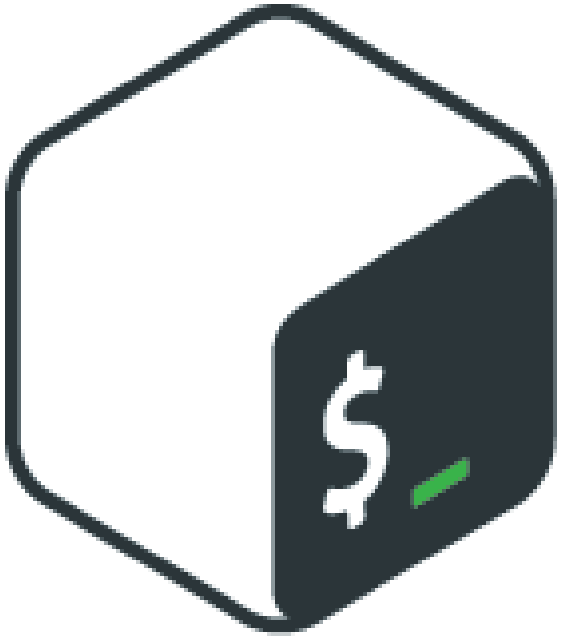
BINF2111 – Introduction to Bioinformatics Computing

BASH 101 – Loops and conditionals



BASH

THE BOURNE-AGAIN SHELL

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RAW Lab

Lecture 9 – Tuesday Sep 20th, 2022

Learning Objectives

- Carnegie Rule

- Review quiz and bonus

- Review assignment 3

- Bash conditionals

- Bash for loops

- Quiz 9

Carnegie rule

Carnegie Rule is a rule of thumb suggesting how much outside-of-classroom study time is required to succeed in an average higher education course in the U.S. system.

Is for every hour spent in the classroom that two or more hours of outside work required.

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Is for every hour spent in the classroom that two or more hours of outside work required.

OUTDATED!

RAW rule of thumb for computational learning is spend quality time at the terminal, googling, and thinking problems at the terminal..

Quiz 8

```
printf '#!/bin/bash\n \n# This is my first comment\n #Wookies rule'
>script.sh

more script.sh

#!/bin/bash

# This is my first comment
# Wookies rule
```

Is that my correct script output?

Quiz 8

```
printf '#!/bin/bash\n \n# This is my first comment\n #Wookies rule'
>script.sh

more script.sh

#!/bin/bash

# This is my first comment
# Wookies rule
```

Is that my correct script output?

Quiz 8

printf '#!/bin/bash\n \n# This is my first comment\n #Wookies rule' >script.sh

more script.sh

#!/bin/bash

This is my first comment
Wookies rule

Is that my correct script output? **FALSE**

Quiz 8

printf '#!/bin/bash\n \n# This is my first comment\n #Wookies rule' >script.sh

more script.sh

#!/bin/bash

This is my first comment
 #Wookies rule

Is that my correct script output? **FALSE**

Quiz 8

This file is an example of a BLANK type file?

@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTT
GTTCAACTCACAGTTT
+
!"*((((***+))%%%++)(%%%%).1***
+*"))**55CCF>>>>>>CCCCCCC65

Quiz 8

This file is an example of a BLANK type file?

@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTT
GTTCAACTCACAGTTT
+
!"*((((***+))%%%++)(%%%%).1***
+*"))**55CCF>>>>>>CCCCCCC65

FASTQ = .fq/.fastq

Assignment 3 lab (most missed)

(Q5) Provide two unique commands to convert a tsv to csv? They cannot start with the same command (For example, sed/tr, grep/tr etc)

- Command 1 here:

- Command 2 here:

- Another way:

Assignment 3 lab (most missed)

(Q5) Provide two unique commands to convert a tsv to csv? They cannot start with the same command (For example, sed/tr, grep/tr etc)

- Command 1 here:

sed 's/\t/,/g' file.tsv >file.csv

- Command 2 here:

- Another way:

Assignment 3 lab (most missed)

(Q5) Provide two unique commands to convert a tsv to csv? They cannot start with the same command (For example, sed/tr, grep/tr etc)

- Command 1 here:

sed 's/\t/,/g' file.tsv >file.csv

- Command 2 here:

cat file.tsv | tr -s '\t' ',' >file.csv

- Another way:

Assignment 3 lab (most missed)

(Q5) Provide two unique commands to convert a tsv to csv? They cannot start with the same command (For example, sed/tr, grep/tr etc)

- Command 1 here:

sed 's/\t/,/g' file.tsv >file.csv

- Command 2 here:

cat file.tsv | tr -s '\t' ',' >file.csv

- Another way:

awk -F '\t' -vOFS=, '{$1=$1}1'

Assignment 3 lab (most missed)

(Q6) Using any command you want convert whitespace into tabs?

- Command 1 here:

```
cat file.txt | tr -s '[:blank:]' '\t' >fixed.txt
```

- Command 2 here:

```
sed 's/[[:blank:]]\+/\t/g' file.txt > fixed.txt
```

- Another way:

```
awk -v OFS="\t" '$1=$1' file.txt > fixed.txt
```

Assignment 3 lab (most missed)

(Q10) Extract the sequence in example2.fasta that has more then one ATG?

```
more example2.fasta
>chr1_geneA
ATGCTAAGGCTATCTTGACAACTGACTGCCTAG
>chr1_geneB
ATGCTAAGGCTATGTTGGCAACTGACTCCCTAG
>chr1_geneC
ATGCTAAGGCTACCTTGACAACTGACTGGGTAG
>chr1_geneD
ATGAAAAGGCTATCTTGACAACTGACTCCCTAG
>chr1_geneX
ATGCTAAGGCTATCTTGATTTCTGACTTTTTAG
>chr1_geneY
ATGGGGGGGCTATCTTGACAACTGACTGCGTAG
>chr1_geneZ
ATGCTAAGGCTATCNNGACAACTGACTAAATAG
```

What is a command to find multiple ‘ATGs’?

- Command:

Assignment 3 lab (most missed)

(Q10) Extract the sequence in example2.fasta that has more then one ATG?

```
more example2.fasta
>chr1_geneA
ATGCTAAGGCTATCTTGACAACTGACTGCCTAG
>chr1_geneB
ATGCTAAGGCTATGTTGGCAACTGACTCCCTAG
>chr1_geneC
ATGCTAAGGCTACCTTGACAACTGACTGGGTAG
>chr1_geneD
ATGAAAAGGCTATCTTGACAACTGACTCCCTAG
>chr1_geneX
ATGCTAAGGCTATCTTGATTTCTGACTTTTTAG
>chr1_geneY
ATGGGGGGGCTATCTTGACAACTGACTGCGTAG
>chr1_geneZ
ATGCTAAGGCTATCNNGACAACTGACTAAATAG
```

What is a command to find multiple ‘ATGs’?

- Command:

grep "ATG" example2.fasta --color

Assignment 3 lab (most missed)

(Q10) Extract the sequence in example2.fasta that has more then one ATG?

```
more example2.fasta
>chr1_geneA
ATGCTAAGGCTATCTTGACAACTGACTGCCTAG
>chr1_geneB
ATGCTAAGGCTATGTTGGCAACTGACTCCCTAG
>chr1_geneC
ATGCTAAGGCTACCTTGACAACTGACTGGGTAG
>chr1_geneD
ATGAAAAGGCTATCTTGACAACTGACTCCCTAG
>chr1_geneX
ATGCTAAGGCTATCTTGATTTCTGACTTTTTAG
>chr1_geneY
ATGGGGGGGCTATCTTGACAACTGACTGCGTAG
>chr1_geneZ
ATGCTAAGGCTATCNNGACAACTGACTAAATAG
```

How do I grab the one with two ATGs?

- Command:

```
grep 'ATG.*ATG' example2.fasta
>extracted.fasta
```

Another way?

Assignment 3 lab (most missed)

(Q10) Extract the sequence in example2.fasta that has more then one ATG?

```
more example2.fasta
>chr1_geneA
ATGCTAAGGCTATCTTGACAACTGACTGCCTAG
>chr1_geneB
ATGCTAAGGCTATGTTGGCAACTGACTCCCTAG
>chr1_geneC
ATGCTAAGGCTACCTTGACAACTGACTGGGTAG
>chr1_geneD
ATGAAAAGGCTATCTTGACAACTGACTCCCTAG
>chr1_geneX
ATGCTAAGGCTATCTTGATTTCTGACTTTTTAG
>chr1_geneY
ATGGGGGGGCTATCTTGACAACTGACTGCGTAG
>chr1_geneZ
ATGCTAAGGCTATCNNGACAACTGACTAAATAG
```

How do I grab the one with two ATGs?

- Command:

```
grep 'ATG.*ATG' example2.fasta
>extracted.fasta
```

Another way?

```
grep '\(.*ATG\)\{2\}' example2.fasta
>extracted.fasta
```

Bonus 7

- Write a bash script that states 150 kg at 178 cm is overweight?

Var1 = ?

Var2 = ?

Bonus 7

- Write a bash script that states 150 kg at 178 cm is overweight?

Var1 = weight
Var2 = height

What are these variables?

Bonus 7

- Write a bash script that states 150 kg at 178 cm is overweight?

Var1 = weight
Var2 = height

What are these variables?

Integer variables!! Whole numbers
1,2,3 etc

Inside a bash script

```
1 #!/bin/bash
2
3 # This script prints a message about your weight if you give it
  your
4
5 # weight in kilos and height in centimeters.
6
7 weight="$1"
8 height="$2"
9 idealweight=$[$height - 110]
10 if [ $weight -le $idealweight ] ; then
11  echo "You should eat a bit more food."
12 else
13  echo "You should eat a bit less food."
14 fi
```

hashbang

Var1

Var2

Inside a bash script


```
bash -x weight.sh 130 178
```

Inside a bash script


```
bash -x weight.sh 130 178
>output.txt
```

Lab Q4


```
bash -x count_fasta.sh  example2.fasta >out.txt
```

```
1 #!/bin/bash
2
3 input=$1
```

What is $1 in this script?

Lab Q4


```
bash -x count_fasta.sh  example2.fasta >out.txt
```

```
1 #!/bin/bash
2
3 input=$1
```

What is $1 in this script? EXAMPLE2.fasta

BASH Variables (By content)

Temporary stores of information

In this respect, variables come in 4 types:

- String variables:

- Integer variables:

- Constant variables:

- Array variables:

BASH Variables (By content)

Temporary stores of information

In this respect, variables come in 4 types:

- String variables: Dog, Cat, Bill, Dave

- Integer variables: 1, 2, 101, 2021, whole numbers

- Constant variables: Pi = 3.14 etc

- Array variables: variable containing multiple values. Any variable may be used as an array. There is no maximum limit to the size

BASH Reserved words

! - Pipelines
[[ ]] - Conditional Constructs
{ } - Command Grouping
break - Looping Constructs
case - Conditional Constructs
continue - Looping Constructs
do - Looping Constructs
done - Looping Constructs
elif - Conditional Constructs
else - Conditional Constructs
esac - Conditional Constructs
fi - Conditional Constructs
for - Looping Constructs
function - Shell Functions
if - Conditional Constructs
in - Conditional Constructs
select - Conditional Constructs
then - Conditional Constructs
time - Pipelines
until - Looping Constructs
while - Looping Constructs

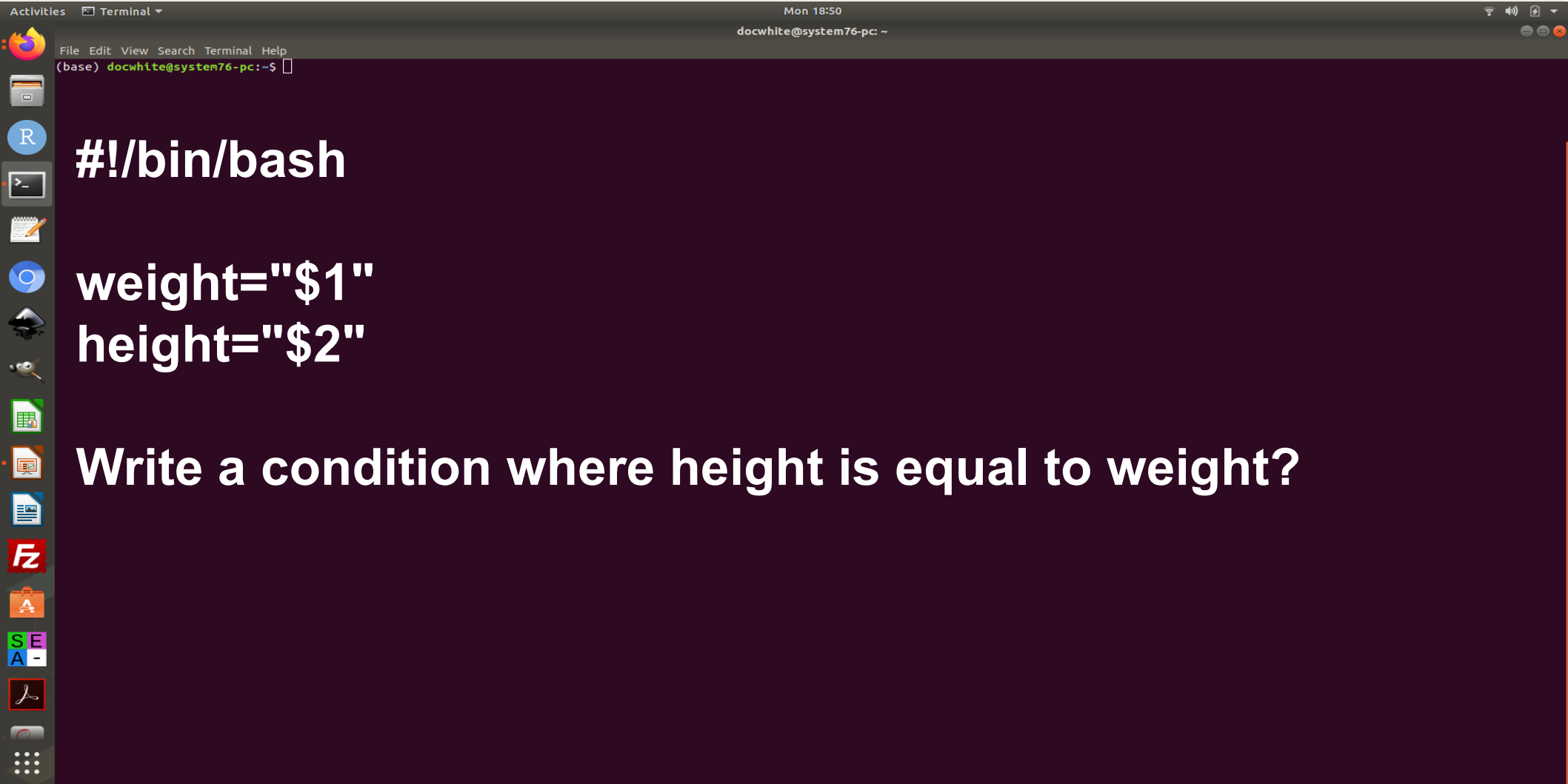
Similar from UNIX
& , | , > , < , ! , =
# , $, (,) , ; , {, } , [,] , \

https://www.gnu.org/software/bash/manual/html_node/Reserved-Word-Index.html

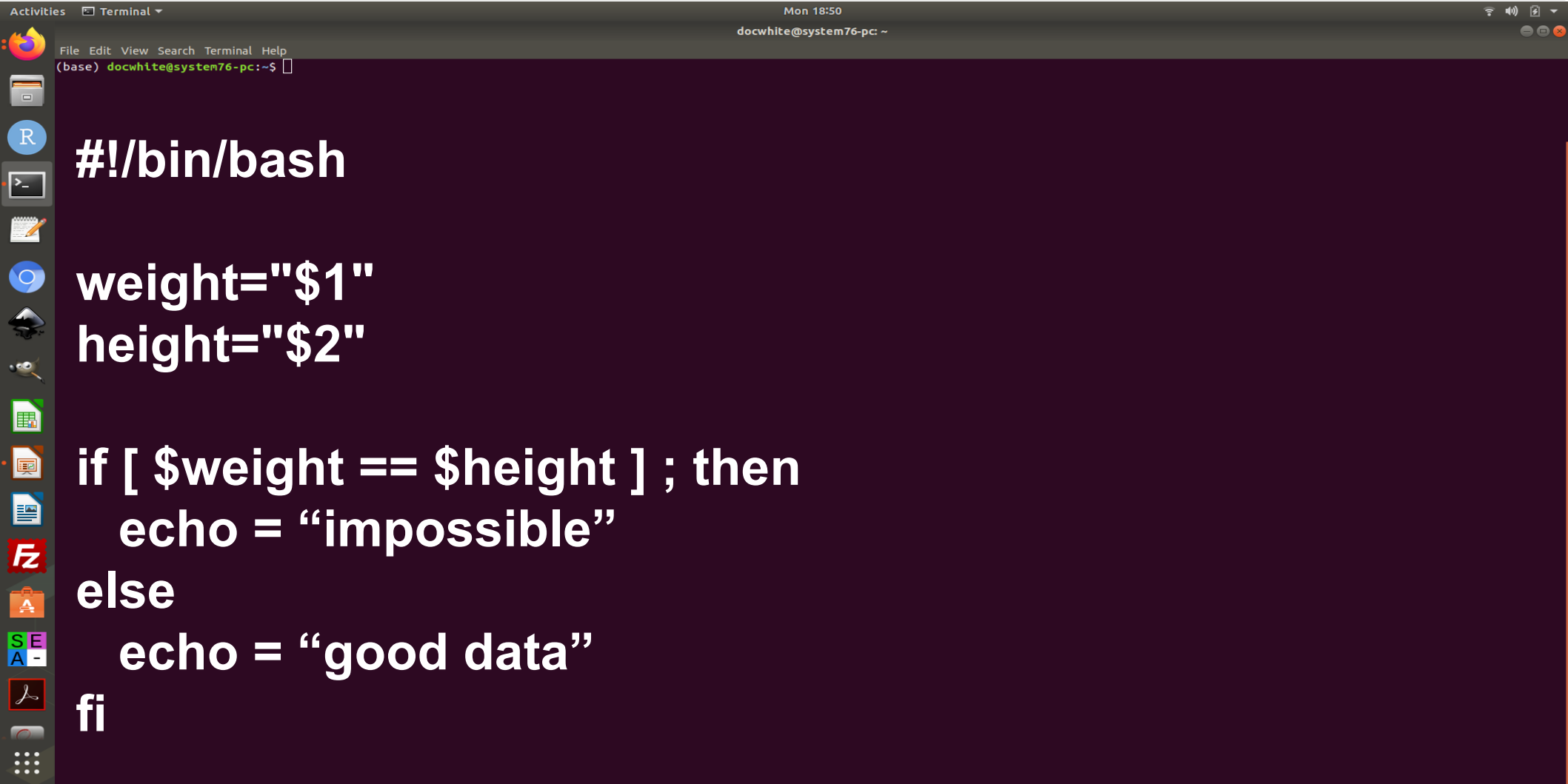
BASH Conditionals (conditions)

[[-z STRING]] Empty string
[[-n STRING]] Not empty string
[[STRING == STRING]] Equal
[[STRING != STRING]] Not Equal
[[NUM -eq NUM]] Equal
[[NUM -ne NUM]] Not equal
[[NUM -lt NUM]] Less than
[[NUM -le NUM]] Less than or equal
[[NUM -gt NUM]] Greater than
[[NUM -ge NUM]] Greater than or equal
[[STRING =~ STRING]] Regexp
((NUM < NUM)) Numeric conditions
[[-o noclobber]] If OPTIONNAME is enabled
[[! EXPR]] Not
[[X && Y]] And
[[X || Y]] Or

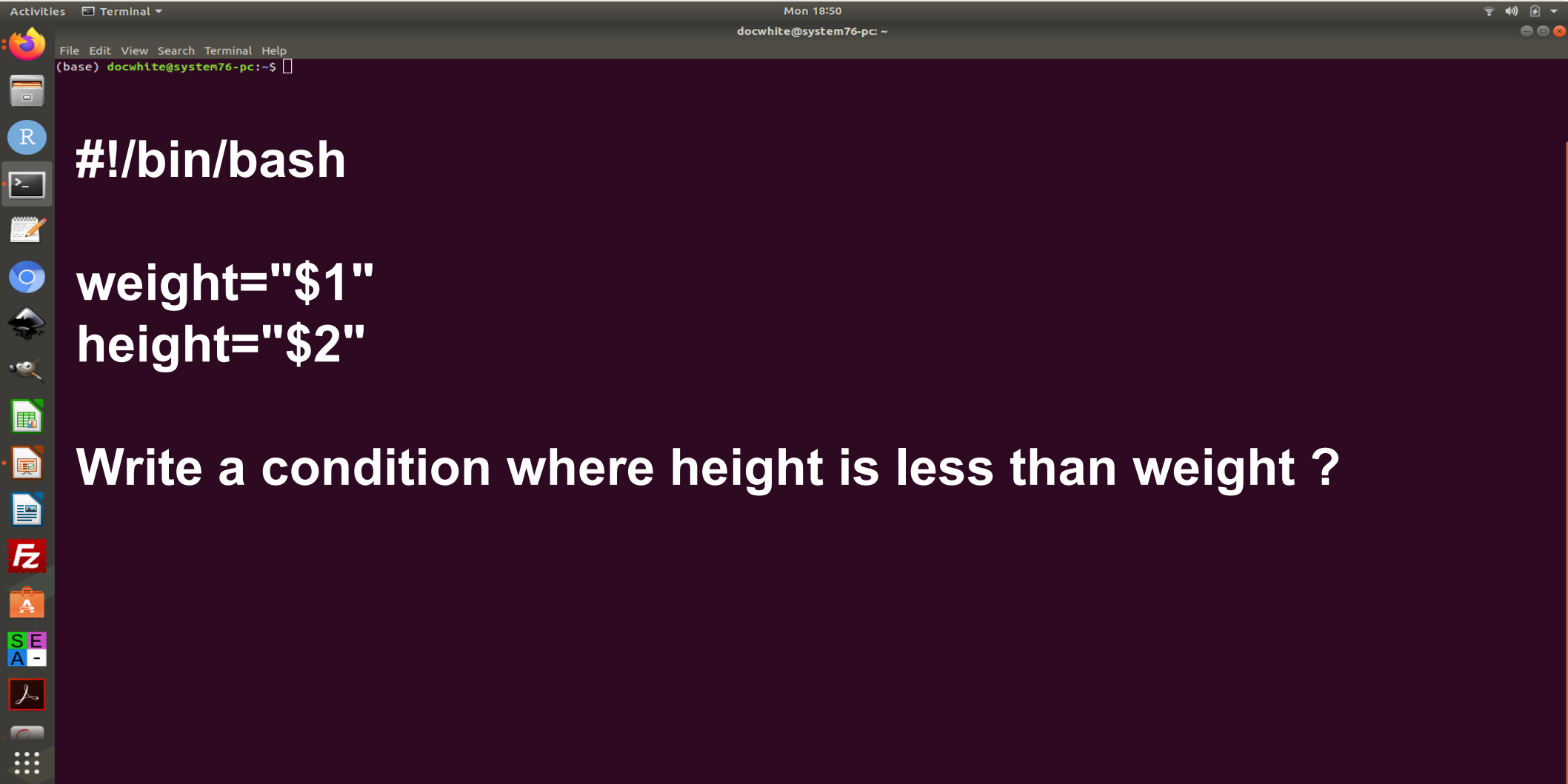
BASH conditions



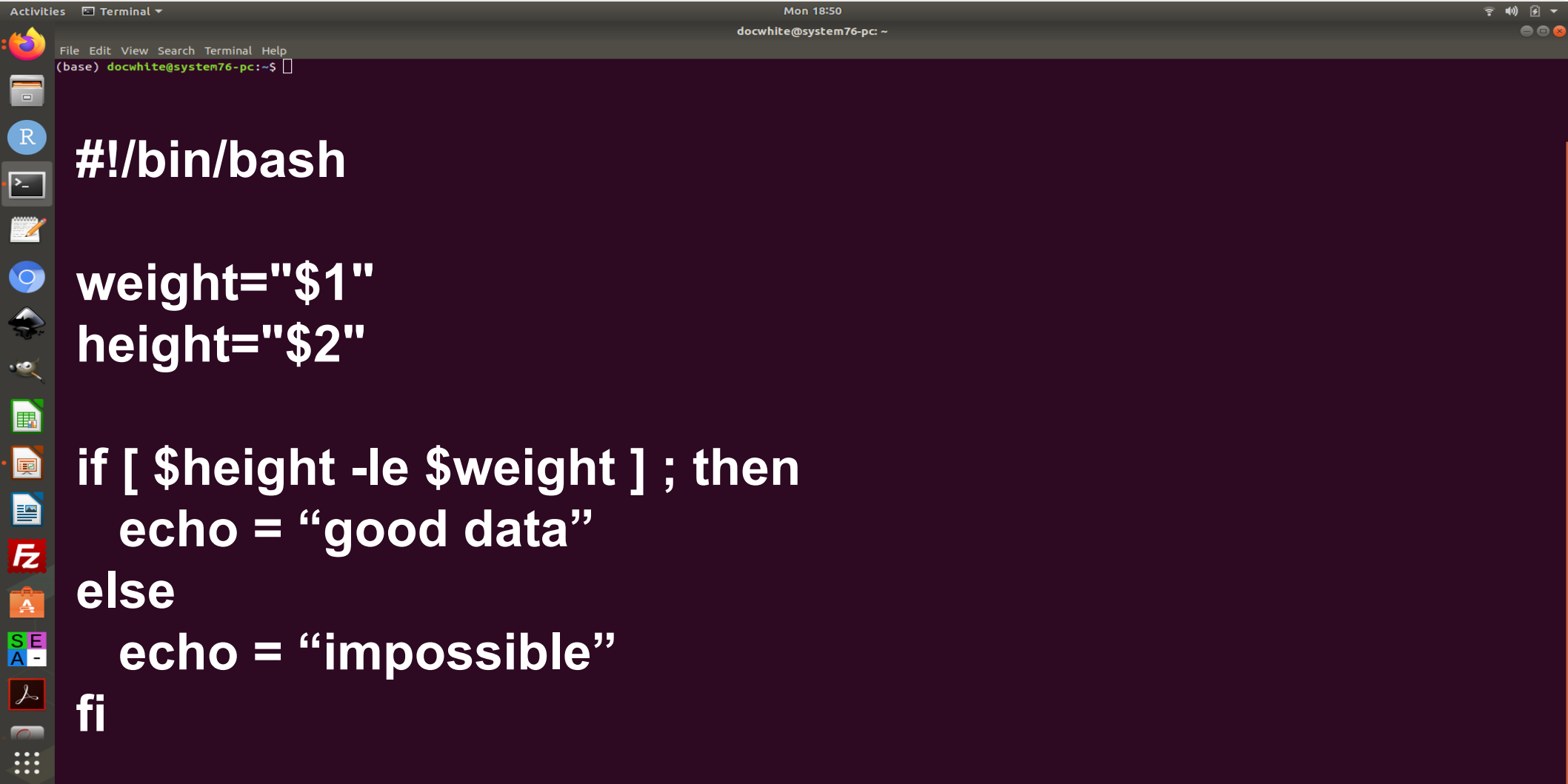
BASH conditions



BASH conditions



BASH conditions



BASH Conditionals (file conditions)

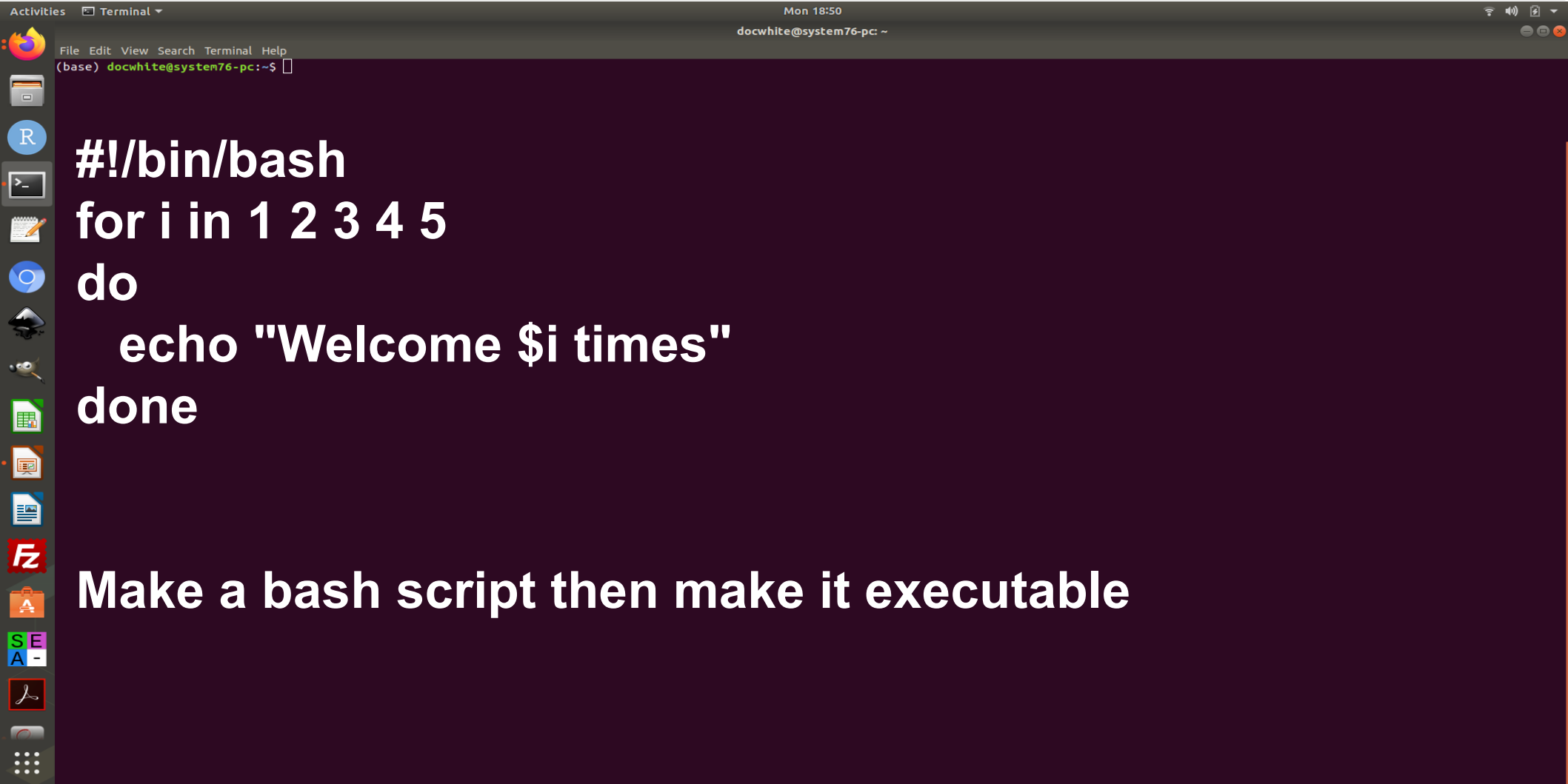
[[-e FILE]]	Exists
[[-r FILE]]	Readable
[[-h FILE]]	Symlink
[[-d FILE]]	Directory
[[-w FILE]]	Writable
[[-s FILE]]	Size is > 0 bytes
[[-f FILE]]	File
[[-x FILE]]	Executable
[[FILE1 -nt FILE2]]	1 is more recent than 2
[[FILE1 -ot FILE2]]	2 is more recent than 1
[[FILE1 -ef FILE2]]	Same files

bash -x weight.sh 130 178

BASH - for loop

```
for i in file.*;do
  command $i
done
```

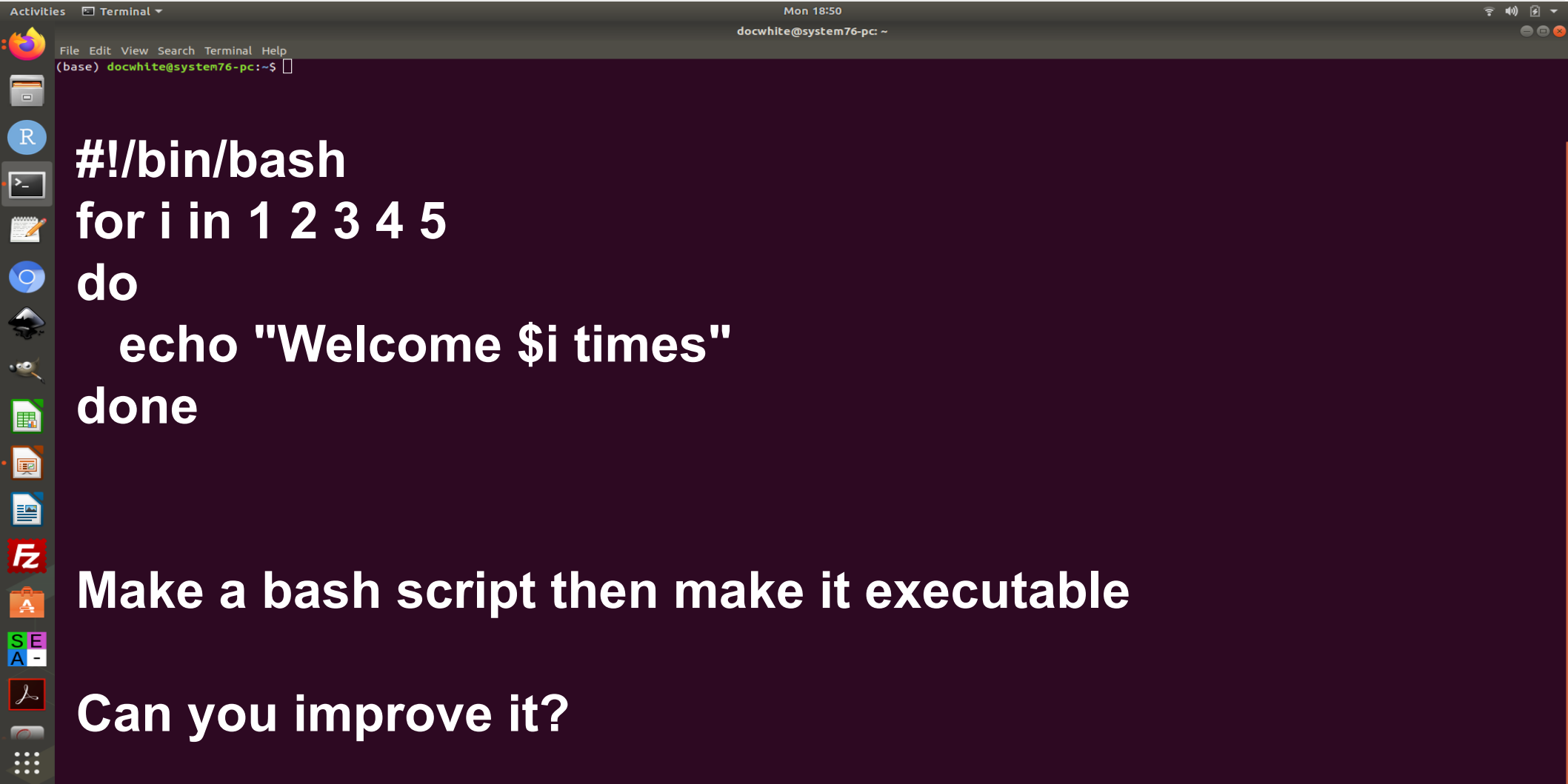
BASH for loops



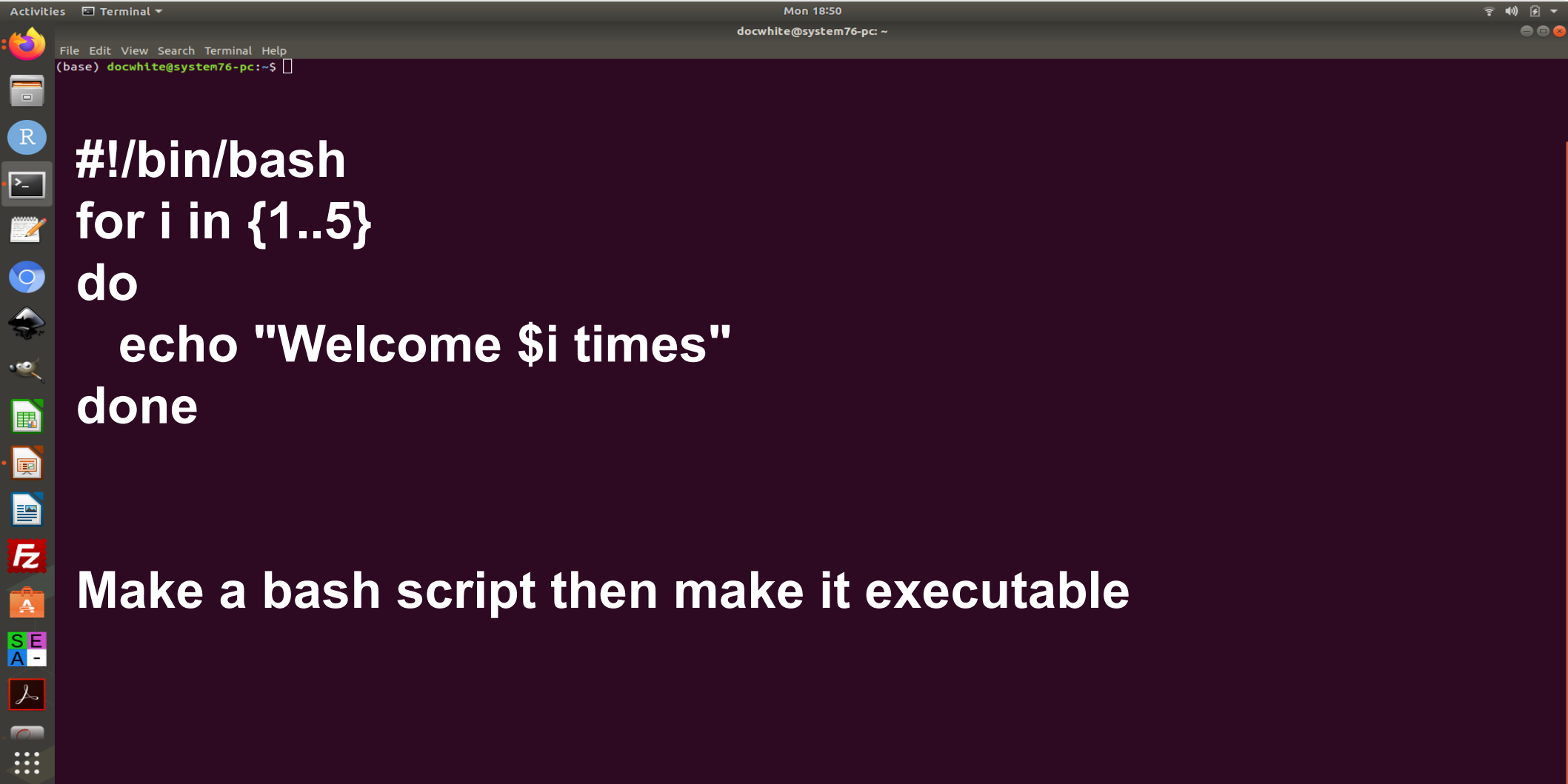

```
#!/bin/bash
for i in 1 2 3 4 5
do
   echo "Welcome $i times"
done
```

Make a bash script then make it executable

BASH for loops



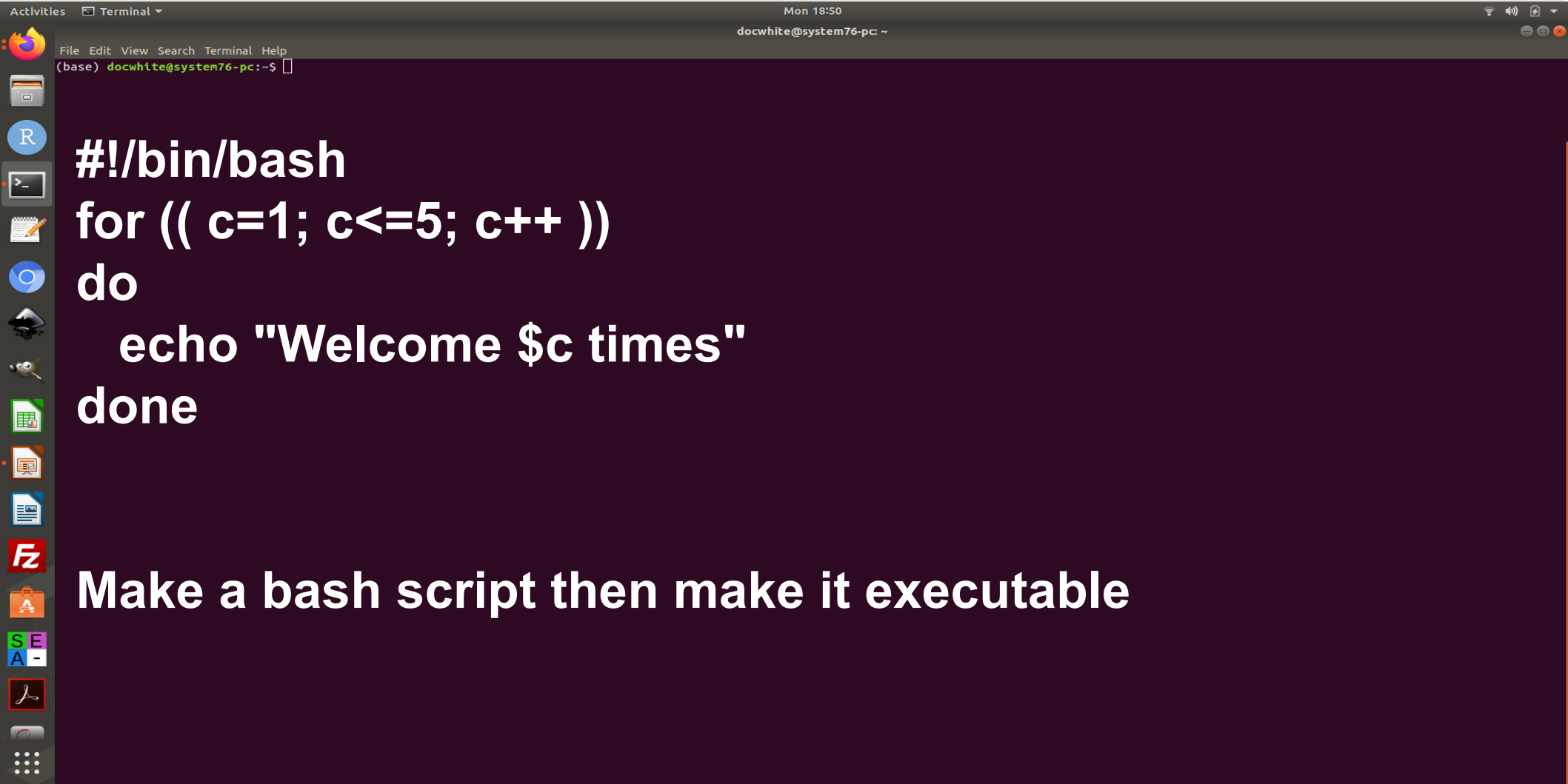
BASH for loops



BASH - for loop (C-style)

```
for ((i = 0 ; i < 100 ; i++)); do
  command $i
done
```

BASH for loops



Quiz 9

- On canvas now

Bonus 9

- Use grep to convert sam file to a fastq file?