Name of the Program: M.Sc. Marine Microbiology
Course Code: MMI-612
Title of the Course: Bioinformatics in Marine Microbiology
Number of Credits: 02
Effective from AY: 2022 - 23

Prerequisites for the course:	Students should have undergone M.Sc. Marine Microbiology/Marine Biotechnology Semester III Courses.	
Objective:	To understand the basics of bioinformatics and learn to analyse phylogeny and metagenomics data for diversity studies.	
Content:	**Module I** Introduction to microbiome research. Data mining – DNA sequence assembly and annotation of genes. Types of User Interface (CUI, GUI). Biological Databases and search tools. Sequence alignment: Pairwise, Multiple. Similarity and homology of sequences. Orthologs, paralogs, analogs. Sequence alignment tools. Similarity and distance, similarity scores, weight matrices, Heuristic method, Hidden Markov Models. Gene annotation, phylogenetics: gene phylogeny versus species phylogeny. Sequence-based classification and identification, Operational Taxonomic Units, rooted and unrooted trees. Approaches in phylogenetic analysis – phenetic, cladistic, evolutionary systematic approach. Methods in tree construction – distance-based methods (UPGMA, NJ, ME), character-based methods (MP, ML).	15 hrs.
	Module II Metagenomics: 16S rRNA amplicon sequencing for metagenomics or targeted metagenomics pipelines to analyse the raw data generated from next generation platforms. Quality check and filtering of sequences, pairing of reads, grouping of reads into OTUs or/and Amplicon Sequence Variants (ASVs). Databases for taxonomic identification. Alignment of OTUs, α-(within group) and β-diversity (between groups) comparison. Full Shotgun DNA metagenomics – de-multiplexing of raw reads, quality check, conversion to FASTQ format files, QIIME/QIIME2, clustering into OTUs, assigning taxonomy to the clusters, Prokka, metAMOS. Introduction to predictive functional analyses and tools for visualization.	15 hrs.
Pedagogy:	Lectures/ assignments/ interactive learning.	
References/ Readings:	1. Lesk, A. M. (2005). *Introduction to bioinformatics.* Oxford University Press. 2. Jean-Michel, C. (2005). *Bioinformatics: a beginner's guide*. India: Wiley Dreamtech. 3. Shanmughavel, P. (2005). *Principles of bioinformatics*.	

	Jaipur: Pointer Publishers.	
	4. Jeremy, J. R., (2004). *Bioinformatics: an introduction*. India: Springer Publishers. 5. Rastogi, C. (2004). *Bioinformatics: concepts, skills & applications.* New Delhi: CBS Publishers. 6. Mount, D. (2000). *Bioinformatics: sequence and genome analysis*. New York: Cold Spring Harbor Laboratory Press. 7. Baxevanis, A. (2001). *Bioinformatics: a practical guide to the analysis of genes and proteins*. New York: John Wiley & Sons. 8. Srinivas, V.R. (2005). *Bioinformatics: a modern approach*. New Delhi: Prentice Hall of India. 9. Ignacimuthu, S. (2008). *Basic bioinformatics.* New Delhi: Narosa Publishing House. 10. Khan, I.A. (2005). *Elementary bioinformatics*. Hyderabad: Pharma Book Syndicate.	
Course Outcomes:	1. Identify various data mining procedures. 2. Apply appropriate models for bioinformatic analysis. 3. Create suitable phylogenetic tree for microbiome analysis. 4. Discuss the workflow for metagenomics analysis of environmental samples. 5. Choose various tools for diversity and functional analyses of environmental samples.	