UCLA QCBio Collaboratory

Day 2: Advanced Command line

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Thank Dr. Lefaudeux and Dr. Guo

Agenda

- Day 0: Preparation

- Day 1: Introduction to Unix Command line
  - Navigating through file system
  - Manipulating files and directories

- Day 2: Advanced Command line
  - Useful commands for file processing
  - sed, awk, grep, and regular expression

- Day 3: Shell scripting and running jobs on hoffman2

Notations of the slides

- `Code chunk` starts with "➢", e.g.
  - ➢ `echo 'Hello world!'`

- Link is underlined

- Practice comes with

Overview

Time

- 3-hour workshop (45min + 45min + 30min + practices/Q&A)

Topics

- ❑ Request resources on hoffman2 cluster
- ❑ Useful commands for file processing
- ❑ sed, awk, grep
- ❑ Regular expression

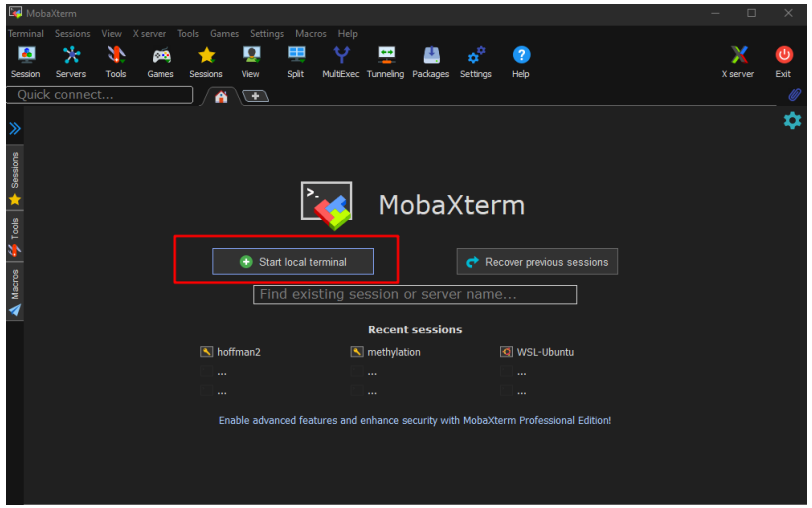
Questions can be put into this Google doc

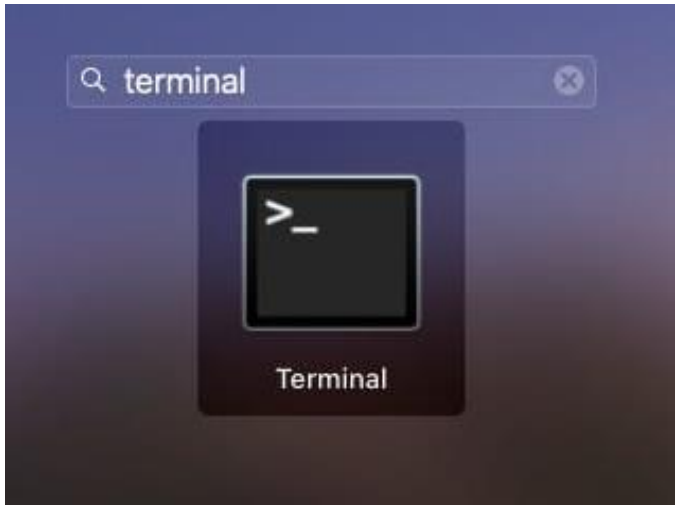
https://www.hostinger.com/tutorials/linux-commands

Summary – Day 1

Connect to hoffman2 cluster through command line interface

- Windows: mobaXterm/WSL open local terminal
- macOS/Linux: open terminal





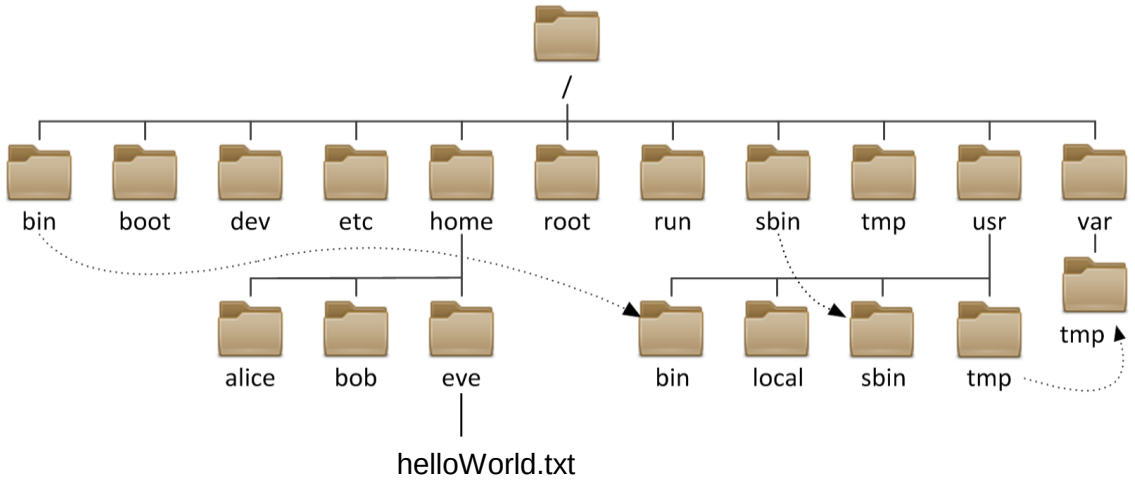
➢ `ssh username@hoffman2.idre.ucla.edu`

(*replace* `username` *with your hoffman2 username, e.g. wbguo*)

Summary – Day 1

Navigate through the file system

- Absolute path & relative path
- The meaning of “~”, “.”, “..”



Command	Function
`ssh`	Connect to hoffman2
`exit`	Close the remote connection
`pwd`	Print working directory
`cd`	Change directory
`ls`	List the information of files/folder (note the flag’s usage)

Tips:

- Use up/down key to browse your command history
- Use Tab key for auto-completion
- Use `clear` to clean screen
- Use `pwd` and `ls` to check

Summary – Day 1

Manipulate with files/directories

Command	Function
`mkdir`	Create a directory
`touch`	Create a file / change the time stamp
`rm`	Delete file or directory
`cp`	Copy file or directory
`mv`	Move file or directory
`cat`	Print the file contents to standard output
`vi`	Modify a file / create a file
`chmod`	Change file permission
`gzip`	Compress/decompress a file
`tar`	Create a compressed archive
`scp/sftp`	File transfer
`man/--help`	Get help

Note:

- command is case-sensitive
- cat file to show the contents

Let’s fight with the dragon!

https://unix.stackexchange.com/questions/620021/what-does-do-in-shell/620058

Request resources on hoffman2

- Connect to hoffman2
  - `ssh username@hoffman2.idre.ucla.edu`

- Request a interactive node
  - `qrsh -l h_rt=03:00:00,h_data=256M`

Note:

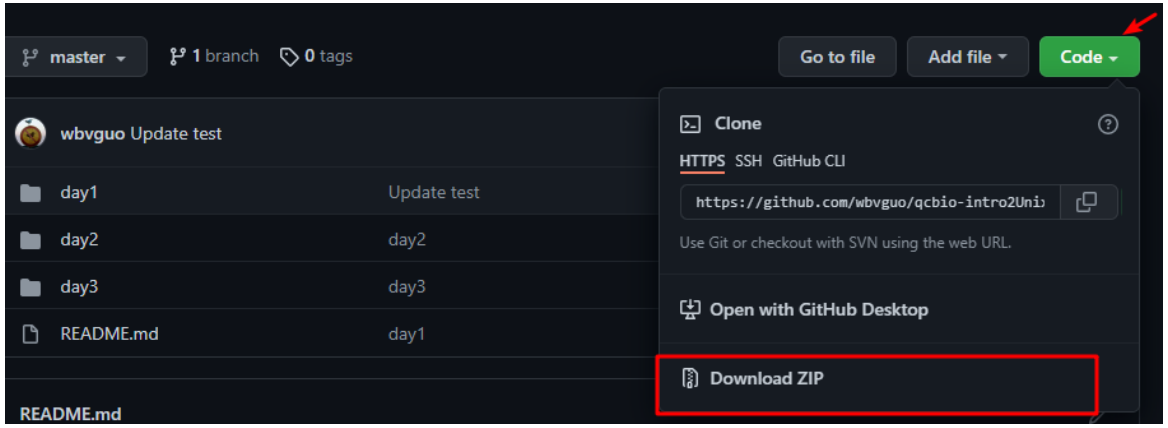
- No space between h_rt and h_data (they are only separated by comma)
- Default h_rt (02:00:00), h_data (1G)
- Make sure to request enough resources for your computing jobs

Get working materials

- Option1: Clone the working materials to your directory
  - ➢ `git clone https://github.com/sergey-knyazev/qcbio-intro2Unix.git`

  (if meet “already exists” problem, try `rm -rf qcbio-intro2Unix` first)

- Option2: download the file and upload to hoffman2
  - Go to `https://github.com/sergey-knyazev/qcbio-intro2Unix.git`
  - Download zip file



Get working materials

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  (if meet “already exists” problem, try `rm -rf qcbio-intro2Unix` first)

- Option2: download the file and upload to hoffman2
  - Go to https://github.com/sergey-knyazev/qcbio-intro2Unix.git
  - Download zip file
  - Upload to hoffman2 using scp or Cyberduck/mobaXterm

Useful commands for file processing

- View/merge
- Sort
- Redirect/pipeline
- Other command lines (`wc/cut/uniq/diff`)

“Everything is a file in Unix”

View a file

- Regular file
  - `cat`
  - `more/less`
  - `head/tail`

- Compressed file
  - `zcat`
  - `zmore`

View (cat)

- `cat`: concatenate files and print on the standard output
- Syntax: `cat <file name>`

```
[wbguo@login2 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3
[wbguo@login2 qcbio-intro2Unix]$ cd day2/
[wbguo@login2 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login2 day2]$ cat chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

- It's not suitable to view very big file

View (more)

- `more`: view the file contents one screen at a time
- Syntax: `more <file name>`

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
```

Scroll option

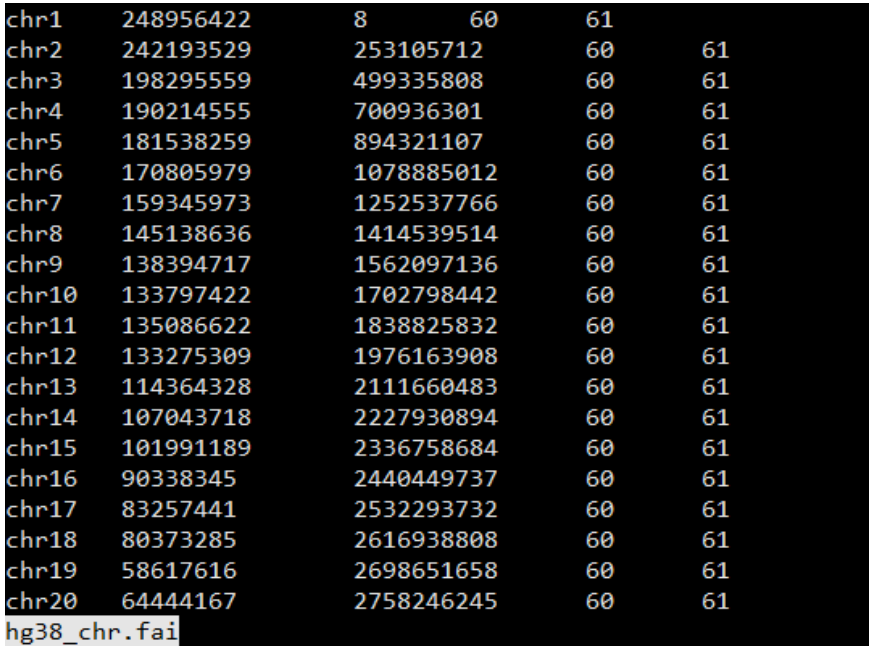
- By line: enter
- By screen: space

Exit Option:

- q (quit)

View (less)

- `less`: display the file in a paginated way
- Syntax: `less <file name>`



```
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
hg38_chr.fai
```

Scroll option

- By line: up/down key
- By page: f or space / b (forward / backward); PgDn/PgUp

Exit Option:

- q (quit)

Search option:

- /string: search string forward
- ?string: search string backward
- n: next occurance
- N: previous occurance

View (head)

- `head`: show the beginning of file
- Syntax: `head -<flag> <file name>`
- Flag option:
  - `-n`: show the first n line of file

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ head -10 hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
```

View (tail)

- `tail`: show the end of the file
- Syntax: `tail -<flag> <file name>`
- Flag option:
  - `-n`: show the last n line of file

```
[wbguo@login1 day2]$ tail -10 hg38_chr.fai
KI270748.1      93321   3150532617      60      61
KI270749.1      158759  3150627517      60      61
KI270750.1      148850  3150788945      60      61
KI270751.1      150742  3150940299      60      61
KI270752.1      27745   3151093577      60      61
KI270753.1      62944   3151121808      60      61
KI270754.1      40191   3151185825      60      61
KI270755.1      36723   3151226709      60      61
KI270756.1      79590   3151264068      60      61
KI270757.1      71251   3151345008      60      61
```

View (zcat/zmore)

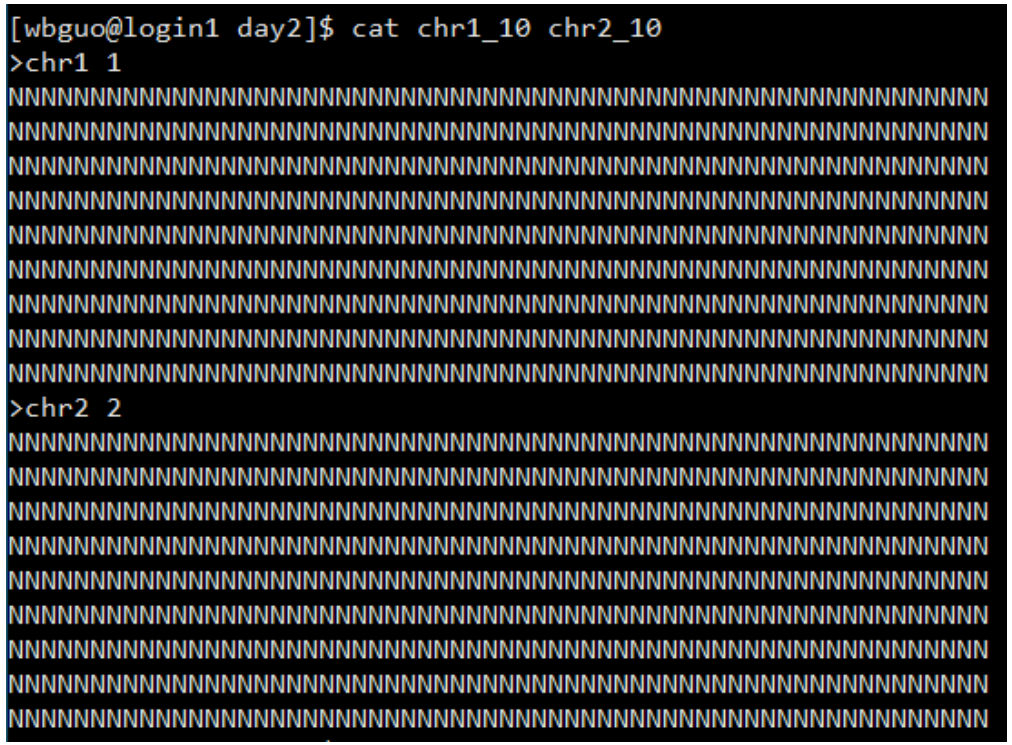
- `zcat`: Decompress and concatenate files to standard output
- Syntax: `zcat <file name>.gz`

- `zmore`: Decompress and view the file contents one screen at a time
- Syntax: `zmore <file name>.gz`

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ zmore sample-A01.gz
------> sample-A01.gz <------
chr3    G       13080   CHH     CA      0.0     0       1
chr3    G       13083   CHH     CT      0.0     0       1
chr3    G       13089   CHG     CA      0.0     0       1
chr3    G       13090   CHH     CC      0.0     0       1
chr3    G       13091   CHH     CC      0.0     0       1
chr3    G       13095   CHG     CT      0.0     0       1
chr3    G       13096   CHH     CC      0.0     0       1
chr3    G       13098   CHH     CA      0.0     0       1
chr3    G       13101   CHG     CT      0.0     0       1
```

Merge (cat)

- `cat`: concatenate files and print on the standard output
- Syntax: `cat <file1> <file2>`



- Question: does the order matter?

Tips: using * as a wildcard in commands

- `cat chr*` concatenates files whose name starts with `chr`
  - Same results as `cat chr1_10 chr2_10`

- `ls *10` outputs files end with `10`

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ ls *10
chr1_10  chr2_10  mod_chr1_10
[wbguo@login1 day2]$
```

- `ls *chr*` outputs files that contains `chr`

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ ls *chr*
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10
[wbguo@login1 day2]$
```

Practice:

- Try less command with file `hg38_chr.fai`
  - Scroll by line/page
  - Search string 'chr’

- Merge `mod_chr1_10` and `chr1_10`

Redirection

- Redirecting the standard output to a file
  - >: output to the file (if file exists, it will overwrite it)
  - >>: append the output to the end of a file (if file doesn't exist, it will create the file)

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt
[wbguo@login1 day2]$ echo "this is day2" > test.txt
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt  test.txt
[wbguo@login1 day2]$ cat test.txt
this is day2
[wbguo@login1 day2]$ echo "add another line" >> test.txt
[wbguo@login1 day2]$ cat test.txt
this is day2
add another line
[wbguo@login1 day2]$
```

Pipeline

- | (pipe): combine multiple commands together
- Syntax: `command1 | command2 | command3`
- The command1's output will be redirected to command2's input, and so on

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt  test.txt
[wbguo@login1 day2]$ zcat sample-A01.gz | head -10
chr3    G       13080   CHH     CA      0.0     0       1
chr3    G       13083   CHH     CT      0.0     0       1
chr3    G       13089   CHG     CA      0.0     0       1
chr3    G       13090   CHH     CC      0.0     0       1
chr3    G       13091   CHH     CC      0.0     0       1
chr3    G       13095   CHG     CT      0.0     0       1
chr3    G       13096   CHH     CC      0.0     0       1
chr3    G       13098   CHH     CA      0.0     0       1
chr3    G       13101   CHG     CT      0.0     0       1
chr3    G       13103   CHH     CA      0.0     0       1
```

Enhance the efficiency:

- Avoid generating the intermediate files

Sort

- `sort`: sort lines in a file
- Syntax: `sort -<flag> <filename>`
- Flag options
  - **-k** col1,col2: Specify a **k**ey to do the sorting, col1 and col2 are used to indicate the starting filed indices and ending field indices (col1 default is 1, col2 can be empty)
  - **-t**: specify the delimiter
  - **-n**: sort based on **n**umerical value (default: alphabetically)
  - **-r**: **r**everse order
  - **-u**: only unique lines
  - **-b**: Ignore blanks at the start of the line
  - **-o**: specify the output file (default is the standard output)

Sort

- `sort`: sort lines in a file
- Syntax: `sort -<flag> <filename>`

original

```
[wbguo@login1 day2]$ head -10 hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
```

sorted

```
[wbguo@login1 day2]$ sort -k 2 -n hg38_chr.fai | head -10
KI270394.1      970     3142567409      60      61
KI270392.1      971     3142565045      60      61
KI270423.1      981     3142587281      60      61
KI270385.1      990     3142554003      60      61
KI270539.1      993     3143532085      60      61
KI270312.1      998     3142429913      60      61
KI270336.1      1026    3142507546      60      61
KI270419.1      1029    3142582335      60      61
KI270329.1      1040    3142499492      60      61
KI270379.1      1045    3142543110      60      61
```

Count

- `wc`: word count for the file
- Syntax: `wc -<flag> <file name>`

- Flag options:
  - -m: show total number of characters
  - -l: show total number of lines
  - -w: show total number of words

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt  test.txt
[wbguo@login1 day2]$ wc -m chr1_10
557 chr1_10
[wbguo@login1 day2]$ wc -l chr1_10
10 chr1_10
[wbguo@login1 day2]$
```

Cut

- `cut`: show the specific parts of the file;
- Syntax:
  - `cut –c <char position> <filename>`
  - `cut –d <delimiter> –f <field position> <filename>`

- Flag options:
  - `-c <char position>`: select only these characters
  - `-d <delimiter> :` separate using delimiter (default tab)
  - `-f <field position>:` extract these fields

Cut

- `cut`: show the specific parts of the file;
- Syntax:
  - `cut –c <char position> <filename>`
  - `cut –d <delimiter> –f <field position> <filename>`

```
[wbguo@login1 day2]$ head -5 seq_file_list.txt
sample-A01_R1_trimmed.fastq.gz
sample-A01_R2_trimmed.fastq.gz
sample-A02_R1_trimmed.fastq.gz
sample-A02_R2_trimmed.fastq.gz
sample-A03_R1_trimmed.fastq.gz
[wbguo@login1 day2]$ cut -c 1-10 seq_file_list.txt | head -5
sample-A01
sample-A01
sample-A02
sample-A02
sample-A03
```

Deduplicate

- `uniq`: extract unique lines
- Syntax: `uniq -<flag> <filename>`

- Flag options:
  - `-c`: count how many times each line occurred
  - `-d`: show only duplicated lines

Deduplicate

- `uniq`: extract unique lines
- Syntax: `uniq -<flag> <filename>`

```
[wbguo@login1 day2]$ cut -c 1-10 seq_file_list.tx
sample-A01
sample-A01
sample-A02
sample-A02
sample-A03
sample-A03
sample-A04
sample-A04
sample-A05
sample-A05
sample-A06
sample-A06
sample-A07
sample-A07
sample-A08
sample-A08
sample-A09
sample-A09
sample-A10
sample-A10
sample-A11
sample-A11
sample-A12
sample-A12
```

```
[wbguo@login1 day2]$ cut -c 1-10 seq_file_list.txt | uniq
sample-A01
sample-A02
sample-A03
sample-A04
sample-A05
sample-A06
sample-A07
sample-A08
sample-A09
sample-A10
sample-A11
sample-A12
```

```
[wbguo@login1 day2]$ cut -c 1-10 seq_file_list.txt | uniq -c
      2 sample-A01
      2 sample-A02
      2 sample-A03
      2 sample-A04
      2 sample-A05
      2 sample-A06
      2 sample-A07
      2 sample-A08
      2 sample-A09
      2 sample-A10
      2 sample-A11
      2 sample-A12
```

Difference

- diff: show differences between files
- Syntax: diff -<flag> <filename1> <filename2>

- Flag options:
  - -c: output with copied context
  - -u: output with unified context
  - -y: side by side

```
[wbguo@login1 day2]$ diff -y mod_chr1_10 chr1_10
>chr1 chr1                                                    | >chr1 1
                                                              > NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  <
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

Practice:

- Perform sorting based on column 3 (numerically decreasing) for file `sample-A01.gz`

- Using `cut` to extract the sample id for file `seq_file_list.txt`
  - e.g. if the file name is `sample-A01_R1_trimmed.fastq.gz`, sample id is `A01`

Advanced Command lines

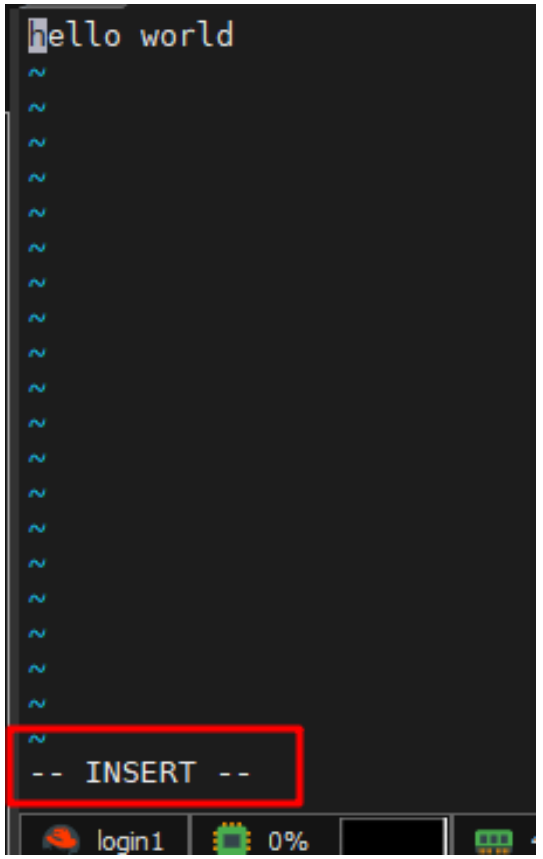
- sed: non-interactively file editing
- awk: scripting language for text processing
- grep: search string/pattern in the file

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

vi: an interactive editor

- Press "**i**" to type in new text (**i**nsertion mode)
- Press "**Esc**" to jump out the insertion mode

- Enter
  - :w (write)
  - :q (quit)
  - :wq (write and quit)
  - :q! (force quit – the modification will not be saved)



vi: an interactive editor

Several scenarios when vi is not suitable

- Files are too large for interactive editing
  - It could be very slow to load them into memory

- Editing is too complicated and tedious
  - After all, you are editing file using hand

sed is very fast and uses little memory,

it can perform multiple editing in one pass

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

sed

- `sed`: stream editor (parse and transform text)
- Syntax: `sed -<flag> 'sed commands' <filename>`

- Editing task: insert / append/ delete / substitute / modify / subset

- Flag options:
  - -i: in place (default is to output to standard output)
  - -e: expression (useful for using multiple sed commands at once)

sed - insert

- Syntax: `sed 'x,y i pattern' <filename>`

- Insert pattern before each line between x and y

```
[wbguo@login1 day2]$ head -5 chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed '1,2 i new_line' chr1_10 | head -5
new_line
>chr1 1
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - insert

- Syntax: sed '/pattern1/ i pattern2' <filename>

- Insert pattern2 before each line when pattern1 is found

```
[wbguo@login1 day2]$ cat chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed '/NNN/ i new_line' chr1_10 | head -10
>chr1 1
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
```

sed - append

- Syntax: sed 'x,y a pattern' <filename>

- Insert pattern after each line between x and y

```
[wbguo@login1 day2]$ sed '1,2 a new_line' chr1_10
>chr1 1
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - append

- Syntax: sed '/pattern1/ a pattern2' <filename>

- Insert pattern2 after each line when pattern1 is found

```
[wbguo@login1 day2]$ sed '/NNN/ a new_line' chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
new_line
```

sed - delete

- Syntax: `sed 'x,y d' <filename>`

- delete lines between x and y

```
[wbguo@login1 day2]$ cat chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed '1,2 d' chr1_10
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - delete

- Syntax: `sed '/pattern/ d' <filename>`

- delete lines when pattern is found

```
[wbguo@login1 day2]$ cat chr1_10
>chr1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed '/>/ d' chr1_10
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - substitute

- Syntax: `sed 's/pattern1/pattern2/' <filename>`
- The substitution only apply to the first match

```
[wbguo@login1 day2]$ sed 's/chr//' mod_chr1_10
>1 chr1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - substitute

- Syntax: sed 's/pattern1/pattern2/' <filename>
- The substitution only apply to the first match

- Syntax: sed 's/pattern1/pattern2/g' <filename>
- Use g (globally) to substitute all the matches

```
[wbguo@login1 day2]$ sed 's/chr//g' mod_chr1_10
>1 1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed - substitute

- Syntax: `sed 'x,y s/pattern1/pattern2/' <filename>`
- Restrict the substitution between line x and y
  - If set y as $, it means the end of the file

```
[wbguo@login1 day2]$ sed '1,5 s/NNNNN//' mod_chr1_10
>chr1 chr1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed – modify a specific line

- Syntax: `sed 'xc\your_new_line' <filename>`
- Change the specific x-th line

```
[wbguo@login1 day2]$ cat mod_chr1_10
>chr1 chr1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed '3c\Hello world!' mod_chr1_10
>chr1 chr1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Hello world!
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed – subset the data

- Syntax example: `sed -n 'x,yp' <filename>`
- Print the file from x-th line to y-th line (both x,y included)

```
[wbguo@login1 day2]$ cat mod_chr1_10
>chr1 chr1
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
[wbguo@login1 day2]$ sed -n '4,6p' mod_chr1_10
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

sed – execute multiple commands in one pass

- Syntax example:
  - sed -e 'x,y d' –e 's,t a pattern' <filename>

```
[wbguo@login1 day2]$ sed -e '1,2 i new_line' -e '3c\Hello world!' mod_chr1_10
new_line
>chr1 chr1
new_line
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Hello world!
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNN_UNIX_IS_COOL_NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

Suggestions

- Do not read and write in the same file

✗ • `sed 'command' file.txt > file.txt`

✔ • `sed -i 'command' file.txt`

- It’s better to backup a file when you use `'sed -i'`

Practice:

- Copy `chr1_10` file as `chr1_test1`, try the following command
  - `sed '1,2 i ooops' chr1_test1 > chr1_test1`
  - `cat chr1_test1`

- Copy `chr1_10` file as `chr1_test2,` try the following command
  - `sed -i '1,2 i ooops' chr1_test2`
  - `cat chr1_test2`

What did you find?

awk

- awk: reads a file line by line, parses the data into fields and allows complex operations to be applied for each line of data
- Syntax: `awk -<flags> 'condition {operation}' <file name>`

- Conditions:
  - Search pattern: /pattern/
  - Comparison: a>b, a==b, a!=b, …
  - Keyword: BEGIN, END
- Operations:
  - Output: e.g. print
  - Arithmetic operation: e.g. c=a*b
  - More complex logic: e.g. if-else

Flag options:

- -F: to specify a delimiter between columns (default is space/tab)
- -v **var=value:** To declare a variable.

awk – print out certain column

- Syntax: `awk '{operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

$1 $2 … $0

- Print column1
  - `awk '{print $1}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{print $1}' hg38_chr.fai | head -10
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
[wbguo@login1 day2]$
```

awk – print out certain column

- Syntax: `awk '{operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

$1 $2 … $0

- Print column1 and column2
  - `awk '{print $1,$2}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{print $1,$2}' hg38_chr.fai | head -10
chr1 248956422
chr2 242193529
chr3 198295559
chr4 190214555
chr5 181538259
chr6 170805979
chr7 159345973
chr8 145138636
chr9 138394717
chr10 133797422
[wbguo@login1 day2]$
```

awk – print out certain column

- Syntax: `awk '{operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Print “contig” and column1
  - `awk '{print "contig",$1}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{print "contig",$1}' hg38_chr.fai | head -10
contig chr1
contig chr2
contig chr3
contig chr4
contig chr5
contig chr6
contig chr7
contig chr8
contig chr9
contig chr10
```

awk – print out certain column

- Syntax: `awk '{operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Print “contig”, column1, column2, and addition of column4 and column5
  - `awk '{print "contig",$1,$2,$4+$5}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{print "contig",$1,$2,$4+$5}' hg38_chr.fai | head -10
contig chr1 248956422 121
contig chr2 242193529 121
contig chr3 198295559 121
contig chr4 190214555 121
contig chr5 181538259 121
contig chr6 170805979 121
contig chr7 159345973 121
contig chr8 145138636 121
contig chr9 138394717 121
contig chr10 133797422 121
```

awk – built-in variables

- NR: Number of Records seen so far
- NF: Number of Fields of current record
- FS: input Field Separator
- OFS: Output Filed Separator

awk – search pattern conditions

- Syntax: `awk 'condition {operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- print the number of line where column1 starts with chr
  - `awk '/chr/ {print NR}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '/chr/ {print NR}' hg38_chr.fai | head -10
1
2
3
4
5
6
7
8
9
10
```

awk – search pattern conditions

- Syntax: `awk -<flags> 'condition {operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- print column1 and column2 if column1 starts with chr, columns are separated by comma

➢ `awk -v FS='\t' -v OFS=',' '/chr/ {print $1,$2}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk -v FS='\t' -v OFS=',' '/chr/ {print $1,$2}' hg38_chr.fai
chr1,248956422
chr2,242193529
chr3,198295559
chr4,190214555
chr5,181538259
chr6,170805979
chr7,159345973
chr8,145138636
chr9,138394717
chr10,133797422
chr11,135086622
chr12,133275309
chr13,114364328
chr14,107043718
chr15,101991189
chr16,90338345
chr17,83257441
chr18,80373285
chr19,58617616
chr20,64444167
chr21,46709983
chr22,50818468
chrX,156040895
chrY,57227415
chrM,16569
```

awk – search pattern conditions

- Syntax: `awk 'condition {operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- print the line where column2 is less than 100,000
  - `awk '$2 < 100000 {print $0}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '$2 < 100000 {print $0}' hg38_chr.fai | more
chrM    16569   3139741236      60      61
GL000208.1      92689   3140745787      60      61
GL000226.1      15008   3142392679      60      61
KI270302.1      2274    3142407961      60      61
KI270303.1      1942    3142410296      60      61
KI270304.1      2165    3142412294      60      61
KI270305.1      1472    3142414519      60      61
KI270310.1      1201    3142416039      60      61
KI270311.1      12399   3142417284      60      61
KI270312.1      998     3142429913      60      61
KI270315.1      2276    3142430951      60      61
KI270316.1      1444    3142433288      60      61
KI270317.1      37690   3142434780      60      61
KI270320.1      4416    3142473122      60      61
KI270322.1      21476   3142477635      60      61
KI270329.1      1040    3142499492      60      61
```

Comparison symbol:

- Equal: ==
- Greater than: >
- Less than: <
- Greater equal: >=
- Less equal: <=

awk – search pattern combined conditions

- Syntax: `awk 'condition {operation}' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- print the line where column2 is less than 100,000, but greater than 10,000

➢ `awk '$2 < 100000 && $2 > 10000 {print $0}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '$2 < 100000 && $2 > 10000 {print $0}' hg38_chr.fai | more
chrM    16569   3139741236      60      61
GL000208.1      92689   3140745787      60      61
GL000226.1      15008   3142392679      60      61
KI270311.1      12399   3142417284      60      61
KI270317.1      37690   3142434780      60      61
KI270322.1      21476   3142477635      60      61
KI270435.1      92983   3142593847      60      61
KI270512.1      22689   3143241452      60      61
KI270538.1      91309   3143439231      60      61
KI270579.1      31033   3143536013      60      61
KI270589.1      44474   3143598397      60      61
KI270707.1      32032   3143835450      60      61
KI270709.1      66860   3143997873      60      61
KI270710.1      40176   3144065871      60      61
```

Combine the conditions:

- And: &&
- Or: ||

awk – if condition

- Syntax: `awk '{if(condition) action}' <filename>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Print column1 and If column 2 is greater than 100,000, print 100,000 as column2
  - `awk '{if ($2 > 100000) print $1, 100000}' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{if ($2 > 100000) print $1, 100000}' hg38_chr.fai | more
chr1 100000
chr2 100000
chr3 100000
chr4 100000
chr5 100000
chr6 100000
chr7 100000
chr8 100000
chr9 100000
chr10 100000
chr11 100000
chr12 100000
chr13 100000
chr14 100000
chr15 100000
chr16 100000
chr17 100000
chr18 100000
chr19 100000
chr20 100000
chr21 100000
chr22 100000
chrX 100000
chrY 100000
GL000008.2 100000
GL000009.2 100000
GL000194.1 100000
```

awk – if-else condition

- Syntax: `awk '{if(condition) action; else (condition) action}' <filename>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Print column1 and If column 2 is greater than 100,000, print “long”, else print “short” as column2
  - `awk '{if ($2 > 100000) print $1,"long"; else print $1,"short" }' hg38_chr.fai`

```
[wbguo@login1 day2]$ awk '{if ($2 > 100000) print $1,"long"; else print $1,"short" }' hg38_chr.fai
chr1 long
chr2 long
chr3 long
chr4 long
chr5 long
chr6 long
chr7 long
chr8 long
chr9 long
chr10 long
chr11 long
chr12 long
```

awk – calculation

- How to calculate the sum of column2 using awk?
  - Define a new variable, and add $2 to it for each line

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

Command:

➢ `awk '{sum+=$2} END {print sum}' hg38_chr.fai`

Variable

`sum=sum+$2`

When you reach to the end of file, then print

```
[wbguo@login1 day2]$ awk '{sum+=$2} END {print sum}' hg38_chr.fai
3099750718
[wbguo@login1 day2]$
```

Practice:

- Use `sample-A01.gz`
  - Print column1 and column2, they are separated by hyphen (-)
  - Filter sites if column4 is not CG
  - calculate the sum of last column

grep

- grep: global regular expression print (search for pattern in the file or standard output)
- Syntax: `grep -<flag> 'Pattern' <file name>`

- Flag options
  - **-v**: print lines that do not contain the string (in**v**ert-match)
  - **-n**: line **n**umbers where the string occurs
  - **-c**: **c**ount number of lines containing the string
  - **-l**: list files that contain the string
  - **-i**: case-**i**nsensitive
  - **-E**: **E**xtended Regular Expression
  - **-B <num>**: **b**efore context, show <num> lines before the match
  - **-A <num>**: **a**fter context, show <num> lines after the match
  - **--color**: color matched string

grep – substring

- Syntax: `grep -<flag> 'Pattern' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Find lines with “chr”
  - `grep 'chr' hg38_chr.fai`

```
[wbguo@login1 day2]$ grep 'chr' hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
```

grep – substring

- Syntax: `grep -<flag> 'Pattern' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Find lines without “chr”
  - `grep -v 'chr' hg38_chr.fai`

```
[wbguo@login1 day2]$ grep -v 'chr' hg38_chr.fai | more
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
GL000195.1      182896  3140371111      60      61
GL000205.2      185591  3140557079      60      61
GL000208.1      92689   3140745787      60      61
GL000213.1      164239  3140840044      60      61
GL000214.1      137718  3141007044      60      61
GL000216.2      176608  3141147081      60      61
GL000218.1      161147  3141326656      60      61
GL000219.1      179198  3141490512      60      61
GL000220.1      161802  3141672720      60      61
GL000221.1      155397  3141837242      60      61
GL000224.1      179693  3141995252      60      61
GL000225.1      211173  3142177963      60      61
GL000226.1      15008   3142392679      60      61
KI270302.1      2274    3142407961      60      61
KI270303.1      1942    3142410296      60      61
```

grep – substring

- Syntax: `grep -<flag> 'Pattern' <file name>`

```
[wbguo@login1 day2]$ more hg38_chr.fai
chr1    248956422       8       60      61
chr2    242193529       253105712       60      61
chr3    198295559       499335808       60      61
chr4    190214555       700936301       60      61
chr5    181538259       894321107       60      61
chr6    170805979       1078885012      60      61
chr7    159345973       1252537766      60      61
chr8    145138636       1414539514      60      61
chr9    138394717       1562097136      60      61
chr10   133797422       1702798442      60      61
chr11   135086622       1838825832      60      61
chr12   133275309       1976163908      60      61
chr13   114364328       2111660483      60      61
chr14   107043718       2227930894      60      61
chr15   101991189       2336758684      60      61
chr16   90338345        2440449737      60      61
chr17   83257441        2532293732      60      61
chr18   80373285        2616938808      60      61
chr19   58617616        2698651658      60      61
chr20   64444167        2758246245      60      61
chr21   46709983        2823764492      60      61
chr22   50818468        2871252985      60      61
chrX    156040895       2922918436      60      61
chrY    57227415        3081560021      60      61
chrM    16569   3139741236      60      61
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000194.1      191469  3140176427      60      61
```

- Count the number of lines that has “chr”
  - `grep -c 'chr' hg38_chr.fai`
  - `grep 'chr' hg38_chr.fai | wc -l`

```
[wbguo@login1 day2]$ grep -c 'chr' hg38_chr.fai
25
[wbguo@login1 day2]$ grep 'chr' hg38_chr.fai | wc -l
25
```

grep – substring in multiple files

- Find lines that contain ‘chr’ in multiple files

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt  test.txt
[wbguo@login1 day2]$ grep -n 'chr' chr1_10 mod_chr1_10
chr1_10:1:>chr1 1
mod_chr1_10:1:>chr1 chr1
[wbguo@login1 day2]$
```

- Find files that have ‘chr’ in their contents

```
[wbguo@login1 day2]$ ls
chr1_10  chr2_10  hg38_chr.fai  mod_chr1_10  sample-A01.gz  seq_file_list.txt  test.txt
[wbguo@login1 day2]$ grep -l 'chr' *
chr1_10
chr2_10
hg38_chr.fai
mod_chr1_10
```

Practice:

- Count the number of lines whose contig contain ‘GL’ in hg38_chr.fai file

- Count the number of lines whose contig doesn’t contain ‘KL’ in hg38_chr.fai file

Practice:

- Count the number of lines whose contig contain ‘GL’ in hg38_chr.fai file

```
[wbguo@login1 day2]$ grep -c 'GL' hg38_chr.fai
16
```

- Count the number of lines whose contig doesn’t contain ‘KL’ in hg38_chr.fai file

```
[wbguo@login1 day2]$ grep -vc 'KL' hg38_chr.fai
194
```

Regular expression

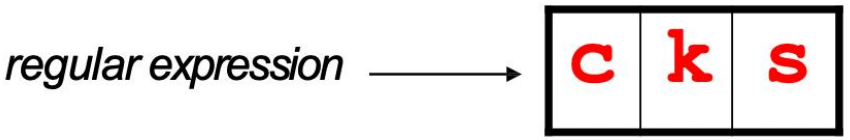
- A regular expression (regex) is a sequence of characters that specifies a search pattern

Example of Patterns

- UID: 123456789, 987654321, ….
  - 9 digits
- Phone number: (123)-456-7890, (987)-654-3210, …
  - 3 digits in parenthesis, followed by hypen, 3 digits, hyphen, 4 digits
- Address: *611 Charles E Young Dr E, 529 Boyer Hall, Los Angeles, CA, 90095*
  - 5 segments separated by comma,
  - 1st and 2nd are a mixture of digits and characters
  - 3rd is a string
  - 4th is a string with 2 capitalized characters
  - 5th is a 5-digit number

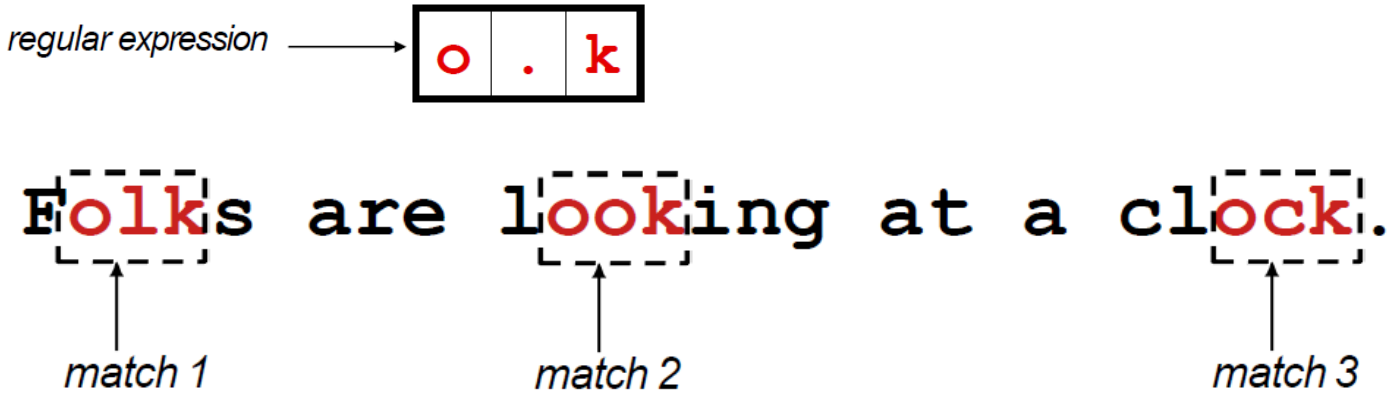
Regular expression:
describe the pattern in a formula
(a sequence of characters)

Regular expression can match multiple places



Rules for writing regular expression

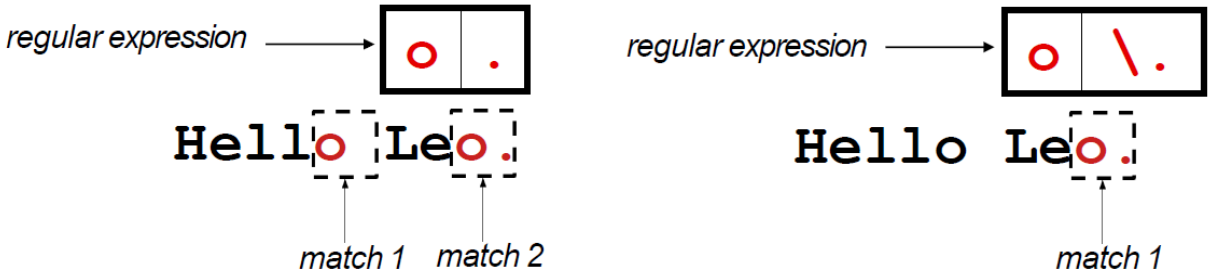
- “.” can be used to match any character




```
[wbguo@login1 day2]$ echo "Folks are looking at a clock" | grep --color 'o.k'
Folks are looking at a clock
```

Rules for writing regular expression

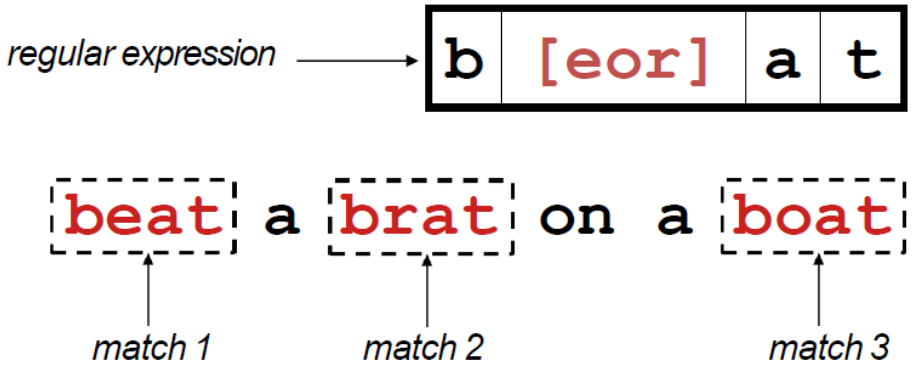
- “.” can be used to match any character
  - If you want to match a “.” itself, use “\” (escape) which removes the specific meaning of the character




```
[wbguo@login1 day2]$ echo "Hello Leo." | grep --color 'o.'
Hello Leo.
[wbguo@login1 day2]$ echo "Hello Leo." | grep --color 'o\.'
Hello Leo.
```

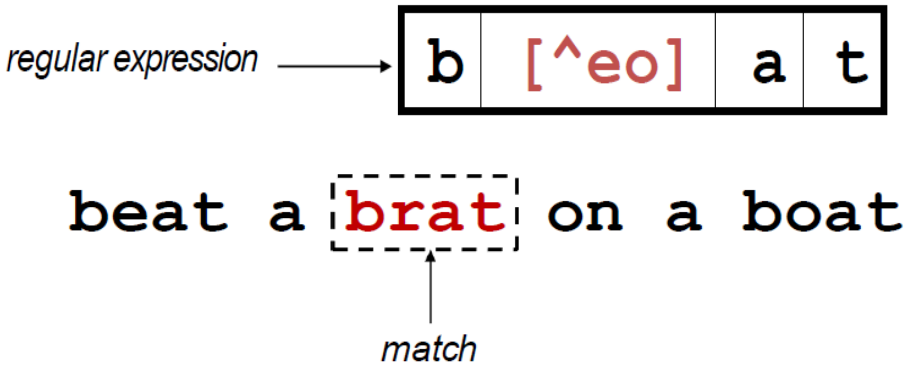
Rules for writing regular expression

- “.” can be used to match any character
  - If you want to match a “.” itself, use “\” (escape) which can remove the specific meaning of the following character
- [] can be used to match any/none of the specified characters



Rules for writing regular expression

- “.” can be used to match any character
  - If you want to match a “.” itself, use “\” (escape) which can remove the specific meaning of the following character
- [] can be used to match any/none of the specified characters



Rules for writing regular expression

- “.” can be used to match any character
  - If you want to match a “.” itself, use “\” (escape) which can remove the specific meaning of the following character
- [] can be used to match any/none of the specified characters
  - Digits: [0-9] or [[:digit:]]
  - Alphabetic characters: [a-zA-Z] or [[:alpha:]]
  - Alphanumeric characters: [a-zA-Z0-9] or [[:alnum:]]

Practice:

- If I want to match both Fastq and fastq, what's the corresponding regular expression?

- Try the following commands on the terminal
  - echo "beat a brat boat" | grep --color 'b[eor]at'
  - echo "beat a brat boat" | grep --color 'b[^eo]at'

Practice:

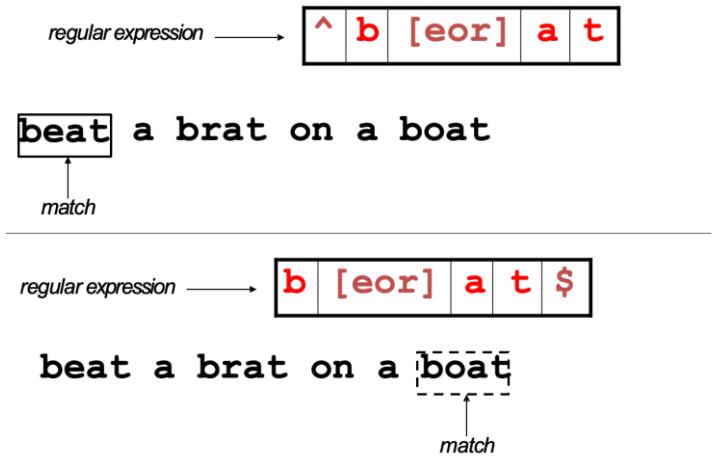
- If I want to match both Fastq and fastq, what's the corresponding regular expression?

  [Ff]astq

- Try the following commands on the terminal
  - echo "beat a brat boat" | grep --color 'b[eor]at'
  - echo "beat a brat boat" | grep --color 'b[^eo]at'

Rules for writing regular expression

- “.” can be used to match any character
  - If you want to match a “.” itself, use “\” (escape) which can remove the specific meaning of the following character
- [] can be used to match any/none of the specified characters
  - Digits: [0-9] or [[:digit:]]
  - Alphabetic characters: [a-zA-Z] or [[:alpha:]]
  - Alphanumeric characters: [a-zA-Z0-9] or [[:alnum:]]
- ^ means the beginning of the string, $ means the end of the string



Rules for writing regular expression

Repetition operators and alternative operators

-E

* : match preceeding pattern 0 or more times (e.g. **el*o** will match H**ello** and vid**eo**)

+ : match preceeding pattern 1 or more time (e.g. **el+o** will match H**ello** but not video)

? : match preceeding pattern 0 or 1 time (e.g. **el?0** will match vid**eo** and dev**elo**p but not Hello)

{n} : match preceeding pattern exactly n times

{n,} : match preceeding pattern exactly at least n times

{,m} : match preceeding pattern exactly at most m times

{n,m} : match preceeding pattern at least n times and at most m times

r1|s2 : alternative, either r1 or s2

Rules for writing regular expression

Groups

- Use () to group the characters

- Examples

a* matches 0 or more occurrences of a
abc* matches ab followed by 0 or more occurences of c: ab, abc, abcc, …
(abc)* matches 0 or more occurences of abc: abc, abcabc, abcabcabc, …

Practice:

- Try to write the regular expression:
  - it starts with 2 capitalized character, and ends with .2, the middle 6 are digits

- Try to apply the regular expression to hg38_chr.fai file

Practice:

- Try to write the regular expression:
  - it starts with 2 capitalized characters, and ends with .2, the middle 6 are digits

    [A-Z]{2}[0-9]{6}\.2

- Try to apply the regular expression to hg38_chr.fai file
  - `cat hg38_chr.fai | grep -E --color '[A-Z]{2}[0-9]{6}\.2'`

```
[wbguo@login1 day2]$ cat hg38_chr.fai | grep -E --color '[A-Z]{2}[0-9]{6}\.2'
GL000008.2      209709  3139758105      60      61
GL000009.2      201709  3139971333      60      61
GL000205.2      185591  3140557079      60      61
GL000216.2      176608  3141147081      60      61
```

Summary

Command	Function
`cat`	Show file contents/merge files
`more/less`	Show file contents
`head/tail`	Show file contents at beginning/end
`zcat/zmore`	Show contents of compressed file
`sort`	Sort a file based on column
`>/>>`	Redirect output to files (write/append)
`|`	Combine commands
`wc`	count
`cut`	Extract a part of string
`uniq`	Show the unique line
`diff`	Show the difference of 2 files
`sed`	Non-interactive editing
`awk`	Text processing
`grep`	search string/pattern in the file

Homework

Credit Card validation

In order to process payments for orders, FAANG needs to validate credit cards entered on the site. Since we are a small company, we will only be accepting Visa and Mastercard Write a command that identifies all well-formatted credit cards in a file called cards.txt that FAANG accepts. The format of these cards are as follows:

Master Card

- Begins with a 5
- Exactly 16 digits long, grouped into sets of 4 separated by a space

Visa

- Begins with a 4
- Between 13 and 16 digits long, grouped into sets of 4 (last may be shorter) separated by a space

You may assume that cards.txt contains one credit card per line.

Q&A

Google doc