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:

Unraveling the diversity and genomic data of marine microbial predators

Keywords:

Single Cell Genomics, Illumina assembling, Gene prediction and function, Microbial eukaryotes, Phagotrophy

Summary:

Molecular surveys of microbial eukaryotic diversity in the past two decades have unveiled many novel and uncharacterized species that are major components of marine ecosystems. The extent of this novelty is particularly dramatic among the heterotrophic and mostly bacterivorous species. These eukaryotic predators play key trophic roles in marine ecosystems but there is little knowledge regarding their ecophysiology and the genomic basis of its bacterivorous activity. In our lab we address this question by using metabarcoding, metagenomics, metatranscriptomics and single-cell genomics on natural microbial communities. In this master project, the student will work in the analysis of a large collection of single-cell amplified genomes (SAGs) collected at the Blanes Bay Microbial Observatory, assisting in the assembly, gene prediction and functional annotation of the partial genomes and identifying the taxonomical affiliation of the SAGs retrieved. Genes related with phagocytosis-related processes, such as digestive enzymes or proton pumps, will be screened in this highly diverse collection of microbial eukaryotic genomes. This offered project will provide to the student an ample overview of genomics and bioinformatics applied to environmental sciences.

References:

Obiol, A., D. López-Escardó, E.D. Salomaki, M.M. Wiśniewska, I. Forn, E. Sà, D. Vaqué, M. Kolísko, and R. Massana. 2023. Gene expression dynamics of natural assemblages of heterotrophic flagellates during bacterivory. Microbiome 11:134. 10.1186/s40168-023-01571-5 Massana, R., and D. López-Escardó. 2022. Metagenome assembled genomes are for eukaryotes too. Cell Genomics 2:100130. doi:10.1016/j.xgen.2022.100130 Labarre, A., D. López-Escardó, F. Latorre, G. Leonard, F. Bucchini, A. Obiol, C. Cruaud, M.E. Sieracki, O. Jaillon, P. Wincker, K. Vandepoele, R. Logares, and R. Massana. 2021. Comparative genomics reveals new functional insights in uncultured MAST species. ISME J. 15:1767–1781. doi:10.1038/s41396-020-00885-8 Massana, R., A. Labarre, D. López-Escardó, A. Obiol, F. Bucchini, T. Hackl, M.G. Fischer, K. Vandepoele, D.V. Tikhonenkov, F. Husnik, and P.J. Keeling. 2021. Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. ISME J. 15:154–167. doi:10.1038/s41396-020-00770-4

Expected skills:

UNIX, bash, python, R programming. Notions of protein databases and functional assignations

Possibility of funding:

To be discussed

Possible continuity with PhD:

Yes