**Smart-seq processing pipeline**

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**TOOLS:**

**FastQC**

Download: <https://www.bioinformatics.babraham.ac.uk/projects/download.html>

Need: v1.6-v1.8 JREs from Oracle.

`java -version`

* openjdk version "1.8.0\_131"

OpenJDK Runtime Environment (build 1.8.0\_131-b12)

OpenJDK 64-Bit Server VM (build 25.131-b12, mixed mode)

`chmod 755 fastqc`

add to PATH

**TopHat**

Download: <https://ccb.jhu.edu/software/tophat/tutorial.shtml>

Need: Bowtie2 (<https://sourceforge.net/projects/bowtie-bio/?source=navbar>)

add to PATH

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**STAR**

Download: <https://github.com/alexdobin/STAR>

git clone https://github.com/alexdobin/STAR.git

`cd STAR/source`

`make STAR`

`cd ..`

`git submodule update --init –recursive`

add to PATH

**HISAT**

Download: <http://www.ccb.jhu.edu/software/hisat/manual.shtml>

add to PATH

**Cufflinks**

Download: <http://cole-trapnell-lab.github.io/cufflinks/getting_started/>

Need: Boost libraries (http://blog.csdn.net/u011641865/article/details/73498533)

SAM tools, Eigen libraries (http://blog.sciencenet.cn/blog-1509670-830821.html)

add to PATH

**HTSeq**

`pip install HTSeq`

**scLVM**

https://github.com/PMBio/scLVM

`conda install -c conda-forge hcephes`

`conda install -c conda-forge liknorm`

`pip install scLVM`

**PCA、tSNE**

Sklearn in Python

**ZIFA**

`git clone https://github.com/epierson9/ZIFA`

`cd ZIFA`

`python setup.py install`

**SCDE**

Download: <http://hms-dbmi.github.io/scde/package.html>

Need: R

**SC3**

Download: <http://bioconductor.org/packages/release/bioc/html/SC3.html>

Need: R

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<https://paste.ubuntu.com/p/7qHMqfVrVB/>

