

# Master project 2020-2021

## Personal Information

<b>Supervisor</b>	Ramiro Logares
<b>Email</b>	ramiro.logares@icm.csic.es
<b>Institution</b>	ICM - CSIC
<b>Website</b>	<a href="http://www.log-lab.barcelona">http://www.log-lab.barcelona</a>
<b>Group</b>	Ecology of Marine Microbes & log-lab

## Project

## Computational genomics

### Project Title:

Population dynamics and evolution of the ocean microbiome

### Keywords:

microbiome, ocean, metagenomics, evolution, ecology

### Summary:

The global ocean and the tiny organisms it contains are crucial for global ecosystem function. Microbial phytoplankton in the ocean fix as much carbon from the atmosphere as land plants, and other heterotrophic microbes guarantee that most of the fixed carbon is circulated through food webs. The genomic machinery that marine microbes use for performing a myriad of metabolic processes remained unknown until ca. 15 years ago, when large-scale DNA sequencing projects became feasible. With the advent of high-throughput DNA sequencing, we started unveiling the ocean microbiome at unprecedented levels of detail. During the last 5 years, very large genomic datasets have been extracted from the global ocean microbiome. In particular, the global expeditions TARA-Oceans (<https://oceans.taraexpeditions.org>) and Malaspina (<http://www.expedicionmalaspina.es>) have produced a goldmine of genomic data that we are continuously explored. This data is the best representation we have of the diversity and function of marine microbes, and considers mostly metagenomes and metatranscriptomes (ca. 30 Terabytes of compressed DNA data). My group at the ICM-CSIC (log-lab <http://www.log-lab.barcelona> at the EMM <https://emm.icm.csic.es>) is involved in both global marine expeditions. The proposed project aims at interrogating these datasets in order to 1) determine the population variation of selected microbes (using mutations; a.k.a. SNPs or Single Nucleotide Polymorphisms) in the global ocean and 2) find out whether some of the previous variation is due to evolutionary processes that occurred relatively recently in geological time. For investigating the above, we will build metagenome-assembled genomes (MAGs) and then map metagenomic or metatranscriptomic reads from the global ocean to a number of selected MAGs. Afterwards, we will perform a SNP calling analysis, aiming to determine fine-grained genomic variation. The analysis of these SNPs is what will indicate how much variation is present in the selected microbial populations and whether part of this variation has emerged through adaptive evolution. Most analyses for this work will be performed at our marine bioinformatics platform Marbits <https://marbits.icm.csic.es>

### References:

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. Logares, R., et al., Disentangling the mechanisms shaping the surface ocean microbiota. 2020. *Microbiome*. In press. <https://www.researchsquare.com/article/rs-7862/v2> Falkowski,

P., The power of plankton. Nature, 2012. 483(7387): p. S17-20. Alberti, A., et al., Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Sci Data, 2017. 4: p. 170093. de Vargas, C., et al., Eukaryotic plankton diversity in the sunlit ocean. Science, 2015. 348(6237): p. 1261605.

**Expected skills::**

Proficiency with bash and R. Familiar with python.

**Possibility of funding::**

To be discussed

**Possible continuity with PhD: :**

To be discussed

**Comments:**

motivation, interest to learn new bioinformatics techniques and to work in clusters

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