* 工具一览

1. Reads Quality Control
   1. Fastqc
   2. Other uninstalled tools
      1. Salmon
      2. KraKen
2. Alignment and Mapping
   1. Tophat
   2. STAR
   3. HISAT
3. Qualification & Normalization
   1. Cufflinks
   2. HT-seq
4. PartA Confounder factor
   1. scLVM
5. PartB-1 Dimension Reduction
   1. PCA
   2. t-sne
   3. ZIFA
6. PartB-2 Clustering
   1. SC3
   2. kmeans
7. PartC Pesudotime
   1. Monocle
8. ParD Differential Expression
   1. SCDE

* 具体安装
* Fastqc
  + Java配置

参考：<https://jingyan.baidu.com/article/4853e1e51d0c101909f72607.html>

         yum -y list java\*

         yum -y install java-1.8.0-openjdk\*

* + Fastqc 安装

参考：<http://www.cnblogs.com/OA-maque/p/4835036.html>

        wget <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.7.zip>

        unzip fastqc\_v0.11.7.zip

        chmod 775 FastQC/fastqc

        [Add to PATH]

* Tophat

参考：<http://blog.sina.com.cn/s/blog_751bd9440102v4lq.html>

解压biowtie2 并 [add to PATH]

解压tophat2 并 [add to PATH]

* STAR
  + 安装 zlib-devel

    yum install zlib-level

* + 安装 STAR

        git clone [https://github.com/alexdobin/STAR.gi](https://github.com/alexdobin/STAR.git)t

        cd STAR/source

        make STAR

        git submodule update --init --recursive

        [add to PATH]

* HISAT

     wget <http://www.ccb.jhu.edu/software/hisat/downloads/hisat-0.1.6-beta-Linux_x86_64.zip>

    [add to PATH]

* Cufflinks

参考：<http://blog.sciencenet.cn/blog-1509670-830821.html>

    wget <http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz>

     tar zxvf cufflinks-2.2.1.Linux\_x86\_64.tar.gz

    [add to PATH]

* HT-seq

查看：<https://github.com/PMBio/scLVM>

    pip install HTSeq

* scLVM

查看：<https://github.com/PMBio/scLVM>

         conda install -c conda-forge hcephes

     conda install -c conda-forge liknorm

pip install scLVM

* PCA

R自带函数

* t-sne

     # in R cmd

Install.package(“tsne”)

* ZIFA

查看：<https://github.com/epierson9/ZIFA>

    git clone <https://github.com/epierson9/ZIFA>

    cd ZIFA

    python setup.py install

* SC3

查看：<http://www.sanger.ac.uk/science/tools/single-cell-consensus-clustering-sc3>

  conda install gxx\_linux-64

     source("[https://bioconductor.org/biocLite.R"](https://bioconductor.org/biocLite.R%22))

     biocLite("SC3")

* k-means

R 自带函数

* Monocle [unsuccessful]
* SCDE [unsuccessful]
* 使用流程

1. 使用数据

Title : Single cell RNA-seq of primary human glioblastomas

SRA : SRP042161

Cite : ingle-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma

Download: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE57872>

Tech : smart2-seq

1. 处理流程

<https://paste.ubuntu.com/p/S2dyBrjW3W/>