



## Master project 2021-2022

### Personal Information

<b>Supervisor</b>	Silvia G. Acinas & Pablo Sanchez
<b>Email</b>	sacinas@icm.csic.es
<b>Institution</b>	Institute of Marine Science (ICM) CSIC
<b>Website</b>	<a href="https://www.icm.csic.es/en">https://www.icm.csic.es/en</a>
<b>Group</b>	Ecology and Genomics of Marine Microbes

### Project

## Computational genomics

#### Project Title:

Revealing active prokaryotic genomes from the global Deep Ocean microbiome.

#### Keywords:

Malaspina Expedition, deep ocean, metagenomes, metatranscriptomes, metagenomic assembled genomes, web development, functional analyses, comparative genomics.

#### Summary:

The Malaspina expedition has represented a milestone in the Spanish science: a unique expedition that has collected biological samples at a global scale. We have sequenced more than 200 metagenomes and 50 metatranscriptomes from all the temperate oceans across the globe, with emphasis in the bathypelagic (between 1000 and 4000 m deep), comprising 7 Terabases and 30.000 million read pairs. This unprecedented dataset has allowed us to generate a marine microbial gene catalog (M-geneDB) of more than 50 million of distinct genes, many of them with still unknown function. We have also generated a first collection of 317 high-quality metagenome-assembled genomes (MAGs) from deep-ocean bacteria and archaea that has allowed us to get a glimpse on the metabolic potential of the keystone prokaryotes in the bathypelagic (Acinas et al., 2019). The MAG collection include potentially chemolithoautotrophic microorganisms - capable to incorporate inorganic carbon in the absence of light, as well as other microorganisms capable of nitrogen fixation - an essential element for life scarce in the ocean. We still don't know how active these microorganisms are in the deep ocean, and therefore their relevance in the biogeochemical cycles as active keyplayers remains unknown. The analysis of the metatranscriptomes of the Malaspina expedition will be crucial to better understand microbial diversity and functioning in this unexplored ecosystem on Earth. The goals of this TFM project would be: 1) to analyze the Malaspina bathypelagic metatranscriptomes, mapping them to the MAG collection and to explore their metabolic activity, 2) to develop a web front-end to query and visualize our MAGs collection from the Malaspina global expedition, 3) to assist in increasing the MAG collection by assembling, binning and annotating metagenomes.

#### References:

1. Acinas, S. et al. Metabolic Architecture of the Deep Ocean Microbiome. bioRxiv 635680 (2019). doi:10.1101/635680

#### Expected skills::

The applicant should be proficient in the unix command line and R. Knowledge of shiny and/or web development tools and MySQL will be a plus. She or he should be pro-active and able to acquire new skills autonomously.

#### Possibility of funding::

To be discussed

**Possible continuity with PhD: :**

To be discussed

**Comments:**

The candidate would be integrated within the team of Dr. Acinas under the close supervision of the bioinformatician Dr. Pablo Sánchez and Dr. Acinas. The candidate would be also interacting with other members of the Acinas' lab and other PIs of the department. The candidate would have an active scientific environment attending to lab meetings and seminars at the ICM.

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