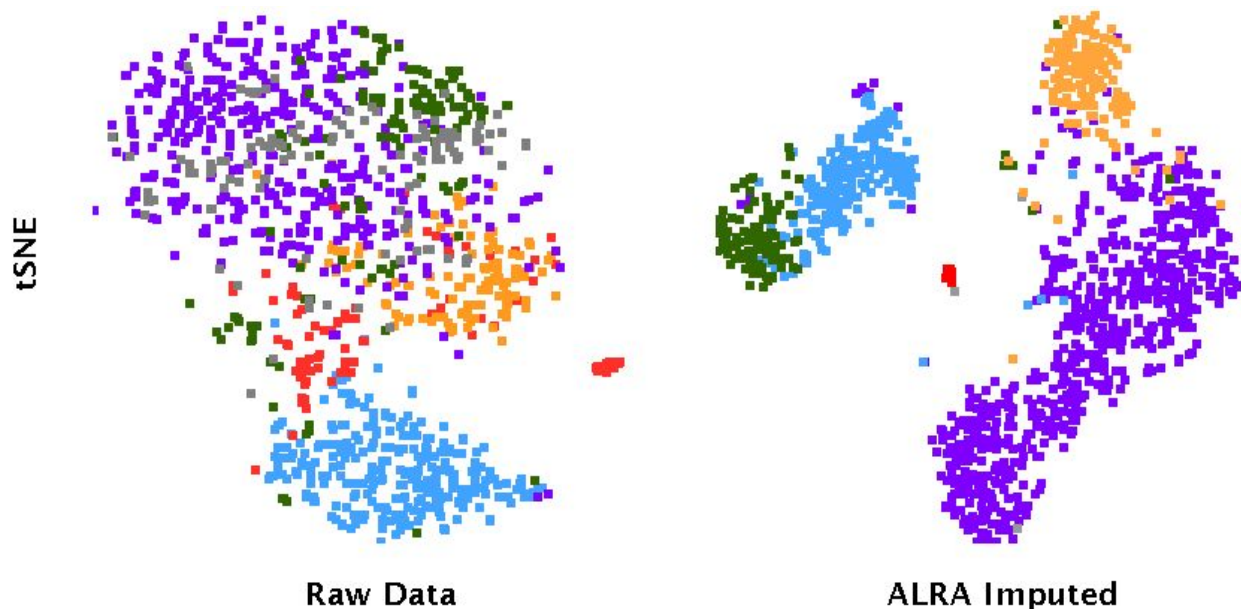# How to ALRA

Introduction

Adaptively-thresholded Low Rank Approximation (ALRA) is an algorithm designed for dropout imputation, developed by the Kluger Lab. (1) The algorithm works by performing low-rank approximation in order to correct for false negative values inherent to single-cell RNA-sequencing, while attempting to maintain true zero values.

One major advantage to this method over other dropout imputing tools such as scImpute(2) is an extremely high performance. The tool was also validated against different datasets by the authors, and this plugin was QC'ed against PBMC data in SeqGeq by the Product Innovation team at FlowJo:

Installation

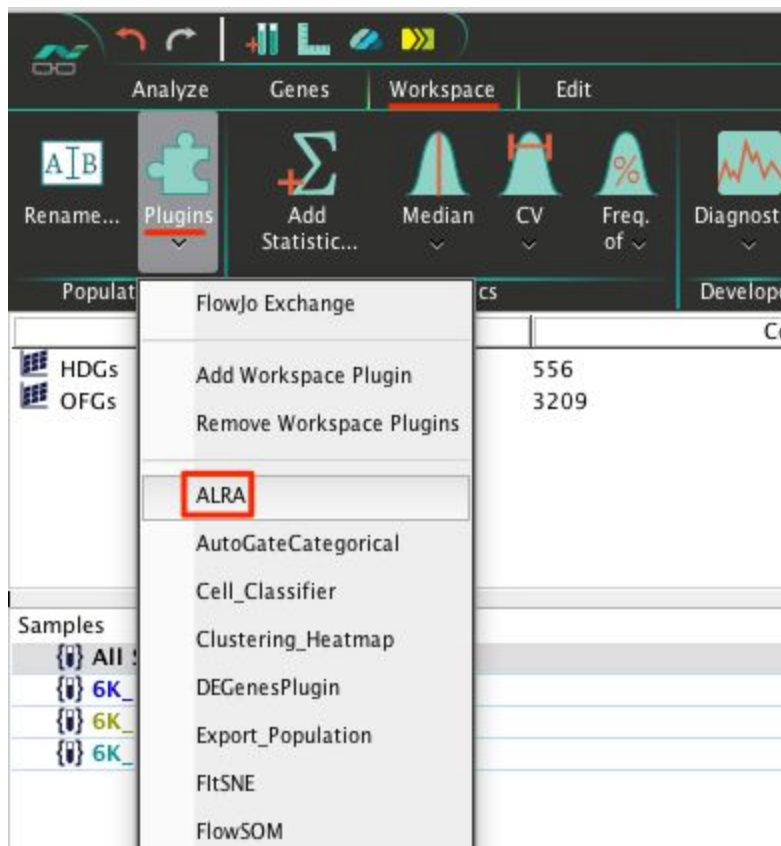Place the ALRA.jar file into your plugins folder.

Install the necessary dependencies for ALRA in R using the following command:
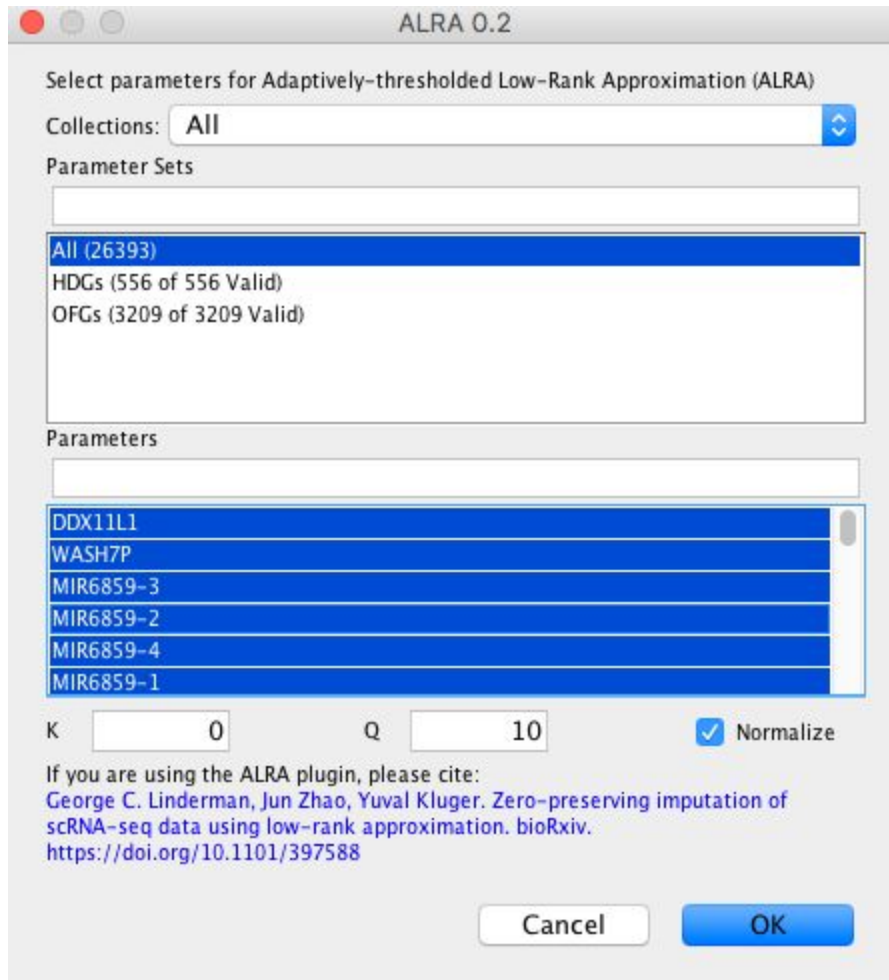
```
install.packages('rsvd')
```

Restart the application.

Running ALRA

Select the population of interest within your workspace, visit the Plugins dropdown within the Workspace tab and choose ALRA:

Within the plugin dialog select the genes to use within dropout imputation and run the tool by clicking, OK:

After the algorithm finishes computing it will create a new data file in the same location as your raw data, appended with .ALRA.csv, and will automatically load this into the workspace.

References:

1. G. Linderman, et al. *Zero-preserving imputation of scRNA-seq data using low-rank approximation*. bioRxiv (2018)
2. W. Li, et al. *scImpute: accurate and robust imputation for single cell RNA-seq data*. bioRxiv (2017)