Single Cell RNA-Seq Analysis (Multiple Samples)

In this tutorial, we demonstrate how to:

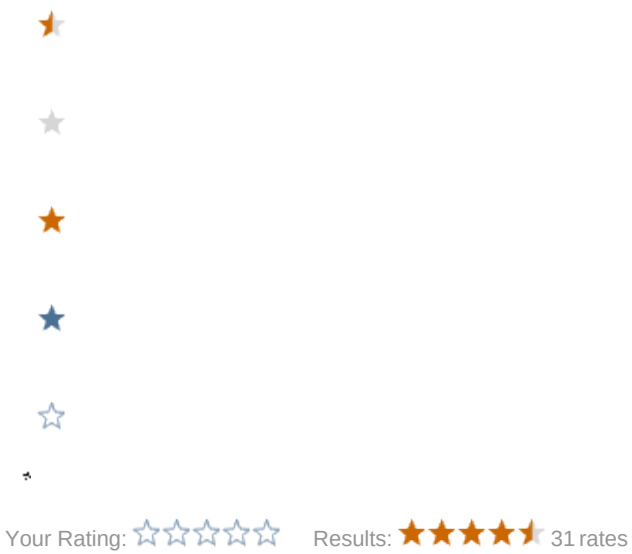
- Getting started with the tutorial data set
- Classify cells from multiple samples using t-SNE
- Compare expression for a cell type between groups
- Compare expression between cell types with multiple samples

Tutorial Data Set

The tutorial is based on the work published by Venteicher and co-workers, on isocitrate dehydrogenase-mutant gliomas. Single cells from tumor biopsies were processed by flow cytometry and the libraries were prepared by Smart-seq2 protocol. The tutorial data set consists of eight expression matrix files, one per patient sample. The tumors were categorized as either astrocytoma or oligodendroglioma glioma subtype by histology. The matrix files contain gene expression values normalized by the following transformation log2[(TPM/10)+1].

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.



Your Rating: Results: 31 rates

Copyright © 2018 by Partek Incorporated. All Rights Reserved. Reproduction of this material without express written consent from Partek Incorporated is strictly prohibited.