Workshop on

“Art of Scientific Writing, Communication and Basics of Computational Biology”

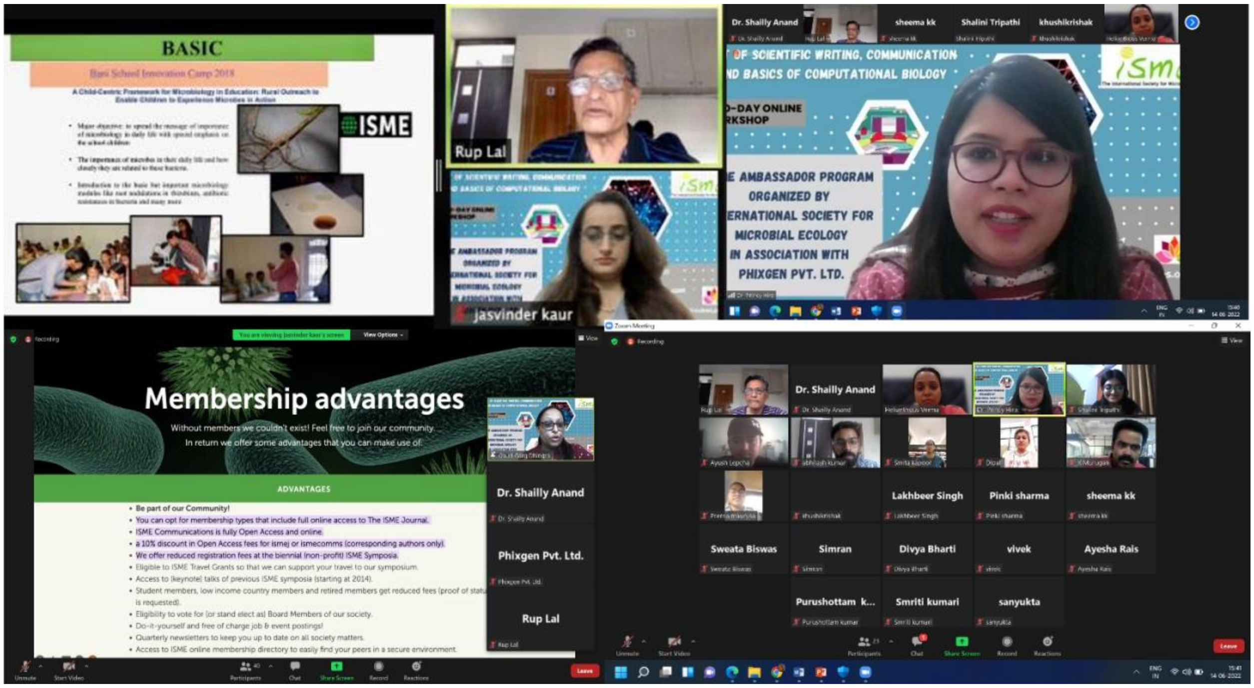
Organized by the International Society for Microbial Ecology (ISME)

under the ISME Ambassador program,

conducted by Phixgen Pvt Ltd. on

<u>DATE: 13-14 June, 2022</u>

ISME's mission is to promote Microbial Ecology research and teaching. On these lines, Dr. Jasvinder Kaur, Gargi College, University of Delhi, opened the session with a welcoming note and an introduction to ISME. Prof. Rup Lal, Senior Ambassador, ISME, made remarks after that (Indian Ocean Region). He discussed the duties of an ISME Ambassador and informed students about the next ISME International Conference in Switzerland. Dr. Gauri Garg Dhingra, Kirori Mal College, University of Delhi, gave an introduction to ISME publications, in which she informed students about the various ISME journals and symposia. Prof. Rup Lal, the workshop's keynote speaker, delivered a session titled "Components of a Manuscript and Their Importance."



Membership advantages

Without members we couldn't exist! Feel free to join our community.
In return we offer some advantages that you can make use of:

ADVANTAGES

- Be part of our Community!
- You can opt for membership types that include full online access to The ISME Journal.
- ISME Communications is fully Open Access and online.
- a 10% discount in Open Access fees for ismej or ismecomms (corresponding authors only).
- We offer reduced registration fees at the biennial (non-profit) ISME Symposia.
- Eligible to ISME Travel Grants so that we can support your travel to our symposium.
- Access to (keynote) talks of previous ISME symposia (starting at 2014).
- Student members, low income country members and retired members get reduced fees (proof of statu is requested).
- Eligibility to vote for (or stand elect as) Board Members of our society.
- Do-it-yourself and free of charge job & event postings!
- Quarterly newsletters to keep you up to date on all society matters.
- Access to ISME online membership directory to easily find your peers in a secure environment.

Day 1: 13 June 2022

The inauguration session was followed by a series of workshop sessions as follows:

Module I- Components of a manuscript and their importance

Resource Person: Prof. Rup Lal, NASI-Senior Scientist Platinum Jubilee Fellow, The Energy and Resources Institute (TERI), New Delhi

Prof. Lal talked on how to write a manuscript that includes carefully all the necessary material so that the research can be understood and replicated by others. He also stressed the importance of a complete, rationally structured, and factual document when presenting any findings. He wrapped off the conversation by emphasizing the need of scientific publications conforming to a precise language and format in order to communicate findings to the scientific community while also complying to ethical rules.

Module II- introduction to scientific writing and designing posters

Resource Person: Dr. Roshan Kumar, P. G. Department of Zoology, Magadh University, Bodh Gaya

Dr. Roshan Kumar provided an in-depth look at the scientific writing and manuscript submission process. He discussed many types of publications, including research papers, reviews, editorials, book reviews, letters to the editor, and book chapters, during his lecture. Following that, he went over the peer review and publication processes in great detail. He commented about the meticulous detailing of the response letter near the end.

Module III: Role of computers and computational languages for studying microbial ecology

Resource Person: Dr. Utkarsh Sood (pHixGen Pvt. Ltd., Gurugram)

The session began with Dr. Utkarsh Sood discussing the use of computers and computational languages in investigating microbial ecology. He covered genetics, microbial ecology, metagenomics, computer hardware, and operating systems fundamentals. Major emphasis was given to Linux operating systems. The Google genomics platform was also explained to the participants. There were also examples of evaluating data that had previously been deposited in public databases and translating the analysis into a useful paper. It was also discussed how important it is to master computational languages like Python and Perl.

Day 2: 14 June 2022

Topic 1: Genome Assembly

Resource Person: Dr. Shailly Anand (Deen Dayal Upadhyaya College, University of Delhi)

In bioinformatics, genome assembly refers to aligning and merging sequencing reads in order to reconstruct the original sequence. In this quest, De novo genome assembly is one of the fundamental problems encountered during sequencing projects. But with the advent of next-generation sequencing (NGS) technologies, which generate large numbers of short (100–400 bp) reads with relatively low sequencing error rates, the past decade has been a witness to the completion of several genome projects with relatively fewer hurdles. There are three main approaches for de novo genome assembly, the greedy strategy, the string overlap graph, and the de Bruijn graph. The session introduced various types of Genome assemblers like Velvet, Celera, Spades, IDBA, Ray, and Abyss. ABySS Assembler was explained in detail. The participants were taught to operate the software and various parameters that need to be taken care of for a good assembly were discussed. At the end of the session, the output files obtained were also discussed in detail with special emphasis on what all information can be deciphered about the assembly.

Topic 2: Genome Annotations

Resource Person: Dr. Princy Hira (Maitreyi College, University of Delhi)

Session on “Genome Annotations” dealt with the basics of annotation like structural and functional annotations, levels of annotation and different tools, hands on exercise on RAST (Rapid Annotation using Subsystem Technology) Server and how it provides a high-quality genome annotation for prokaryotes across the whole phylogenetic tree were explained. Once annotation is completed, genomes can be downloaded in a variety of formats or viewed online. The genome annotation provided does include a mapping of genes to subsystems and a metabolic reconstruction. In addition, students were also taught how to predict closest neighbors for the bacterial genome using RAST.

Topic 3: Phylogenomics

Resource Person: Dr. Helianthous (Ramjas College, University of Delhi)

Dr. Helianthous talked about the concepts of phylogeny and taxonomy. Following that, the students were taught about the genotypic, phenotypic, and chemotaxonomic markers used to classify bacterial species into taxa using a polyphasic approach. The importance and drawbacks of using the 16S rRNA gene sequence to create phylogenetic trees were next discussed. The benefits of employing genomic-based approaches to analyze the 16S rRNA gene sequence were then described, including two types of Phylogenomic methods: whole genome and core genome.

Following that, approaches based on the entire genome, such as Average Nucleotide Identity (ANI), Average Amino acid Identity (AAI), and Genome to Genome Distance Calculator (GGDC), were discussed. These analyses were demonstrated to the students using previously saved data, followed by the creation of a heat map and dual dendrogram using the multi-experiment viewer (MeV). After that, students were asked to raise any questions they had and to practice on their own systems.

The workshop ended with concluding remarks by Prof. Rup Lal.