Master project 2021-2022

Personal Information	
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Project

Web development & bioinformatic tools

Project Title:

Shiny Tree

Keywords:

reference databases, shiny, eDNA, microbiome

Summary:

The laboratory The del Campo Lab is based at the Institut de Biologia Evolutiva (UPF-CSIC) in Barcelona. The research at the del Campo Lab is focused on the study of host-associated microbes and the effect of global warming on the microbiomes of benthic and planktonic marine animals. We have a wet and dry lab, to perform experiments and bioinformatics analysis, enabling the broadest possible goals. The ongoing climate change and its effects on the environment, such as rising sea temperature, has strong impacts on free-living marine microbial communities. However, the effects of global warming have not been properly studied on host-associated microbiomes. Microbiomes (both prokaryotic and eukaryotic) associated with host organisms have a strong influence on host evolution, physiology, and ecological functions. We study how environmental changes resulting from global warming affect the composition and function of the microbiomes in key members of the marine fauna and consequently how these changes affect the hosts. Currently, our study focuses on these impacts on corals, teleost fish, and zooplankton. To tackle this novel research topic, we use a combination of molecular biology, ecophysiology, and bioinformatics. The proposed project Phylogenetic trees are essential to interpret evolutionary relationships and have become crucial in order to curate taxonomically the references databases used for microbiome and eDNA (biomonitoring) analysis. However, not all the researchers that keep the have the neeeded taxonomic know-how to properly curate the aforementioned databases are familiar with the use of the terminal or the use of phylogenetic tree building software. The aim of the proposed project is to build a Shiny app to facilitate tree building, edition and manipulation to non-experts in a user-friendly manner. Using established tools such as fasttree, RAxML or ggtree we will build a Shiny app that will be integrated into a reference database curation pipeline that we are designing in collaboration with The Carpentries (https://carpentries.org/) as part of the EukRef project (https://pr2-database.org/eukref/about/).

References:

del Campo, J. et al. (2018) EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. PLOS Biol. 16, e2005849 Yu, G. et al. (2017) Ggtree: an R Package for Visualization and Annotation of Phylogenetic Trees With Their Covariates and Other Associated Data. Methods Ecol. Evol. 8, 28–36

Expected skills::

R, Shiny

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed