

Advanced Linux Usage

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Enabler for Life Sciences

- Same program, many files

```
$ ls -l
total 0
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_9.bam
$ my_prog sample_1.bam
```

- Same program, many files

```
$ ls -l
total 0
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_9.bam
$ my_prog sample_1.bam
$ my_prog sample_2.bam
```

- Same program, many files

```
$ ls -l
total 0
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 16:42 sample_9.bam
$ my_prog sample_1.bam
$ my_prog sample_2.bam
$ my_prog sample_3.bam
$ my_prog sample_4.bam
$ my_prog sample_5.bam
$ my_prog sample_6.bam
$ my_prog sample_7.bam
$ my_prog sample_8.bam
$ my_prog sample_9.bam
$
```

Multiple files

- Same program, many files
 - 10 files? Ok
 - 1000 files? Not ok

Multiple files

- Same program, many files
 - 10 files? Ok
 - 1000 files? Not ok
- Reproducibility
 - Self and others

Multiple files

- Same program, many files
 - 10 files? Ok
 - 1000 files? Not ok
- Reproducibility
 - Self and others

A solution - write a script!


```
total 0
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo 0 Sep  1 17:18 sample_9.bam
$ nano analysis.sh
```

GNU nano 2.0.9

File: analysis.sh

Modified

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.0.9

File: analysis.sh

Modified

my_prog sample_1.bam

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.0.9

File: analysis.sh

Modified

```
my_prog sample_1.bam  
my_prog sample_2.bam
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.0.9

File: analysis.sh

Modified

```
my_prog sample_1.bam
my_prog sample_2.bam
my_prog sample_3.bam
my_prog sample_4.bam
my_prog sample_5.bam
my_prog sample_6.bam
my_prog sample_7.bam
my_prog sample_8.bam
my_prog sample_9.bam
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

Basic script

```
$ l
total 4,0K
-rw-rw-r-- 1 dahlo dahlo 267 Sep  7 09:34 analysis.sh
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_9.bam
$
```

Basic script

```
$ l
total 4,0K
-rw-rw-r-- 1 dahlo dahlo 267 Sep  7 09:34 analysis.sh
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_9.bam
$ bash analysis.sh
```

```
$ l
total 4,0K
-rw-rw-r-- 1 dahlo dahlo 267 Sep  7 09:34 analysis.sh
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_1.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_2.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_3.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_4.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_5.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_6.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_7.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_8.bam
-rw-rw-r-- 1 dahlo dahlo   0 Sep  1 17:18 sample_9.bam
$ bash analysis.sh
```

Still not OK for 1000 or more files!

GNU nano 2.0.9

File: analysis.sh

Modified

```
my_prog sample_1.bam
my_prog sample_2.bam
my_prog sample_3.bam
my_prog sample_4.bam
my_prog sample_5.bam
my_prog sample_6.bam
my_prog sample_7.bam
my_prog sample_8.bam
my_prog sample_9.bam
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.5.3

File: analysis.sh

```
my_prog -r references/human_genome.fa sample_1.bam
my_prog -r references/human_genome.fa sample_2.bam
my_prog -r references/human_genome.fa sample_3.bam
my_prog -r references/human_genome.fa sample_4.bam
my_prog -r references/human_genome.fa sample_5.bam
my_prog -r references/human_genome.fa sample_6.bam
my_prog -r references/human_genome.fa sample_7.bam
my_prog -r references/human_genome.fa sample_8.bam
my_prog -r references/human_genome.fa sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
my_prog -r references/human_genome.fa sample_1.bam
my_prog -r references/human_genome.fa sample_2.bam
my_prog -r references/human_genome.fa sample_3.bam
my_prog -r references/human_genome.fa sample_4.bam
my_prog -r references/human_genome.fa sample_5.bam
my_prog -r references/human_genome.fa sample_6.bam
my_prog -r references/human_genome.fa sample_7.bam
my_prog -r references/human_genome.fa sample_8.bam
my_prog -r references/human_genome.fa sample_9.bam
```

Same for all

Unique

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

- **Assigning**

```
my_variable=5
```

```
my_variable="nice text"
```

- **Assigning**
`my_variable=5`
`my_variable="nice text"`
- **Using**
`$my_variable`

- **Assigning**

```
my_variable=5
```

```
my_variable="nice text"
```

- **Using**

```
$my_variable
```

```
$ my_variable="Martin"
```

- **Assigning**

```
my_variable=5
```

```
my_variable="nice text"
```

- **Using**

```
$my_variable
```

```
$ my_variable="Martin"
```

```
$ echo "Hello $my_variable."
```

- **Assigning**

```
my_variable=5
```

```
my_variable="nice text"
```

- **Using**

```
$my_variable
```

```
$ my_variable="Martin"
```

```
$ echo "Hello $my_variable."
```

```
Hello Martin.
```


GNU nano 2.5.3

File: analysis.sh

```
my_prog -r references/human_genome.fa sample_1.bam
my_prog -r references/human_genome.fa sample_2.bam
my_prog -r references/human_genome.fa sample_3.bam
my_prog -r references/human_genome.fa sample_4.bam
my_prog -r references/human_genome.fa sample_5.bam
my_prog -r references/human_genome.fa sample_6.bam
my_prog -r references/human_genome.fa sample_7.bam
my_prog -r references/human_genome.fa sample_8.bam
my_prog -r references/human_genome.fa sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/human_genome.fa
```

```
my_prog -r $ref sample_1.bam
my_prog -r $ref sample_2.bam
my_prog -r $ref sample_3.bam
my_prog -r $ref sample_4.bam
my_prog -r $ref sample_5.bam
my_prog -r $ref sample_6.bam
my_prog -r $ref sample_7.bam
my_prog -r $ref sample_8.bam
my_prog -r $ref sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^ Replace

[Read 12 lines]

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
```

```
my_prog -r $ref sample_1.bam  
my_prog -r $ref sample_2.bam  
my_prog -r $ref sample_3.bam  
my_prog -r $ref sample_4.bam  
my_prog -r $ref sample_5.bam  
my_prog -r $ref sample_6.bam  
my_prog -r $ref sample_7.bam  
my_prog -r $ref sample_8.bam  
my_prog -r $ref sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
```

```
my_prog -r $ref sample_1.bam  
my_prog -r $ref sample_2.bam  
my_prog -r $ref sample_3.bam  
my_prog -r $ref sample_4.bam  
my_prog -r $ref sample_5.bam  
my_prog -r $ref sample_6.bam  
my_prog -r $ref sample_7.bam  
my_prog -r $ref sample_8.bam  
my_prog -r $ref sample_9.bam
```

Unique

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

```
for var in 1 2 3;  
do  
    echo $var  
done
```

```
$ bash loop_test.sh  
1  
2  
3  
$
```

```
for var in text works too;  
do  
    echo $var  
done
```

```
$ bash loop_test.sh  
text  
works  
too  
$
```

```
for var in mix them 5;  
do  
    echo $var  
done
```

```
$ bash loop_test.sh  
mix  
them  
5  
$
```

```
for var in *.txt;  
do  
    echo $var  
done
```

```
$ bash loop_test.sh  
all.txt  
examples.txt  
readme.txt
```


GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
```

```
my_prog -r $ref sample_1.bam  
my_prog -r $ref sample_2.bam  
my_prog -r $ref sample_3.bam  
my_prog -r $ref sample_4.bam  
my_prog -r $ref sample_5.bam  
my_prog -r $ref sample_6.bam  
my_prog -r $ref sample_7.bam  
my_prog -r $ref sample_8.bam  
my_prog -r $ref sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
for file in *.bam ;
do
    my_prog -r $ref $file
done
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
for file in *.bam ;
do
    echo my_prog -r $ref $file
done
```

Debugging!

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
for file in *.bam ;
do
    echo my_prog -r $ref $file
done
```

```
$ bash analysis.sh
my_prog -r references/goat_genome_version4.1.fa sample_1.bam
my_prog -r references/goat_genome_version4.1.fa sample_2.bam
my_prog -r references/goat_genome_version4.1.fa sample_3.bam
my_prog -r references/goat_genome_version4.1.fa sample_4.bam
my_prog -r references/goat_genome_version4.1.fa sample_5.bam
my_prog -r references/goat_genome_version4.1.fa sample_6.bam
my_prog -r references/goat_genome_version4.1.fa sample_7.bam
my_prog -r references/goat_genome_version4.1.fa sample_8.bam
my_prog -r references/goat_genome_version4.1.fa sample_9.bam
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Te

GNU nano 2.5.3

File: analysis.sh

```
ref=references/goat_genome_version4.1.fa
for file in *.bam ;
do
    my_prog -r $ref $file
done
```

^G Get Help
^X Exit

^O Write Out
^R Read File

^W Where Is
^_ Replace

^K Cut Text
^U Uncut Text

^J Justify
^T To Spell

^C Cur Pos
^_ Go To Line

^Y Prev Page
^V Next Page

Arguments

```
$ bash analysis.sh
```

Arguments

```
$ bash analysis.sh data/
```

```
$ bash analysis.sh data/
```

\$1


```
$ bash analysis.sh data/ second_argument
```

\$1

\$2

```
$ bash analysis.sh data/ second_argument third
```

\$1

\$2

\$3

Arguments

```
$ bash analysis.sh data/ second_argument third "fourth argument"
```

\$1

\$2

\$3

\$4

GNU nano 2.3.1

File: analysis.sh

Modified

```
ref=references/goat_genome_version4.1.fa  
  
for file in *.bam;  
do  
    my_prog -r $ref $file  
done
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.3.1

File: analysis.sh

Modified

```
ref=references/goat_genome_version4.1.fa  
for file in $1/*.bam;  
do  
    my_prog -r $ref $file  
done
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.3.1

File: analysis.sh

Modified

```
ref=references/goat_genome_version4.1.fa
for file in $1/*.bam;
do
    my_prog -r $ref $file
done
```

```
$ bash analysis.sh /path/to/my/data
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

GNU nano 2.3.1

File: analysis.sh

Modified

```
ref=references/goat_genome_version4.1.fa
for file in /path/to/my/data/*.bam;
do
    my_prog -r $ref $file
done
```

```
$ bash analysis.sh /path/to/my/data
```

^G Get Help
^X Exit

^O WriteOut
^J Justify

^R Read File
^W Where Is

^Y Prev Page
^V Next Page

^K Cut Text
^U UnCut Text

^C Cur Pos
^T To Spell

- Control statement

```
if condition; then  
    action  
fi
```


- Control statement

```
if true; then  
    echo "This is true"  
fi
```

result:
This is true

- Control statement

```
if false; then  
    echo "This is true"  
fi
```

result:

- Control statement

```
if [[ "Hello" == "Hello" ]]; then  
    echo "This is true"  
fi
```

result:
This is true

- Control statement

```
if [[ "Hello" == "Hi" ]]; then  
    echo "This is true"  
fi
```

result:

- Control statement

```
if [[ "Hello" == "Hel"* ]]; then  
    echo "This is true"  
fi
```

result:
This is true

- Control statement

```
if [[ 5 == 9 ]]; then  
    echo "This is true"  
fi
```

result:

- Control statement

```
if [[ 5 -lt 9 ]]; then  
    echo "This is true"  
fi
```

result:
This is true

- Control statement

```
if [[ 5 -gt 9 ]]; then  
    echo "This is true"  
fi
```

result:

- Control statement (math context)

```
if ( ( 5 > 9 ) ) ; then  
    echo "This is true"  
fi
```

result:

- For all dog samples

```
for file in $1/*.bam ;  
do  
    echo my_prog $file  
done
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then

        echo my_prog $file

    fi
done
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then

        echo my_prog $file

    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*  FALSE
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then

        echo my_prog $file

    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*  FALSE
/path/to/my/data/dog_sample_01.bam == *dog*  TRUE
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then

        echo my_prog $file

    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*  FALSE
/path/to/my/data/dog_sample_01.bam == *dog*  TRUE
/dog_and_more/lizard_sample_01.bam == *dog*  TRUE
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then
        echo my_prog $file
    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*    FALSE
/path/to/my/data/dog_sample_01.bam == *dog*    TRUE
/dog_and_more/lizard_sample_01.bam == *dog*    TRUE

$ basename /path/to/my/data/dog_sample_01.bam
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then
        echo my_prog $file
    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*  FALSE
/path/to/my/data/dog_sample_01.bam == *dog*  TRUE
/dog_and_more/lizard_sample_01.bam == *dog*  TRUE

$ basename /path/to/my/data/dog_sample_01.bam
dog_sample_01.bam
```


- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then
        echo my_prog $file
    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*    FALSE
/path/to/my/data/dog_sample_01.bam == *dog*    TRUE
/dog_and_more/lizard_sample_01.bam == *dog*    TRUE

$ basename /path/to/my/data/dog_sample_01.bam
dog_sample_01.bam

$(basename data/dog_sample_01.bam) == dog*    TRUE
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $file == dog* ]];
    then
        echo my_prog $file
    fi
done
```

```
/path/to/my/data/dog_sample_01.bam == dog*    FALSE
/path/to/my/data/dog_sample_01.bam == *dog*    TRUE
/dog_and_more/lizard_sample_01.bam == *dog*    TRUE

$ basename /path/to/my/data/dog_sample_01.bam
dog_sample_01.bam

$(basename data/dog_sample_01.bam) == dog*    TRUE
dog_sample_01.bam == dog*                     TRUE
```

- For all dog samples

```
for file in $1/*.bam;
do
    if [[ $(basename $file) == dog* ]];
    then

        echo my_prog $file

    fi
done
```

- For all dog samples

```
for file in $1/*.bam;
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    my_prog $file

  fi
done
```

Different languages

- Programming is programming
 - Perl, Python, Bash, and more

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 - Perl, Python, **Bash**, and more

```
for file in $1/*.bam;
do
    if [[ $(basename $file) == dog* ]];
    then

        my_prog $file

    fi
done
```

Different languages

- Programming is programming
 - **Perl**, Python, Bash, and more

```
for file in $1/*.bam;
do
    if [[ $(basename $file) == dog* ]];
    then

        my_prog $file

    fi
done
```

```
use strict;
use warnings;
use File::Basename;

foreach my $file (glob("$ARGV[0]/*.bam")) {

    if(basename($file) =~ "^dog.*") {

        system("my_prog", $file)

    }

}
```

Different languages

- Programming is programming
 - Perl, **Python**, Bash, and more

```
for file in $1/*.bam;
do
    if [[ $(basename $file) == dog* ]];
    then

        my_prog $file

    fi
done
```

```
import glob
import sys
import subprocess
import os

for file in glob.glob( sys.argv[1] + "/*.bam" ):

    if os.path.basename(file).startswith("dog"):

        subprocess.call( ["my_prog", file] )
```


Different languages

- Programming is programming
 - Perl, Python, Bash, and more
- Start with one, git gud, (learn another)

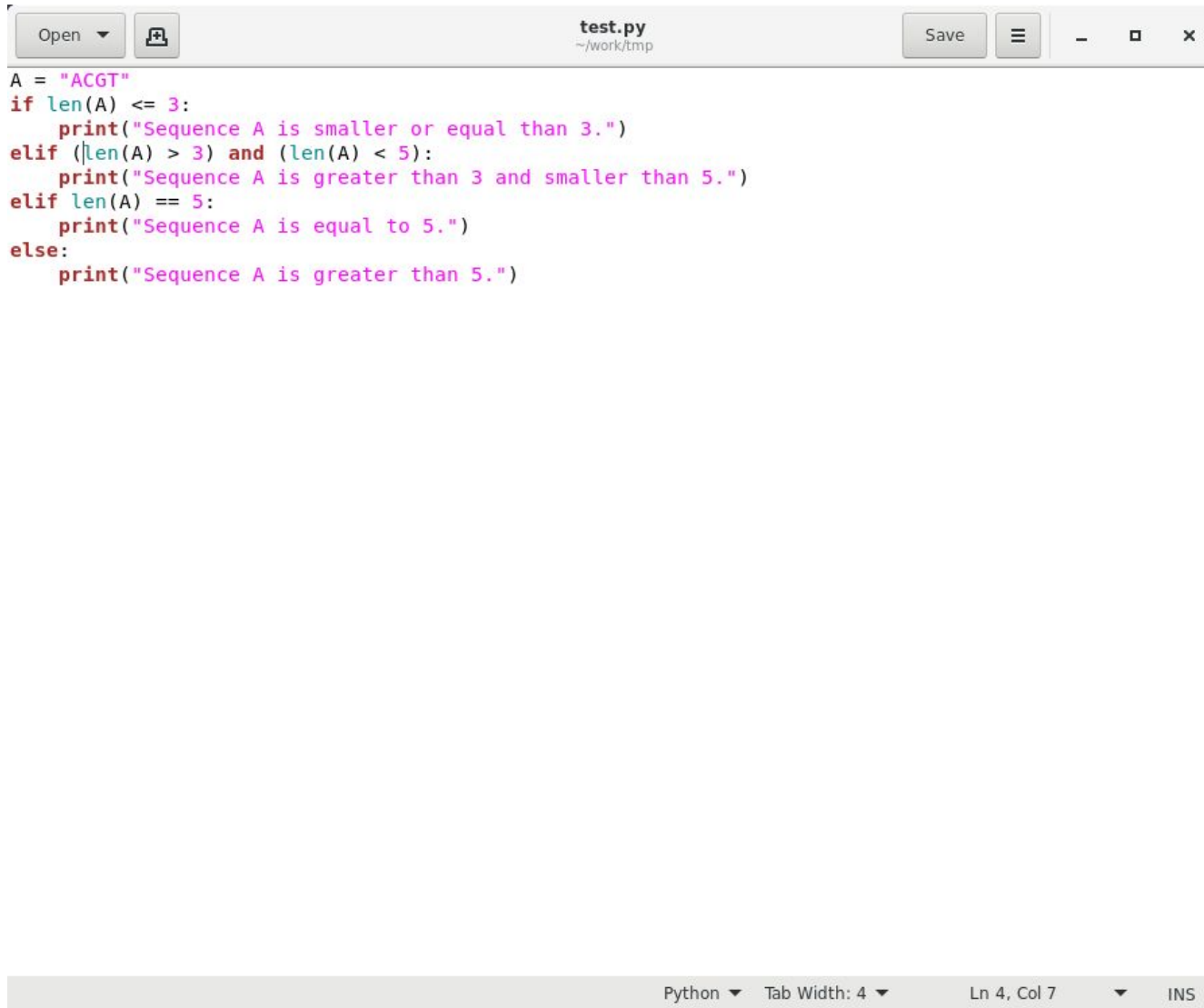
Different languages

- Programming is programming
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- Start with one, git gud, (learn another)

PYTHON

- Graphical text editor more similar to what you might be used to
- Launch through command line:

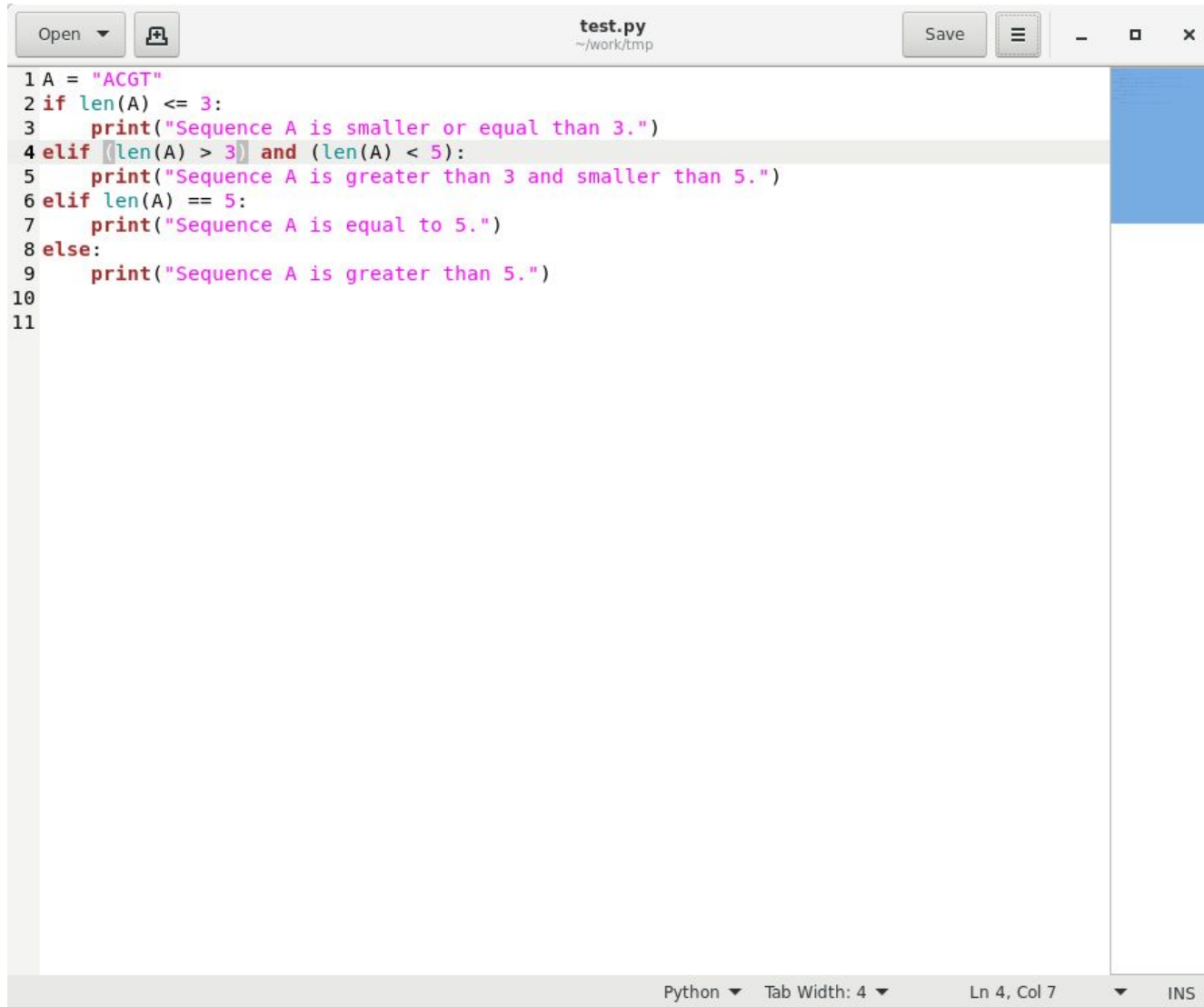
```
$ gedit
```



The image shows a screenshot of the Gedit text editor interface. The title bar at the top indicates the file is named 'test.py' and is located at '~/.work/tmp'. The editor contains a Python script that checks the length of a string 'A' and prints messages based on its length. The script is as follows:

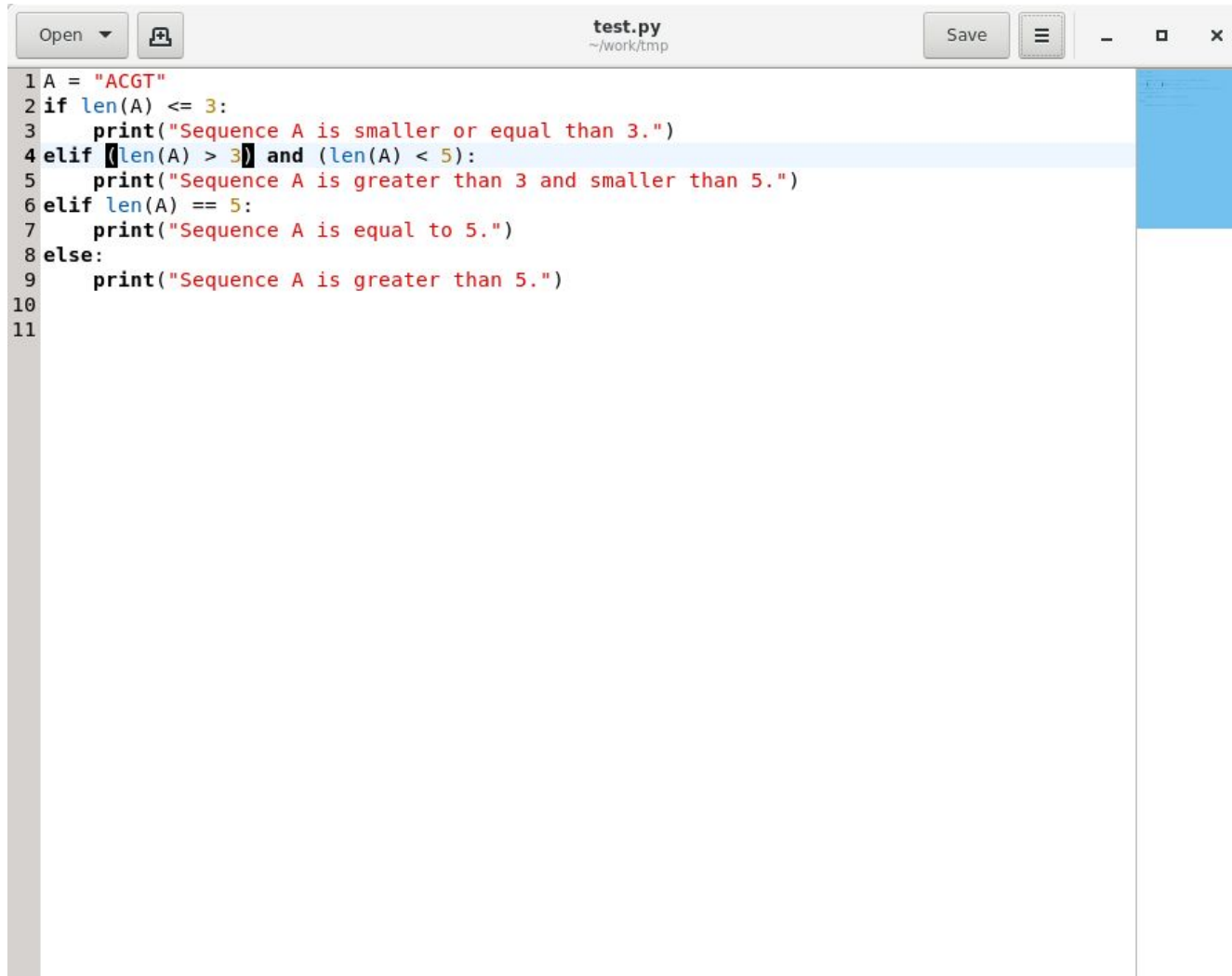
```
A = "ACGT"
if len(A) <= 3:
    print("Sequence A is smaller or equal than 3.")
elif (len(A) > 3) and (len(A) < 5):
    print("Sequence A is greater than 3 and smaller than 5.")
elif len(A) == 5:
    print("Sequence A is equal to 5.")
else:
    print("Sequence A is greater than 5.")
```

The status bar at the bottom of the window shows 'Python' as the selected language, 'Tab Width: 4', the current cursor position 'Ln 4, Col 7', and the input mode 'INS'.



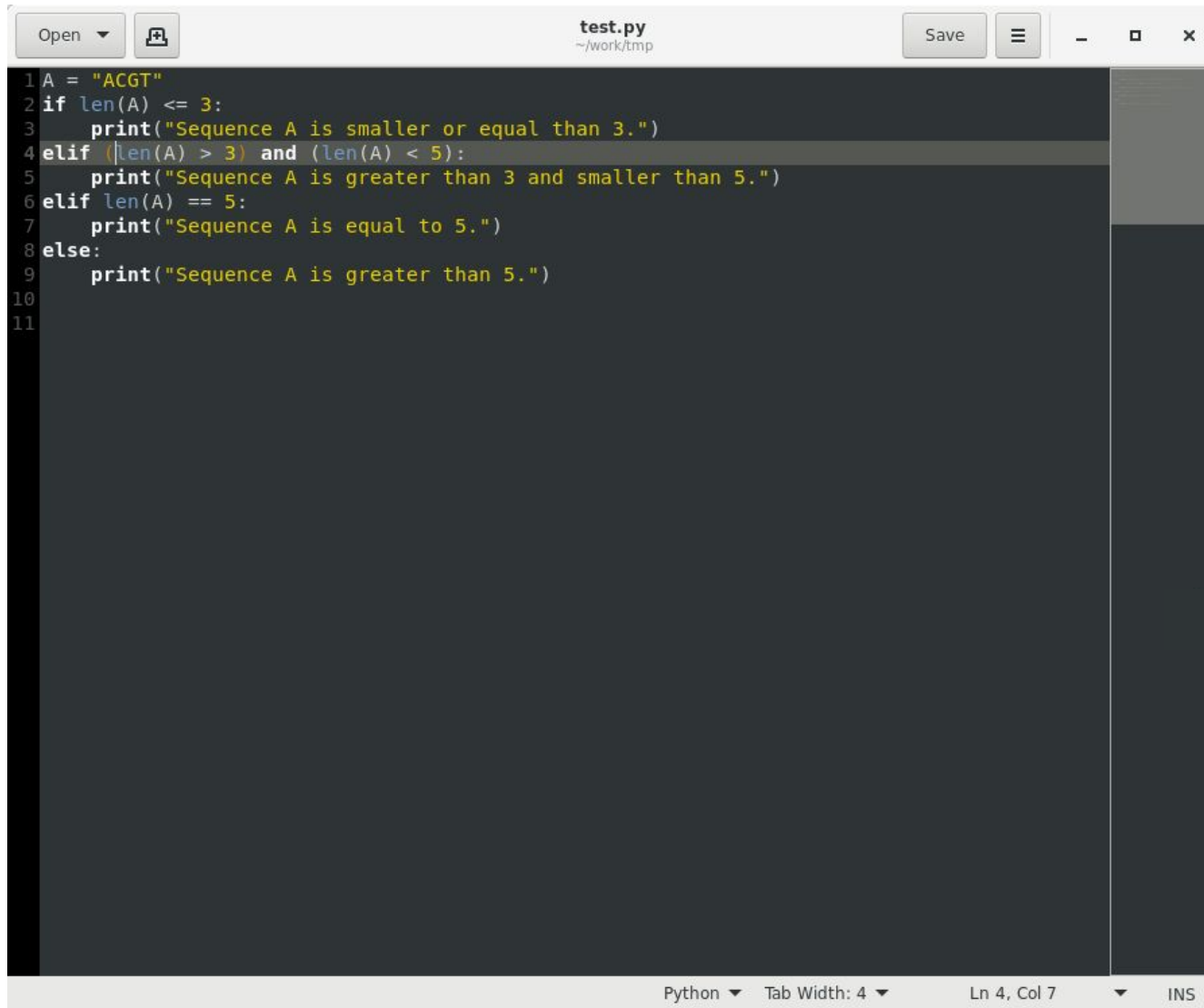
```
1 A = "ACGT"
2 if len(A) <= 3:
3     print("Sequence A is smaller or equal than 3.")
4 elif len(A) > 3 and (len(A) < 5):
5     print("Sequence A is greater than 3 and smaller than 5.")
6 elif len(A) == 5:
7     print("Sequence A is equal to 5.")
8 else:
9     print("Sequence A is greater than 5.")
10
11
```

Python Tab Width: 4 Ln 4, Col 7 INS



```
1 A = "ACGT"
2 if len(A) <= 3:
3     print("Sequence A is smaller or equal than 3.")
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11
```

Theme: Kate



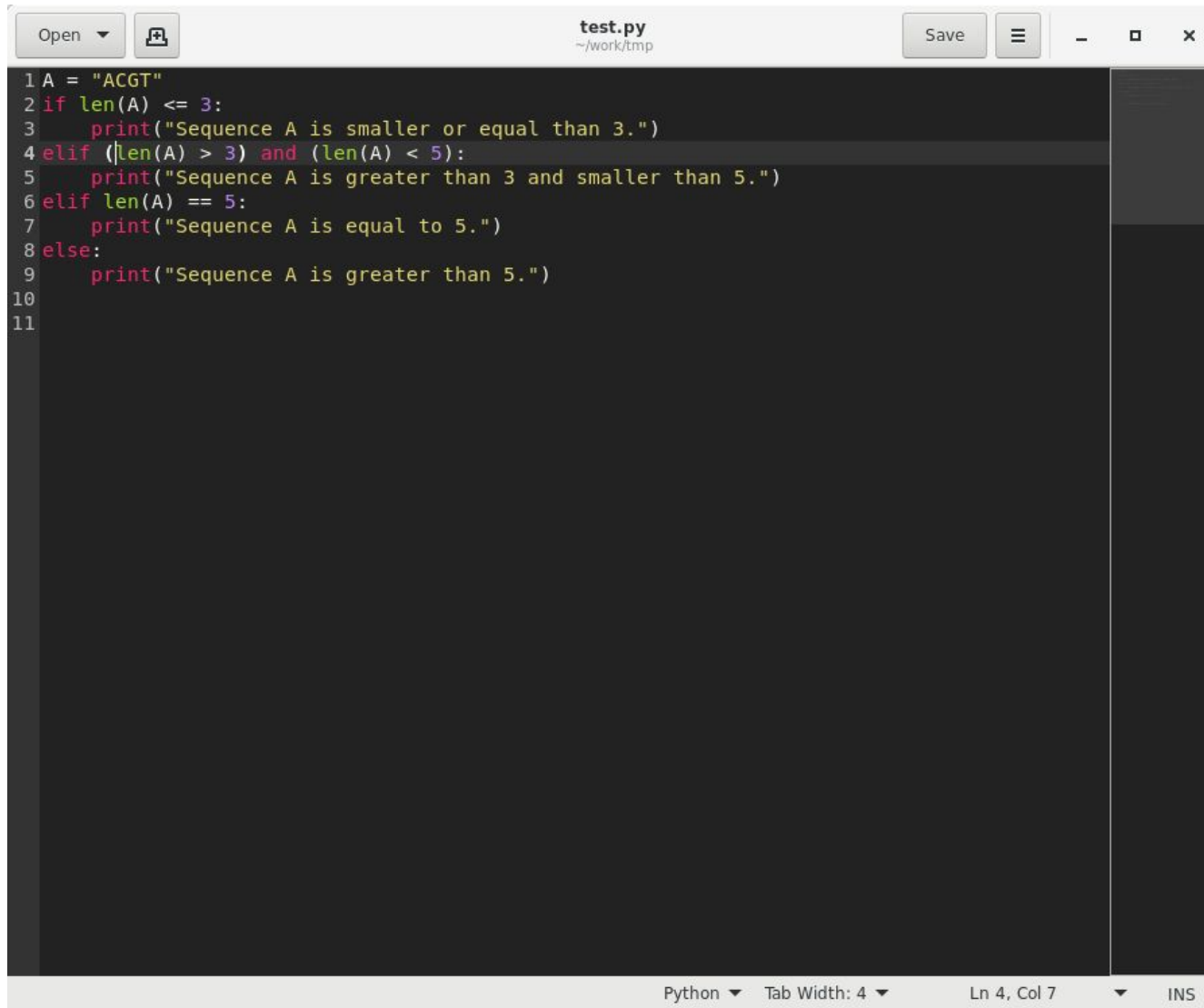
```

1 A = "ACGT"
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```

Python Tab Width: 4 Ln 4, Col 7 INS

Theme: Oblivion



```
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11
```

Python Tab Width: 4 Ln 4, Col 7 INS

Theme: Monokai

- Menu - Preferences - View
 - Display line numbers
 - Display overview map
 - Highlight current line
 - Highlight matching brackets
- Menu - Preferences - Editor
 - Tab width 4
 - Insert spaces instead of tabs
- Menu - Preferences - Fonts & Colors
 - Kate or Oblivion

Laboratory time once again!

https://nbisweden.github.io/workshop-ngsintro/2411/topics/linux/lab_linux_advanced.html