July 21, 2019

Dear Editor,

I submit the manuscript entitled “scGEAToolbox: a Matlab toolbox for single-cell RNA sequencing data analysis” that I wish to be considered for publication as an *Applications Note* article in *Bioinformatics*.

Given scRNA-seq data is increasing exponentially over time, I believe a new Matlab toolbox for scRNA-seq data analysis is highly desired. Today most tools for analyzing scRNA-seq data are developed in R and Python. Matlab, however, as a high-level scientific computational language has many advantages. The toolbox I developed contains a comprehensive set of functions that are useful for seasoned developers to take advantage of Matlab itself to develop new algorithms for scRNA-seq data analyses. Furthermore, there is an application with graphic user interfaces I designed for biologists who work with scRNA-seq data with limited expertise of command line-based software tools.

I shall appreciate your consideration of my manuscript and look forward to receiving constructive comments from reviewers.

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)