



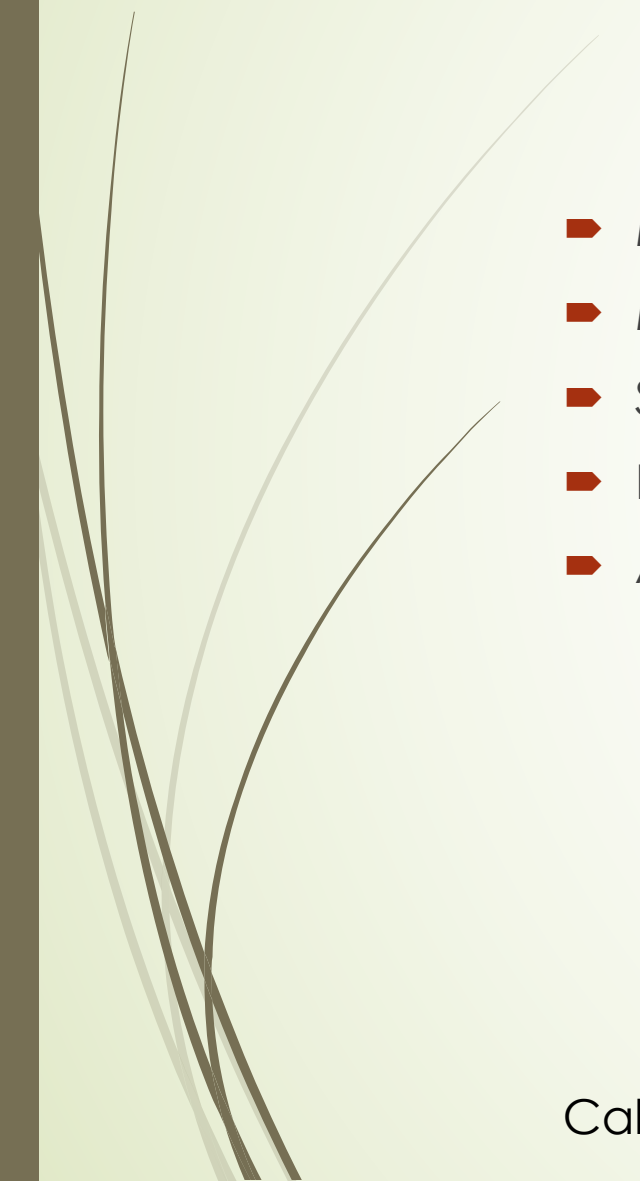
BASH FOR THE VIRTUOUS

where our hero discovers *the virtuous cycle*



Ok, why automate

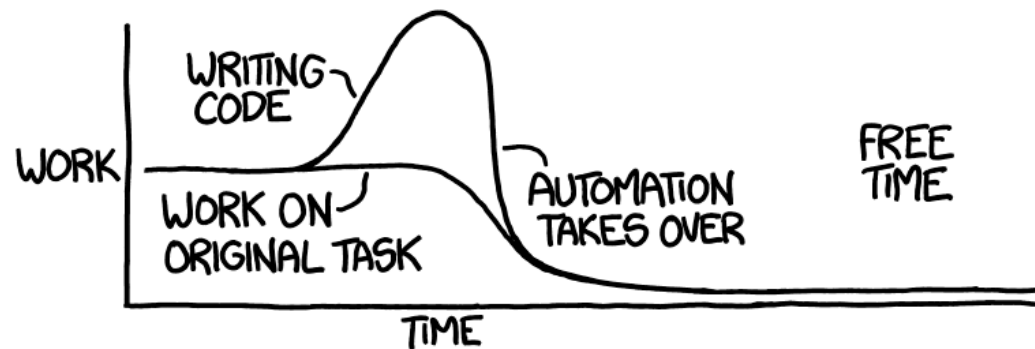
- Making a task as frictionless as possible allows you to keep in Flow
- Most people underestimate how many times they will do a task
- Saving time leads to a virtuous cycle
- Reduces mistakes...generally
- About time...



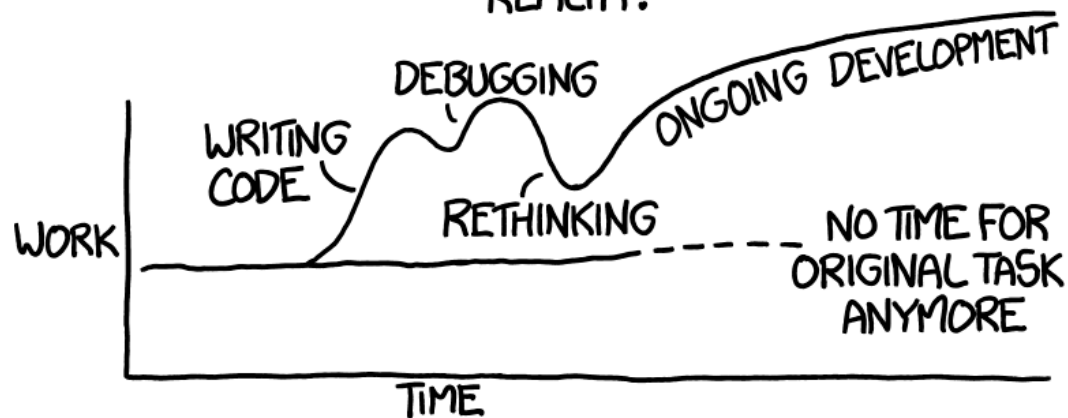
Call me #lshmael

"I SPEND A LOT OF TIME ON THIS TASK.
I SHOULD WRITE A PROGRAM AUTOMATING IT!"

THEORY:



REALITY:



HOW LONG CAN YOU WORK ON MAKING A ROUTINE TASK MORE
EFFICIENT BEFORE YOU'RE SPENDING MORE TIME THAN YOU SAVE?
(ACROSS FIVE YEARS)

		HOW OFTEN YOU DO THE TASK					
		50/DAY	5/DAY	DAILY	WEEKLY	MONTHLY	YEARLY
HOW MUCH TIME YOU SHAVE OFF	1 SECOND	1 DAY	2 HOURS	30 MINUTES	4 MINUTES	1 MINUTE	5 SECONDS
	5 SECONDS	5 DAYS	12 HOURS	2 HOURS	21 MINUTES	5 MINUTES	25 SECONDS
	30 SECONDS	4 WEEKS	3 DAYS	12 HOURS	2 HOURS	30 MINUTES	2 MINUTES
	1 MINUTE	8 WEEKS	6 DAYS	1 DAY	4 HOURS	1 HOUR	5 MINUTES
	5 MINUTES	9 MONTHS	4 WEEKS	6 DAYS	21 HOURS	5 HOURS	25 MINUTES
	30 MINUTES		6 MONTHS	5 WEEKS	5 DAYS	1 DAY	2 HOURS
	1 HOUR		10 MONTHS	2 MONTHS	10 DAYS	2 DAYS	5 HOURS
	6 HOURS				2 MONTHS	2 WEEKS	1 DAY
	1 DAY					8 WEEKS	5 DAYS



Before we begin... make life easier with tab completion

- Get a terminal window open preferable on the cluster
- Type in `$ so` [hit the tab twice]
- You should see all of the commands that start with `so`:
- Now type an `r` [hit the tab once]
- It should complete the command and give you:
 - `sort`
- type `ls ~/virtuous_bash/mis` [hit tab once]
 - It will complete the directory to `~/virtuous_bash/misnamed_files/`

The `#sun` shone, having no alternative, on the nothing new.



Life easier with... bash editing shortcuts

- ▶ Type: `$ do ri me fa sol la ti` (or any nonsense consisting of multiple words)
- ▶ Use alt left key and alt right key on the mac to move between words
 - ▶ On other systems, you can also try ALT +f and ALT+b
- ▶ Move the cursor to the end of the line with CTRL+e
- ▶ Move the cursor to the beginning of the line with CTRL+a
- ▶ Type CTRL-c to clear



Bash Profile - Basics

- The bash profile you will want to edit in command line osX is `.bash_profile`, `.bash_login`, or `.profile`.
- The bash profile you will want to edit on the clusters is `.bash_profile`
- You must reboot for the profile to take effect

Dr. Weiss, at #forty, knew that her life had been ruined by literature.

Aliases

- Aliases allow you to tie a command to a different command string
- I use this to make ssh into longleaf quicker
 - alias longleaf="ssh -X paulcotn@longleaf.unc.edu"
- By typing in the command `$ longleaf`, I log into longleaf
- Other good commands would be:

```
alias pine="~/pine/scr/p/a/paulcotn"
```

```
alias dor = 'srun --mem 40G --pty R'
```

```
alias showqueue='squeue -u YOUR_ONYEN -O JobID:8,PARTITION:10,name:30,state:10,REASON'
```




Rule of thumb

- When the command is **long**
- You do it a **lot**
- You aren't realistically going to **remember** it

Time is not a line but a dimension, like the dimensions of space.



Practice

- Type in
 - \$ **alias** ltr='ls -ltr'
- Run the command ltr in any directory
- You should now have a list of files in the long format with the latest files at the bottom.
- To see the list of aliases type:
 - \$ alias
- To see remove the alias type:
 - \$ unalias ltr

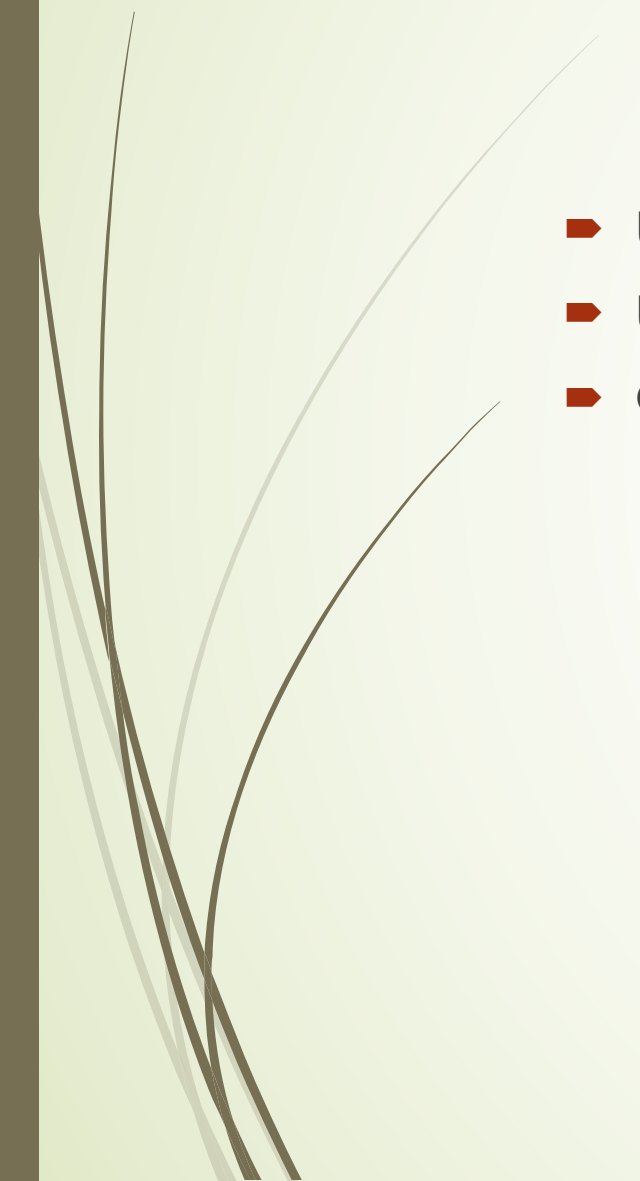


Functions in bash profiles

- ▶ Functions can work like aliases except you can pass parameters
 - ▶ Functions can be more powerful than that...
- ▶ A typical function
 - ▶ `function xferll () { rsync -vac "$1" paulcotn@longleaf.unc.edu:/pine/scr/p/a/paulcotn; }`
 - ▶ `$ xferll .profile`
 - ▶ Transfer a file or directory to my scratch space on longleaf
 - ▶ `function search () { egrep -roil $1 . | sort | uniq; }`
 - ▶ `$ search "Mary's Lamb"`
 - ▶ Find files that have the string in them



Alias vs Function

- Use an alias when you **don't need** to pass a variable unless it is at the end
 - Use a function when you **do need** to pass a variable
 - OR you want to do something more sophisticated
- 



The Path

- Another really common change made in the profile is the path.
- If you open up, your `.bash_profile` or `.profile` now you will probably see a `PATH` being set. My cluster environment Path is set this way:
 - `export PATH=$PATH:$HOME/.local/bin:$HOME/bin`
- With this anything in the `~/.local/bin` or the `~/bin` can be called from anywhere
- Why would we do this...



Write your own scripts

- As you progress through life, you will probably find or in fact write your own scripts to extend what the environment can do.
- I am actually going to show one of the most helpful scripts I have ever found... with a caveat.



Practice


- First lets change the path temporarily:

```
$ export PATH=$PATH:$HOME/virtuous_bash/bin
```

- Type in:

```
$ which renamepl  
/Users/paul/virtuous_bash/bin/renamepl
```

- Open up the file ~/virtuous_bash/bin/renamepl in your favorite text editor



```
#!/usr/bin/perl
#
# Usage: rename perlexpr [files]

($regexp = shift @ARGV) || die "Usage:  rename perlexpr
[filenames]\n";

if (!@ARGV) {
    @ARGV = <STDIN>;
    chomp(@ARGV);
}

foreach $_ (@ARGV) {
    $old_name = $_;
    eval $regexp;
    die "$@" if $@;
    rename($old_name, $_) unless $old_name eq $_;
}

exit(0);
```




Practice

➤ Type in:

```
$ ls -1 ~/virtuous_bash/misnamed_files/
```

➤ Looking at the directory you should see something like this:



```
FureyLab-JMS-iMac:misnamed_files paul$ ls -l
~/virtuous_bash/misnamed_files/
outBD_ChIP_H3K27me3_106_kidney.txt
outCHIPKID106-CTL_ChIP_106_kidney_GTGAAA_L002_R1_001.txt
outCHIPKID4-CTL_ChIP_K27ac_4_kidney_ACAGTG_L006_R1_001.txt
outCHIPKID4-CTL_ChIP_K27ac_4_kidney_ACAGTG_L008_R1_001.txt
outCHIPKID6-CTL_ChIP_6_kidney_v2_AGTTCC_L005_R1_001.txt
```

OOPS... The files **should not have** the out at the beginning, and should have the fastq extension and not the txt extension




Practice

➤ Type in

```
$ renamepl 's/out(.*)\.txt/\1.fastq/' ~/virtuous_bash/misnamed_files/*
```

➤ This should correct all of the files in that directory such that...



```
FureyLab-JMS-iMac:~ paul$ ls -1 ~/virtuous_bash/misnamed_files/  
BD_ChIP_H3K27me3_106_kidney.fastq  
CHIPKID106-CTL_ChIP_106_kidney_GTGAAA_L002_R1_001.fastq  
CHIPKID4-CTL_ChIP_K27ac_4_kidney_ACAGTG_L006_R1_001.fastq  
CHIPKID4-CTL_ChIP_K27ac_4_kidney_ACAGTG_L008_R1_001.fastq  
CHIPKID6-CTL_ChIP_6_kidney_v2_AGTTCC_L005_R1_001.fastq
```

OK! Now the files look like what I want them to be!!!!





How did that work exactly?

- Rename takes a perl regular expression:
 - In our case : `s/out(.*)\.txt/\1.fastq/`
- And applied it to the files we gave it.
- The regex above says take all of the files that start with **out** and ends with **.txt** rename them such that the out is stripped and the **.txt** is changed to **.fastq**



The other rename

- Ok there is a caveat...
- Some systems where Perl is installed will have a more powerful rename command installed called rename.
- Also, some version of Linux will have a less flexible rename tool called well rename. The longleaf cluster has this one.



Practice

- ▶ Type in
 - ▶ `$ ls ~/virtuous_bash/no_leading_zero`
- ▶ Take a look at the file names and note none of them having leading zeros:
 - ▶ `file1.txt, file2.txt, ... file19.txt, file20.txt`
- ▶ I want to rename the files to have leading zeros:
 - ▶ `file01.txt, file02.txt, ... file19.txt, file20.txt`



If you are on longleaf

- Now type:
 - `$ rename file file0`
`~/virtuous_bash/no_leading_zero/file?.txt`
- Now type:
 - `$ ls ~/virtuous_bash/no_leading_zero/`
- You should see names with leading zeros.



Regex give renamepl a lot of flexibility

- To change files in this pattern: 01-paul.txt 04-clock.txt
- To this pattern: paul-01.txt clock-04.txt
- `$renamepl 's/(\d+)-(.*)\.txt/\2-\1\3/' *.txt`
- As long as you know the syntax for Perl regex than you can rename long lists of files easily



An example of why regex is useful to know


- For this next set of slides I am going to be work in BBedit and Sublime Text
- If you are using a different text editor we may have to work a bit to do these examples.
- Any text editor will do this as long as you have regex find and replace.
- The syntax however can be different



The problem

- I have a list of fastq file names in the /proj/fureylab area.
- I want to run these files through the pipeline by changing each line, which contains a filename into a three lines of commands.
- The list of fastq files are long.

Miss Brooke had that kind of beauty which seems to be thrown into relief by poor #dress.



/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/fastq/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz



```
mkdir -p $TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_00
```

```
cd $TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001
```

```
python atac_v_1_1.py --out-dir
```

```
/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/out2/ --tmp-  
dir $TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001/tmp --group-  
name ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001 --max-nhits 1 --  
config config.cfg --slurm --section C57BL6 --run
```

```
/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/fastq/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz
```

Breakdown the first two lines

- First thing first I want to create a directory off of \$TMP_DIR with the base name of the original file
- **ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz**



- **mkdir \$TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001**
- **cd \$TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001**

The third line -\1

- ▶ Ok this is the tricky bit so lets break the third line down to this format
- ▶ `python atac_v_1_1.py --out-dir \1 --tmp-dir \2 --group-name \3 --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run \4`
- ▶ Where
 - ▶ \1 is the name of the directory UNDER the fastq directory in the name script with an out2 appended

`/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/fastq/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz`



`/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/out2`



The third line -\2

- ▶ `python atac_v_1_1.py --out-dir \1 --tmp-dir \2 --group-name \3 --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run \4`
- ▶ Where
 - ▶ \2 is `$TMP_DIR/[BASENAME] /tmp`

ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz



`$TMP_DIR/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001/tmp`



The third line \3

- ▶ `python atac_v_1_1.py --out-dir \1 --tmp-dir \2 --group-name \3 --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run \4`
- ▶ \3 is just the base name

ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz



ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001

The third line \4

- ▶ `python atac_v_1_1.py --out-dir \1 --tmp-dir \2 --group-name \3 --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run \4`
- ▶ \4 is just the original file name

`/proj/fureylab/data/ATAC/mouse/C57BL6/CTL_kidney/BD_ATAC_5_kidney/fastq/ATAC_BD_10-BD_ATAC_5_kidney_re_AGGCAGA_L004_R1_001.fastq.gz`



Two step process: Step 1

- I am now going to take the text file and produce a line for every filename into 3 columns:
- Column 1 is the name of the directory UNDER the fastq directory in the name script with an out2 appended (**\1 in the previous**)
- Column 2 is just the base name (**\2 in the previous**)
- Column 3 is just the original name (**\4 in the previous**)

The past is a foreign #country; they do things differently there.



Open the file:

`~/virtuous_bash/CAST_rerun/source.txt`

source.txt

Evaluation (30 days left)

Currently Open Documents

ATAC_C57BL6_DO.txt

ATAC_C57BL6_SCRATCH.txt

ATAC_C57BL6_SKIP.txt

ATAC_C57BL6.sh

ATAC_C57BL6.txt

ATAC_CAST_SCRATCH.txt

ATAC_CAST_TERRY.sh

ATAC_CAST.bash

ATAC_CAST.sh

ATAC_CAST.txt

automation2017_09_02.txt

Awk example.txt

ChIP.sh

ChIP.txt

dbGap_notes.txt

untitled text 15

untitled text 21

NovelFirstLines.txt

untitled text 26

untitled text 27

source.txt

five_columns.txt

~/virtous_bash/CAST_rerun.txt/source.txt

1

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz

2

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq

3

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz

4

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz

5

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/fastq/ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001.f

6

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/fastq/ATACKD102-BD_ATAC_102_kidney_cat_060315.

7

/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/fastq/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002

8

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat091516.fastq.gz

9

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat012016.fastq.gz

10

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/fastq/ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R

11

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/fastq/CAST_BD_liver_ATAC_7_cat012016.fastq.gz

12

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/fastq/ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_

13

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/fastq/CAST_BD_liver_ATAC_9_cat012016.fastq.gz

14

/proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/fastq/ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_

15

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/fastq/Lung_103_ATAC.fastq.gz

16

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/fastq/Lung_104_ATAC.fastq.gz

17

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/fastq/Lung_2_ATAC.fastq.gz

18

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_1_lung/fastq/ATACLU1-BD_ATAC_1_lung_cat.fastq.gz

19

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_105_lung/fastq/Lung_105_ATAC.fastq.gz

20

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_101_lung/fastq/Lung_101_ATAC.fastq.gz

21

/proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_102_lung/fastq/Lung_102_ATAC.fastq.gz

22

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_8_lung/fastq/Lung_8_ATAC.fastq.gz

23

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_9_lung/fastq/Lung_9_ATAC.fastq.gz

24

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_7_lung/fastq/ATACLU7-BD_ATAC_7_lung_cat.fastq.gz

25

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_11_lung/fastq/Lung_11_ATAC.fastq.gz

26

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_12_lung/fastq/Lung_12_ATAC.fastq.gz

27

/proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_10_lung/fastq/Lung_10_ATAC.fastq.gz

28

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_1_liver/fastq/ATAC_BD_16-BD_ATAC_1_liver_re_TAAGGCG_L005_R

29

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_105_liver/fastq/Liver_105_ATAC.fastq.gz

30

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_102_liver/fastq/Liver_102_ATAC.fastq.gz

31

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_104_liver/fastq/Liver_104_ATAC.fastq.gz

32

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_2_liver/fastq/ATAC_BD_17-BD_ATAC_2_liver_re_CGTACTA_L006_R

33

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_103_liver/fastq/Liver_103_ATAC.fastq.gz

34

/proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_101_liver/fastq/Liver_101_ATAC.fastq.gz

35

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_7_kidney/fastq/ATACKID7-BD_ATAC_7_kidney_cat_060315.fastq.

36

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_12_kidney/fastq/ATACKID12-BD_ATAC_12_2ndPrep_kidney_AGGCAG

37

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_9_kidney/fastq/ATAC_BD_20-BD_ATAC_9_kidney_re_GGACTCC_L006_

38

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_8_kidney/fastq/ATAC_BD_11-BD_ATAC_8_kidney_re_TCCTGAG_L003_

39

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_11_kidney/fastq/ATAC_BD_27-BD_ATAC_11_kidney_re_TCCTGAG_L0

40

/proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_10_kidney/fastq/CAST_BD_kidney_ATAC_10_cat012016.fastq.gz

+

🕒

L: 14 C: 72

Text File

Unicode (UTF-8)

Unix (LF)

📄

Saved: 9/5/17, 3:12:11 PM

📄

4,242 / 415 / 40

100%



TEXTWRANGLER OR BBEDIT



Now bring up the find and replace window
(META KEY)+F

ATAC_C57BL6_DO.txt
ATAC_C57BL6_SCRATCH.txt
ATAC_C57BL6_SKIP.txt
ATAC_C57BL6.sh
ATAC_C57BL6.txt
ATAC_CAST_SCRATCH.txt
ATAC_CAST_TERRY.sh
ATAC_CAST.bash
ATAC_CAST.sh
ATAC_CAST.txt
automation2017_09_02.txt
Awk example.txt
ChIP.sh
ChIP.txt
dbGap_notes.txt
untitled text 15
untitled text 21
NovelFirstLines.txt
untitled text 26
untitled text 27
source.txt
five_columns.txt

```
1 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz
2 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq
3 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz
```

Find

Evaluation (30 days left)

Find:

```
^(.*/)(fastq/)(.*/)(\..fastq\..gz)$
```

Replace:

```
\1\t\3\t\1\2\3\4
```

Matching: ☐ Case sensitive ☐ Entire word ☒ GrepSearch in: ☐ Selected text only ☐ Wrap around

Next



Previous

Find All

Extract

Replace

Replace All

Replace & Find

```
19 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_105_lung/fastq/Lung_105_ATAC.fastq.gz
20 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_101_lung/fastq/Lung_101_ATAC.fastq.gz
21 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_102_lung/fastq/Lung_102_ATAC.fastq.gz
22 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_8_lung/fastq/Lung_8_ATAC.fastq.gz
23 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_9_lung/fastq/Lung_9_ATAC.fastq.gz
24 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_7_lung/fastq/ATACLU7-BD_ATAC_7_lung_cat.fastq.gz
25 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_11_lung/fastq/Lung_11_ATAC.fastq.gz
26 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_12_lung/fastq/Lung_12_ATAC.fastq.gz
27 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_10_lung/fastq/Lung_10_ATAC.fastq.gz
28 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_1_liver/fastq/ATAC_BD_16-BD_ATAC_1_liver_re_TAAGGCG_L005_R
29 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_105_liver/fastq/Liver_105_ATAC.fastq.gz
30 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_102_liver/fastq/Liver_102_ATAC.fastq.gz
31 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_104_liver/fastq/Liver_104_ATAC.fastq.gz
32 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_2_liver/fastq/ATAC_BD_17-BD_ATAC_2_liver_re_CGTACTA_L006_R
33 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_103_liver/fastq/Liver_103_ATAC.fastq.gz
34 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_101_liver/fastq/Liver_101_ATAC.fastq.gz
35 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_7_kidney/fastq/ATACKID7-BD_ATAC_7_kidney_cat_060315.fastq.gz
36 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_12_kidney/fastq/ATACKID12-BD_ATAC_12_2ndPrep_kidney_AGGCAG
37 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_9_kidney/fastq/ATAC_BD_20-BD_ATAC_9_kidney_re_GGACTCC_L006
38 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_8_kidney/fastq/ATAC_BD_11-BD_ATAC_8_kidney_re_TCCTGAG_L003
39 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_11_kidney/fastq/ATAC_BD_27-BD_ATAC_11_kidney_re_TCCTGAG_L0
40 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_10_kidney/fastq/CAST_BD_kidney_ATAC_10_cat012016.fastq.gz
```



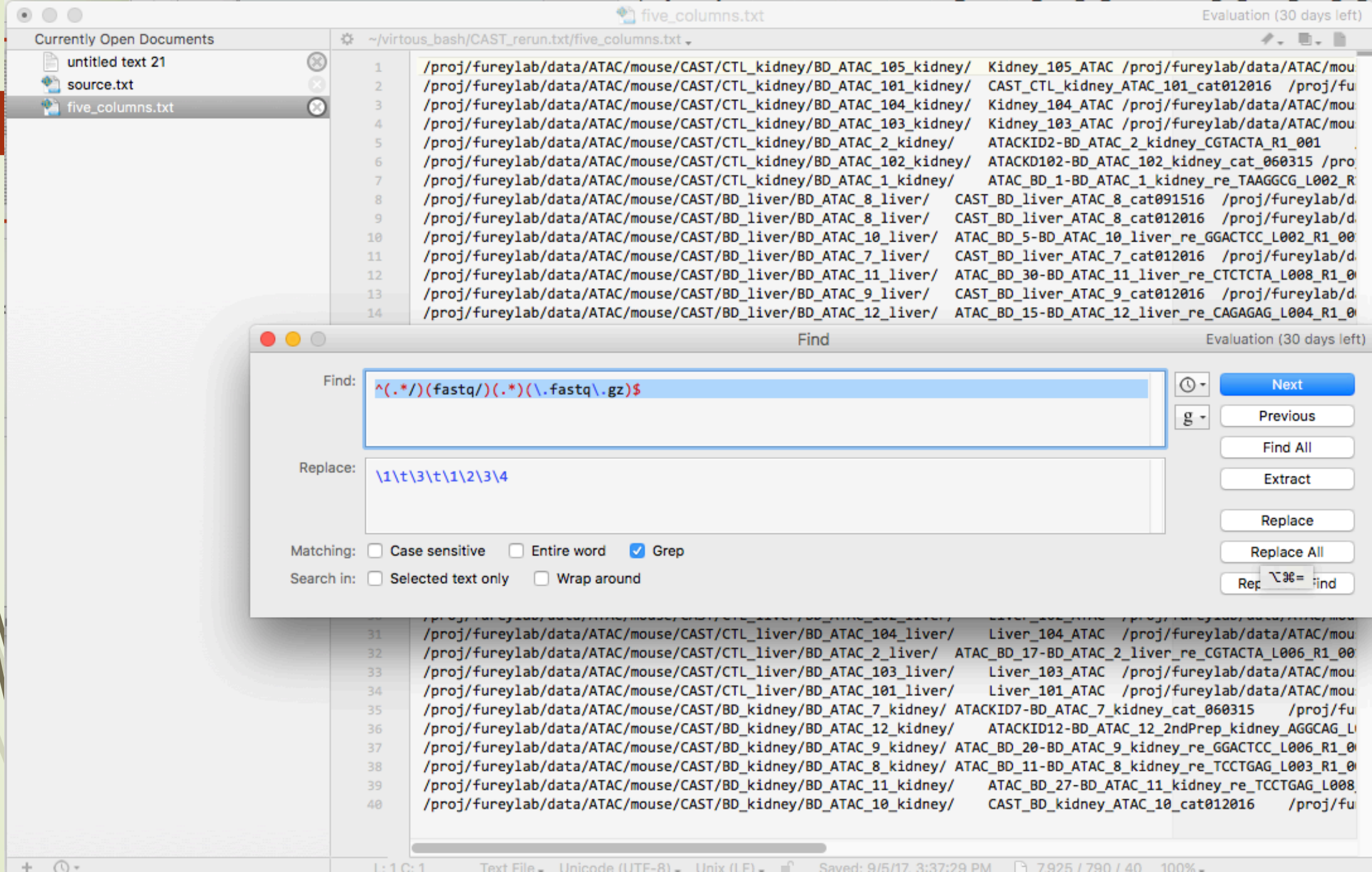
Type in the find window:

`^(.*\/)(fastq\/)(.*)(\.fastq\.gz)$`

Type in the replace window

`\1\t\3\t\1\2\3\4`

Press **Replace All**





SUBLIME TEXT



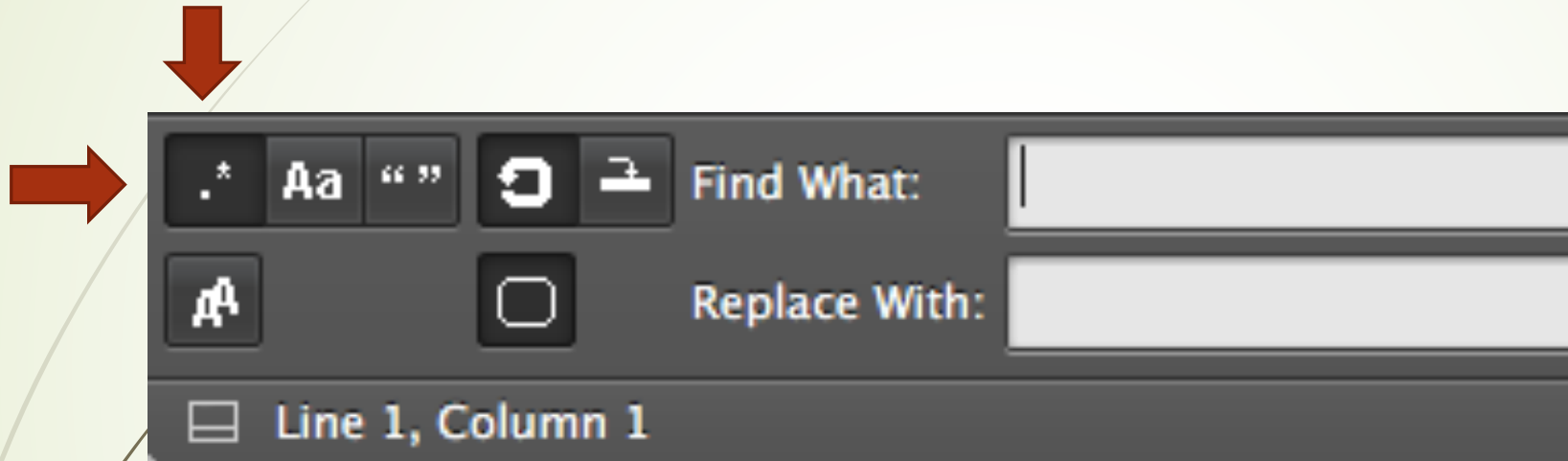
Open the file:

`~/virtuous_bash/CAST_rerun/source.txt`

source.txt

```
1 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz
2 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq.gz
3 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz
4 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz
5 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/fastq/ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001.fastq.gz
6 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/fastq/ATACKID102-BD_ATAC_102_kidney_cat_060315.fastq.gz
7 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/fastq/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001.fastq.gz
8 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat091516.fastq.gz
9 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat012016.fastq.gz
10 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/fastq/ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001.fastq.gz
11 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/fastq/CAST_BD_liver_ATAC_7_cat012016.fastq.gz
12 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/fastq/ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_R1_001.fastq.gz
13 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/fastq/CAST_BD_liver_ATAC_9_cat012016.fastq.gz
14 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/fastq/ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_R1_001.fastq.gz
15 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/fastq/Lung_103_ATAC.fastq.gz
16 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/fastq/Lung_104_ATAC.fastq.gz
17 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/fastq/Lung_2_ATAC.fastq.gz
18 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_1_lung/fastq/ATACLU1-BD_ATAC_1_lung_cat.fastq.gz
19 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_105_lung/fastq/Lung_105_ATAC.fastq.gz
20 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_101_lung/fastq/Lung_101_ATAC.fastq.gz
21 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_102_lung/fastq/Lung_102_ATAC.fastq.gz
22 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_8_lung/fastq/Lung_8_ATAC.fastq.gz
23 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_9_lung/fastq/Lung_9_ATAC.fastq.gz
24 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_7_lung/fastq/ATACLU7-BD_ATAC_7_lung_cat.fastq.gz
25 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_11_lung/fastq/Lung_11_ATAC.fastq.gz
26 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_12_lung/fastq/Lung_12_ATAC.fastq.gz
27 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_10_lung/fastq/Lung_10_ATAC.fastq.gz
28 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_1_liver/fastq/ATAC_BD_16-BD_ATAC_1_liver_re_TAAGGCG_L005_R1_001.fastq.gz
29 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_105_liver/fastq/Liver_105_ATAC.fastq.gz
30 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_102_liver/fastq/Liver_102_ATAC.fastq.gz
31 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_104_liver/fastq/Liver_104_ATAC.fastq.gz
32 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_2_liver/fastq/ATAC_BD_17-BD_ATAC_2_liver_re_CGTACTA_L006_R1_001.fastq.gz
33 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_103_liver/fastq/Liver_103_ATAC.fastq.gz
34 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_101_liver/fastq/Liver_101_ATAC.fastq.gz
35 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_7_kidney/fastq/ATACKID7-BD_ATAC_7_kidney_cat_060315.fastq.gz
36 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_12_kidney/fastq/ATACKID12-BD_ATAC_12_2ndPrep_kidney_AGGCAG_L006_R1_001.fastq.gz
37 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_9_kidney/fastq/ATAC_BD_20-BD_ATAC_9_kidney_re_GGACTCC_L006_R1_001.fastq.gz
38 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_8_kidney/fastq/ATAC_BD_11-BD_ATAC_8_kidney_re_TCCTGAG_L003_R1_001.fastq.gz
39 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_11_kidney/fastq/ATAC_BD_27-BD_ATAC_11_kidney_re_TCCTGAG_L008_R1_001.fastq.gz
40 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_10_kidney/fastq/CAST_BD_kidney_ATAC_10_cat012016.fastq.gz
```


Select replace from the find menu
Make sure the regex button is selected



source.txt

```
1 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz
2 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq.gz
3 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz
4 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz
5 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/fastq/ATACKID2-BD_ATAC_2_kidney_CGACTA_R1_001.fastq.gz
6 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/fastq/ATACKID2-BD_ATAC_102_kidney_cat_060315.fastq.gz
7 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/fastq/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001.fastq.gz
8 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat091516.fastq.gz
9 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat012016.fastq.gz
10 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/fastq/ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001.fastq.gz
11 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/fastq/CAST_BD_liver_ATAC_7_cat012016.fastq.gz
12 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/fastq/ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_R1_001.fastq.gz
13 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/fastq/CAST_BD_liver_ATAC_9_cat012016.fastq.gz
14 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/fastq/ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_R1_001.fastq.gz
15 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/fastq/Lung_103_ATAC.fastq.gz
16 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/fastq/Lung_104_ATAC.fastq.gz
17 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/fastq/Lung_2_ATAC.fastq.gz
18 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_1_lung/fastq/ATACLU1-BD_ATAC_1_lung_cat.fastq.gz
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25 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_11_lung/fastq/Lung_11_ATAC.fastq.gz
26 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_12_lung/fastq/Lung_12_ATAC.fastq.gz
27 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_10_lung/fastq/Lung_10_ATAC.fastq.gz
28 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_1_liver/fastq/ATAC_BD_16-BD_ATAC_1_liver_re_TAAGGCG_L005_R1_001.fastq.gz
29 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_105_liver/fastq/Liver_105_ATAC.fastq.gz
30 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_102_liver/fastq/Liver_102_ATAC.fastq.gz
31 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_104_liver/fastq/Liver_104_ATAC.fastq.gz
32 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_2_liver/fastq/ATAC_BD_17-BD_ATAC_2_liver_re_CGACTA_L006_R1_001.fastq.gz
33 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_103_liver/fastq/Liver_103_ATAC.fastq.gz
34 /proj/fureylab/data/ATAC/mouse/CAST/CTL_liver/BD_ATAC_101_liver/fastq/Liver_101_ATAC.fastq.gz
35 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_7_kidney/fastq/ATACKID7-BD_ATAC_7_kidney_cat_060315.fastq.gz
36 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_12_kidney/fastq/ATACKID12-BD_ATAC_12_2ndPrep_kidney_AGGCAG_L006_R1_001.fastq.gz
37 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_9_kidney/fastq/ATAC_BD_20-BD_ATAC_9_kidney_re_GGACTCC_L006_R1_001.fastq.gz
38 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_8_kidney/fastq/ATAC_BD_11-BD_ATAC_8_kidney_re_TCCTGAG_L003_R1_001.fastq.gz
39 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_11_kidney/fastq/ATAC_BD_27-BD_ATAC_11_kidney_re_TCCTGAG_L008_R1_001.fastq.gz
40 /proj/fureylab/data/ATAC/mouse/CAST/BD_kidney/BD_ATAC_10_kidney/fastq/CAST_BD_kidney_ATAC_10_cat012016.fastq.gz
```

.*

Aa

"



Find What:

^(.*)/(fastq/)(.*)\\.fastq\\.gz\$

Find

Replace



Replace With:

\\1\\t\\3\\t\\1\\2\\3\\4

Find All

Replace All



Type in the find window:

`^(.*\/)(fastq\/)(.*)(\.fastq\.gz)$`

Type in the replace window

`\1\t\3\t\1\2\3\4`

Press **Replace All**

source.txt

```
1 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/ Kidney_105_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/  
BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz  
2 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/ CAST_CTL_kidney_ATAC_101_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/  
CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq.gz  
3 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/ Kidney_104_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/  
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4 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/ Kidney_103_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/  
BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz  
5 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/ ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/  
CTL_kidney/BD_ATAC_2_kidney/fastq/ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001.fastq.gz  
6 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/ ATACKD102-BD_ATAC_102_kidney_cat_060315 /proj/fureylab/data/ATAC/mouse/CAST/  
CTL_kidney/BD_ATAC_102_kidney/fastq/ATACKD102-BD_ATAC_102_kidney_cat_060315.fastq.gz  
7 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/ ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001 /proj/fureylab/data/ATAC/  
mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/fastq/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001.fastq.gz  
8 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/ CAST_BD_liver_ATAC_8_cat091516 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/  
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9 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/ CAST_BD_liver_ATAC_8_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/  
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10 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/ ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001 /proj/fureylab/data/ATAC/mouse/  
CAST/BD_liver/BD_ATAC_10_liver/fastq/ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001.fastq.gz  
11 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/ CAST_BD_liver_ATAC_7_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/  
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12 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/ ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_R1_001 /proj/fureylab/data/ATAC/mouse/  
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13 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/ CAST_BD_liver_ATAC_9_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/  
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14 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/ ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_R1_001 /proj/fureylab/data/ATAC/mouse/  
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15 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/ Lung_103_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/fastq/  
Lung_103_ATAC.fastq.gz  
16 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/ Lung_104_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/fastq/  
Lung_104_ATAC.fastq.gz  
17 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/ Lung_2_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/fastq/  
Lung_2_ATAC.fastq.gz  
18 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_1_lung/ ATACLU1-BD_ATAC_1_lung_cat /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/  
BD_ATAC_1_lung/fastq/ATACLU1-BD_ATAC_1_lung_cat.fastq.gz  
19 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_105_lung/ Lung_105_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_105_lung/fastq/  
Lung_105_ATAC.fastq.gz  
20 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_101_lung/ Lung_101_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_101_lung/fastq/  
Lung_101_ATAC.fastq.gz  
21 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_102_lung/ Lung_102_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_102_lung/fastq/  
Lung_102_ATAC.fastq.gz  
22 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_8_lung/ Lung_8_ATAC /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_8_lung/fastq/  
Lung_8_ATAC.fastq.gz  
23 /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_9_lung/ Lung_9_ATAC /proj/fureylab/data/ATAC/mouse/CAST/BD_lung/BD_ATAC_9_lung/fastq/  
Lung_9_ATAC.fastq.gz
```



An example of the finished file is in:
~/virtuous_bash/CAST_rerun/five_columns.txt

Two step process: Step 2

- Take the columns from Step 1 and slot them into the string:

```
mkdir -p $TMPDIR/\2
```

```
cd $TMPDIR/\2
```

```
python atac_v_1_1.py --out-dir \1\out2 --tmp-dir $TMPDIR/\2tmp  
-group-name \2 --max-nhits 1  
-config config.cfg --slurm --section C57BL6 -run \3
```

Mrs. Dalloway said she would buy the #flowers herself.



Type in the find window:

```
^(.*)/(fastq/)(.*)(\.fastq\.gz)$
```

Type in the replace window

```
mkdir -p $TMPDIR/\2\n
```

```
cd $TMPDIR/\2
```

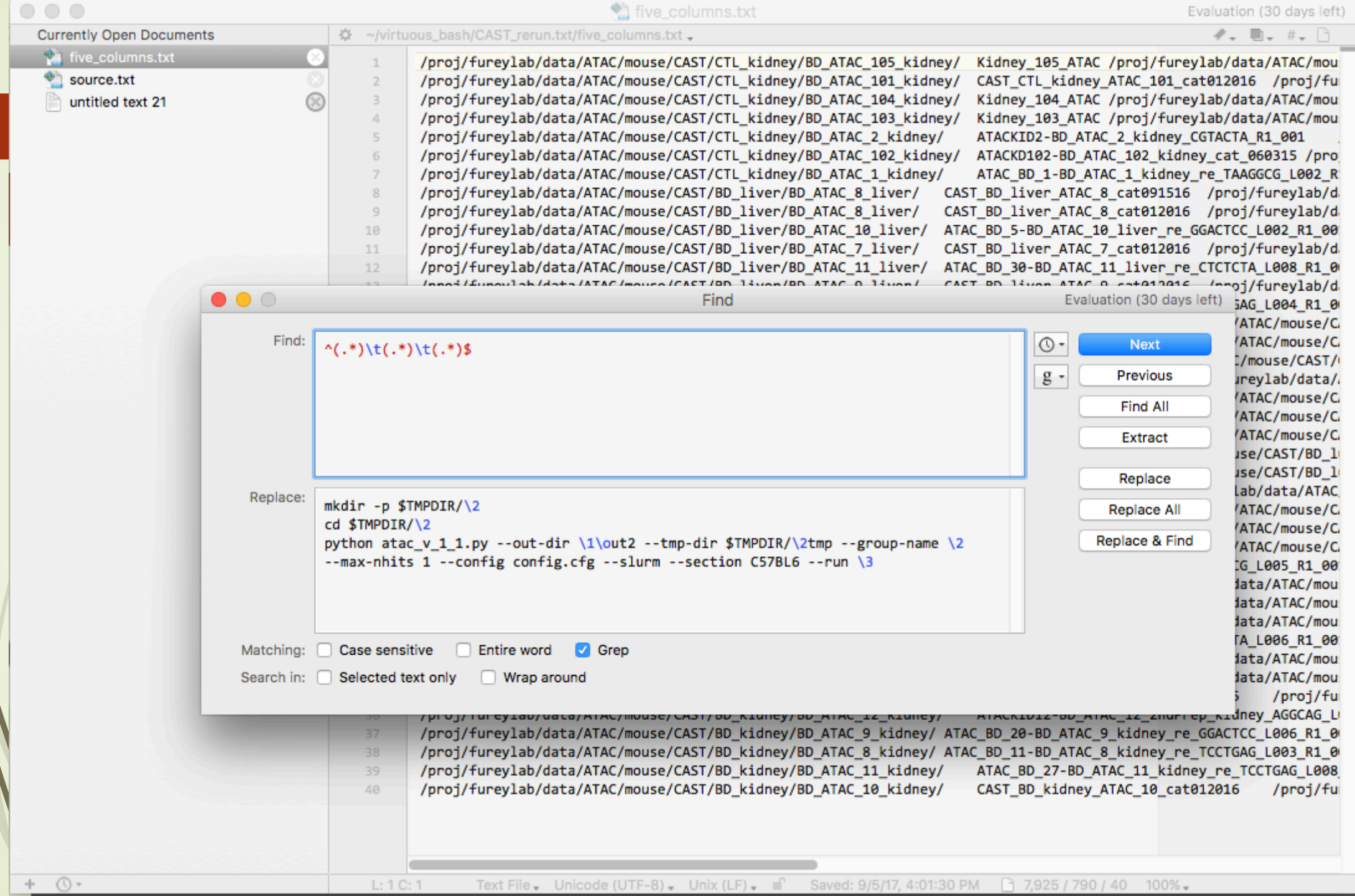
```
python atac_v_1_1.py --out-dir \1\out2
```

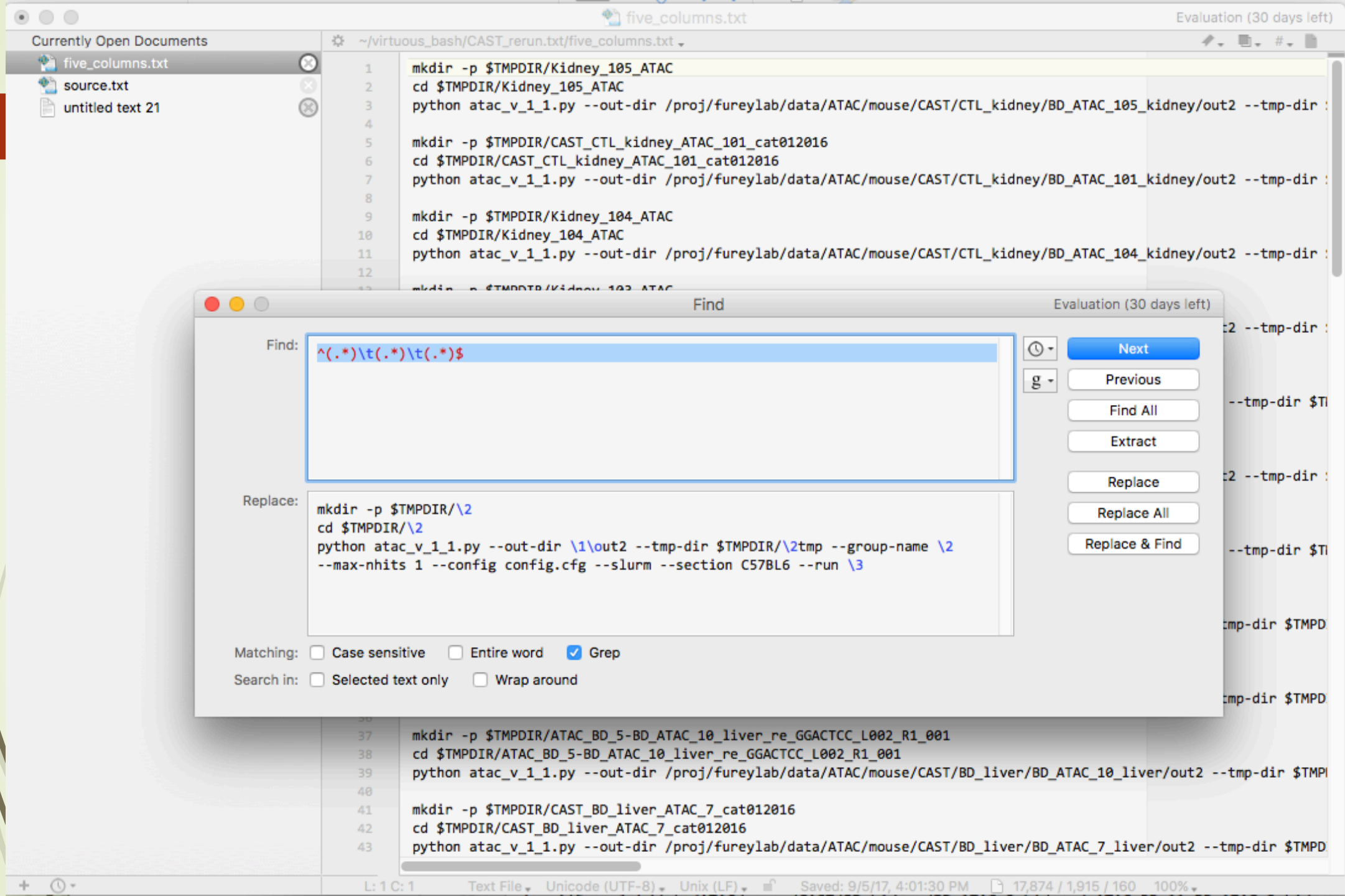
```
--tmp-dir $TMPDIR/\2tmp --group-name \2
```

```
--max-nhits 1 --config config.cfg
```

```
--slurm --section C57BL6 --run \3
```

Press Replace All





```
1 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/—Kidney_105_ATAC-/proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz
2 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/ CAST_CTL_kidney_ATAC_101_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq.gz
3 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/ Kidney_104_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz
4 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/ Kidney_103_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz
5 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/ ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/fastq/ATACKID2-BD_ATAC_2_kidney_CGTACTA_R1_001.fastq.gz
6 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/ ATACKD102-BD_ATAC_102_kidney_cat_060315 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/fastq/ATACKD102-BD_ATAC_102_kidney_cat_060315.fastq.gz
7 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/ ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/fastq/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001.fastq.gz
8 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/ CAST_BD_liver_ATAC_8_cat091516 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat091516.fastq.gz
9 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/ CAST_BD_liver_ATAC_8_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_8_liver/fastq/CAST_BD_liver_ATAC_8_cat012016.fastq.gz
10 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/ ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_10_liver/fastq/ATAC_BD_5-BD_ATAC_10_liver_re_GGACTCC_L002_R1_001.fastq.gz
11 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/ CAST_BD_liver_ATAC_7_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_7_liver/fastq/CAST_BD_liver_ATAC_7_cat012016.fastq.gz
12 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/ ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_11_liver/fastq/ATAC_BD_30-BD_ATAC_11_liver_re_CTCTCTA_L008_R1_001.fastq.gz
13 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/ CAST_BD_liver_ATAC_9_cat012016 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_9_liver/fastq/CAST_BD_liver_ATAC_9_cat012016.fastq.gz
14 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/ ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_R1_001 /proj/fureylab/data/ATAC/mouse/CAST/BD_liver/BD_ATAC_12_liver/fastq/ATAC_BD_15-BD_ATAC_12_liver_re_CAGAGAG_L004_R1_001.fastq.gz
15 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/ Lung_103_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_103_lung/fastq/Lung_103_ATAC.fastq.gz
16 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/ Lung_104_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_104_lung/fastq/Lung_104_ATAC.fastq.gz
17 /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/ Lung_2_ATAC /proj/fureylab/data/ATAC/mouse/CAST/CTL_lung/BD_ATAC_2_lung/fastq/Lung_2_ATAC.fastq.gz
```

* Aa " " 🔍 ↺

Find What:

^(.*)\t(.*)\t(.*)\$

Find

Replace



Replace With:

```
mkdir -p $TMPDIR/\2
cd $TMPDIR/\2
python atac_v1_1.py --out-dir \1\out2 --tmp-dir $TMPDIR/\2tmp --group-name \2 --max-nhits 1 --config config.cfg
```

Find All

Replace All

untitled

five_columns.txt

```
1 mkdir -p $TMPDIR/Kidney_105_ATAC
2 cd $TMPDIR/Kidney_105_ATAC
3 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_105_kidney/out2 --tmp-dir $TMPDIR/Kidney_105_ATACtmp
  --group-name Kidney_105_ATAC --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/
  BD_ATAC_105_kidney/fastq/Kidney_105_ATAC.fastq.gz
4
5
6 mkdir -p $TMPDIR/CAST_CTL_kidney_ATAC_101_cat012016
7 cd $TMPDIR/CAST_CTL_kidney_ATAC_101_cat012016
8 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/out2 --tmp-dir $TMPDIR/
  CAST_CTL_kidney_ATAC_101_cat012016tmp --group-name CAST_CTL_kidney_ATAC_101_cat012016 --max-nhits 1 --config config.cfg --slurm --section C57BL6
  --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_101_kidney/fastq/CAST_CTL_kidney_ATAC_101_cat012016.fastq.gz
9
10
11 mkdir -p $TMPDIR/Kidney_104_ATAC
12 cd $TMPDIR/Kidney_104_ATAC
13 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_104_kidney/out2 --tmp-dir $TMPDIR/Kidney_104_ATACtmp
  --group-name Kidney_104_ATAC --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/
  BD_ATAC_104_kidney/fastq/Kidney_104_ATAC.fastq.gz
14
15
16 mkdir -p $TMPDIR/Kidney_103_ATAC
17 cd $TMPDIR/Kidney_103_ATAC
18 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_103_kidney/out2 --tmp-dir $TMPDIR/Kidney_103_ATACtmp
  --group-name Kidney_103_ATAC --max-nhits 1 --config config.cfg --slurm --section C57BL6 --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/
  BD_ATAC_103_kidney/fastq/Kidney_103_ATAC.fastq.gz
19
20
21 mkdir -p $TMPDIR/ATAKID2-BD_ATAC_2_kidney_CGTACTA_R1_001
22 cd $TMPDIR/ATAKID2-BD_ATAC_2_kidney_CGTACTA_R1_001
23 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/out2 --tmp-dir $TMPDIR/
  ATAKID2-BD_ATAC_2_kidney_CGTACTA_R1_001tmp --group-name ATAKID2-BD_ATAC_2_kidney_CGTACTA_R1_001 --max-nhits 1 --config config.cfg --slurm
  --section C57BL6 --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_2_kidney/fastq/ATAKID2-BD_ATAC_2_kidney_CGTACTA_R1_001.fastq.gz
24
25
26 mkdir -p $TMPDIR/ATAKD102-BD_ATAC_102_kidney_cat_060315
27 cd $TMPDIR/ATAKD102-BD_ATAC_102_kidney_cat_060315
28 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/out2 --tmp-dir $TMPDIR/
  ATAKD102-BD_ATAC_102_kidney_cat_060315tmp --group-name ATAKD102-BD_ATAC_102_kidney_cat_060315 --max-nhits 1 --config config.cfg --slurm
  --section C57BL6 --run /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_102_kidney/fastq/ATAKD102-BD_ATAC_102_kidney_cat_060315.fastq.gz
29
30
31 mkdir -p $TMPDIR/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001
32 cd $TMPDIR/ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001
33 python atac_v_1_1.py --out-dir /proj/fureylab/data/ATAC/mouse/CAST/CTL_kidney/BD_ATAC_1_kidney/out2 --tmp-dir $TMPDIR/
  ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001tmp --group-name ATAC_BD_1-BD_ATAC_1_kidney_re_TAAGGCG_L002_R1_001 --max-nhits 1 --config
```

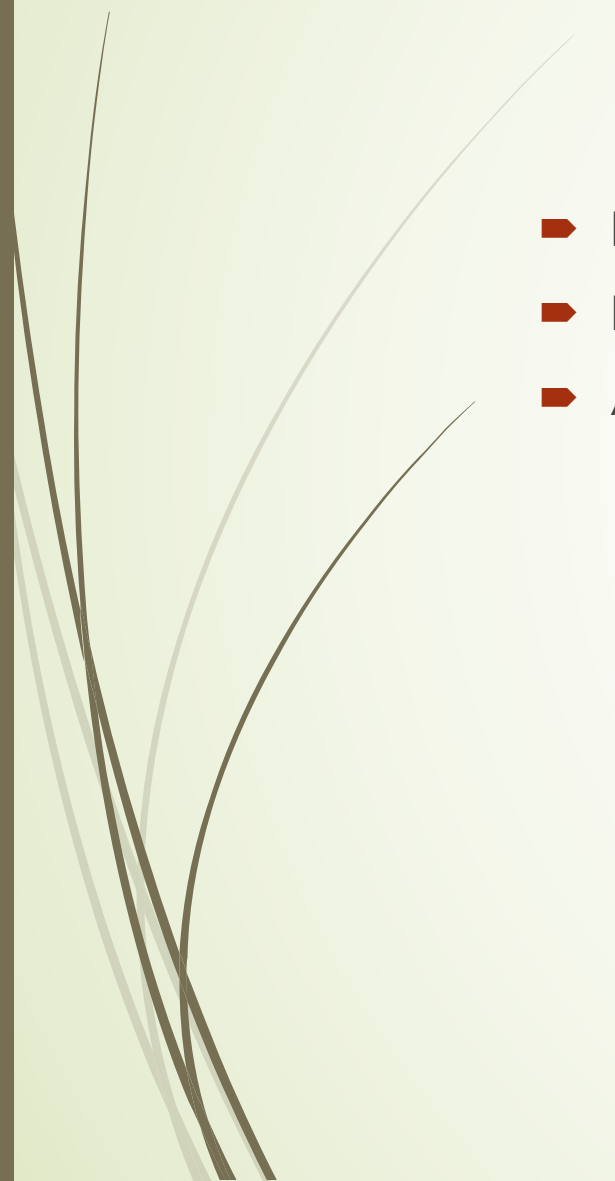
Other uses for the technique

- ▶ Formatting the genome browsers *.ra files (or any large config file)

```
track CC001_Control_LUNG_ATAC_14
shortLabel CC001_Control_LUNG_ATAC_14
longLabel CC001_Control_LUNG_ATAC_14
parent BD_ATAC_LUNG_CC
visibility full
type bigWig
priority 25
maxHeightPixels 100:32:32
autoScale on
windowingFunction maximum
color 0,0,128
bigDataUrl CC_ATAC/bacCC001_Control_LUNG_ATAC_14.bw
```



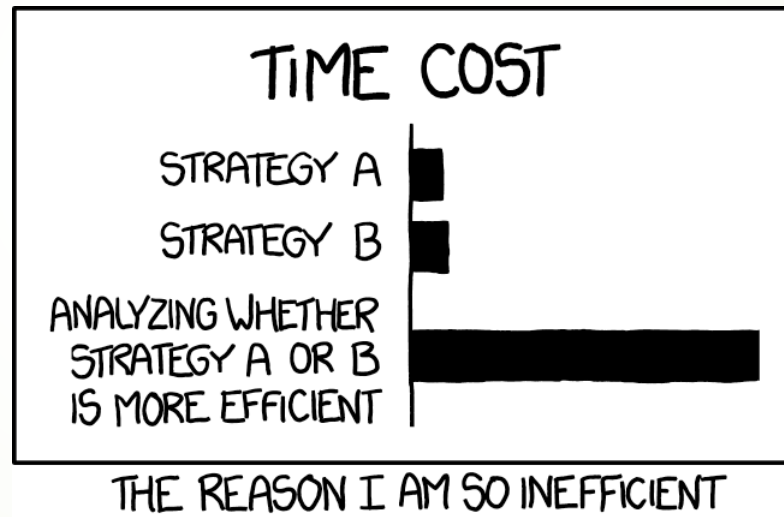
Other uses for the technique

- Large bulk move scripts
 - Bulk changing file formats in situ
 - And others...
- 

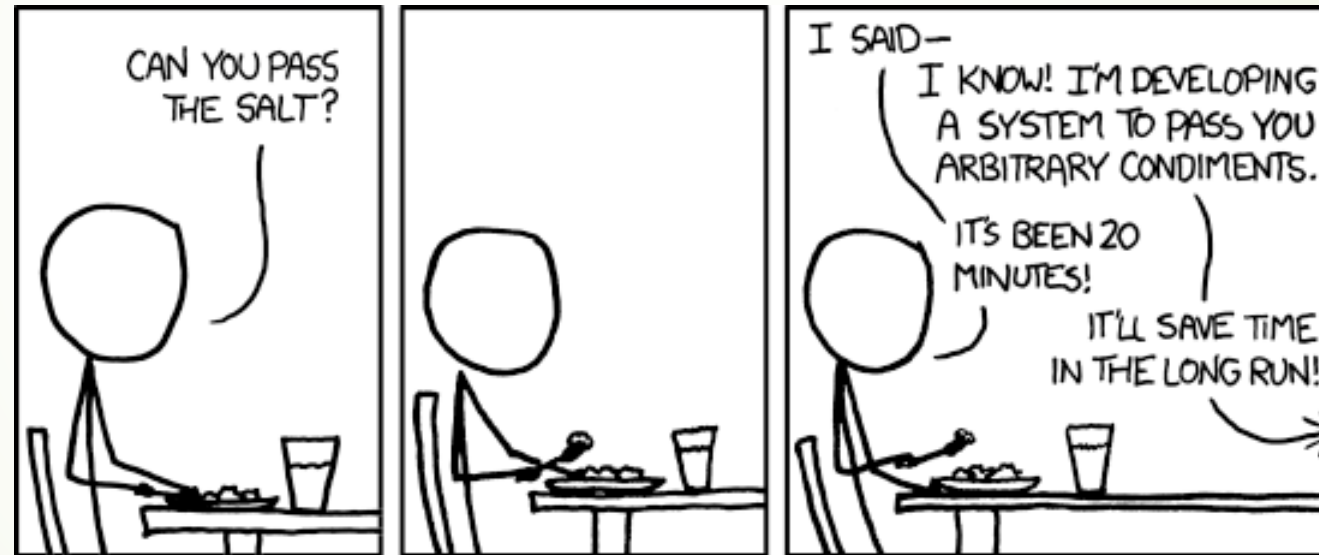
Pitfalls



Choose with prejudice

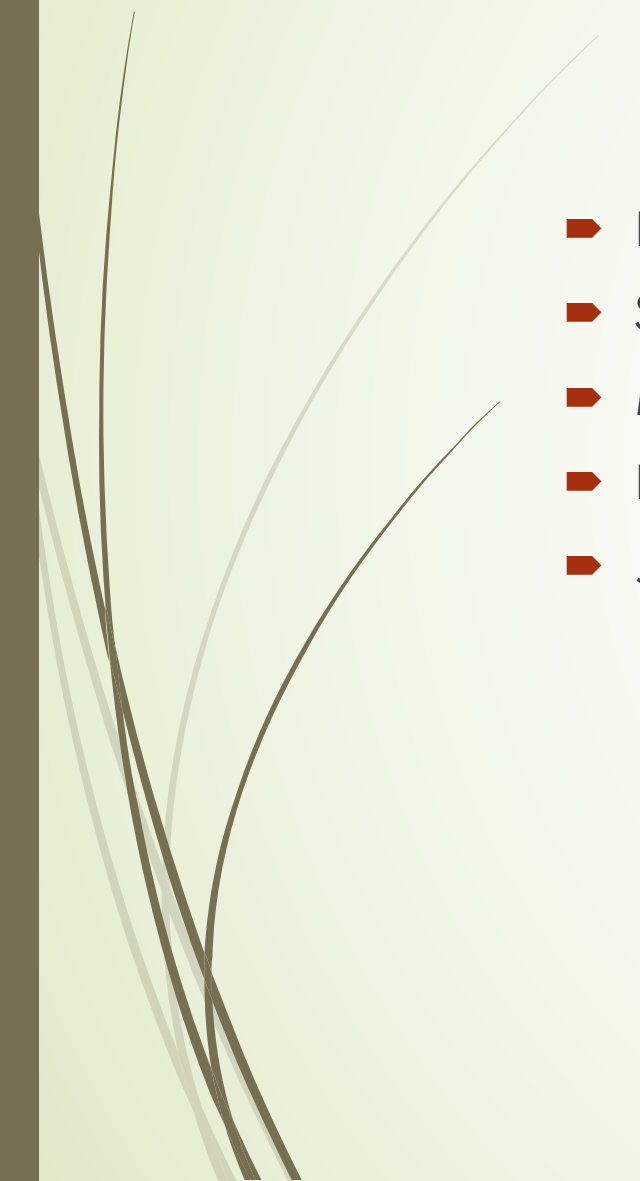


The general solution can be expensive





Thanks Everyone

- Furey Lab
 - Sheikh Lab
 - Mohlke Lab
 - Karl Eklund and Research Computing
 - Jeremy Simon for the Genome Browser Example
- 



Unused Material





For loops

- Remember the files in `~/virtuous_bash/no_leading_zero/?`
- How did I create them easily:
 - `for i in $(seq 1 20); do touch "file$i.txt"; done`