

February 3, 2020

Dear *Bioinformatics* Editor,

Please find enclosed our manuscript entitled “**CONSTAX2: Improved taxonomic classification of environmental DNA markers**” that we would like to have considered for publication in the *Bioinformatics* journal as an *Application Note*.

This paper is on a major update of the software *CONSTAX* (*CON*Sensus *TAX*onomy classifier for taxonomic annotation of fungal rDNA amplicons based upon a consensus approach of RDP, SINTAX and UTAX algorithms). *CONSTAX2* can be used to classify prokaryotes and incorporates BLAST-based classifiers to reduce classification errors. Additionally, *CONSTAX2* implements a conda-installable, command line tool with improved classification metrics, faster training, multithreading support, capacity to incorporate external taxonomic databases, new isolate matching and high-level taxonomy tools, and replete with documentation and example tutorials.

This manuscript is 1057 words in main body length and includes 1 figure, 1 supplemental file, 3 supplemental figures, and 1 supplemental table. This manuscript version has been approved by all authors and has not been published or submitted elsewhere for review, and if accepted we will adhere to the copyright guidelines established by the *Bioinformatics* journal.

We also suggest James Cole (colej@msu.edu) at Michigan State University, Irina M. Velsko at the Max Planck Institute, Richard Allen White III at the University of North Carolina at Charlotte, and Nicholas Bokulich at ETH Zürich as potential good reviewers for this manuscript.

Thank you again for considering this manuscript for publication in the *Bioinformatics* journal.

With best regards,

Julian A. Liber

A handwritten signature in black ink, appearing to read 'Julian A. Liber', written in a cursive style.

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