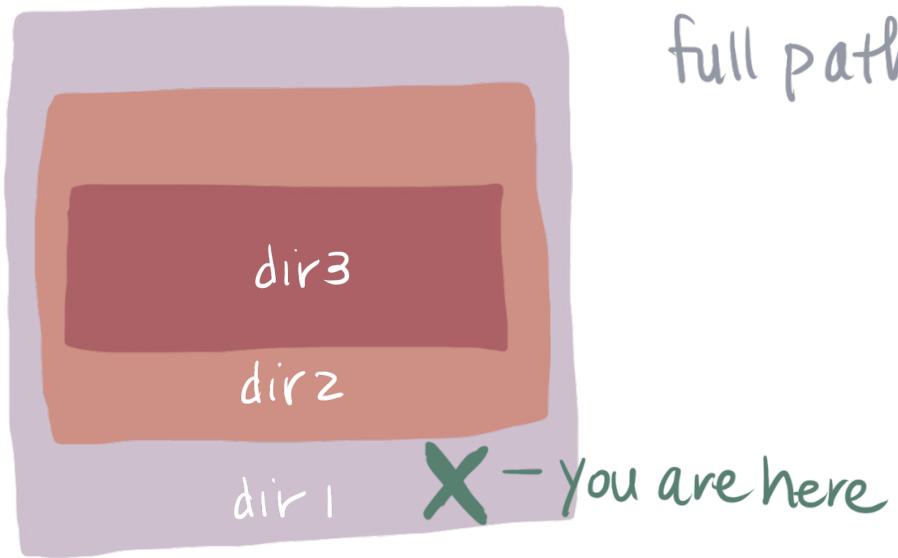


Introduction to bash and the CLI

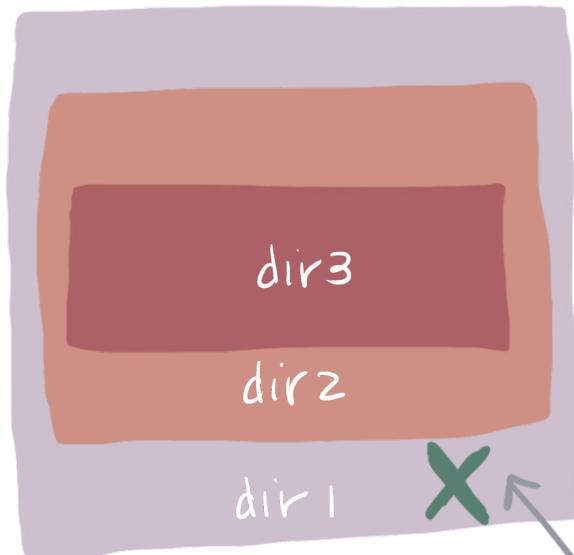


Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories

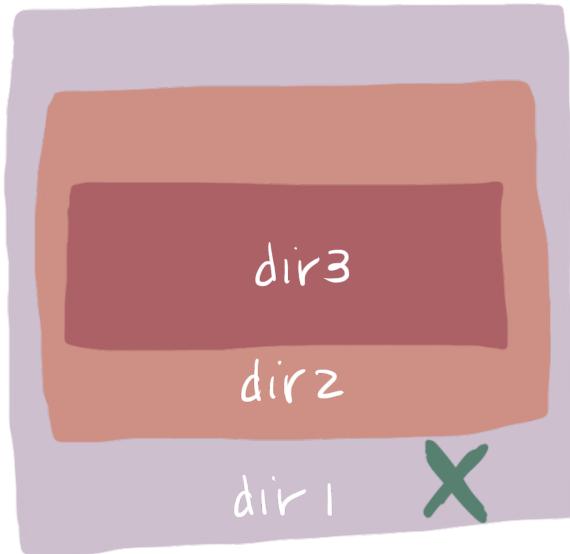


full path: ~/Desktop/dir1/dir2/ dir3

pwd ~/Desktop/dir1/

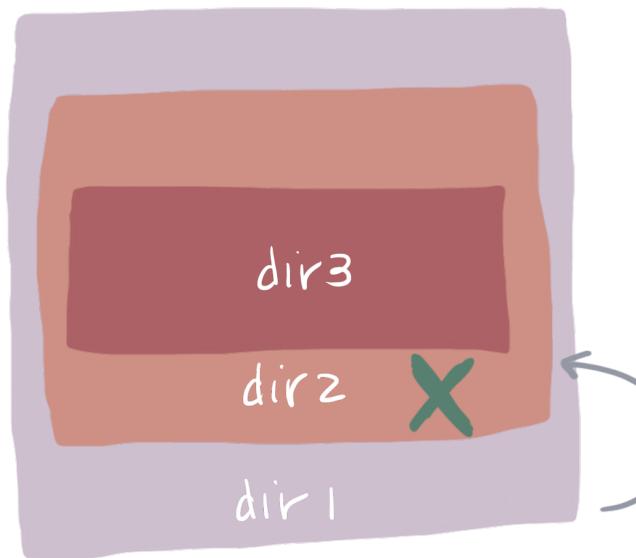
present working directory

Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

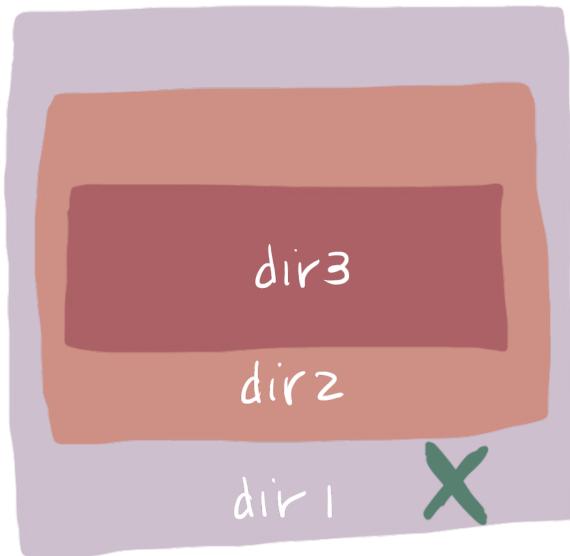
Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

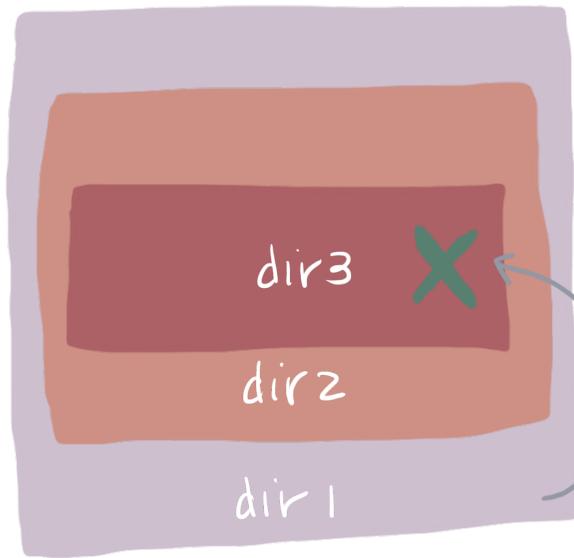
cd dir2
change directory

Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

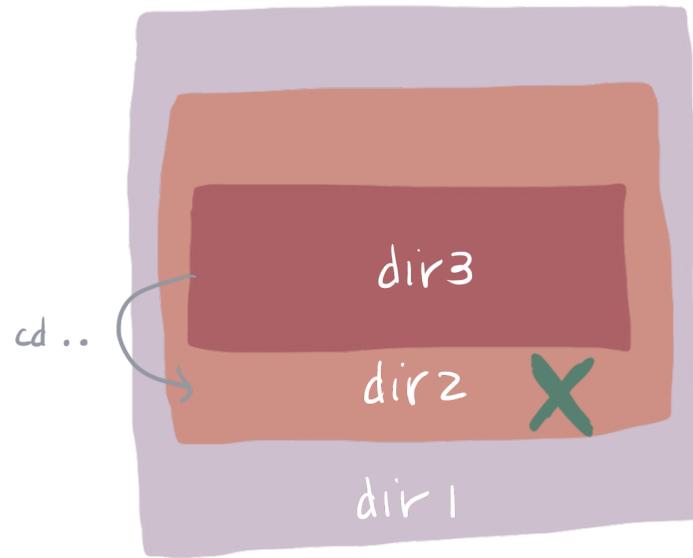
Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

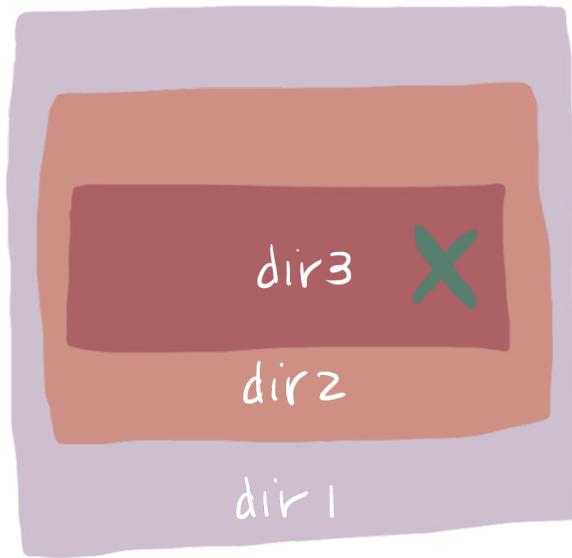
cd dir2/dir3

Navigation: file paths and directories



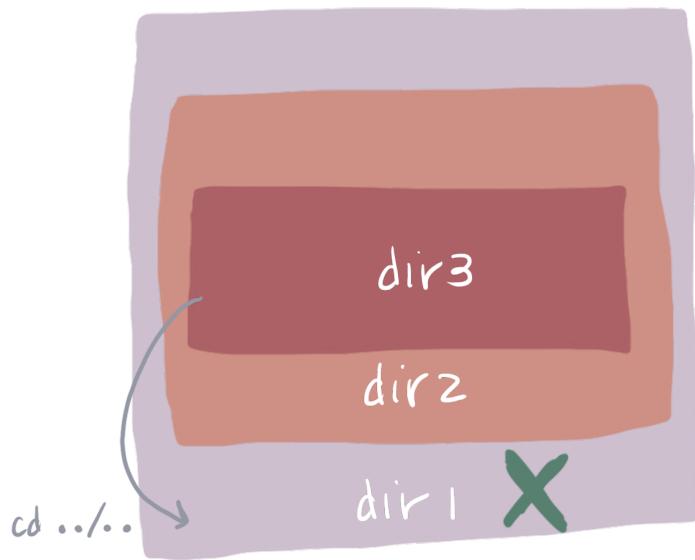
full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories



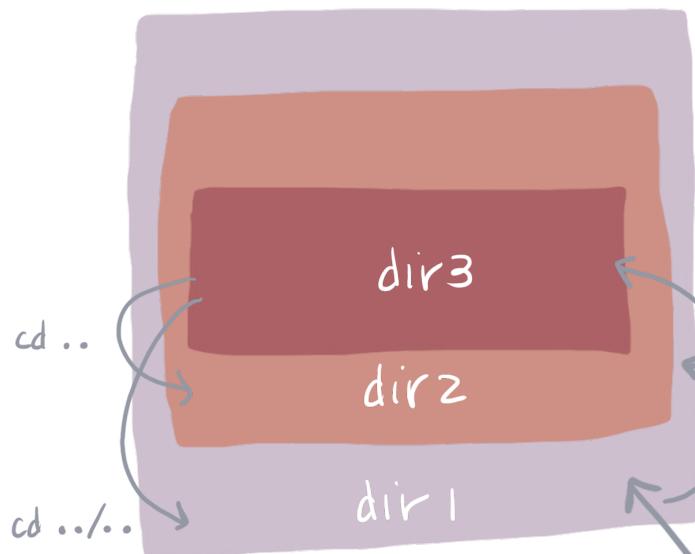
full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories



full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories



pwd lists your current location

cd (change directory):

cd dir goes deeper into directories
.. goes backwards

Working with files in bash: basics

ls or **ll** (only on Linux/TACC)

lists all files in your current directory

```
(base) login1.ls5(1004)$ ls
clust_80_outfiles    clust_84_parameters  clust_89_outfiles        clust_91_parameters
clust_80_parameters  clust_85_outfiles    clust_89_parameters  clust_91_whole_outfiles
clust_81_outfiles    clust_85_parameters  clust_89_whole_outfiles  clust_91_whole_parameters
clust_81_parameters  clust_86_outfiles    clust_89_whole_parameters  clust_92_outfiles
clust_82_outfiles    clust_86_parameters  clust_90_outfiles    clust_92_parameters
clust_82_parameters  clust_87_outfiles    clust_90_parameters   clust_92_whole_outfiles
clust_83_outfiles    clust_87_parameters  clust_90_whole_outfiles  clust_92_whole_parameters
clust_83_parameters  clust_88_outfiles    clust_90_whole_parameters  clust_93_outfiles
clust_84_outfiles    clust_88_parameters  clust_91_outfiles    clust_93_parameters
```

wc word count

```
Annes-MacBook-Pro:pool1 eac$ wc JA19528_barcodes_pool1.txt
 23      48     392 JA19528_barcodes_pool1.txt
```

lines words characters

```
(base) login1.ls5(1005)$ ll
total 176
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_80_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_80_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_81_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_81_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_82_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_82_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_83_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_83_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_84_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_84_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_85_outfiles
drwx----- 2 eac3496 G-817611 4096 Feb  8 2018 clust_85_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_86_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_86_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_87_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_87_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_88_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_88_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_89_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_89_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_89_whole_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_89_whole_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_90_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_90_parameters
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_90_whole_outfiles
drwx----- 2 eac3496 G-817611 4096 May 25 2018 clust_90_whole_parameters
```

Working with files in bash: basics

```
cp [file to copy] [new copied file name]
```

copies file you specify and makes a copy with a different filename

```
$ mv params.txt directory/  
$ mv ./directory/params.txt .  
$ mv params.txt paramsnewname.txt
```

Working with files in bash: basics

```
mv [file] [to]
```

moves file you specify to new location; can also use this to **rename** files if you don't move them

```
$ mv params.txt directory/  
$ mv ./directory/params.txt .  
$ mv params.txt paramsnewname.txt
```

Working with files in bash: basics

`cat [file]`

prints out the contents of a file

But, sometimes the contents of a file are way too big (10s of Gb!) and we only need to see part of the file

`head [file]` prints out first 10 lines of file

`tail [file]` prints out last 10 lines of file

Working with files in bash: basics

`rm -r` remove with flag

What is a flag?

option following a command

How do we use flags?

`ls -ll` gives you additional details of the files (ll on TACC)

Let me give you an example: ls

```
[Annes-MacBook-Pro:pool1 eac$ ls  
JA19528_barcodes_pool1.txt
```

Let me give you an example: ls

```
[Annes-MacBook-Pro:pool1 eac$ ls  
JA19528_barcodes_pool1.txt  
[Annes-MacBook-Pro:pool1 eac$ ll  
-bash: ll: command not found
```

Let me give you an example: ls

```
[Annes-MacBook-Pro:pool1 eac$ ls  
JA19528_barcodes_pool1.txt  
[Annes-MacBook-Pro:pool1 eac$ ll  
-bash: ll: command not found  
[Annes-MacBook-Pro:pool1 eac$ ls -l  
total 8  
-rw-rw-r--@ 1 eac  staff  392 Dec  9  2020 JA19528_barcodes_pool1.txt
```

Let me give you an example: cat

```
[Annes-MacBook-Pro:pool1 eac$ cat JA19528_barcodes_pool1.txt
```

Let me give you an example: cat

```
[Annes-MacBook-Pro:pool1 eac$ cat JA19528_barcodes_pool1.txt
alt16wlm_TX      GCATG
alt16w2m_TX      AACCA
alt17w2f_TX      CGATC
alt95w2f_TX      TCGAT
alt17w4f_TX      TGCAT
CAS178_KS        CAACC
CAS265A_KS       GGTTG
CAS276_KS        AAGGA
CAS277_KS        AGCTA
CAS298_KS        ACACA
CAS299_KS        AATTA
```

Let me give you an example: cat

```
[Annes-MacBook-Pro:pool1 eac$ wc JA19528_barcodes_pool1.txt  
      23      48     392 JA19528_barcodes_pool1.txt
```

```
cat filename | wc -l    lines
```

the **pipe** chains commands
together

word count

Let me give you an example: cat

```
[Annes-MacBook-Pro:pool1 eac$ wc JA19528_barcodes_pool1.txt
     23      48    392 JA19528_barcodes_pool1.txt
[Annes-MacBook-Pro:pool1 eac$ wc -l JA19528_barcodes_pool1.txt
     23 JA19528_barcodes_pool1.txt
```

```
cat filename | wc -l      lines
```

the **pipe** chains commands
together word count

Let me give you an example: cat

```
[Annes-MacBook-Pro:pool1 eac$ wc JA19528_barcodes_pool1.txt
 23      48    392 JA19528_barcodes_pool1.txt
[Annes-MacBook-Pro:pool1 eac$ wc -l JA19528_barcodes_pool1.txt
 23 JA19528_barcodes_pool1.txt
[Annes-MacBook-Pro:pool1 eac$ cat JA19528_barcodes_pool1.txt | wc -l
 23
```

```
cat filename | wc -l
```

the **pipe** chains commands together

Working with files in bash: basics

Cat allows you to view the contents of a file, but how do you actually edit the contents?

```
nano [filename]
```

To exit the text editor, do ctrl+K; a series of prompts will appear

Annes-MacBook-Pro:ddRADseq eac\$ nano ped_info.txt

this is your cursor) navigate w arrow keys

```
GNU nano 2.0.6                               File: ped_info.txt

ll_lampro_pruned.ped

CAS178_KS    CAS178_KS    0      0      0      0      G      G      T      A      T      T      T
CAS265A_KS   CAS265A_KS   0      0      0      0      G      G      T      T      T      T      T
CAS276_KS   CAS276_KS    0      0      0      0      G      G      T      T      T      T      T
CAS277_KS   CAS277_KS    0      0      0      0      G      G      T      T      T      T      T
CAS298_KS   CAS298_KS    0      0      0      0      G      G      T      A      T      T      T
CAS299_KS   CAS299_KS    0      0      0      0      G      G      T      T      T      T      T
CSA144_TX   CSA144_TX    0      0      0      0      G      G      T      T      T      T      T
CSA151_TX   CSA151_TX    0      0      0      0      0      0      0      0      0      0      0
CSA208_TX   CSA208_TX    0      0      0      0      G      G      T      T      T      T      T
CSA402_TX   CSA402_TX    0      0      0      0      G      G      T      T      T      T      T

ll_lampro_pruned.map

0      loc0_pos11     0      12
0      loc0_pos14     0      15
0      loc0_pos22     0      23
0      loc0_pos24     0      25
0      loc0_pos40     0      41
0      loc0_pos42     0      43
0      loc0_pos52     0      53
0      loc0_pos66     0      67
0      loc0_pos71     0      72
0      loc0_pos93     0      94

chrom-map.txt

Save modified buffer (ANSWERING "No" WILL DESTROY CHANGES) ?
Y Yes
N No
C Cancel

RAD_0    RAD_0

[ Read 30 lines ]
^G Get Help      ^O WriteOut     ^R Read File     ^Y Prev Page    ^K Cut Text      ^C Cur Pos
^X Exit         ^J Justify       ^W Where Is      ^V Next Page    ^U UnCut Text   ^T To Spell
```

exit txt editor

Annes-MacBook-Pro:ddRADseq eac\$ nano ped_info.txt

```
GNU nano 2.0.6                                File: ped_info.txt

ll_lampro_pruned.ped

CAS178_KS      CAS178_KS      0      0      0      0      G      G      T      A      T      T      T
CAS265A_KS     CAS265A_KS     0      0      0      0      G      G      T      T      T      T      T
CAS276_KS      CAS276_KS      0      0      0      0      G      G      T      T      T      T      T
CAS277_KS      CAS277_KS      0      0      0      0      G      G      T      T      T      T      T
CAS298_KS      CAS298_KS      0      0      0      0      G      G      T      A      T      T      T
CAS299_KS      CAS299_KS      0      0      0      0      G      G      T      T      T      T      T
CSA144_TX      CSA144_TX      0      0      0      0      G      G      T      T      T      T      T
CSA151_TX      CSA151_TX      0      0      0      0      0      0      0      0      0      0      0
CSA208_TX      CSA208_TX      0      0      0      0      G      G      T      T      T      T      T
CSA402_TX      CSA402_TX      0      0      0      0      G      G      T      T      T      T      T

ll_lampro_pruned.map

0      loc0_pos11    0      12
0      loc0_pos14    0      15
0      loc0_pos22    0      23
0      loc0_pos24    0      25
0      loc0_pos40    0      41
0      loc0_pos42    0      43
0      loc0_pos52    0      53
0      loc0_pos66    0      67
0      loc0_pos71    0      72
0      loc0_pos93    0      94

chrom-map.txt

RAD_0      RAD_0
Save modified buffer (ANSWERING "No" WILL DESTROY CHANGES) ?
Y Yes
N No      ^C Cancel
```

Working with files in bash: basics

- `ls` or `ls -ll`
- `cp`
- `mv`
- `cat`, `head`, `tail`
- `wc -l`
- `nano`
- `rm (-r flag)` <- be careful!

Getting a little more complicated...

- **wildcards**: special characters that replace specific strings of text
- We'll mostly just be dealing with the * symbol
- * replaces *any string*

```
[(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam  epi.fq_GACT.trim.sam  epi.fq_TCAG.trim.sam  rana.fq_CATC.trim.sam  rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam  epi.fq_GCTT.trim.sam  epi.fq_TGTC.trim.sam  rana.fq_CTAC.trim.sam  rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam  epi.fq_GTGA.trim.sam  rana.fq_ACCA.trim.sam  rana.fq_GACT.trim.sam  rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam  epi.fq_GTGT.trim.sam  rana.fq_AGAC.trim.sam  rana.fq_GCTT.trim.sam  rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam  epi.fq_TCAC.trim.sam  rana.fq_AGTG.trim.sam  rana.fq_GTGA.trim.sam
```

```
[(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam

[(base) login2.frontera(1057)$ ls epi*
epi.fq_ACCA.trim.sam epi.fq_CATC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TCAC.trim.sam
epi.fq_AGAC.trim.sam epi.fq_CTAC.trim.sam epi.fq_GTGA.trim.sam epi.fq_TCAG.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GACT.trim.sam epi.fq_GTGT.trim.sam epi.fq_TGTC.trim.sam
```

```
[(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam

[(base) login2.frontera(1057)$ ls epi*
epi.fq_ACCA.trim.sam epi.fq_CATC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TCAC.trim.sam
epi.fq_AGAC.trim.sam epi.fq_CTAC.trim.sam epi.fq_GTGA.trim.sam epi.fq_TCAG.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GACT.trim.sam epi.fq_GTGT.trim.sam epi.fq_TGTC.trim.sam

[(base) login2.frontera(1058)$ ls rana*
rana.fq_ACCA.trim.sam rana.fq_CATC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TCAC.trim.sam
rana.fq_AGAC.trim.sam rana.fq_CTAC.trim.sam rana.fq_GTGA.trim.sam rana.fq_TCAG.trim.sam
rana.fq_AGTG.trim.sam rana.fq_GACT.trim.sam rana.fq_GTGT.trim.sam rana.fq_TGTC.trim.sam
```

```
[(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam

[(base) login2.frontera(1057)$ ls epi*
epi.fq_ACCA.trim.sam epi.fq_CATC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TCAC.trim.sam
epi.fq_AGAC.trim.sam epi.fq_CTAC.trim.sam epi.fq_GTGA.trim.sam epi.fq_TCAG.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GACT.trim.sam epi.fq_GTGT.trim.sam epi.fq_TGTC.trim.sam

[(base) login2.frontera(1058)$ ls rana*
rana.fq_ACCA.trim.sam rana.fq_CATC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TCAC.trim.sam
rana.fq_AGAC.trim.sam rana.fq_CTAC.trim.sam rana.fq_GTGA.trim.sam rana.fq_TCAG.trim.sam
rana.fq_AGTG.trim.sam rana.fq_GACT.trim.sam rana.fq_GTGT.trim.sam rana.fq_TGTC.trim.sam

[(base) login2.frontera(1059)$ ls *.sam
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam
```

```
[(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam

[(base) login2.frontera(1057)$ ls epi*
epi.fq_ACCA.trim.sam epi.fq_CATC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TCAC.trim.sam
epi.fq_AGAC.trim.sam epi.fq_CTAC.trim.sam epi.fq_GTGA.trim.sam epi.fq_TCAG.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GACT.trim.sam epi.fq_GTGT.trim.sam epi.fq_TGTC.trim.sam

[(base) login2.frontera(1058)$ ls rana*
rana.fq_ACCA.trim.sam rana.fq_CATC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TCAC.trim.sam
rana.fq_AGAC.trim.sam rana.fq_CTAC.trim.sam rana.fq_GTGA.trim.sam rana.fq_TCAG.trim.sam
rana.fq_AGTG.trim.sam rana.fq_GACT.trim.sam rana.fq_GTGT.trim.sam rana.fq_TGTC.trim.sam

[(base) login2.frontera(1059)$ ls *.sam
epi.fq_ACCA.trim.sam epi.fq_GACT.trim.sam epi.fq_TCAG.trim.sam rana.fq_CATC.trim.sam rana.fq_GTGT.trim.sam
epi.fq_AGAC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TGTC.trim.sam rana.fq_CTAC.trim.sam rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GTGA.trim.sam rana.fq_ACCA.trim.sam rana.fq_GACT.trim.sam rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam epi.fq_GTGT.trim.sam rana.fq_AGAC.trim.sam rana.fq_GCTT.trim.sam rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam epi.fq_TCAC.trim.sam rana.fq_AGTG.trim.sam rana.fq_GTGA.trim.sam

[(base) login2.frontera(1060)$ ls epi*sam
epi.fq_ACCA.trim.sam epi.fq_CATC.trim.sam epi.fq_GCTT.trim.sam epi.fq_TCAC.trim.sam
epi.fq_AGAC.trim.sam epi.fq_CTAC.trim.sam epi.fq_GTGA.trim.sam epi.fq_TCAG.trim.sam
epi.fq_AGTG.trim.sam epi.fq_GACT.trim.sam epi.fq_GTGT.trim.sam epi.fq_TGTC.trim.sam
```

We can use wildcards for directories, too!

```
(base) login2.frontera(1062)$ ls
angsd
AUTHORS
bowtie2
bowtie2-align-l
bowtie2-align-l-debug
bowtie2-align-s
bowtie2-align-s-debug
bowtie2-build
bowtie2-build-l
bowtie2-build-l-debug
bowtie2-build-s
bowtie2-build-s-debug
bowtie2-inspect
bowtie2-inspect-l
bowtie2-inspect-l-debug
bowtie2-inspect-s

        bowtie2-inspect-s-debug  clust_95      epi_95_maps      MANUAL.markdown  rana_95_maps
        BOWTIE2_VERSION          doc          epi_80_maps      NEWS
clust_80          epi_81_maps      epi_80_maps      rana_80_maps
clust_81          epi_82_maps      epi_81_maps      rana_81_maps
clust_82          epi_83_maps      epi_82_maps      rana_82_maps
clust_83          epi_84_maps      epi_83_maps      rana_83_maps
clust_84          epi_85_maps      epi_84_maps      rana_84_maps
clust_85          epi_86_maps      epi_85_maps      rana_85_maps
clust_86          epi_87_maps      epi_86_maps      rana_86_maps
clust_87          epi_88_maps      epi_87_maps      rana_87_maps
clust_88          epi_89_maps      epi_88_maps      rana_88_maps
clust_89          epi_90_maps      epi_89_maps      rana_89_maps
clust_90          epi_91_maps      epi_90_maps      rana_90_maps
clust_92          epi_92_maps      epi_91_maps      rana_92_maps
clust_93          epi_93_maps      epi_92_maps      rana_93_maps
clust_94          epi_94_maps      LICENSE        rana_94_maps
                           MANUAL
```

each of these directories (which is also why they're blue)
has the same set of samples in it:

```
(base) login2.frontera(1056)$ ls
epi.fq_ACCA.trim.sam  epi.fq_GACT.trim.sam  epi.fq_TCAG.trim.sam  rana.fq_CATC.trim.sam  rana.fq_GTTG.trim.sam
epi.fq_AGAC.trim.sam  epi.fq_GCTT.trim.sam  epi.fq_TGTC.trim.sam  rana.fq_CTAC.trim.sam  rana.fq_TCAC.trim.sam
epi.fq_AGTG.trim.sam  epi.fq_GTGA.trim.sam  rana.fq_ACCA.trim.sam  rana.fq_GACT.trim.sam  rana.fq_TCAG.trim.sam
epi.fq_CATC.trim.sam  epi.fq_GTTG.trim.sam  rana.fq_AGAC.trim.sam  rana.fq_GCTT.trim.sam  rana.fq_TGTC.trim.sam
epi.fq_CTAC.trim.sam  epi.fq_TCAC.trim.sam  rana.fq_AGTG.trim.sam  rana.fq_GTGA.trim.sam
```

We can use wildcards for directories, too!

```
(base) login2.frontera(1062)$ ls
angsd           bowtie2-inspect-s-debug   clust_95      epi_95_maps      MANUAL.markdown  rana_95_maps
AUTHORS         BOWTIE2_VERSION          doc          epi.fq_ACCA.trim NEWS          rana.fq_ACCA.trim
bowtie2          clust_80                epi_80_maps    epi.fq_AGAC.trim rana_80_maps    rana.fq_AGAC.trim
bowtie2-align-l  clust_81                epi_81_maps    epi.fq_AGTG.trim rana_81_maps    rana.fq_AGTG.trim
bowtie2-align-l-debug  clust_82                epi_82_maps    epi.fq_CATC.trim rana_82_maps    rana.fq_CATC.trim
bowtie2-align-s  clust_83                epi_83_maps    epi.fq_CTAC.trim rana_83_maps    rana.fq_CTAC.trim
bowtie2-align-s-debug  clust_84                epi_84_maps    epi.fq_GACT.trim rana_84_maps    rana.fq_GACT.trim
bowtie2-build    clust_85                epi_85_maps    epi.fq_GCTT.trim rana_85_maps    rana.fq_GCTT.trim
bowtie2-build-l  clust_86                epi_86_maps    epi.fq_GTGA.trim rana_86_maps    rana.fq_GTGA.trim
bowtie2-build-l-debug  clust_87                epi_87_maps    epi.fq_GTGT.trim rana_87_maps    rana.fq_GTGT.trim
bowtie2-build-s  clust_88                epi_88_maps    epi.fq_TCAC.trim rana_88_maps    rana.fq_TCAC.trim
bowtie2-build-s-debug  clust_89                epi_89_maps    epi.fq_TCAG.trim rana_89_maps    rana.fq_TCAG.trim
bowtie2-inspect   clust_90                epi_90_maps    epi.fq_TGTC.trim rana_90_maps    rana.fq_TGTC.trim
bowtie2-inspect-l  clust_92                epi_92_maps    example          rana_92_maps    README.md
bowtie2-inspect-l-debug  clust_93                epi_93_maps    LICENSE          rana_93_maps    scripts
bowtie2-inspect-s  clust_94                epi_94_maps    MANUAL          rana_94_maps    TUTORIAL
```

How do we ask the computer to print out all files from those directories that look like this? **epi.fq_TCAG.trim.sam**

```
(base) login2.frontera(1063)$ ls clust*/epi.fq_TCAG.trim.sam
clust_80/epi.fq_TCAG.trim.sam  clust_88/epi.fq_TCAG.trim.sam
clust_81/epi.fq_TCAG.trim.sam  clust_89/epi.fq_TCAG.trim.sam
clust_82/epi.fq_TCAG.trim.sam  clust_90/epi.fq_TCAG.trim.sam
clust_83/epi.fq_TCAG.trim.sam  clust_92/epi.fq_TCAG.trim.sam
clust_84/epi.fq_TCAG.trim.sam  clust_93/epi.fq_TCAG.trim.sam
clust_85/epi.fq_TCAG.trim.sam  clust_94/epi.fq_TCAG.trim.sam
clust_86/epi.fq_TCAG.trim.sam  clust_95/epi.fq_TCAG.trim.sam
clust_87/epi.fq_TCAG.trim.sam
```

Remember, Google is your best friend!

The screenshot shows a Stack Exchange question page. The title of the question is "how to count total number of words in a file?". It was asked 8 years, 4 months ago and has been viewed 92k times. A user named don_crissti (70.2k reputation) edited the question on Aug 20 '16 at 14:29. The question text is: "I am looking for a command to count number of all words in a file. For in this," followed by a code block: "today is a good day". A comment below says: "then it should print 5, since there are 5 words there." The question is tagged with "text-processing" and "wc".

Questions

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TEAMS

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Answers

7 Have you tried `wc -w $FILE`? – don_crissti Jun 19 '13 at 17:07

2 Don't solve what's been solved. – Prasanth Jun 19 '13 at 17:31

Add a comment

5 Answers

42 \$ wc -w <file>