January 21, 2019

Dear Editor,

I submit the manuscript entitled “scGEApp: a Matlab app for single-cell gene expression analysis” that I wish to be considered for publication as Applications Note in *Bioinformatics*.

This is a small application with graphic user interfaces I designed for biologists who work with single-cell RNA-seq data with limited expertise of command line-based software tools. It is developed with the current version of Matlab and users will benefit most from having such an environment, although I do provide a stand-alone application for those users who do not use Matlab. One of the most important features of my application is that I implement a new feature selection algorithm. This is a simple, nonparametric, but effective method based on 3D spline fit of the data. It takes three key parameters: mean, the coefficient of variation, and dropout rate, into account and uses distance to the spline curve as the metric. As all three parameters are inter-correlated and many parametric methods that suffer from poor modeling often fall in capturing features of genes. I use real data examples show the application of my method. Importantly, the full process of the analysis can be done through the graphic user interfaces. These including downstream analysis such as GSEA and GOrilla.

I shall appreciate your consideration of my manuscript and look forward to receiving constructive comments from reviewers. We provide the following list of potential reviewers who all qualified in reviewing our work and are likely to be interested in our results.

Sincerely,



James Cai, Ph.D.

Associate Professor

Faculty of Genetics

Department of Veterinary Integrative Biosciences

Department of Electrical & Computer Engineering (affiliated)

Texas A&M University

4458 TAMU

College Station, TX 77843-4458

Tel (979) 458-5482 | Fax (979) 847-8981

[jcai@tamu.edu](mailto:jcai@tamu.edu)