30 May 2018

Dear Editor,

We are pleased to submit our manuscript entitled “Keeping it light: (Re)analyzing community-wide datasets without major infrastructure” for consideration as an commentary in *GigaScience* Journal.

# We recently submitted an article for review at GigaScience entitled “Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes” (Johnson et al., *Submitted*) detailing the re-analysis of 678 transcriptomes. While working on the project, we discovered that this type of re-analysis is not really commonplace outside of computational labs. Given the concomitant growth of publicly available DNA sequence data and advancement of computational tools and approaches we believe that this type of study will become more commonplace.

# In this paper, we outline what we found to be best practices for dealing with re-analysis projects and detail some areas where we might grow as a community to better facilitate these types of studies. This discussion, however, we felt fell outside of the research article (Johnson et al.) which was submitted separately to *GigaScience*.

The content of this submission to *GigaScience* has been approved by all of the authors and has not been submitted elsewhere.

Thank you for your time and consideration of our manuscript.

Sincerely,



Dr. Harriet Alexander

Department of Population Health and Reproduction

1 Shields Ave.

Vetinerary Medicine

University of California, Davis

Davis, CA 95616

(479) 200-6104

hxander@ucdavis.edu