

SHOGUN: Simeaultaneous

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Abstract

SHOGUN is a software pipeline for simultaneous taxonomic and functional abundance profiling of metagenomics datasets with Bayesian redistribution of ambiguous mapping. The pipeline is built in a modular fashion so that it may be run in its entirety or individual parts may be flexible allowing for user creation of a reference database and selection of the alignment tool that best fits a given users data and computational resources. The package allows users to efficiently go from quality-controlled sequences to abundance profiles consistently and accurately, enabling reproducible metagenomic sequencing research.

Hello World

References
