upf. Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2024-2025

Personal Information

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Project

Computational genomics

Project Title:

The Ocean Microbiome: Exploring Population Dynamics and Evolutionary Adaptations in a Changing Ocean

Keywords:

ocean, microbiome, population genomics, evolution

Summary:

The oceans play a crucial role in Earth's functioning and climate regulation, and the microscopic organisms they harbor are critical for this role. Microbial phytoplankton in the ocean, for instance, fix as much carbon from the atmosphere as terrestrial plants, while other heterotrophic microbes ensure that a portion of the fixed carbon circulates through food webs, supporting animal life. In the face of global change, we must deepen our understanding of marine microbes and their potential response to an increasingly warm ocean. Over the past 15 years, the genomic machinery of the ocean microbiome has been extensively researched, thanks to the emergence of High Throughput DNA Sequencing. This technology has facilitated the discovery of millions of new genes in the ocean, subsequently linked to metabolisms and genomes. However, our grasp of the fine-grained genomic variation typically associated with populations remains limited. Investigating these populations could reveal specific adaptations to varying oceanic conditions, enabling a better understanding of natural selection and the identification of gene variants that may code for proteins with functional variation. Furthermore, our current understanding of how this fine variation behaves across time and space, due to selection or drift, leading to evolutionary change, remains rudimentary. As a result, exploring population genomics and fine evolutionary change are among the most significant challenges in ocean microbiome research for the coming decade. The proposed master's project aims to: 1. Determine the population variation of selected ocean microbes using Single Nucleotide Variants (SNVs). 2. Investigate whether some of the observed variants can be attributed to evolutionary processes that occurred relatively recently in geological time. This project will utilize short (Illumina) and long-read (PacBio HiFi) metagenome datasets from two global ocean expeditions (Tara Oceans and Malaspina) as well as monthly metagenomes from two coastal microbial observatories in the Mediterranean Sea over twenty (BBMO) and seven (SOLA) years. Together, these datasets comprise terabytes of genomic data, being possibly the best representation we have so far of the diversity and function of marine microbes. We will analyze metagenome-assembled genomes (MAGs) and map short metagenomic reads from the global ocean or time-series datasets to a selection of ecologically significant MAGs. Subsequently, we will perform SNV calling analysis to delve into population genomics, with the goal of linking populations with environmental or geographic features. SNV analyses will help determine whether part of the detected variation has emerged through adaptive evolution. The majority of the work will involve bioinformatics, statistics, and machine learning, with analyses being conducted at our marine bioinformatics platform Marbits (https://marbits.icm.csic.es) and the Finisterrae III supercomputer at CESGA in Galicia, through CSIC agreements. This project is an excellent opportunity for a motivated student interested in working at the intersection of microbiology, meta-omics, bioinformatics, and oceanography. Participation in this project may lead to future opportunities in the EU's prioritized research area of blue biotechnology through bioprospecting gene variants from the ocean microbiome for industrial applications (https://ec.europa.eu/maritimeaffairs/policy/biotechnology_en). Financial support may be available through the CSIC's JAE intro program or other projects (subject to discussion). The Log-Lab has previously hosted seven master's students from the Master in Bioinformatics for Health Sciences program, with most continuing their PhD studies at the Institute of Marine Sciences (ICM-CSIC) or abroad, or working as bioinformaticians at the ICM-CSIC. The ICM-CSIC is the largest marine research center in Spain and a leader in its field, having received the Severo Ochoa excellence distinction. The ICM provides a dynamic, stimulating, and multidisciplinary research environment that is committed to promoting the career development of young researchers (https://www.icm.csic.es/en). This project offers a unique opportunity for a dedicated student to contribute to the growing field of

marine microbiome research and potentially make a lasting impact on our understanding of marine microbes and their role in our changing world.

References:

Falkowski, P. The power of plankton. Nature, 2012. 483(7387): p. S17-20. Logares R, et al. (2020) Disentangling the mechanisms shaping the surface ocean microbiota. Microbiome 8:55 Santos-Júnior CD, etal. (2020) Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. Microbiome 8:151 Sunagawa, S., et al., Structure and function of the global ocean microbiome. Science, 2015. 348(6237): p. 1261359. Carradec, Q., et al., A global ocean atlas of eukaryotic genes. Nat Commun, 2018. 9(1): p. 373. de Vargas, C., et al., Eukaryotic plankton diversity in the sunlit ocean. Science, 2015. 348(6237): p. 1261605. Junger, P. C., Sarmento, H., Giner, C. R., Mestre, M., Sebastián, M., Morán, X. A. G., Arístegui, J., Agustí, S., Duarte, C. M., Acinas, S. G., Massana, R., Gasol, J. M., & Logares, R. (2023). Global biogeography of the smallest plankton across ocean depths. Science Advances, 9(45), eadg9763. https://doi.org/10.1126/sciadv.adg9763

Expected skills:

R or Python, familiar with Bash. To have basic notions of ecology and evolution

Possibility of funding:

To be discussed

Possible continuity with PhD:

To be discussed

Comments:

Flexibility for remote and in-person work