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September 9, 2016

Dear Bioinformatics editor,

We are submitting for your consideration in Bioinformatics a manuscript entitled *phyx: Phylogenetic tools for Unix*. We have developed a set of programs that perform many functions essential for phylogenetics and phylogenomics directly from the command line that are significantly more efficient in both memory and computational time than most, and in many cases, than all other available software packages. The vast majority of the programs in *phyx* can also be piped together, allowing for quick and easy pipelines to be constructed. We are confident that these programs will allow for more convenient and efficient computation and communication of phylogenomic and phylogenetic analyses. This software package is well suited for publication in Bioinformatics as it improves significantly upon many software packages including *Phyutility*, published in Bioinformatics with hundreds of citations by the corresponding author of this manuscript.

Thank you for considering our manuscript for Bioinformatics.

Sincerely,

Stephen Smith, Joseph Brown, and Joseph Walker