

Manubot Rootstock: Manuscript Title

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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.

Manubot Rootstock Information

Note: Manubot instances should delete this file.

The Manubot is a system for automating scholarly publishing. Content is written in [Pandoc Markdown](#) source files. See `USAGE.md` for more information on how to use the Manubot.

The Manubot project began with the [Deep Review](#), where it was used to compose a highly-collaborative review article [1]. Other manuscripts that were created with Manubot include:

- The Sci-Hub Coverage Study ([GitHub](#), [HTML manuscript](#))
- Michael Zietz's Report for the Vagelos Scholars Program ([GitHub](#), [HTML manuscript](#)) [2]

If you notice a problem with Manubot, it's best to submit an upstream fix to the appropriate repository: `greene1ab/manubot-rootstock` for the git repository stub or `greene1ab/manubot` for the Python package.

References

1. Opportunities And Obstacles For Deep Learning In Biology And Medicine

Travers Ching, Daniel S. Himmelstein, Brett K. Beaulieu-Jones, Alexandr A. Kalinin, Brian T. Do, Gregory P. Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M Hoffman, ... Casey S. Greene

Cold Spring Harbor Laboratory (2017-05-28) <https://doi.org/10.1101/142760>

2. Vagelos Report Summer 2017

Michael Zietz

Figshare (2017) <https://doi.org/10.6084/m9.figshare.5346577>