

Name of the Program: M.Sc. Marine Microbiology

Course Code: MMI-613

Title of the Course: Bioinformatics in Marine Microbiology Practical

Number of Credits: 01

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 database search, sequence-based identification and phylogenetic tree construction for evolutionary studies.	
Content:	Module I 1. NCBI search tool, nBLAST (2 hrs, Ref. 1-6). 2. Downloading type sequences, creating FASTA files for alignment, sequence alignment (2 hrs, Ref. 1-6). 3. Construction of phylogenetic trees (4 hrs, Ref. 1-6). 4. Introduction to Galaxy workflow (10 hrs, Ref. 7-10). 5. QIIME2 workflow (12 hrs, Ref. 7-10).	30 hrs.
Pedagogy:	Experiments/ videos/ tutorials in the laboratory.	
References/Readings:	1. Lesk, A. M. (2005). <i>Introduction to bioinformatics</i>. Oxford University Press. 2. Jean-Michel, C. (2005). <i>Bioinformatics: a beginner's guide</i>. India: Wiley Dreamtech. 3. Jeremy, J. R., (2004). <i>Bioinformatics: an introduction</i>. India: Springer Publishers. 4. Mount, D. (2000). <i>Bioinformatics: sequence and genome analysis</i>. New York: Cold Spring Harbor Laboratory Press. 5. Baxevanis, A. (2001). <i>Bioinformatics: a practical guide to the analysis of genes and proteins</i>. New York: John Wiley & Sons. 6. Ignacimuthu, S. (2008). <i>Basic bioinformatics</i>. New Delhi: Narosa Publishing House. 7. Greenwald, W. W., Klitgord, N., Seguritan, V., Yooseph, S., Venter, J. C., Gamer, C., Nelson, K.E., & Li, W. (2017). Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. <i>BMC Genomics</i>, 18, 296. 8. Sczyrba, A. et al. (2017). Critical assessment of metagenome interpretation – a benchmark of computational metagenomics software. <i>Nature Methods</i>, 14(11), 1063-1073. 9. Vollmers, J., Wiegand, S., & Kaaster, A-K. (2017). Comparing and evaluating metagenome assembly tools from a microbiologist's perspective – not only size matters! <i>PloS One</i>, 12 (1), e0169662.	

	10. Hiltemann, S. D., Boers, S. A., van der Spek, P. J., Jansen, R., Hays, J. P., & Stubbs, A. P. (2019). Galaxy mothur toolset (GmT): a user-friendly application for 16S rRNA gene sequencing analysis using mothur. <i>GigaScience</i> , 8, 1-5.	
Course Outcomes:	1. Design workflow for phylogenetic analysis of microbial cultures. 2. Discuss metagenomics workflow for environmental studies. 3. Apply open-source bioinformatics software for use in microbiome analysis. 4. Design a roadmap for analysis of high throughput sequence data.	