

# sclmpute a SeqGeq™ Plugin

## Introduction

- sclmpute is a novel statistical method developed by Wei Vivian Li and Jingyi Jessica Li to impute the dropout values in scRNA-seq data. sclmpute tries to identify gene expression values affected by dropout events and performs imputation on these values without introducing new bias to the whole data matrix. Sclmpute may be an effective tool to recover transcriptome dynamics masked by dropout events, and that sclmpute can correct false zero counts, enhance the clustering of cell populations and subpopulations, improve the accuracy of differential expression analysis, and aid the study of gene expression dynamics.
- We have developed a sclmpute plugin that integrates this method into SeqGeq™. A video tutorial is available [here](#).

## Download and installation

- Download and install [SeqGeq™](#) 1.1+ (**plugin is not compatible with SeqGeq 1.0.1**)
- Download the sclmpute plugin from [here](#) and place it in your SeqGeq plugins directory.
- Review [FlowJo documentation in installing plugins](#). Remember to set your R in Preferences/Diagnostics/R Path as shown in that

document; except do that in SeqGeq™ (not FlowJo)

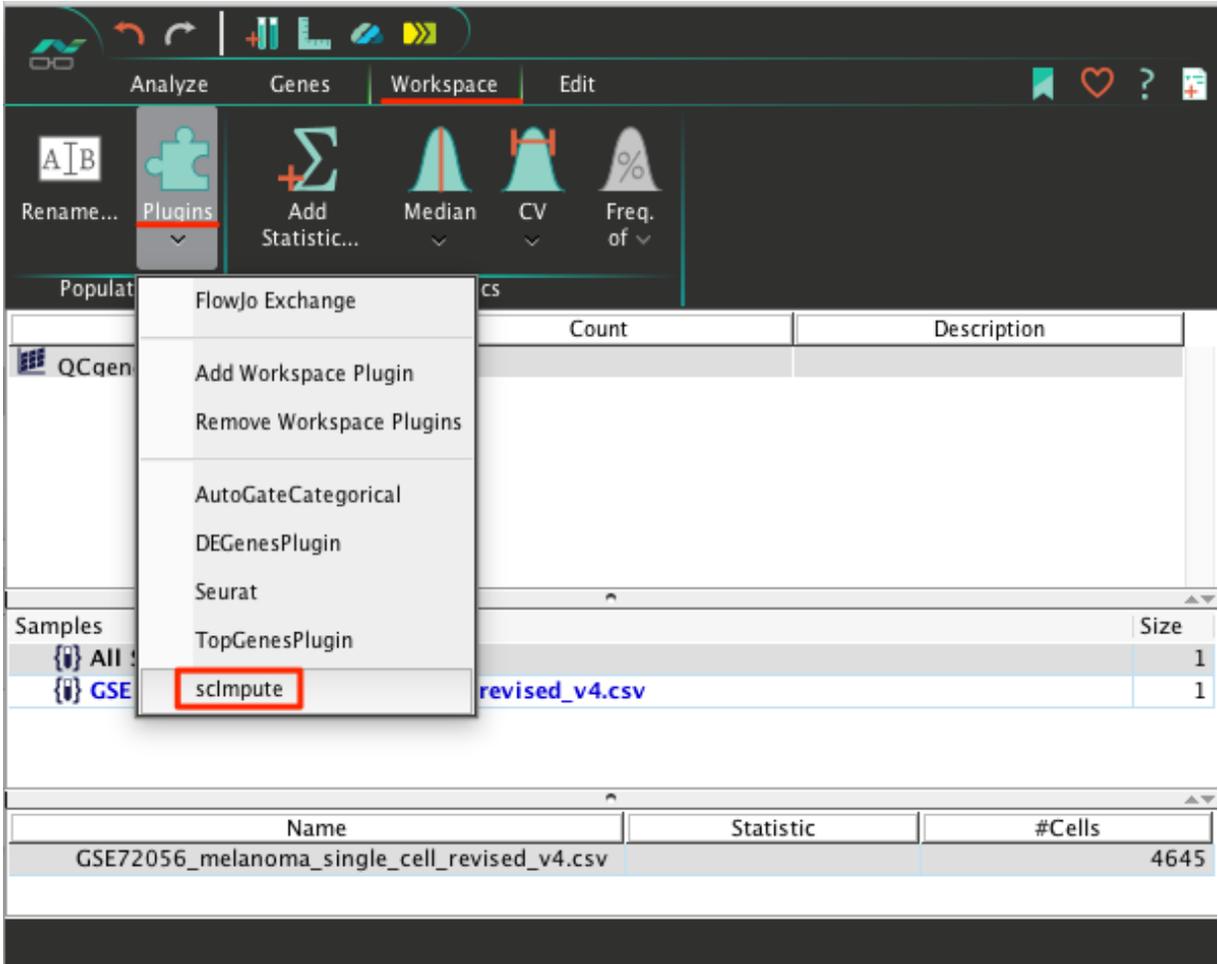
- You will also need R, and the [scImpute](#) library (version 0.0.4). This can be installed using devtools directly from Github by typing the following in your R console:

```
install.packages("devtools")  
library(devtools)  
install_github("Vivianstats/scImpute")
```

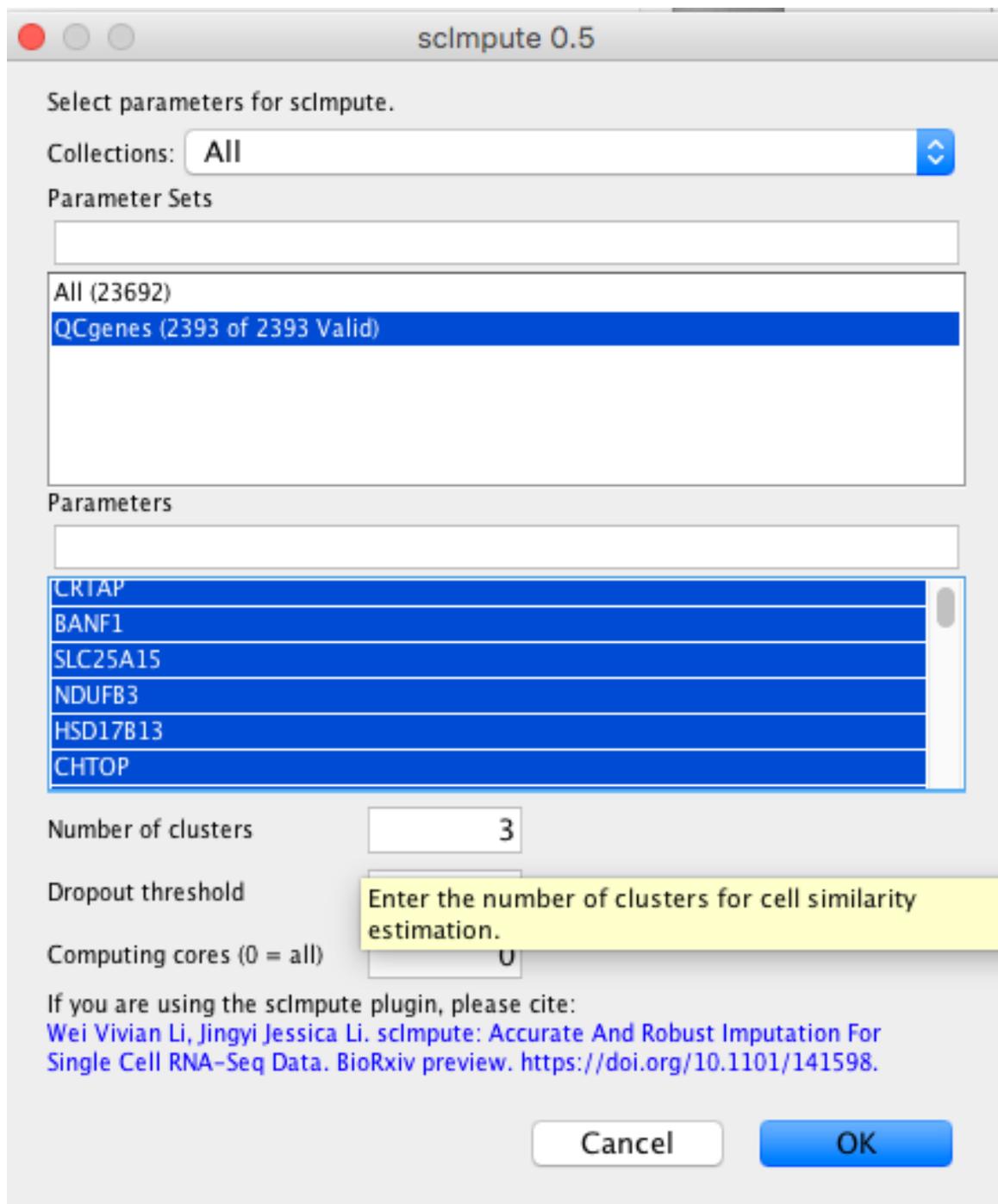
- Note: On a Mac, R-based plugins may fail to calculate if the file path to either the data or the workspace contains a space or other special characters. Sorry, we will fix that. In the meantime, please avoid spaces and special characters in your path.

## How-To

- After setting up the plugin in R and the plugins directory, simply open SeqGeq and load your data set there.
- After selecting the data file you'll be able to run the plugin by selecting it within the Workspace section of SeqGeq's workspace:



- This will open the scImpute plugin dialog, where you can adjust settings for the calculation. Mousing over any of the options there will give a tool-tip describing the function:



- Once the calculation has completed (this can take some time), you'll get a new version of the data matrix within SeqGeq, in which normalization of drop-out events is calculated for all genes selected in the plugin dialog:

The screenshot displays the SeqGeq software interface. At the top, there are tabs for 'Analyze', 'Genes', 'Workspace', and 'Edit'. Below these are icons for 'Rename...', 'Plugins', 'Add Statistic...', 'Median', 'CV', and 'Freq. of'. The main area shows a table with the following data:

Name	Count	Description
QCgenes	2393	

Below this table is a 'Samples' section with the following data:

Sample Name	Size
All Samples	2
GSE72056_melanoma_single_cell_revised_v4.csv	1
GSE72056_melanoma_single_cell_revised_v4.sclmpute.csv	1

At the bottom, there is a detailed view of the sample processing status:

Name	Statistic	#Cells
GSE72056_melanoma_single_cell_revised_v4.csv		4645
sclmpute		DONE!
GSE72056_melanoma_single_cell_revised_v4.sclmpute.csv		4645

If you have any questions or concerns regarding SeqGeq or the sclmpute plugin, please reach out to: [seqgeq@flowjo.com](mailto:seqgeq@flowjo.com)