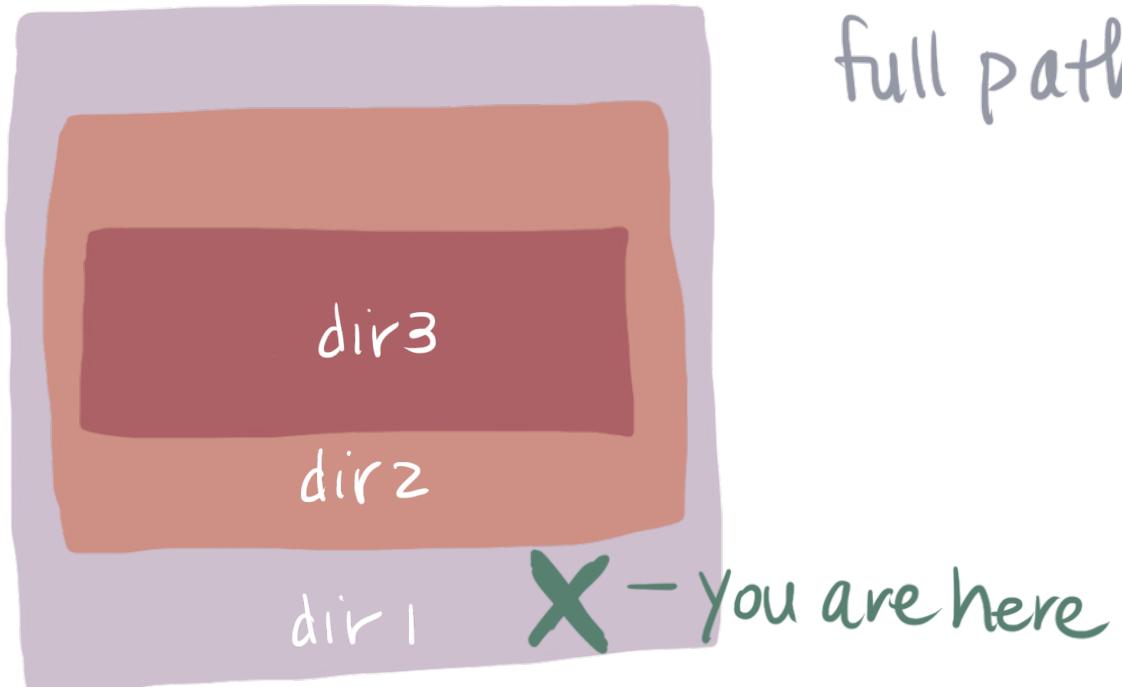


Introduction to bash and the CLI



Navigation: file paths and directories



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

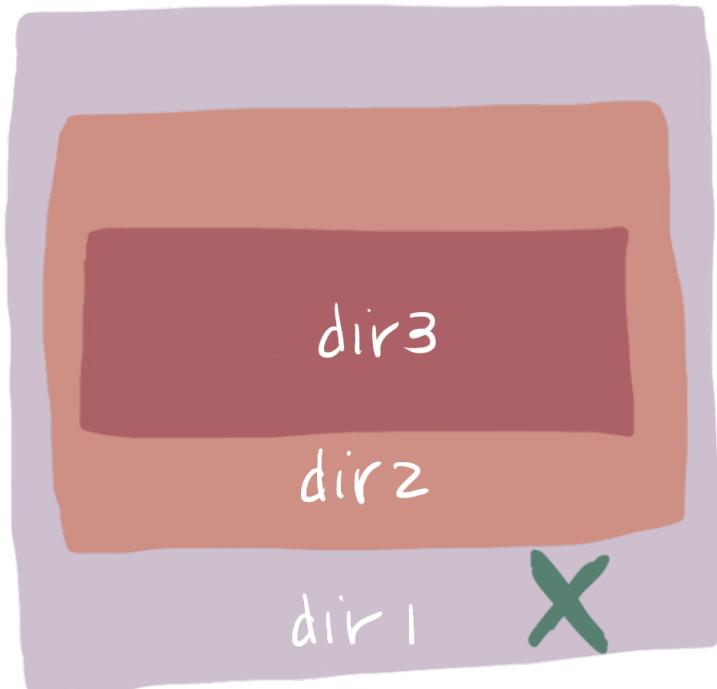
Navigation: file paths and directories



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

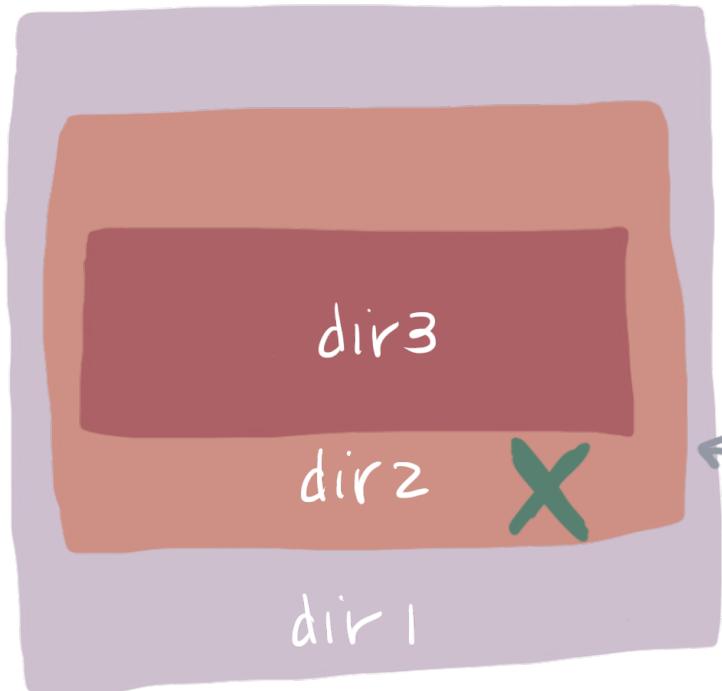
`pwd ~/Desktop/dir1/`
present working directory

Navigation: file paths and directories



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

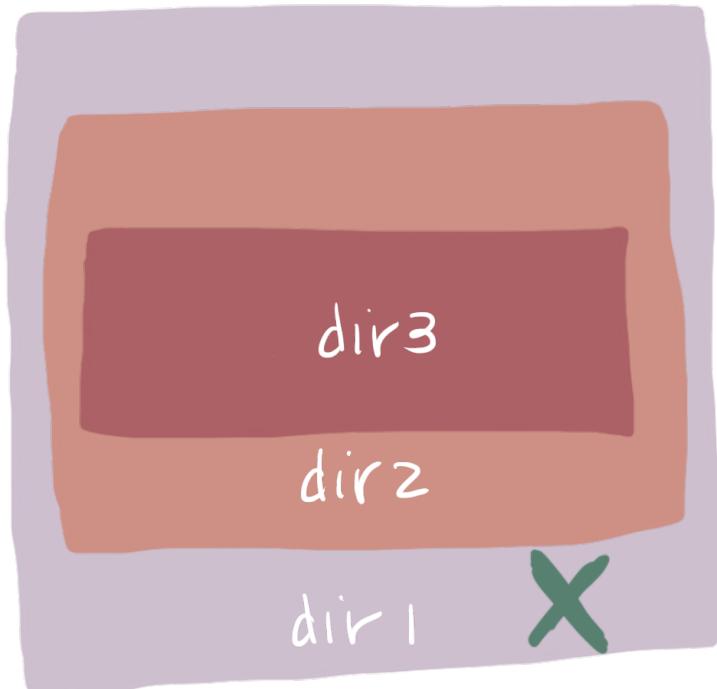
Navigation: file paths and directories



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

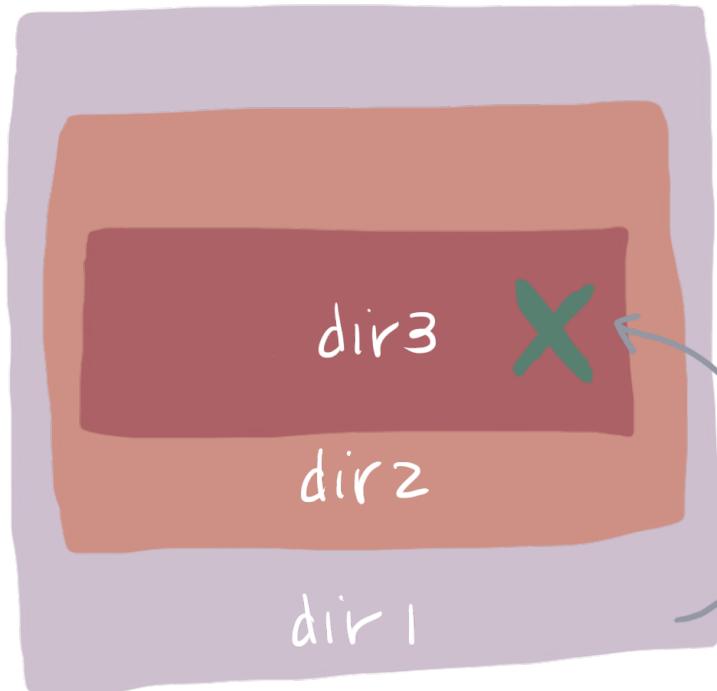
`cd dir2`
change directory

Navigation: file paths and directories



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

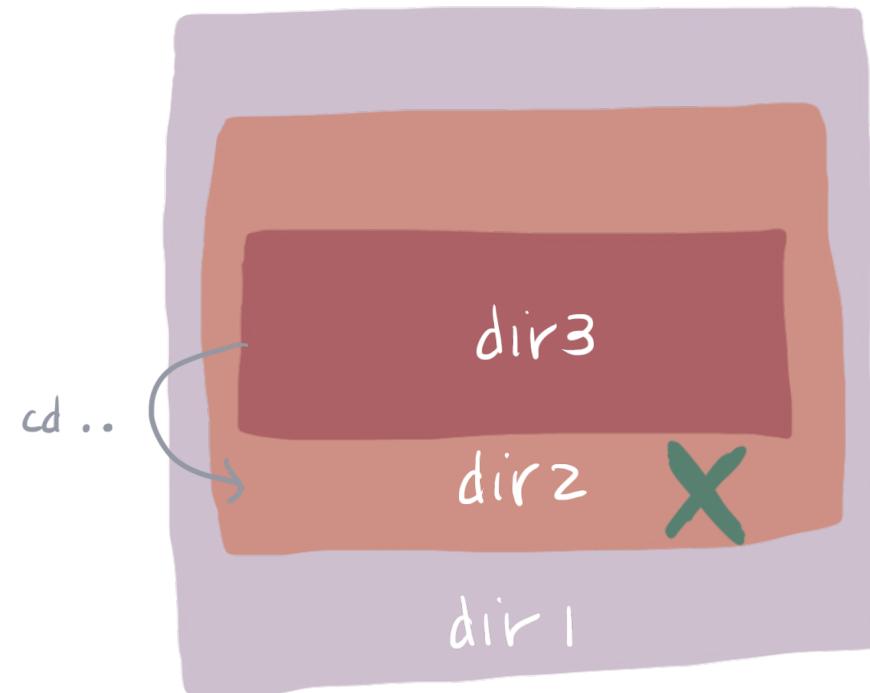
Navigation: file paths and directories



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

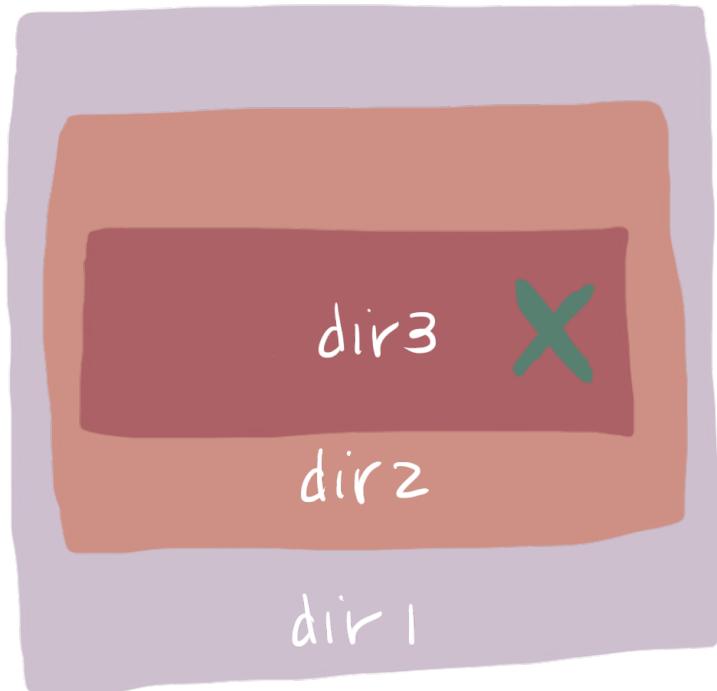
`cd dir2/dir3`

Navigation: file paths and directories



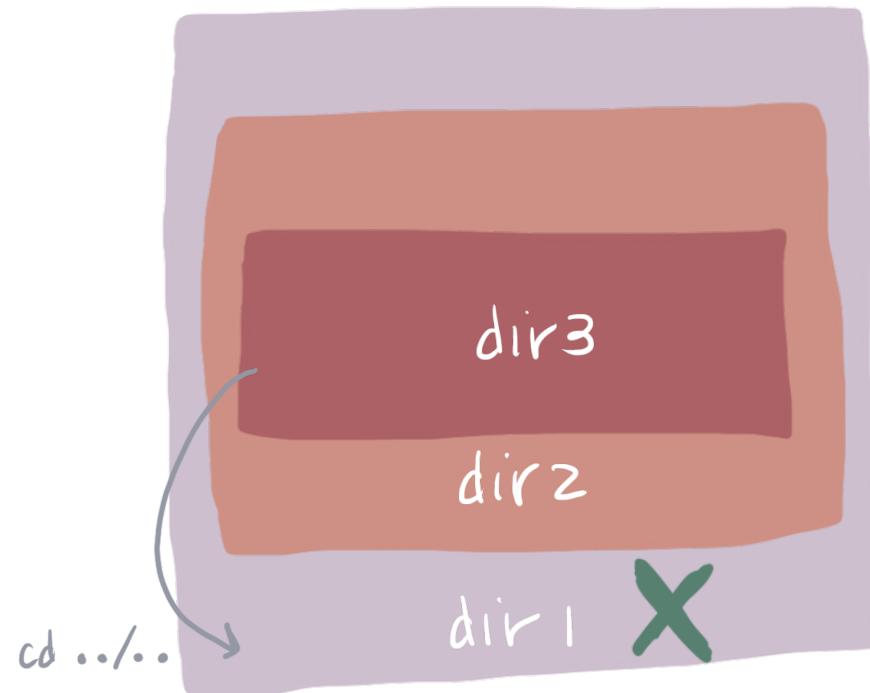
full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories



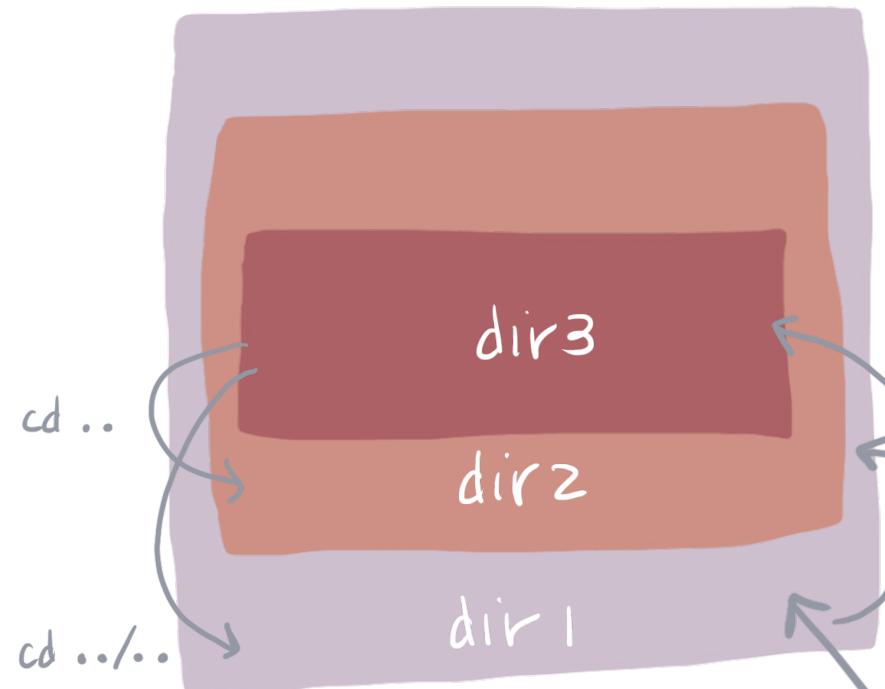
full path: ~/Desktop/dir1/dir2/ dir3

Navigation: file paths and directories



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

Navigation: file paths and directories



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

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

```
$ cp params.txt directory/params2.txt
```

```
$ cp ./directory/params.txt ./directory/params2.txt
```

```
$ cp 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 word count
together

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	TT	TT	TT	TT	TT
CAS276_KS	CAS276_KS	0	0	0	0	G	G	TT	TT	TT	TT	TT
CAS277_KS	CAS277_KS	0	0	0	0	G	G	TT	TT	TT	TT	TT
CAS298_KS	CAS298_KS	0	0	0	0	G	G	TT	A	T	T	T
CAS299_KS	CAS299_KS	0	0	0	0	G	G	TT	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

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

exit txt editor

navigate quickly delete lines

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

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

```
(base) login2.friontera(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
```

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
bowtie2          clust_80                epi_80_maps   epi.fq_AGAC.trim rana_80_maps
bowtie2-align-l  clust_81                epi_81_maps   epi.fq_AGTG.trim rana_81_maps
bowtie2-align-l-debug  clust_82                epi_82_maps   epi.fq_CATC.trim rana_82_maps
bowtie2-align-s  clust_83                epi_83_maps   epi.fq_CTAC.trim rana_83_maps
bowtie2-align-s-debug  clust_84                epi_84_maps   epi.fq_GACT.trim rana_84_maps
bowtie2-build    clust_85                epi_85_maps   epi.fq_GCTT.trim rana_85_maps
bowtie2-build-l  clust_86                epi_86_maps   epi.fq_GTGA.trim rana_86_maps
bowtie2-build-l-debug  clust_87                epi_87_maps   epi.fq_GTGT.trim rana_87_maps
bowtie2-build-s  clust_88                epi_88_maps   epi.fq_TCAC.trim rana_88_maps
bowtie2-build-s-debug  clust_89                epi_89_maps   epi.fq_TCAG.trim rana_89_maps
bowtie2-inspect  clust_90                epi_90_maps   epi.fq_TGTC.trim rana_90_maps
bowtie2-inspect-l  clust_92                epi_92_maps   example          rana_92_maps
bowtie2-inspect-l-debug  clust_93                epi_93_maps   LICENSE          rana_93_maps
bowtie2-inspect-s  clust_94                epi_94_maps   MANUAL          rana_94_maps
                                         
```

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_87/epi.fq_TCAG.trim.sam
```

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how to count total number of words in a file?

Asked 8 years, 4 months ago Active 5 years, 1 month ago Viewed 92k times

I am looking for a command to count number of all words in a file. For in this,

19 today is a good day

5 then it should print 5, since there are 5 words there.

text-processing wc

Share Improve this question Follow edited Aug 20 '16 at 14:29 don_crissti 70.2k ● 27 ● 194 ● 219 asked

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

The command `wc` aka. word count can do it:

42 \$ `wc -w <file>`