. CSIR-CIMAP has played a key role in positioning India as a global leader in production of mints, vetiver and other aromatic grasses, and in ensuring indigenous production of artemisinin – a WHO approved antimalarial. CSIR-CIMAP houses a National Gene Bank on MAPs, which is one of the three of its kind in India. CSIR-CIMAP has played a key role in successfully commercializing an ayurvedic herbs based antidiabetic formulation, which has now benefitted millions. The institute is presently accredited by ICS-UNIDO and Indian-Ocean Rim Association (IORA) as a focal point for research and training on Medicinal Plants among 21 participating member countries.

About the Workshop

'Omic' technologies cover universal detection of genes (genomics), mRNA (transcriptomics), proteins (proteomics) and metabolites (metabolomics) in a specific biosample. Data analysis is complicated as a massive amount of data generated, and bioinformatician involvement in the process is essential. Transcriptomics data mining is an efficient way to discover genes or gene families encoding enzymes involved in various metabolic pathways. High-throughput next-generation sequencing (NGS) technologies have revolutionized transcriptomics especially with the advent of RNA-sequencing (RNA-seq). This technology can be used to obtain RNA sequences on a massive scale with enormous sequencing depth. Plants produce a vast array of specialized metabolites, many of which used as pharmaceuticals, flavors, fragrances, and other high-value fine chemicals. Most of these compounds occur in non-model plants for which genomic sequence information is not yet available. The production of a large amount of nucleotide sequence data using next-generation technologies is now relatively fast and cost-effective, especially when using the latest Roche-454 and Illumina sequencers with enhanced base-calling accuracy. To investigate specialized metabolite biosynthesis in plants establishment of data-mining framework required by employing next-generation sequencing and computational algorithms, to construct and analyze the transcriptomes of plants that produce compounds of interest for biotechnological applications. After sequence assembly an extensive annotation approach required to assign functional information to transcripts. The annotation based on direct searches against public databases, e.g., RefSeq, InterPro, GO, EC, and associated KEGG pathway maps. This study aims to identify biosynthetic gene candidates related to specific metabolic pathways. These assembled transcriptome data access through web-based BLAST server. Transcriptomes are studied for interpreting functional elements of the genome and revealing molecular constituents of cells and tissues.

The aim of Workshop

To familiarize researchers/students with advances in Bioinformatics tools/methods and its application in plant's transcriptome data mining and analysis. The workshop would cover the following aspects:

- Bioinformatics databases and data sources
- Biological sequence analysis
- Sequence families, alignment, and phylogeny
- Domain families and databases
- Transcript profiling
- Statistical issues in Transcriptomics analysis
- Analyzing differential gene expression

The participants may access online bioinformatics resources related to genomics, transcriptomics, sequence analysis, and functional annotation. The hands-on training gained may help in enhancing their bioinformatics knowledge and tools handling skill.

Registration Fee

Rs.1000/- for faculty/scientists/academicians & Rs.500/- for students/research scholars. The registration fee includes lectures/training manual, brochure, stationery items, lunch, and tea. Fee is to be pay through online to bank A/c No. 00000030267691783, SBI main branch, Hazratganj, Lucknow (IFSC code: SBIN0000125) or Demand Draft in favor of '**Director, CIMAP**'. Complete registration form along with the fee details should reach us on or before March 16, 2019. Registration to the workshop will be on 'First-come-First-serve' basis. For any query, please contact Dr. Feroz Khan (f.khan@cimap.res.in, Mob.9415538701).

For further details please contact:

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Registration Form

Name: _____

Designation: _____

Affiliation: _____

Address: _____

Area of interest: _____

E-mail: _____

Mobile/Phone No.: _____

Payment Details:

Registration Fee: Rs. _____

Mode of payment (Cash/Online/DD): _____

Online Transaction/DD No. _____ Date _____ Bank _____

Signature