

OptiFit: a fast method for fitting amplicon sequences to existing OTUs

2020-12-08

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¹ **Abstract**

² **Importance**

3 Introduction

4 Results

- 16S rRNA gene sequence datasets from human gut, mouse gut, marine, and soil environments were downloaded, processed with mothur, and clustered *de novo* with OptiClust.
- Independent reference databases (greengenes, silva, and RDP) were clustered *de novo*, then query datasets were fit to the *de novo* OTUs using OptiFit.
 - In open-reference mode, OTU quality as measured by the MCC score was similar between fitting the datasets to reference OTUs with OptiFit and clustering the datasets *de novo* with OptiClust.
 - However, in closed-reference mode, OTU quality was slightly worse when fitting to greengenes and silva, and much worse when fitting to RDP as compared to OptiClust. OptiFit was able to map more query sequences to reference OTUs created with the greengenes and silva databases than with RDP.
 - These results held true for all four datasets and all three reference databases.
- Datasets were randomly split into a reference fraction and a query fraction.
 - Reference sequences were clustered *de novo* with OptiClust.
 - Query sequences were then fit to the *de novo* OTUs with OptiFit.
 - Reference sizes from 10% to 80% of the sequences were created, with the remaining sequences used for the query.
 - OTU quality from fitting split datasets was highly similar to that from *de novo* clustering the whole dataset.
 - Closed-reference OptiFit with split datasets was faster than OptiClust on whole datasets.
 - * OptiClust performed faster than open-reference OptiFit only when the OptiFit reference fraction was 30% or less.

– Different methods for selecting the sequences to be used as the reference were tested; simple random sample, weighting sequences by relative abundance, and weighting by similarity to other sequences in the dataset.

* OTU quality was similar with the simple and abundance-weighted sampling, but slightly worse with similarity-weighted sampling.

- vsearch with greengenes

Discussion

Materials and Methods

Acknowledgements

KLS received support from the NIH Training Program in Bioinformatics (T32 GM070449).

The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

Author Contributions

References