Alignment-free distance estimation ...

This manuscript ([permalink](#)) was automatically generated from [bluegenes/2021-ani-paper@de414d1](#) on December 28, 2020.

Authors

- **N. Tessa Pierce Ward**
  [0000-0002-2942-5331](#) · [bluegenes](#) · [saltyscientist](#)
  Department of Population Health and Reproduction, University of California, Davis · Funded by NSF 1711984, NSF 2018911

- **C. Titus Brown**
  [0000-0001-6001-2677](#) · [ctb](#) · [ctitusbrown](#)
  Department of Population Health and Reproduction, University of California, Davis · Funded by Moore Foundation GBMF4551

Abstract

Introduction

Pairwise overall genome relatedness forms the basis genome-based taxonomic classification and phylogentic analysis. Average Nucleotide Identity (ANI) is a widely-accepted method for estimating genome similarity. Massive-scale sequencing of microbial genomes has necessitated a transition to alignment-free estimation of genome relatedness. A number of alignment-free similarity estimates exist, including several that closely approximate ANI.

Acknowledgements

Author Contributions

Author	Contributions
NTP	Conceptualization; Methodology; Writing - Original Draft; Writing - Review and Editing; Visualization; Supervision; Funding Acquisition
...	...
CTB	Conceptualization; Methodology; Writing - Original Draft; Writing - Review and Editing; Visualization; Supervision; Funding Acquisition

Competing Interests

The authors declare no competing interests.

References

1. **Open collaborative writing with Manubot**
   Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter
   PLOS Computational Biology (2019-06-24) https://doi.org/c7np
   DOI: 10.1371/journal.pcbi.1007128 · PMID: 31233491 · PMCID: PMC6611653

2. https://github.com/bluegenes/2021-ani-paper