

Ubuntu Install Shell Script for Heaney et al. 2021

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This file contains the shell commands followed on a fresh Ubuntu install to add all software used during RNAseq analysis. This is provided for reproducibility. Note that the shell commands here do not form a complete shell script so they should not be run directly. Please modify as needed.

System basics

```
# Install Zshell
sudo apt-get install zsh
sudo apt-get install git-core
sudo wget https://github.com/robbyrussell/oh-my-zsh/raw/master/tools/install.sh -O - | zsh
chsh -s 'which zsh'
sudo shutdown -r 0

# Install dropbox
sudo apt-get install nautilus-dropbox

# Run dropbox to initiate download

# Install Java/Oracle 8
sudo apt-get update
sudo apt-get install default-jre
sudo apt-get install default-jdk
sudo add-apt-repository ppa:webupd8team/java
sudo apt-get update
sudo apt-get install oracle-java8-installer
```

Python and pip

```
# Install pip
sudo apt-get update
sudo apt-get upgrade
sudo apt-get install python-pip

# Install python 2.7.10
sudo apt-get install build-essential checkinstall
sudo apt-get install libreadline-gplv2-dev libncursesw5-dev libssl-dev libsqlite3-dev tk-dev libgdbm-dev
cd /usr/src
```

```

sudo wget https://www.python.org/ftp/python/2.7.10/Python-2.7.10.tgz
sudo tar xzf Python-2.7.10.tgz
cd Python-2.7.10
sudo ./configure
sudo make altinstall
sudo apt-get install python-dev

```

R and R studio

```

# Install R Base
sudo echo "deb http://cran.rstudio.com/bin/linux/ubuntu xenial/" | sudo tee -a /etc/apt/sources.list
gpg --keyserver keyserver.ubuntu.com --recv-key E084DAB9
gpg -a --export E084DAB9 | sudo apt-key add -
sudo apt-get update
sudo apt-get install r-base r-base-dev

# Install R Studio 0.99.903
sudo apt-get install gdebi-core
wget https://download1.rstudio.org/rstudio-0.99.903-amd64.deb
sudo gdebi -n rstudio-0.99.903-amd64.deb
rm rstudio-0.99.903-amd64.deb

```

RNAseq tools

```

# Install FastQC 0.11.5
cd /usr/src
sudo curl -O http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.5.zip
sudo unzip fastqc_v0.11.5.zip
sudo ln -sf /usr/src/FastQC/fastqc /usr/bin/fastqc
sudo chmod +x /usr/bin/fastqc

# Install cutadapt 1.11
sudo -H pip install cutadapt

# Install Trim Galore 0.4.1
cd /usr/src
sudo curl -O http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/trim_galore_v0.4.1.zip
sudo unzip trim_galore_v0.4.1.zip
sudo ln -sf /usr/src/trim_galore_zip/trim_galore /usr/bin/trim_galore

# Install Tophat 2.1.1
cd /usr/src
sudo curl -O https://ccb.jhu.edu/software/tophat/downloads/tophat-2.1.1.Linux_x86_64.tar.gz
sudo tar xzvf tophat-2.1.1.Linux_x86_64.tar.gz

# Install Bowtie 2.2.9
cd /usr/src
sudo curl -OL http://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.2.9/bowtie2-2.2.9-linux-x86_64
sudo unzip bowtie2-2.2.9-linux-x86_64.zip

```

```

# Install samtools 0.1.19
cd /usr/src
sudo curl -OL https://sourceforge.net/projects/samtools/files/samtools/0.1.19/samtools-0.1.19.tar.bz2
sudo tar jxvf samtools-0.1.19.tar.bz2
sudo chown $USER -R /usr/src/samtools-0.1.19
cd samtools-0.1.19
sudo make

# Install Piranha 1.2.1
cd /usr/src
sudo curl -O http://smithlabresearch.org/downloads/piranha-1.2.1.tar.gz
sudo tar xzvf piranha-1.2.1.tar.gz
cd piranha-1.2.1
sudo ./configure --with-bam_tools_headers="/usr/src/BAMTools/include/" \
    --with-bam_tools_library="/usr/src/BAMTools/lib/"
sudo make all
sudo make install

# Add the following paths to the zshell profile:
export PATH=/usr/src/tophat-2.1.1.Linux_x86_64:$PATH
export PATH=/usr/src/bowtie2-2.2.9:$PATH
export PATH=/usr/src/samtools-0.1.19:$PATH
export PATH=/usr/src/piranha-1.2.1:$PATH

gedit /home/sanjeev/.zshrc

# Install RSeQC 2.6.4
sudo -H pip install RSeQC

# Install CMake 3.6.2
cd /usr/src
sudo curl -O https://cmake.org/files/v3.6/cmake-3.6.2.tar.gz
sudo tar xzvf cmake-3.6.2.tar.gz
cd cmake-3.6.2
sudo chmod u+x bootstrap
sudo ./bootstrap
sudo make
sudo make install

# Install BAMtools 2.4.1
cd /usr/src
sudo git clone git://github.com/pezmaster31/bamtools.git
cd bamtools
sudo mkdir build
cd build
cd cmake ..
sudo make

# Install GSL-2.2.1
cd /usr/src
sudo curl -O http://gnu.mirrors.pair.com/gnu/gsl/gsl-2.2.1.tar.gz
sudo tar xzvf gsl-2.2.1.tar.gz
sudo ./configure

```

```

sudo make
sudo make install
sudo apt-get install libgs10-dev

# Install BEDtools 2.25.0-1
sudo apt-get install bedtools

```

R and Bioconductor packages

```

# Prepare to install R/Bioconductor packages
sudo chown $USER -R /usr/lib/R
sudo chown $USER -R /usr/share/R
sudo apt-get update
sudo apt-get install r-base-html r-base-latex r-cran-rgtk2 r-cran-rggobi r-cran-rgl libxml2-dev libcurl4-openssl-dev

# Install R packages
install.packages("R.utils")
install.packages("ggplot2")
install.packages("RColorBrewer")
install.packages("pheatmap")
install.packages("reshape2")

# Install Bioconductor and related packages
source("http://bioconductor.org/biocLite.R")
biocLite("org.Mm.eg.db")
biocLite("DESeq2")
biocLite("Rsubread")
biocLite("genefilter")
biocLite("edgeR")
biocLite("AnnotationDbi")
biocLite("RIPSeeker")
biocLite("biomaRt")
biocLite("ChIPpeakAnno")

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```

```
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