

## 1. Basics of kallisto single cell — introduction

Overview of kallisto single cell: <https://pachterlab.github.io/kallisto/singlecell.html>

Quick start of kallisto: <https://pachterlab.github.io/kallisto/starting>

Presentation materials: <https://github.com/caltech-bioinformatics-resource-center/bioinformatics-symposium-2019>

## 2. Hands-on exercise

### 2.1 Software installation and configuration

This exercise covers installation of **kallisto**, **bustools**, **Jupyter Notebook**, **R-studio**, **Scanpy** and **Seurat** software tools and download of demo datasets.

**Bioinformatics server users, please open a terminal window (install putty on Windows <https://www.putty.org>)**

```
ssh user@bioinformatics.caltech.edu
```

**Mac and Linux laptop users, please open a terminal window.**

#### 2.1.1 Installation of **kallisto**

Visit <http://pachterlab.github.io/kallisto/download> from any web browser

Download **Mac** or **Linux** executables from the version: **v0.45.0**

##### **Mac users**

```
cd /home/user
wget https://github.com/pachterlab/kallisto/releases/download/v0.45.0/kallisto_mac-v0.45.0.tar.gz
tar -xvzf kallisto_mac-v0.45.0.tar.gz
```

##### **Linux (server and laptop) users**

```
cd /home/user
wget https://github.com/pachterlab/kallisto/releases/download/v0.45.0/kallisto_linux-v0.45.0.tar.gz
tar -xvzf kallisto_linux-v0.45.0.tar.gz
```

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Test executable **kallisto**

```
export PATH="/home/user/kallisto_linux-v0.45.0:$PATH"  
kallisto bus
```

### 2.1.2 Installation of **bustools**

```
git clone https://github.com/BUStools/bustools.git  
cd bustools  
mkdir build  
cd build  
cmake ..  
make
```

Test executable bustools

```
cd /home/user  
export PATH="/home/user/bustools/build/src:$PATH"  
bustools
```

### 2.1.3 Installation of **Anaconda** (<https://repo.continuum.io/archive/>)

We have tested **Anaconda3-5.2.0-Linux-x86\_64.sh** (Linux)

**Bioinformatics Server Users:**

```
export PATH="/home/software/anaconda3.5.2/bin:$PATH"
```

**Linux laptop users:**

```
cd /home/user  
wget https://repo.continuum.io/archive/Anaconda3-5.2.0-Linux-x86.sh  
bash Anaconda3-5.2.0-Linux-x86.sh
```

### 2.1.4 Installation of **R / R-studio** (not necessary for Bioinformatics Server Users)

R (<https://www.r-project.org/>)

R-studio (<https://www.rstudio.com/products/rstudio/download/>)

### 2.1.5 Installation of **Scanpy** (not necessary for Bioinformatics Server Users)

Scanpy <https://scanpy.readthedocs.io/en/latest/installation.html>

### 2.1.6 Installation of **Seurat** (not necessary for Bioinformatics Server Users)

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Seurat <https://satijalab.org/seurat/install.html>

## 2.2 Bash command lines for data processing

Download demo scripts and data in the terminal

```
cd /home/user
```

```
svn checkout https://github.com/caltech-bioinformatics-resource-center/bioinformatics-symposium-2019/trunk/Hands-on%20Part1%20BASH/demo
```

```
cd demo
```

```
more run_script
```

Copy/paste to run each line of **run\_script** to process the demo data.

**Please feel free to ask the tutors if you have problems!**