Methods to compare with

1. Quality Control:

Scater: <http://www.biorxiv.org/content/biorxiv/early/2016/08/15/069633.full.pdf>

sinQC:

https://academic.oup.com/bioinformatics/article/32/16/2514/1743129/Quality-control-of-single-cell-RNA-seq-by-SinQC

[Classification of low quality cells from single-cell RNA-seq data](http://xueshu.baidu.com/s?wd=paperuri%3A%284a340fc832d6c1d76ddd4b0a0bb7ed52%29&filter=sc_long_sign&tn=SE_xueshusource_2kduw22v&sc_vurl=http%3A%2F%2Fwww.ncbi.nlm.nih.gov%2Fpubmed%2F26887813&ie=utf-8&sc_us=14966880579612825054):

http://xueshu.baidu.com/s?wd=paperuri%3A%284a340fc832d6c1d76ddd4b0a0bb7ed52%29&filter=sc\_long\_sign&tn=SE\_xueshusource\_2kduw22v&sc\_vurl=http%3A%2F%2Flink.springer.com%2Fcontent%2Fpdf%2F10.1186%2Fs13059-016-0888-1.pdf&ie=utf-8&sc\_us=14966880579612825054

1. Differential Expression

MAST: http://xueshu.baidu.com/s?wd=paperuri%3A%288d490597554defee105d6c0efeaec351%29&filter=sc\_long\_sign&tn=SE\_xueshusource\_2kduw22v&sc\_vurl=http%3A%2F%2Flink.springer.com%2Fcontent%2Fpdf%2F10.1186%252Fs13059-015-0844-5.pdf&ie=utf-8&sc\_us=2365272210134243314

DEseq2: http://www.bioconductor.org/packages/release/bioc/html/DESeq2.html

SCDE: http://www.bioconductor.org/packages/release/bioc/html/scde.html

D3E: http://www.biorxiv.org/content/biorxiv/early/2015/10/29/020735.full.pdf

1. Dimensionality Reduction:

Fastproject: <http://www.biorxiv.org/content/biorxiv/early/2016/03/12/043463.full.pdf>

ZIFA: <http://xueshu.baidu.com/s?wd=paperuri%3A%28b6f77c8cb095503fe6f7147e96a09eab%29&filter=sc_long_sign&tn=SE_xueshusource_2kduw22v&sc_vurl=http%3A%2F%2Flink.springer.com%2Farticle%2F10.1186%2Fs13059-015-0805-z&ie=utf-8&sc_us=3700730146798537728>

PCA

(with different normalization methods)

Datasets to use:

All datasets used by our referred papers (like Zhang’s paper and ZINB). We can also try on datasets used by the papers mentioned above. Use the datasets easy to download and preprocess firstly.