Manubot Rootstock: Manuscript Title

This manuscript ([permalink](https://bhillmann.github.io/SHOGUN-paper/v/04663593b0fc028b730834c98489bb4d63d29e77/)) was automatically generated from [bhillmann/SHOGUN-paper@0466359](https://github.com/bhillmann/SHOGUN-paper/tree/04663593b0fc028b730834c98489bb4d63d29e77) on May 18, 2018.

## Authors

* **John Doe** ORCID icon [XXXX-XXXX-XXXX-XXXX](https://orcid.org/XXXX-XXXX-XXXX-XXXX) · GitHub icon [johndoe](https://github.com/johndoe) · Twitter icon [johndoe](https://twitter.com/johndoe) Department of Something, University of Whatever · Funded by Grant XXXXXXXX
* **Jane Roe** ORCID icon [XXXX-XXXX-XXXX-XXXX](https://orcid.org/XXXX-XXXX-XXXX-XXXX) · GitHub icon [janeroe](https://github.com/janeroe) Department of Something, University of Whatever; Department of Whatever, University of Something

## 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 indivual 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](http://pandoc.org/MANUAL.html#pandocs-markdown) source files. See [USAGE.md](https://github.com/greenelab/manubot-rootstock/blob/master/USAGE.md) for more information on how to use the Manubot.

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

* The Sci-Hub Coverage Study ([GitHub](https://github.com/greenelab/scihub-manuscript), [HTML manuscript](https://greenelab.github.io/scihub-manuscript/))
* Michael Zietz’s Report for the Vagelos Scholars Program ([GitHub](https://github.com/zietzm/Vagelos2017), [HTML manuscript](https://zietzm.github.io/Vagelos2017/)) [[2](#ref-15nwuvjrA)]

If you notice a problem with Manubot, it’s best to submit an upstream fix to the appropriate repository: [greenelab/manubot-rootstock](https://github.com/greenelab/manubot-rootstock) for the git repository stub or [greenelab/manubot](https://github.com/greenelab/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>