SciLifeLab
UPPSALA

Advanced Linux Usage

2017-09-26

Martin Dahlö
martin.dahlo@scilifelab.uu.se

Valentin Georgiev
valentin.georgiev@farmbio.uu.se

Enabler for Life Sciences

SciLifeLab UPPSALA

Shell and Bash

the Shell is a Command Line Interface (CLI)

Bash is one particular shell

tcsh, zsh are also shell programs

SciLifeLab UPPSALA

Multiple files

- 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
```

Multiple files

- 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
```

SciLifeLab UPPSALA

Multiple files

- 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
```

SciLifeLab UPPSALA

Multiple files

- 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
$
```

SciLifeLab UPPSALA

Multiple files

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

SciLifeLab UPPSALA

Multiple files

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

SciLifeLab UPPSALA

Multiple files

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

The answer - write a script!

SciLifeLab UPPSALA

Basic 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
```

SciLifeLab UPPSALA

Basic script

```
 GNU nano 2.0.9                File: analysis.sh                          Modified


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

SciLifeLab UPPSALA

Basic script

```
 GNU nano 2.0.9                File: analysis.sh                      Modified

my_prog sample_1.bam

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

SciLifeLab UPPSALA

Basic script

```
 GNU nano 2.0.9                File: analysis.sh                      Modified

my_prog sample_1.bam
my_prog sample_2.bam




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

SciLifeLab UPPSALA

Basic script

```
 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  ^O WriteOut  ^R Read File  ^Y Prev Page  ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is   ^V Next Page  ^U UnCut Text ^T To Spell
```

SciLifeLab UPPSALA

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
$
```

SciLifeLab UPPSALA

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
```

SciLifeLab UPPSALA

Variables

- Assigning

```
my_variable=5
my_variable=”nice text”
```

SciLifeLab UPPSALA

Variables

- Assigning

```
my_variable=5
my_variable=”nice text”
```

- Using

```
$my_variable
```

SciLifeLab UPPSALA

Variables

- Assigning

```
my_variable=5
my_variable=”nice text”
```

- Using

```
$my_variable
```

```
$ my_variable=”Pia”
```

SciLifeLab UPPSALA

Variables

- Assigning

```
my_variable=5
my_variable=”nice text”
```

- Using

```
$my_variable
```

```
$ my_variable=”Pia”
$ echo “Hello, $my_variable! ”
```

SciLifeLab UPPSALA

Variables

- Assigning

```
my_variable=5
my_variable=”nice text”
```

- Using

```
$my_variable
```

```
$ my_variable=”Pia”
$ echo “Hello, $my_variable! ”
Hello, Pia!
```

SciLifeLab UPPSALA

Variables

```
 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  ^O WriteOut  ^R Read File  ^Y Prev Page  ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is   ^V Next Page  ^U UnCut Text ^T To Spell
```

SciLifeLab UPPSALA

Variables

```
 GNU nano 2.0.9                File: analysis.sh                          Modified

prefix="sample"

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  ^O WriteOut  ^R Read File  ^Y Prev Page  ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is   ^V Next Page  ^U UnCut Text ^T To Spell
```

SciLifeLab UPPSALA

Variables

```
 GNU nano 2.0.9                File: analysis.sh                          Modified

prefix="sample"

my_prog ${prefix}_1.bam
my_prog ${prefix}_2.bam
my_prog ${prefix}_3.bam
my_prog ${prefix}_4.bam
my_prog ${prefix}_5.bam
my_prog ${prefix}_6.bam
my_prog ${prefix}_7.bam
my_prog ${prefix}_8.bam
my_prog ${prefix}_9.bam

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

SciLifeLab UPPSALA

Variables

```
 GNU nano 2.0.9                File: analysis.sh                          Modified

prefix="dog"

my_prog ${prefix}_1.bam
my_prog ${prefix}_2.bam
my_prog ${prefix}_3.bam
my_prog ${prefix}_4.bam
my_prog ${prefix}_5.bam
my_prog ${prefix}_6.bam
my_prog ${prefix}_7.bam
my_prog ${prefix}_8.bam
my_prog ${prefix}_9.bam

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

SciLifeLab UPPSALA

Loops

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

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

SciLifeLab UPPSALA

Loops

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

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

Loops

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

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

SciLifeLab UPPSALA

Loops

```
 GNU nano 2.0.9                File: analysis.sh

prefix="sample"

for i in 1 2 3 4 5 6 7 8 9;
do
    my_prog ${prefix}_$i.bam
done
```

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

SciLifeLab UPPSALA

Loops

```
 GNU nano 2.0.9                File: analysis.sh

prefix="sample"

for i in 1 2 3 4 5 6 7 8 9;
do
    echo my_prog ${prefix}_$i.bam
done


                        [ Wrote 7 lines ]
^G Get Help  ^O WriteOut  ^R Read File ^Y Prev Page ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is  ^V Next Page ^U UnCut Text ^T To Spell
```

SciLifeLab
UPPSALA

Loops

```
 GNU nano 2.0.9                File: a

prefix="sample"

for i in 1 2 3 4 5 6 7 8 9;
do
    echo my_prog ${prefix}_$i.bam
done
```

```
$ bash analysis.sh
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    ^O WriteOut    ^R Read Fi
^X Exit        ^J Justify     ^W Where I
```

Loop over files

```
$ ls *.bam
sample_1.bam  sample_3.bam  sample_5.bam  sample_7.bam  sample_9.bam
sample_2.bam  sample_4.bam  sample_6.bam  sample_8.bam
$
```

Loop over files

```
 GNU nano 2.0.9                File: analysis.sh

prefix="sample"

for file in $( ls *.bam );
do
    echo my_prog $file
done


                              [ Wrote 7 lines ]
^G Get Help    ^O WriteOut    ^R Read File   ^Y Prev Page   ^K Cut Text    ^C Cur Pos
^X Exit        ^J Justify     ^W Where Is    ^V Next Page   ^U UnCut Text  ^T To Spell
```

Loop over files

```
 GNU nano 2.0.9                File: analysis.sh


for file in $( ls *.bam );
do
    echo my_prog $file
done


                          [ Wrote 7 lines ]
^G Get Help  ^O WriteOut  ^R Read File ^Y Prev Page ^K Cut Text  ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is  ^V Next Page ^U UnCut Text ^T To Spell
```

Loop over files

```
 GNU nano 2.0.9                    File:
```

```
for file in $( ls *.bam );
do
    echo my_prog $file
done
```

```
$ bash analysis.sh
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    ^O WriteOut    ^R Read
^X Exit        ^J Justify     ^W Where
```

Loop over files

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

Loop over files

```
 GNU nano 2.0.9                File: analysis.sh                          Modified

for file in $( ls $1/*.bam );
do
    echo my_prog $file
done

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

SciLifeLab
UPPSALA

Loop over files

```
 GNU nano 2.0.9                    File:

for file in $( ls $1/*.bam );
do
    echo my_prog $file
done


^G Get Help    ^O WriteOut    ^R Read F
^X Exit        ^J Justify     ^W Where
```

```
$ bash analysis.sh .
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
$
```

SciLifeLab
UPPSALA

Loop over files

```
 GNU nano 2.0.9                    File:

for file in $( ls $1/*.bam );
do
    echo my_prog $file
done


^G Get Help    ^O WriteOut    ^R Read F
^X Exit        ^J Justify     ^W Where
```

```
$ bash analysis.sh /path/to/my/bams
my_prog /path/to/my/bams/sample_1.bam
my_prog /path/to/my/bams/sample_2.bam
my_prog /path/to/my/bams/sample_3.bam
my_prog /path/to/my/bams/sample_4.bam
my_prog /path/to/my/bams/sample_5.bam
my_prog /path/to/my/bams/sample_6.bam
my_prog /path/to/my/bams/sample_7.bam
my_prog /path/to/my/bams/sample_8.bam
my_prog /path/to/my/bams/sample_9.bam
$
```

Loop over files

```
 GNU nano 2.0.9                File: analysis.sh                          Modified

for file in $( ls $1/*.bam );
do
    my_prog $file
done

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

SciLifeLab UPPSALA

Loop over files

```
$ 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
```

```
for file in $( ls $1/*.bam );
do
    my_prog $file
done
```

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

```
if [[ 5 > 9 ]]; then
  echo ”This is true”
fi
```

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

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

SciLifeLab UPPSALA

If

- Control statement

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

- For all samples except dog

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

- For all samples except dog

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

        echo my_prog $file

    fi
done
```

- For all samples except dog

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

        echo my_prog $file

    fi
done
```

Ex: `$file` is `/path/to/dog_1.bam`

- For all samples except dog

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

        echo my_prog $file

    fi
done
```

Ex: `$file` is `/path/to/dog_1.bam`

`basename $file`

- For all samples except dog

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

        echo my_prog $file

    fi
done
```

Ex: `$file` is `/path/to/dog_1.bam`

`basename $file`

`dog_1.bam`

- For all samples except dog

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

        echo my_prog $file

    fi
done
```

Ex: `$file` is `/path/to/dog_1.bam`

`basename $file`

`dog_1.bam`

- For all samples except dog

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

        my_prog $file

    fi
done
```

Ex: `$file` is `/path/to/dog_1.bam`

`basename $file`

`dog_1.bam`

SciLifeLab UPPSALA

Different languages

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

SciLifeLab UPPSALA

Different languages

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

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

        my_prog $file

    fi
done
```

SciLifeLab UPPSALA

Different languages

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

```
for file in $( ls $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);
    }
}
```

SciLifeLab UPPSALA

Different languages

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

```
for file in $( ls $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 not os.path.basename(file).startswith("dog"):

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

SciLifeLab UPPSALA

Different languages

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

SciLifeLab UPPSALA

Different languages

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

PYTHON

SciLifeLab
UPPSALA

Laboratory time! (yet again)