Registration Details

Registration Fee : Rs.1500/-

Account Name **MAHER Professional Development Programme**

Registration link: **https://forms.gle/SMpRusEsNBYaZZe97**

Maximum Number of Seats : 30

Last Date for Registration : **18th February, 2025**

Participants should E-mail the transaction details to

crlmaher@maher.ac.in
for confirmation of registration

Organizing Chairs

Dr. N. Arunagirinathan
Dean Research

Dr. P. Balakrishnan
Chief Scientist

Co-organizing Secretaries

Dr. Pavithra Amritkumar
Associate Dean - Consultancy

Dr. D. Thirumal Kumar
Assistant Registrar (Administration)

Organizing Team

Dr. C. Valli Nachiyar
Dean Publication

Dr. D. Nalini
Research Scientist

Dr. S. Sivamalar
Research Scientist

Dr. D. Nallusamy
Research Scientist

Dr. Tharani Munusamy
Research Scientist

Dr. K. Karunanidhi
Research Associate

Dr. S. Suvaithenamudhan
Assistant Professor

Dr. Indhu Purushothaman
Assistant Professor

MEENAKSHI
ACADEMY OF HIGHER EDUCATION & RESEARCH
(DEEMED TO BE UNIVERSITY U/S 3 OF UGC ACT 1956)
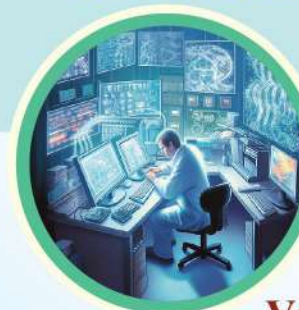
DEPARTMENT OF RESEARCH

MAHER ADVANCED RESEARCH CENTRE
FOR HEALTH SCIENCES (MARCH)

Cordially invite you all for

Two-day Hands-on Bioinformatics Workshop on

VIRAL DIVERSITY, SEQUENCE ANALYSIS, PHYLOGENETICS & MOLECULAR DOCKING

Hybrid Mode (Online or Offline)
Date : 21 & 22 February, 2025

Venue

**3rd FLOOR, DEPARTMENT OF RESEARCH
MEENAKSHI ACADEMY FOR HIGHER EDUCATION AND RESEARCH
DEEMED TO BE UNIVERSITY**

No.12, Vembuliamman Koil Street, West K.K.Nagar, Chennai - 600 078

BENEFITS OF ATTENDING THIS WORKSHOP:

Attending this workshop provides participants with hands-on experience in analyzing viral sequences, constructing phylogenetic trees, understanding viral evolution and basic concepts of molecular docking using freely available online tools. Participants will gain practical skills in sequence alignment, metadata analysis, visualization and molecular docking enhancing their ability to apply bioinformatics techniques in research or public health contexts.

WHO CAN ATTEND THIS WORKSHOP?

This workshop is ideal for researchers, students, and professionals seeking to deepen their knowledge of viral genomics and computational biology.

PROGRAMME SCHEDULE

VIRAL DIVERSITY, SEQUENCE ANALYSIS, PHYLOGENETICS

Workshop Schedule - Day 1 (21.02.2025)

Time	Activity
09:30 AM – 10:00 AM	Registration & Inauguration
10:00 AM – 11:00 AM	Viral Diversity and Evolutionary Concepts
11:00 AM – 11:15 AM	Tea Break
11:15 AM – 01:00 PM	Sequence Databases and Evolutionary Analysis
01:00 PM – 02:00 PM	Lunch Break
02:00 PM – 05:00 PM	Advanced Topics: Drug Resistance, Vaccine Escape, and Recombination

Workshop Schedule - Day 2 (22.02.2025)
MOLECULAR DOCKING

Time	Activity
10.00 AM – 11:15 AM	Protein structure- Modelling and Validation
11:15 AM – 11:30 AM	Tea Break
11:30 AM – 01:00 PM	Ligand Modelling and Toxicity analysis
01:00 PM – 02:00 PM	Lunch Break
02:00 PM – 05:00 PM	Advanced Topics: Molecular Docking and Analysis
05:00 PM – 05:30 PM	Valedictory Program

For all Communications and Queries Contact :

Dr. Pavithra Amritkumar
Mobile: **9940052696**

Dr. D.Thirumal Kumar
Mobile: **8056295915**

ABOUT THE RESOURCE PERSONS:

Dr. Jason Blackard, Professor, University of Cincinnati College of Medicine, Cincinnati, USA leads a research laboratory focused on understanding interactions between viral pathogens, particularly hepatitis C virus (HCV), HIV, and other hepatitis viruses like HBV, HEV, and GBV-C. Dr. Blackard holds a doctoral degree in Biological Sciences in Public Health from Harvard University and completed a research fellowship at the Gastrointestinal Unit of Harvard Medical School/Massachusetts General Hospital. His present work investigates the mechanisms of viral pathogenesis, genetic diversity, and co-infections using cell culture, molecular virology, and patient-derived samples. Current projects include modeling HCV replication, studying HIV replication in hepatocytes, exploring novel systems for HIV/HCV co-infection, and characterizing the genetic and phenotypic properties of viral polymerases. With over 186 peer-reviewed publications predominantly in virology, he is a leading expert in the field.Dr. Blackard's research has significant implications for understanding viral evolution, co-infections, and disease progression

Dr. Daniel Alex Anand, Associate Professor at Sathyabama Institute of Science and Technology, Chennai, brings two decades of expertise in bioinformatics and computational systems biology to address challenges in informatics, data science, and systems medicine. With a PhD specializing in sequence analysis and molecular phylogenetics, his research spans neurological disorders, pharmacogenomics, and bioinformatics algorithm development. Dr. Anand's 100+ peer-reviewed publications and extensive experience mentoring over 300 students underscore his dedication to advancing science and education. His integrative approaches to molecular interaction mapping and big data analytics have significant implications for understanding and treating complex disorders, making him a leading resource in bioinformatics and personalized medicine.