Documentation for Bash

# 1st Bash Shell

Set run Bash as default.

<https://unix.stackexchange.com/questions/50264/how-to-fix-bash-or-auto-run-bin-bash-on-ssh-login/50265>

Set PATH for all users.

<https://stackoverflow.com/questions/14637979/how-to-permanently-set-path-on-linux-unix>

## **Sample**

|  |  |
| --- | --- |
| Command | Explanation |
|  | head $(find -name metrics\_summary.csv) | sed -e 's,,/, ,/g' | column -s, -t > summary.log |
| sudo netstat -lntp | *# look for listening on the port* |
| sudo ps -aux | grep 'rserver' | *look for the rserver process* |
| sudo cat /var/log/syslog | Tar -xvz a.tar.gz |
|  |  |
|  |  |
|  | xx=$(pgrep -u fanyh sshd)  for x in ${xx[\*]}; do kill -9 $x; done |
|  |  |

## **Jupyter Notebook**

To check running jupyter server: jupyter notebook list

|  |  |
| --- | --- |
| Server run: | nohup jupyter notebook --no-browser --port=8890 & |
| Local Run: | ssh -N -f -L localhost:8887:localhost:8890 lxiang@shang.phys.gwu.edu |
| Local Browser: | localhost:8887 |
| Find process | ps aux | grep "ssh -N -f -L localhost:8887:localhost:8890 |
| -N | Do not execute a remote command, this is useful for just forwarding ports. |
| -f | Requests **ssh** to go to background just before command execution. This is useful if **ssh** is going to ask for passwords or passphrases, but the user wants it in the background. This implies **-n**. The recommended way to start X11 programs at a remote site is with something like **ssh -f host xterm**. |
| Man ssh | https://man.openbsd.org/ssh |
|  |  |

## **Rstudio**

Install: <https://rstudio.com/products/rstudio/download-server/debian-ubuntu/>

<https://support.rstudio.com/hc/en-us/articles/200532327-Managing-the-Server>

<https://support.rstudio.com/hc/en-us/articles/200552316-Configuring-the-Server>

ssh -N -f -L localhost:7777:localhost:8787 [lxiang@shang.phys.gwu.edu](mailto:lxiang@shang.phys.gwu.edu)

|  |  |
| --- | --- |
| sudo rstudio-server verify-installation | sudo rstudio-server start |
|  |  |
|  |  |
|  |  |

## **R**

<https://stackoverflow.com/questions/17473547/error-with-readline-yes-default-and-headers-libs-are-not-available>

<https://twilightbbs.wordpress.com/2017/07/04/compiling-cran-r-from-scratch-and-possible-workarounds/> ## configure error fix

# cross compiler error !!! conda install gcc\_linux-64

|  |  |
| --- | --- |
| Command | Explanation |
| Tar -xvz a.tar.gz | ## |
| ./configure **--enable-R-shlib**  **Make** | ln -s /opt/vertica/R/bin/R /usr/bin/R  **Make check**  **Make install** |

## **Jupyter Switch Kernel**

|  |  |
| --- | --- |
| conda create -n py36 python=3.6  conda activate py36  conda install notebook ipykernel  ipython kernel install --user | jupyter kernelspec list (find available kernels)  locate “kernel.json” and replace  “argv”:[  “python\_wrong\_version”, with “correct version”  ] |
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## **Conda**

https://conda.io/docs/user-guide/getting-started.html

|  |  |
| --- | --- |
| conda –version | conda update conda |
| conda list |  |
| Make Conda package for everyone | So for ~/.bashrc, you could edit the system wide config files /etc/bash.bashrc (for functions/aliases) or /etc/profile (for environment stuff) - you can the full list from man bash |
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## **User and Group**

<https://www.tecmint.com/add-users-in-linux/>

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| --- | --- |
| 1.sudo useradd -m user\_name | Sudo passwd user\_name |
| 2. addgroup A | Sudo usermod -a -G A user\_name (put user into A) |
|  |  |
| 1. Edit /etc/default/useradd, and change the value of SHELL | 1. Override the shell's value when adding user with: useradd -D -s /bin/bash |
|  |  |

## **SSH Key**

Make bash default log in sudo chsh acao -s /bin/bash

sudo apt install openssh-server

global /etc/ssh/ssh\_config

<https://help.ubuntu.com/community/SSH/OpenSSH/Keys#keys-with-specific-commands>

<https://www.cyberciti.biz/faq/how-to-disable-ssh-password-login-on-linux/>

## Reload new setting: /etc/init.d/ssh reload

|  |  |
| --- | --- |
| The private key is kept on the computer you log in from, while the public key is stored on the **.ssh/authorized\_keys** file on all the computers you want to log in to. | |
| ssh-keygen -t rsa -b 4096 | Generate key in 4096 bits. |
| SSH clients will typically use ~/.ssh/identity (ssh v1) or one of~/.ssh/id\_rsa or ~/.ssh/id\_dsa (v2) as the default private key. You can change this in ~/.ssh/config (the IdentityFile parameter - the -i option to SSH actually overrides this. See man ssh\_config for details). | |
| Ssh-copy-id <username>@<host> |  |
|  |  |
| Change SSH log-off time  sshd\_config: | ClientAliveInterval 300  ClientAliveCountMax 3  After 3 times(per 300 seconds) test with no response, log off. |
|  |  |
|  |  |
| Tips: Use default name for generated id\_rsa. So that there is no issue with denied PublicKey | |

## **Quota System**

https://www.digitalocean.com/community/tutorials/how-to-enable-user-and-group-quotas

|  |  |
| --- | --- |
| 1. apt-get install quota | 2.sudo vim /etc/fstab  ADD: usrquota,grpquota of mount point: /home |
| LABEL=DOROOT / ext4 errors=remount-ro,usrquota 0 1  UUID=9bc6af63-9ac4-4e66-82b9-f0a2ef6148dd /home ext4 errors=remount-ro,usrquota 0 1  /home/tmp /tmp none bind 0 0 ## This is for increase /tmp space | |
| 3. mount -o remount /home  4. quotacheck -cugm /home | 5.quotaon /home  6. edquota user\_name |
|  |  |
|  |  |
| Grace Period: edquota -t days, hours, minutes, seconds.  Filesystem blocks soft hard inodes  /dev/disk/by-label/DOROOT 8 10000 10240 2  sudo repquota -as (Check quota table) ***one block is 1kb***  1 Terabytes = 1073741729.88 Kilobytes 2 Terabytes = 2147483459.76 Kilobytes  3 Terabytes = 3221225189.65 Kilobytes 4 Terabytes = 4294966919.53 Kilobytes  “Looks like the maximum number of sections is around 4TB.  4294966919 ”  https://convertlive.com/u/convert/terabytes/to/kilobytes | |
| https://www.server-world.info/en/note?os=Ubuntu\_16.04&p=quota | |
|  |  |
| sudo mount -o rw,remount / |  |
|  |  |
|  |  |

**Memory Management**

<https://unix.stackexchange.com/questions/34334/how-to-create-a-user-with-limited-ram-usage>

|  |  |
| --- | --- |
| Nice value for users | etc/security/limits.conf  luser memory memlimit/ |
|  |  |

**CPU Management**

<https://bencane.com/2013/09/30/changing-the-default-nice-value-for-a-user-or-group/>

|  |  |
| --- | --- |
| Nice value for users |  |
|  |  |

## **Mount Outside Drive**

|  |  |
| --- | --- |
| lsblk | “list block devices) shows all attached drives.” |
| Blkid | Find UUID for mount |
| /etc/fstab | defines what should be mounted. It is read at system start. |
| mount -a | That reads /etc/fstab as system start |
|  |  |
| Mount a disk more than 20 TBs. | https://unix.stackexchange.com/questions/29078/how-to-partition-22tb-disk |
| **XFS:** | **https://linux.die.net/man/8/mkfs.xfs** |
| **umount** | **https://unix.stackexchange.com/questions/107885/busy-device-on-umount** |

## **Amazon AWS**

|  |  |
| --- | --- |
| S3 command line introduction | https://docs.aws.amazon.com/cli/latest/userguide/cli-services-s3-commands.html |
| aws s3 cp --recursive Jianxu s3://xianglilab/tracks\_hub/ | **aws s3 cp LARP4\_IRI.tar.gz s3://xianglilab/Shared/** |

## **Google Download large files:**

## the simple gdown --id file\_id will do, no need to the full url

**Illumina:**

Run CLI: $HOME/bin/bs

List all runID ~/bin/bs list appsessions

<https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview#InstallBaseSpaceSequenceHubCLI>

## **System\_Check**

|  |  |
| --- | --- |
| lscpu | lshw / hwinfo / lspci / fdisk |
| Cat /proc/version |  |
| landscape-sysinfo | Display important info |
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## **Variable Substitution**

var=0123456789

|  |  |
| --- | --- |
| ${var} | 0123456789 |
| ${var:1} | 123456789 |
| ${var:1 :-1} | 12345678 |
| ${var:?”message”} | If var is null or unset, message is printed as err. |
| ${var:+word} |  |
| Export $Variables | Export MYVAR EXPORT NAME=value |
| ${var[\*]} ${var[@]} |  |
| $(seq 1.0 0.01 1.1) | Generating a sequence of floating point values. |
| ${var/pattern/string}  ${var//pattern/string} | Replace the first occurrence pattern with a given string, replace all occurrences.  echo "${message//[0-9]/X}" |
|  |  |

## **Special Variable**

|  |  |
| --- | --- |
| $0 | The filename of the current script. |
| $n | These variables correspond to the arguments with which a script was invoked. |
| $# | The number of arguments supplied to a script. |
| $\* | All the arguments are double quoted |
| $@ | All the arguments are individually double quoted. |
| $? | The exit status of the last command executed. |
| $$ | The process number of the current shell |
| $! | The process number of the last background command. |

## **Quoting Mechanisms**

|  |  |
| --- | --- |
| Echo hello\; World or “I have \$1200” | Print: Hello; World and I have $1200 |
| ‘ ’ | All special characters lose their special meaning. |
| “ “ | Lose special meaning except $ ` \$ \’ \” \\ |
| After \ |  |
|  |  |

## **O/I**

|  |  |
| --- | --- |
| Who > users.log | Output Saving a new file .log |
| Who >> users.log | Append the output in an existing file. |
| printf |  |
| Let / $(( )) | Conducting the arithmetic operation. |
| History | Return your command history with line number  And using !$number to re-run that command |
| Sudo dpkg –get-selections | grep python | Search all the installed package related to python |
| Apt-get remove $packagename |  |
|  |  |

## Files and Directories

|  |  |
| --- | --- |
| Cat | Displays file contents |
| scp | cp --parents $(find -name \*.html) ~/Data/Haihui/  Hdac/RNA\_seq/Aug2018/CELLRANGER/output/ |
| Chgrp | Changes file group |
| Less | Displays file contents only for one screen |
| File | Determines file type |
| Grep | Searches files for regular expression |
| In | Creates softlink on old name |
| More | Displays data in paginated form |
| Rmdir | Deletes an existing directory provided it is empty |
| Tail | Prints last few lines in a file |
| Touch | Updates access and modification time of a file |
| Df -k / du -sh | Display the disk space |
| Test -d dir | Dir is a directory |
| -f file | If file |
| -e file | If exists |
| -h link | If link |
| -r file | If readable |
| -w file | If writable |
| -x file | If executable |

## **File System Basics**

|  |  |
| --- | --- |
| / | The root directory, contain only the directories for top level. |
| /bin | Contain executables files. Available to all users. |
| /dev | Device drivers |
| /etc | Supervisor directory commands |
| /lib | Shared library files |
| /mnt | Mount other temporary file systems. |
| /proc | All processes marked as a file by process number |
| /usr | Used for miscellaneous purposes. |
| /var | Variable-length files. |
| /sbin | System administration executable files. |
|  |  |

## **Processes**

|  |  |
| --- | --- |
| PID/PPID/init/daemon/zombie | Pidof “NAME\_Process” |
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## **Linux Update**

|  |  |
| --- | --- |
| sudo apt-get update | sudo apt-get upgrade |
|  | sudo apt-get dist-upgrade |
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## **Grep**

|  |  |
| --- | --- |
| -v | Invert |
| -w | Matches entire words |
| -B | Before |
| -A | After |
| -C | Before and after |
| Grep -n input1 input2 | cut -f1 -d:> | Only get the line number |
| -G basic regular expression | -P Perl Regular expression |
|  |  |

**Regular Expression:**

<https://www.rexegg.com/regex-quickstart.html>

## **Sed**

|  |  |
| --- | --- |
| -n –quiet –silent | By default sed prints out the pattern space at the end. |
| -e script –expression=script |  |
| Scripts |  |
| Sed ’30,35d’ input > output | 30,35 is an address range, d is the delete command. |
| sed -i $'1i #chr\tstart\tend\tgene\_id' test.txt | Add first row |
| sed -i -e 's/^/chr/' \*.bdg | Add chr to each row |
| sed -i '/Match Partern/d' \*.bed | Delete match to a partern |
| sed -n '1,3p' < file.txt | Display line 1 up to line 3 |

## **Awk**

se the -v option to declare an awk variable holding the value of the function argument.

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| --- | --- |
| Awk ‘program’ input1 input 2 | Awk -f program-file input1 input2… |
| Awk ‘{print}’ | awk ’BEGIN { print "Don\47t Panic!" }’ |
| awk -F '\t' 'BEGIN{OFS=FS}{if( NR > 1) print $1,$2,$3,NR+1,$5,$6 }' | |
|  |  |
| delete-lines-containing-empty-fields | https://unix.stackexchange.com/questions/347843/delete-lines-containing-empty-fields |
|  |  |
| Using Awk to do some calculation | cat WT-na1\_20180709000.bedpe | awk '{print $3-$2}' | sort -n | awk '{print NR"\t"$1}' > distribution\_framentsize.txt & |
|  | awk '{if ($3-$2 < 50) {print $3-$2"\t"$4}}' |

## **R**

https://stackoverflow.com/questions/9789806/command-line-utility-to-print-statistics-of-numbers-in-linux

|  |  |
| --- | --- |
| Get V1  Min. : 1.00 1st Qu.: 3.25  Median : 5.50 Mean : 5.50  3rd Qu.: 7.75 Max. :10.00 | R -q -e "x <- read.csv('nums.txt', header = F); summary(x); sd(x[ , 1])" |
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## **tr**

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| tr ‘;’ ‘,’ < be.fore > af.ter | convert ; into , in all of your text. |
| tr 'A-Z' 'a-z' <be.fore >af.ter | Conver Upper into lower |
| tr -d '\r' <file.dos >file.txt | Converting DOS Files to Linux Format |
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## **Colonial One**

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| --- | --- |
| Ssh [lux@login.colonialone.gwu.edu](mailto:lux@login.colonialone.gwu.edu) |  |
| Module avail $name | Display the modules in server. |
| Module load R/3.3.3  Module unload R/3.3.3  Module purge | Load module R/3.3.3  Unload module  Unload all loaded modules |
| Module list | List all module loaded |
| Module spider \*name\* | Vague search |
|  |  |
| Lustre file is only kept for 60 days |  |
| Sinfo | Slurmd information (idle= avaliable) |
| salloc -t 120 -p debug -N 1 |  |
| srun hostname |  |
| Squeue | Display the job-id |
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| **Parallel Module** |  |
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## **Git**

**https://linuxhint.com/git\_tutorial\_beginners/**

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| --- | --- |
| git config --global color.ui "auto"  core.editor=vim -w | user.name=lux563624348  user.email=lux@gwu.edu |
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## **Scripts**

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| --- | --- |
| Self-contained executable command | #! /usr/bin/awk -f |
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## **Tar**

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| --- | --- |
| **create** a **tar**.**gz** | . **tar** -zcvf **tar**-archive-name.**tar**.**gz**source-folder-name. |
|  |  |
| extract a **tar**.**gz** | **tar** -zxvf **tar**-archive-name.**tar**.**gz**. |
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## **Fastqc(v0.11.7)**

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| --- | --- |
| Fastqc |  |
| multiqc \*fastqc.zip --ignore \*.html |  |
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## **Backup and Recover with Rsync**

<https://www.sanitarium.net/golug/rsync_backups_2010.html>

All these commands are under sudo su authorization.

|  |  |
| --- | --- |
| Crontab -e | rsync --delete -az --exclude 'cloud\_research' -e ssh /home/ xli@128.164.54.240:/home/back\_up\_daily > /home/crontab\_log/Tang.daily.backup\_$(date +%Y%m%d).log |
|  |  |
| Full backup | rsync --compress --archive --verbose --exclude={"dev/","proc/","sys/","tmp/","run/","mnt/","media/","lost+found/","cloud\_research/",”home/data”} --hard-links --human-readable --inplace --numeric-ids --delete --link-dest=/home/back\_up/201809 -e ssh / xli@128.164.54.240:/home/back\_up/201809 > /home/crontab\_log/Tang.daily.backup\_$(date +%Y%m%d\_%H.%M).log |
|  |  |
| Create folder | ssh xli@128.164.54.240 "mkdir -p /home/back\_up/Weekly\_Backup/$(date +%Y%m%d)" |
|  |  |
| Incremental Backup | http://www.clipular.com/c/5875563890475008.png?k=XSK0qYpVB78Xj_AEbzgrttsSVTI |
| Recover  Do not Directly rsync to /home | rsync --compress --archive --verbose --exclude={"dev","proc","sys","tmp","run","mnt","media","lost+found","cloud\_research"} --hard-links --human-readable --inplace --numeric-ids --delete -e ssh /home/back\_up/Tang/Daily\_Backup/05252019/ root@tang.phys.gwu.edu:/ > /home/back\_up/Tang/Tang.recover.$(date +%m%d%Y\_%H.%M).log |
|  | Recover to a third path first, then move. |

## **Sample**

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| --- | --- |
|  | head $(find -name metrics\_summary.csv) | sed -e 's/,,/, ,/g' | column -s, -t > summary.log |
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## **Tensorflow**

conda create -n tensorflow\_env python=3.6 tensorflow keras pandas numpy matplotlib scikit-learn

|  |  |
| --- | --- |
| To activate this environment, use:  # > source activate tensorflow\_env | # To deactivate an active environment, use:  # > source deactivate |
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## Convert gtf to bed format.

sed '1d;' filename.gff | awk '{print $1}' | tr -s [:] '\t' | tr -s '-' '\t' |

Shell Substitutions

Echo -e “It is $a \n”

|  |  |
| --- | --- |
| \n | A new line |
| \a | Alert (BEL) |
| \b | backspace |
| \c | Suppress trailing newline |
| \f | Form feed |
| \r | Carriage return |
| \t | Horizontal tab |
| \v | Vertical tab |
| \\ | backslash |

`command`

When performing the command substitution make sure that you use the backquote, not the single quote character.

# 2nd Sequencing

## **Bowtie**

(http://bowtie-bio.sourceforge.net/bowtie2/manual.shtml#getting-started-with-bowtie-2-lambda-phage-example)

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## **Tophat**

(https://ccb.jhu.edu/software/tophat/manual.shtml)

|  |  |
| --- | --- |
| Test Data Link: | http://shang.phys.gwu.edu/Test\_Data/ |
| Command | Explanation |
|  | head $(find -name metrics\_summary.csv) | sed -e 's/,,/, ,/g' | column -s, -t > summary.log |
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# Computational Server Check

cat /proc/cpuinfo |grep process |wc -l

free -g

df -h

#check (core, memory, storage)

# Download\_fastqc\_lx

Some basic command lines:

1. Back ground running and log: nohup bash XX.sh > XX.log &
2. In Win 10 bash environment, only trying to modify the files between windows and bash via DIR:

/mnt/c/Users/USER\_NAME/

/mnt/c/Users/Xiang\ Li/Dropbox/AResearch/

## Md5 check

md 5sum -c

# Saving DIR

No DIR:

if [ ! -d $OUTPUTDIR ]; then

mkdir -p $OUTPUTDIR

# run\_fastqc\_lx.sh

Multiple Line comment:

If false

Then

…code…

fi

# Samtools:

<http://www.htslib.org/doc/samtools.html>

samtools view [options] in.sam|in.bam|in.cram [region...]

Specify one or more space-separated region specifications after the input filename to restrict output to only those alignments which overlap the specified region(s). Use of region specifications requires a coordinate-sorted and indexed input file (in BAM or CRAM format).

Sort alignments by leftmost coordinates, or by read name when **-n** is used

samtools sort -o output.sam input.bam

Create a BAI index

Samtools index -b input.bam

Samtools view -h input.bam MMLV -o MMLV.sam

Bedtools bamtofastq -I MMLV.bam -fq MMLV\_R1.fastq # -fq2 MMLV\_R2.fastq

# BOWTIE2

bowtie2-build [options]\* <reference\_in> <bt2\_base>

bowtie2-inspect [options]\* <bt2\_base>

bowtie2-inspect -s <> ##summary

You are aligning paired end reads, so I think you need to specify the parameters --un-conc and --al-conc . Check here just in case:   
[http://bowtie-bio.sourceforge.net/bo...output-options](http://bowtie-bio.sourceforge.net/bowtie2/manual.shtml#output-options)

--un-conc-gz <path>

# If a percent symbol, %, is used in <path>, the percent symbol is replaced with 1 or 2to make the per-mate filenames.

# bowtie2\_SingleEnd.sh

BOWTIEINDEXES Changed.

After fastqc. Fastq.zip file and the DIR of raw\_data

# BBDuk

bbduk.sh in1=read1.fq in2=read2.fq out1=clean1.fq out2=clean2.fq

 “bbduk.sh -Xmx1g in=reads.fq”. That command will force it to use 1 GB.

# check on Specific gene.

grep AVPR1

Sicer:

Islandfilter.wig for visualization.

Four .bed files plus one input as background.

# Set up Hub Tracks:

1. Converting wig files to BigWig files via using WigToBigWig;

# wigToBigwig

./wigToBigWig ${SAMPLENAME}.wig $WIG2BIGWIG/UCSC/genome\_sizes/mm9.genome ${SAMPLENAME}.bw

1. Create a directory which contains hub.txt, genomes.txt TrackDb.txt and all BigWig files.
2. hub.txt – a short description of hub properties.
3. genomes.txt – list of genome assemblies included in the hub data
4. trackDb.txt (Under a specific genome assembly directory) – display properties for tracks in this directory.
5. All the BigWig files are not necessarily on the same location as above files as long as they can be accessed via internet.

Addition: groups - a file which defines the track groups on this Genome Browser. Track groups are the sections of related tracks grouped together under the primary genome browser graphics display image. The groups.txt file defines the grouping of track controls under the primary Genome Browser image display. The example referenced here has the usual definitions as found in the UCSC Genome Browser. Each group is defined, for example the Mapping group:

Setting Detail of TrackDb.txt: (<https://genome.ucsc.edu/goldenPath/help/trackDb/trackDbHub.html>)

Summary:

For: Dropbox

https://dl.dropboxusercontent.com/s/7sjfbknsqhq6xfw/test.bed”, which can be loaded by the UCSC Genome Browser automatically.

track macs2\_single\_end\_Eed(GFP-)1

shortLabel Eed(GFP-)1

longLabel Eed(GFP-)1

type bigWig

bigDataUrl https://s3.amazonaws.com/xianglilab/tracks\_hub/Haihui/Treg\_cell\_transcriptome\_RNA\_seq/BigWigs/GK1\_20190114000\_treat\_pileup.bw

visibility full

color 0,128,0

autoScale on

alwaysZero on

maxHeightPixels 100:24:8

windowingFunction mean+whiskers

### Multi sub tracks

track Eed(GFP-)

container multiWig

shortLabel Eed(GFP-)

longLabel Eed(GFP-)

aggregate none

visibility full

autoScale on

type bigWig

maxHeighPixels 100:32:8

track macs2\_single\_end\_Eed(GFP-)1

shortLabel Eed(GFP-)1

longLabel Eed(GFP-)1

parent Eed(GFP-)

type bigWig

bigDataUrl https://s3.amazonaws.com/xianglilab/tracks\_hub/Haihui/Treg\_cell\_transcriptome\_RNA\_seq/BigWigs/GK1\_20190114000\_treat\_pileup.bw

visibility full

color 0,128,0

autoScale on

alwaysZero on

maxHeightPixels 100:24:8

windowingFunction mean+whiskers

## **Single cell**

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| Check summary | head $(find -name metrics\_summary.csv) | sed -e 's/,,/, ,/g' | column -s, -t > summary.log |
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