**New Employee Guidance**

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**Before start, you should get your CHOP ID and on a CHOP computer.**

**Set up your account (Assuming your CHOP ID is *demo1*):**

1. Apply Admin Access to your PC/Mac:
2. Login to [http://serviceportal.chop.edu](http://serviceportal.chop.edu/)
3. Search “Administrative Access – Workstation”
4. Fill the form, wait for IT guy. If you are in a hurry, contact Andrew or it will take up to one week for them to approve your request (but you do not need admin access for the rest of this guidance).
5. Login to Cirrus: <https://ris.research.chop.edu/systems/cirrus> (Make sure you selected the right domain: chop.edu)
6. In catalog page, find “Respublica Access Request”
7. Fill the form using cost center 27085 and activity 7225380000.
8. After your HPC account set up, go back to Cirrus and find “Request Fileshare Access”
9. Fill the form and request ReadWrite access to FileShare “xing\_lab”
10. After your request was permitted, write to John Daniels (<DANIELSJ1@chop.edu>) to ask for make your own directory under xing\_lab (/mnt/isilon/xing\_lab/demo1/, BTW, everyone in our lab is able to access /mnt/isilon/xing\_lab/aspera/).
11. **CAUTION: YOU SHOULD NOT DEPOSITE ANY DATA OR PROGRAM UNDER */home/demo1* DIRECTORY, ALL FILES SHOULD LOCATE IN */mnt/isilon/xing\_lab/demo1/*.**
12. Apply your PENNKEY on <https://pennkey.research.chop.edu/>

**Set up environment for m6a analysis:**

*All software should be installed under /mnt/isilon/xing\_lab/demo1. Although you can use module load to load needed module like STAR, R, Kallisto, et. al., it is recommended to install and use your own version.*

**Install dependent:**

1. Samtools
2. Bedtools
3. Bcftools
4. Latest Curl
5. Add bin directory of all tools above to ~/.bashrc

**Install R**

1. Download R packages from <https://cran.r-project.org/src/base/R-3/R-3.5.3.tar.gz>
2. Unzip to installing folder: tar –xzvf R-3.5.3.tar.gz
3. Enter source code folder: cd R-3.5.3
4. Configure: ./configure –prefix=/absolute/path/to/install/folder
5. Make: make
6. Install: make install
7. Add to user path: vim ~/.bashrc
8. Add path to environment: export PATH="/absolute/path/to/install/folder/bin":$PATH
9. Apply bashrc: source ~/.bashrc
10. Install ggplot2 and sleuth:

R

Install.packages(“ggplot2”)

source("http://bioconductor.org/biocLite.R")

biocLite("rhdf5")

install.packages("devtools")

devtools::install\_github("pachterlab/sleuth")

**Install Anaconda2:**

1. Download
2. Set environment: export PATH="/path/to/anaconda2/bin":$PATH
3. Remove obsoleted pysam and libcurl: conda remove pysam/libcurl
4. Install all packages listed below (pip was recommended):

pysam

PyPDF2

PyYAML

bs4

lxml

pybedtools

pathlib

pyBigWig

GEOparse

Bio

Pdfkit

libcurl

**Install STAR** (<https://github.com/alexdobin/STAR>)

They provided pre-compiled bin, you can also compile from source. Add the bin folder to .bashrc.

**Install Kallisto** (<https://pachterlab.github.io/kallisto>)

They provided pre-compiled bin, you can also compile from source. Add the bin folder to .bashrc.

**Install CLAM** (<https://github.com/Xinglab/CLAM>)

Follow the installation guide.

**Install Homer** (<http://homer.ucsd.edu/homer/download.html>)

Install Homer and required genome build files by:

perl configureHomer.pl -install homer

perl configureHomer.pl -install hg19

perl configureHomer.pl -install mm10

**Install wkhtmltopdf** ([https://wkhtmltopdf.org](https://wkhtmltopdf.org/))

They only provide RPM packages, you will need to install by extracting RPM using CPIO:

rpm2cpio to-install.rpm | cpio –idv

Remember to add the path to .bashrc file.

**Congratulations! You are all set!!**