scImpute a SeqGeq™ Plugin

Introduction

- scImpute is a novel statistical method developed by Wei Vivian Li and Jingyi Jessica Li to impute the dropout values in scRNA-seq data. scImpute 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. ScImpute may be an effective tool to recover transcriptome dynamics masked by dropout events, and that scImpute 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 scImpute 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 scImpute plugin from 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
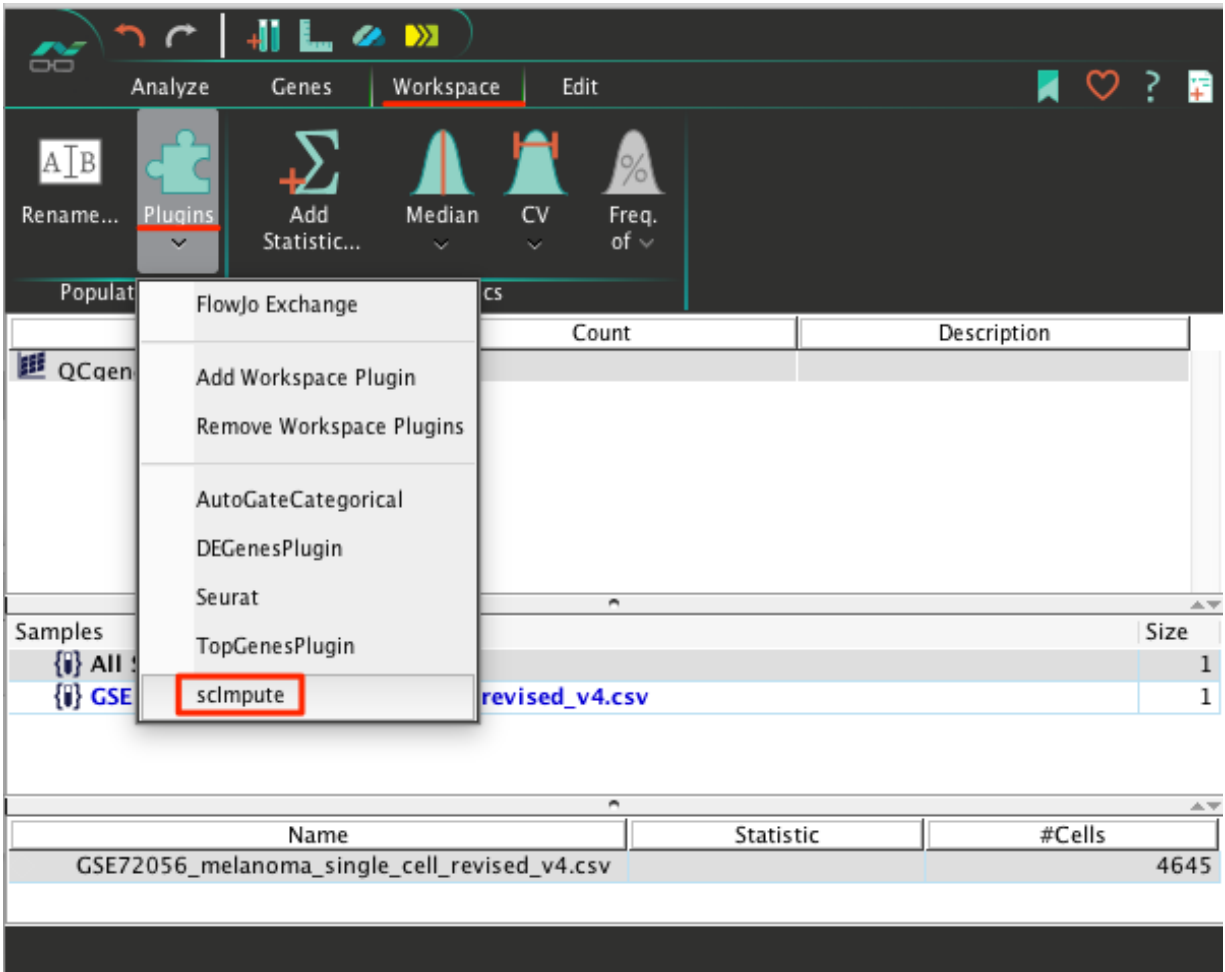
document; except do that in SeqGeq™ (not FlowJo)

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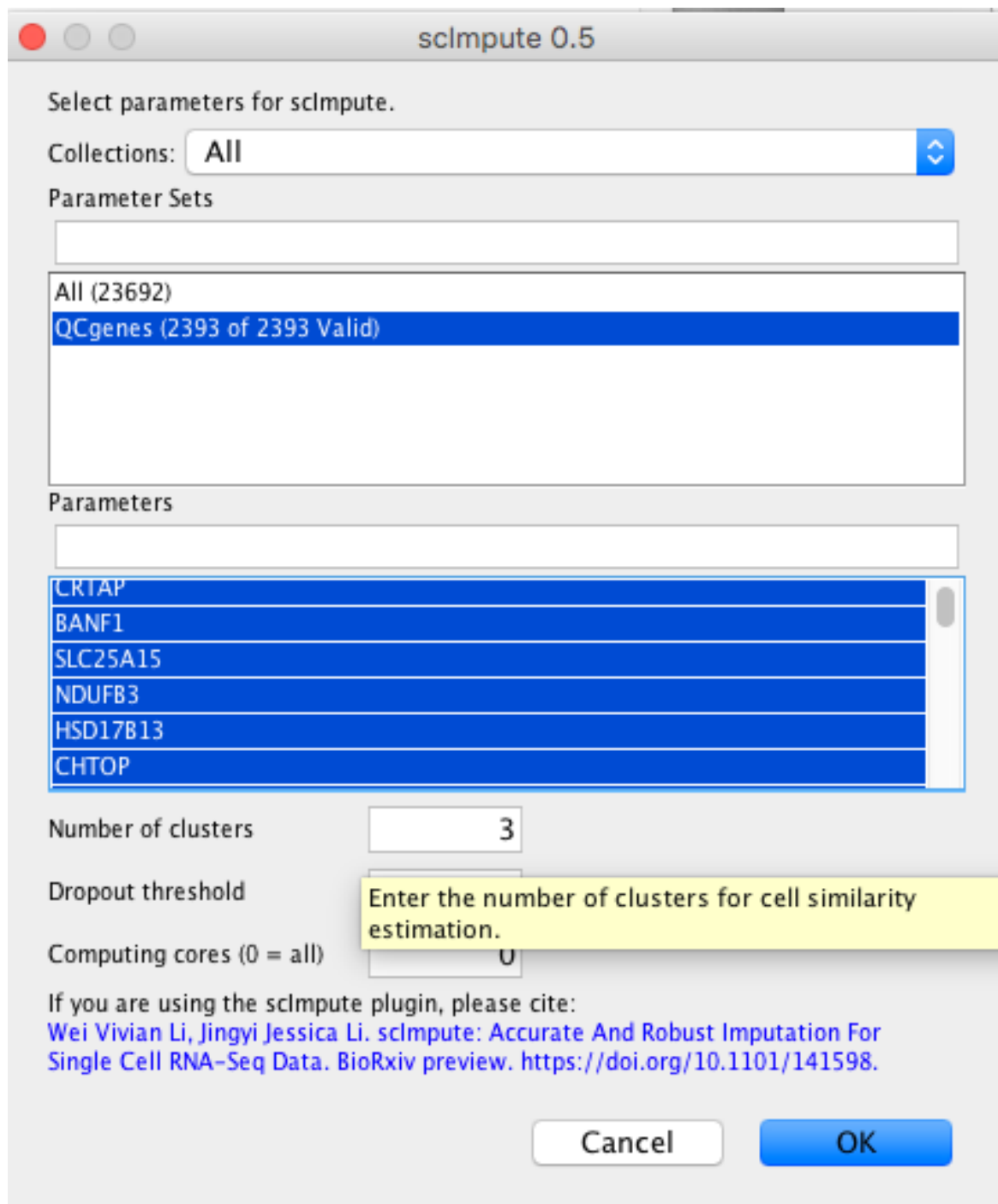
- Note: On a Mac, R-based plugins may fail to calculate if the file path to either the data or the workspace contains a space or other special characters. Sorry, we will fix that. In the meantime, please avoid spaces and special characters in your path.

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 selecing 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:

If you have any questions or concerns regarding SeqGeq or the scImpute plugin, please reach out to: seqgeq@flowjo.com