

June 1, 2021

Dear Editors of the *R Journal*,

Enclosed for find our manuscript "PSweight: An R Package for Propensity Score Weighting Analysis" for consideration for publication in R Journal.

The development of the R package PSweight is to provide a comprehensive design and analysis platform for drawing causal inference based on propensity score weighting. As we elaborate in the manuscript, this is the first R package to accommodate a variety of balancing weighting schemes with both binary and multiple treatments. In addition, it allows for flexible specifications to meet different user needs such as constructing simple and augmented (doubly-robust) weighting estimators, estimating nuisance-adjusted sandwich variances of the causal effects, calculating ratio estimands for binary and count outcomes. Finally, the package also accommodates the need for estimating propensity scores and outcome models through external machine learning R routines.

The development of PSweight was initiated in May 2020 and has by far received over 7,000 downloads with steady increase. In its most current version 1.1.4, we have integrated the machine learning methods for estimating model components, optimal trimming strategies of the propensity scores, and further improved the user interface such that the output format resembles existing R packages. During this one-year period, we have continuously received inquiries from users regarding the application of the package to a variety of causal inference applications. In this manuscript, we aim to provide a broad and general perspective on the functionality of PSweight and hope to attract a wider readership than current package users with well-annotated details. Beyond describing the content of the package, we further demonstrate its application using a real-world data example from the National Child Development Survey (NCDS) with multiple treatments.

Please feel free to let us know if there are any questions regarding our manuscript and package. We thank the editors for consideration of our manuscript.

Sincerely,

On behalf of all co-authors

Tianhui Zhou, PhD Candidate, Department of Biostatistics and Bioinformatics,

Duke University,

Trahi Um

Email: tianhui.zhou@duke.edu