

Resource Summary Report

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Bioinformatic analysis of biomarker genes using metagenomic shotgun sequence datasets

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Type: Protocol

Proper Citation

Fernando Espinola 2018. Bioinformatic analysis of biomarker genes using metagenomic shotgun sequence datasets. protocols.io dx.doi.org/10.17504/protocols.io.u32eyqe

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.u32eyqe>

Authors: Fernando Espinola

Summary: This protocol describes the steps used to analyze shotgun sequences deposited in Integrated Microbial Genomes and Microbiomes (IMG/M) by using functional annotation evidences. KEGG orthology terms and pathways are used as evidence. The abundance of each of the corresponding biomarker genes is estimated by calculating the proportion of amino acid sequences assigned to the KO of interest (estimated gene copies, assembled and unassembled metagenomes, as retrieved from IMG/M) and normalized with respect to the total number of sequences assigned to KOs in each metagenome.

Associated Publications: Calderoli PA, Espinola FJ, Dionisi HM, Gil MN, Jansson JK, Lozada M (2018) Predominance and high diversity of genes associated to denitrification in metagenomes of subantarctic coastal sediments exposed to urban pollution. PLoS ONE 13(11): e0207606. doi: [10.1371/journal.pone.0207606](https://doi.org/10.1371/journal.pone.0207606)

Affiliations: CESIMAR-CENPAT-CONICET

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