Lawrence Berkeley National Laboratory

Recent Work

Title

MicroPheno: predicting environments and host phenotypes from 16S rRNA gene sequencing using a k-mer based representation of shallow sub-samples.

Permalink https://escholarship.org/uc/item/39t3r53h

Journal Bioinformatics (Oxford, England), 35(6)

ISSN 1367-4803

Authors

Asgari, Ehsaneddin Garakani, Kiavash McHardy, Alice C <u>et al.</u>

Publication Date 2019-03-01

DOI

10.1093/bioinformatics/bty652

Peer reviewed

1082

Corrigendum

MicroPheno: predicting environments and host phenotypes from 16S rRNA gene sequencing using a k-mer based representation of shallow sub-samples

Ehsaneddin Asgari^{1,2}, Kiavash Garakani¹, Alice C. McHardy², Mohammad R.K. Mofrad^{1,3,*}

¹Molecular Cell Biomechanics Laboratory, Departments of Bioengineering and Mechanical Engineering, University of California, Berkeley, CA, 94720, USA, ²Computational Biology of Infection Research, Helmholtz Center for Infection Research, 38124 Braunschweig, Germany and ³Molecular Biophysics and Integrated Bioimaging, Lawrence Berkeley National Lab, Berkeley, CA, 94720, USA

Bioinformatics, bty296, https://doi.org/10.1093/bioinformatics/bty296

The author wishes to inform readers that the affiliations for the authors were incorrect in the original paper. They appear correctly above.

The paper has been corrected online.

© The Author(s) 2018. Published by Oxford University Press.

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License(http://creativecommons.org/licenses/by-nc/4.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contactjournals.permissions@oup.com