

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
```

^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

```
$ 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
$
```

```
$ 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

```
$ bash analysis.sh
```

```
$ 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

```
$ 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

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^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
```

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


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$ 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

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dog_sample_01.bam == dog*                     TRUE
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Different languages

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

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- 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)

  }

}
```

- 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

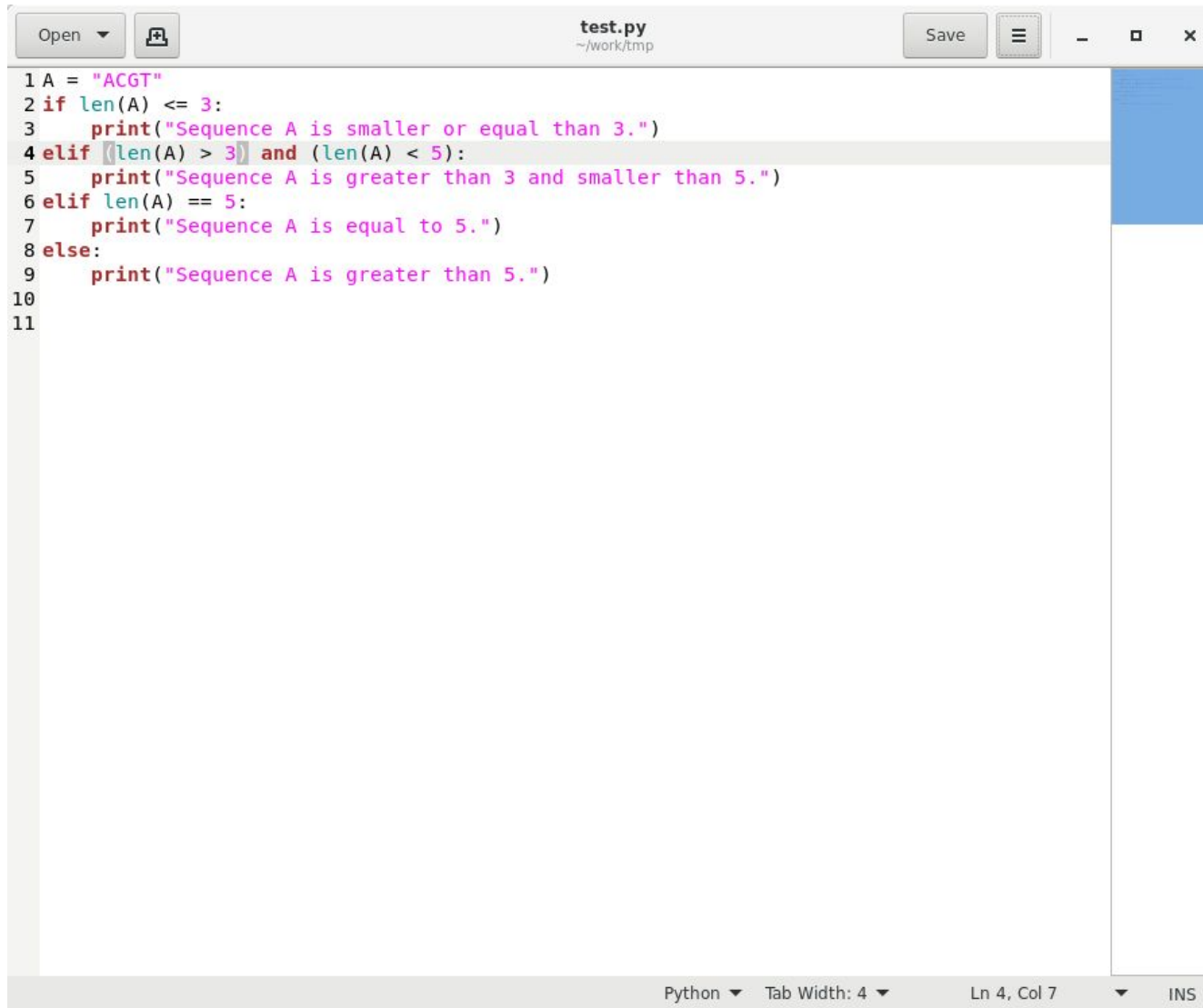
- Programming is programming
 - Perl, Python, Bash, and more
- Start with one, git gud, (learn another)

PYTHON

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

```
$ gedit
```

```
Open [icon] test.py ~/.work/tmp Save [icon] - □ ×  
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.")  
  
Python Tab Width: 4 Ln 4, Col 7 INS
```

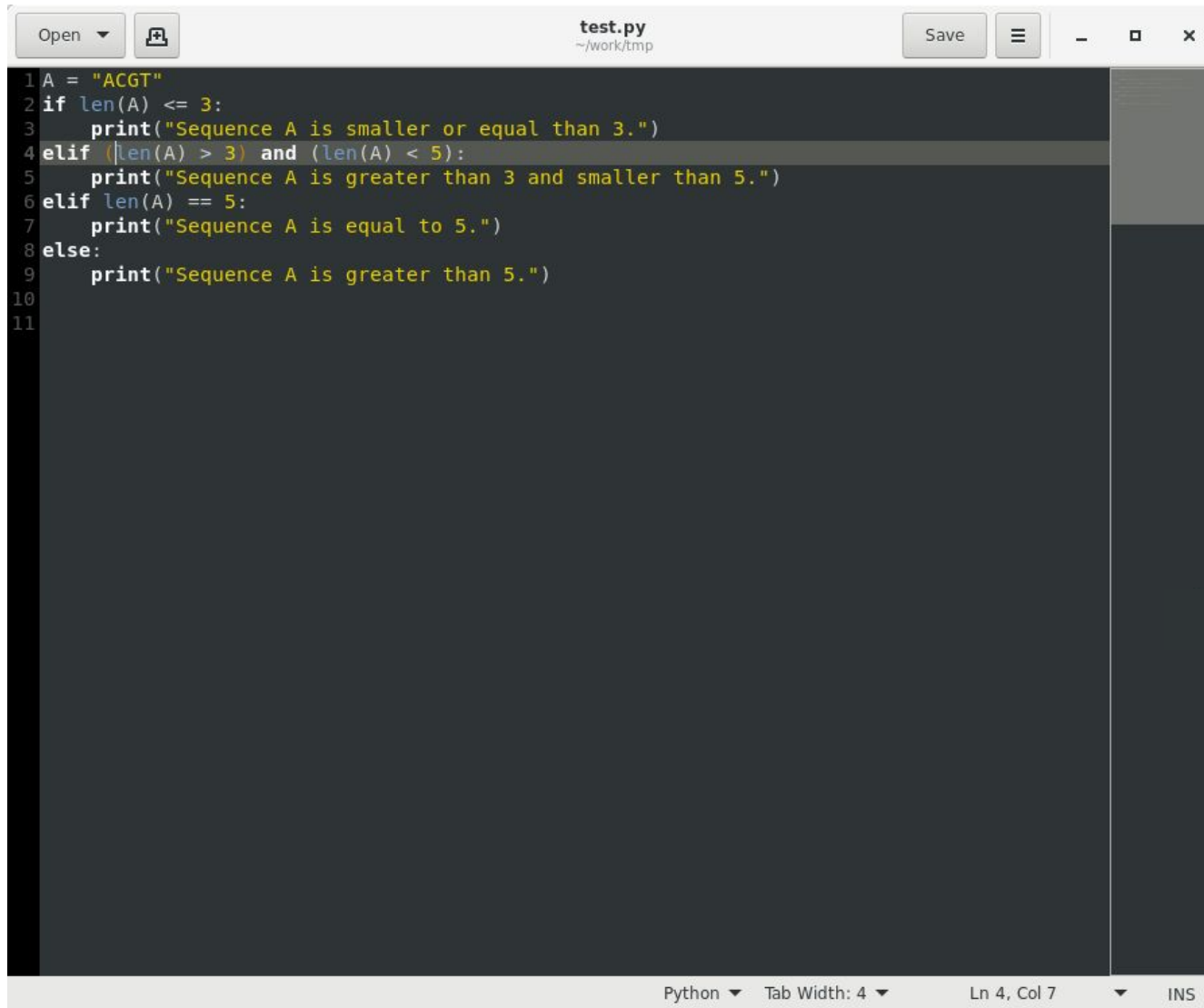


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6 elif len(A) == 5:
7     print("Sequence A is equal to 5.")
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9     print("Sequence A is greater than 5.")
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```

Python ▾ Tab Width: 4 ▾ Ln 4, Col 7 ▾ INS

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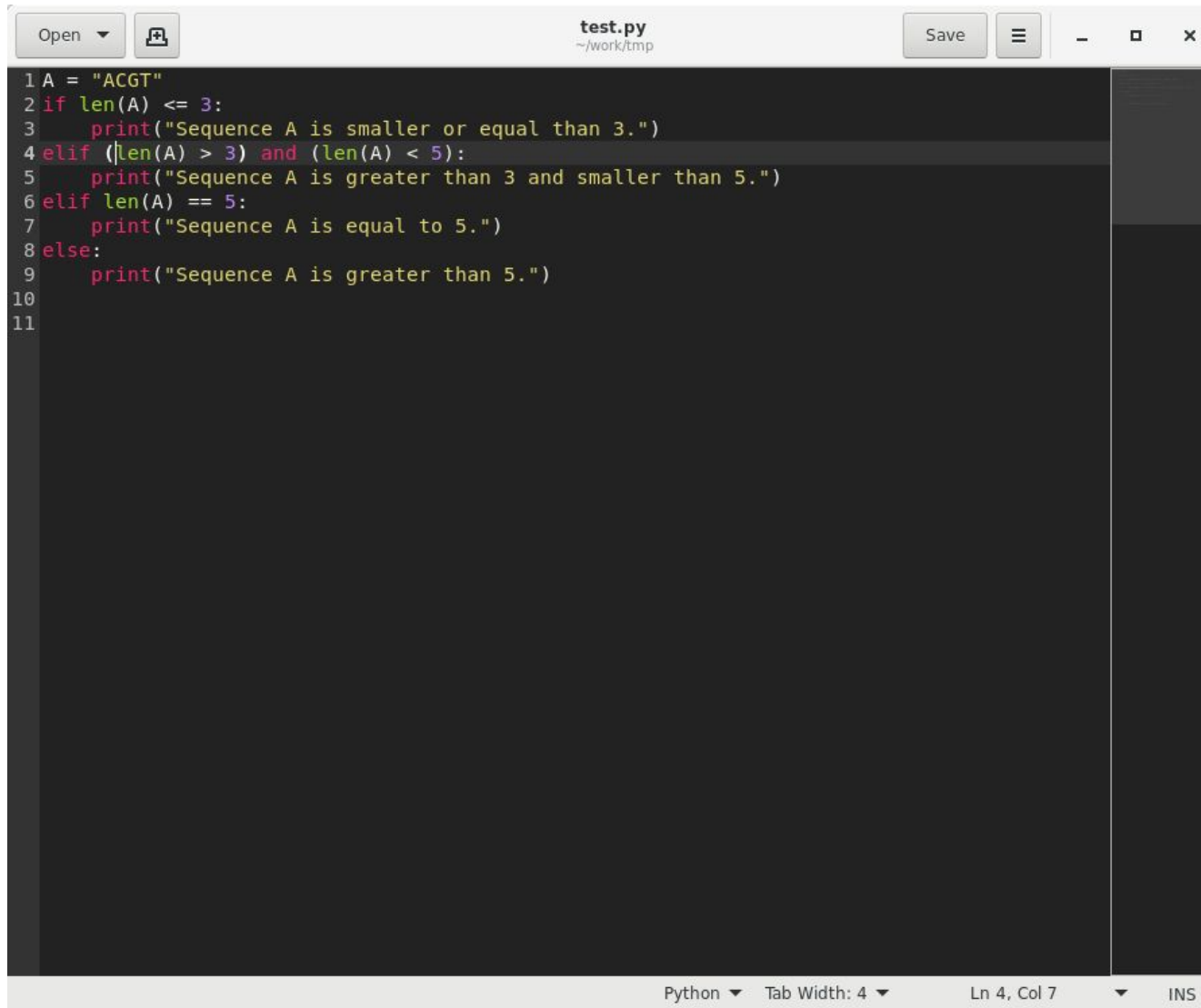
Theme: Kate



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Python ▾ Tab Width: 4 ▾ Ln 4, Col 7 ▾ INS

Theme: Oblivion



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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/2311/topics/linux/lab_linux_advanced.html