Programming Linux environment

Variables

Basic Input/output

Permissions

Download data files

Environment variables

- How does the terminal know **where to look** for executables? (e.g. how does it know `ls` is in `/usr/bin`?)
- A **variable** is a word that represents/contains a value or string. Environment variables describe your system
- `MY_SYSTEM=Ubuntu-Linux`

Set of variables: environment

- Try this command

```
env
```

- What do you see?
- Look for PATH variable

```
PATH=/usr/bin:/usr/local/bin:/usr/sbin
```

- Try the command:

```
echo $PATH
```

PATH environment variable

- `echo $PATH`
- `/home/toni/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games`
- Path contains a list of directories separated by the symbol “:”

Installing an application in a local folder

- You **copy** the executable to one of the folders in PATH

```
$ sudo cp /home/toni/Downloads/app /usr/local/bin
$ sudo chmod +x /usr/local/bin/app
```

- You **create a sym(bolic) link** to an executable in the one of the folders in PATH
- You **add a directory to the PATH variable**

```
Export PATH=/home/masterbio/myapp/app:$PATH
```

Example: installing Blast

Steps to have a local Blast in your home

- **Download blast and md5 files**
- **Check file integrity**
- **Unpack file**
- **Copy blast to installation folder (/home/toni/myblast)**
- **Check permissions and execution of myblast**
- **Create a symlink in home folder**
- **Add new blast tool to $PATH variable**

Blast download links:

ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.5.0+-src.tar.gz

ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.5.0+-src.tar.gz.md5

Installing apps in the system

- What if a new version comes up?
- How to make application available for other users?
- What if I need shared system libraries for my application?

```
sudo apt-get update
sudo apt-get install blast
```

Variables and scripts

- You can write a list of commands one after the other in a **text file**, and let bash execute it.
- Let's try!
  - Create a file in your home called "**space_left**" with text editor
  - Enter two following bash commands in this file:

```
df -h .
du -sh */
```

  - Then write at the console: **`bash ./space_left`**

Bash script

- Simple text files become Bash scripts when adding a **shebang** line as first line
- Shebang states which program should read and execute the text file

```
#!/bin/bash
#!/usr/bin/perl
#!/usr/bin/python
```

WORK!

- Write a script with two variables and two messages
- Use the command echo to print message, name and the variable USER

```
message="hello"
name="toni"
echo "$message, $USER !"
echo "my name is $name"
```

WORK!

- Modify your script to:
  - save the date of today in a variable
  - print a hello message with the date
  - use **read** command to get the name of the user

```
read –p “please tell me your name: ” user_name
```

  - print a hello message with the user name you just read

File permissions

- `chown user:group filename`
- `chmod [ugo][+-][rwx] filename`
- `chmod [0-7][0-7][0-7] filename`
  - 1 stands for execute
  - 2 stands for write
  - 4 stands for read
  - any number from 0 to 7 is a unique combination of 1, 2 and 4.

File permissions

- Can you run your script?
- What’s missing?

Script arguments

- We can pass on **arguments** to our scripts: they are subsequently stored in variables called $1, $2, $3,...
- **Edit a new file called 'arguments.sh'** with following contents (be aware of the “)

```
#!/bin/bash
firstArg=$1
secondArg=$2
echo “You have entered \”$firstArg\” and
\”$secondArg\””
```

Script arguments

- Make your script executable

```
chmod +x arguments.sh
```

- Run your script

```
./arguments.sh first second
```

WORK!

- Modify your hello script to:
  - get the user name from an argument
  - print the argument received from the user
  - make your script executable

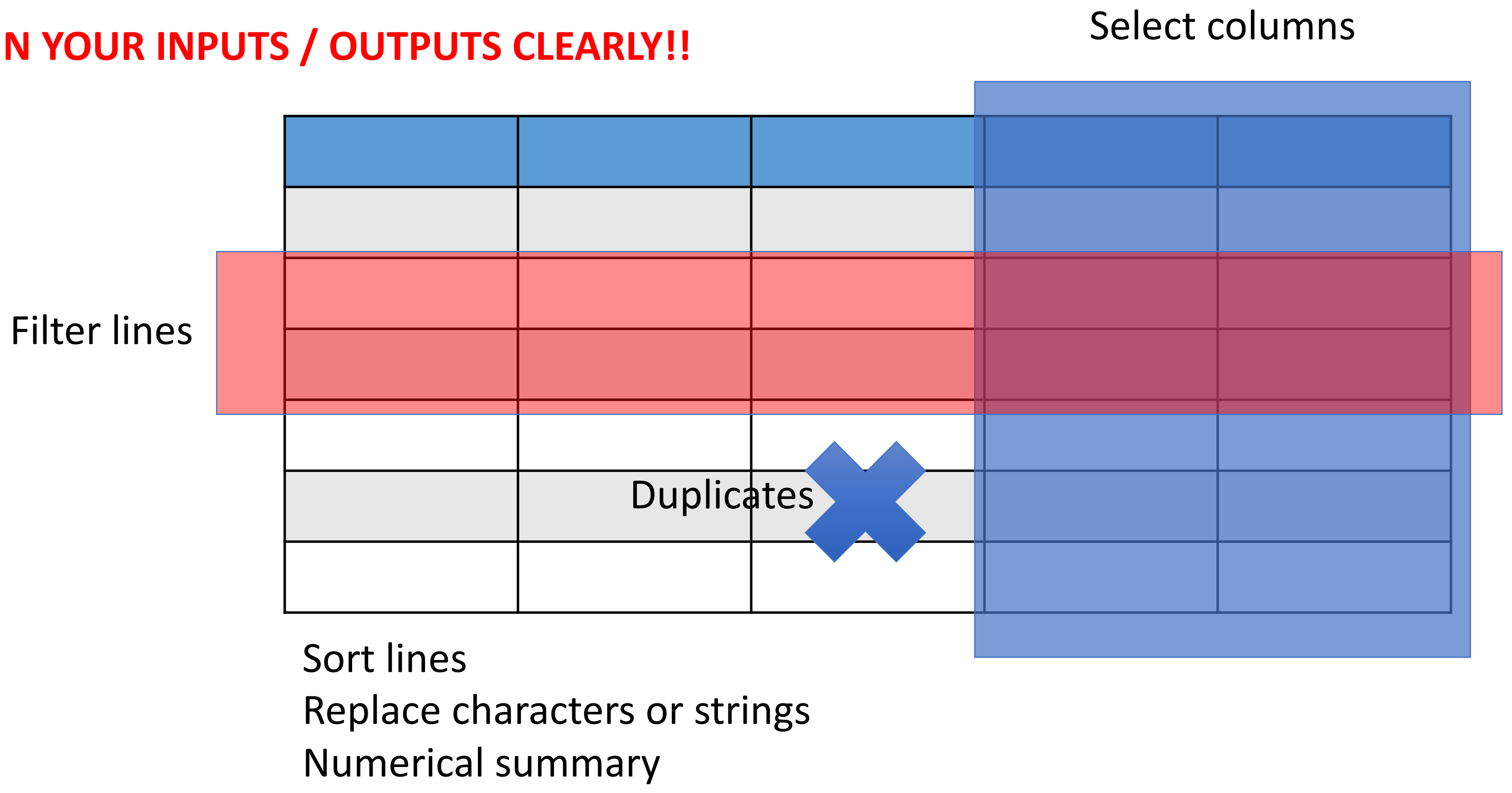
Linux text tools and scripting

General text manipulation

- Matrix of text
    - Each element is a line
    - Each feature is a column
- Typical operations
    - Count, filter, select, summarize, search, …

Script=Designing filters

DESIGN YOUR INPUTS / OUTPUTS CLEARLY!!



Choose your weapon

- UNIX has an extensive toolkit for **text** analysis:
  - **Extraction**: head, tail, grep, awk
  - **Reporting**: wc
  - **Manipulation**: sort, tr, sed
- Complex text parsing needs more specific programming: **Python, Go, Ruby, …**

Output redirection

- Output from script must be saved in a new file
- Example: sort list of search results by score
- The output of a program can be saved to a file

```
ls -lR /home/toni > /tmp/ls-dump.txt
less /tmp/ls-dump.txt
```

Not overwriting output

- If you write to a file with “**>**”, contents are replaced
- You can append to a file using >>

```
echo “hello” >> /tmp/hello-test.txt
echo “world” >> /tmp/hello-test.txt
cat /tmp/hello-test.txt
wc /tmp/hello-test.txt
```

- `What is` **`wc`** `doing?`

Doing many things at the same time

- Dump the output of an **`ls`** command to a file
- Open the generated text and read it
- Remove the file

```
ls –lR /home/toni/dataset1 > /tmp/ls-dump.txt
cat /tmp/ls-dump.txt
rm /tmp/ls-dump.txt
```

Too much typing!!

La parte de imagen con el identificador de relación rId2 no se encontró en el archivo.

Building pipelines of commands

- A pipeline reads a file and then processes it using the output of a tool as the input to the next
- Dump the output of an `ls` command to a file
- Open the generated text and read it
- Remove the file

```
ls -lR | less
```

BEWARE!->Output of **`ls -lR`** is the input of **`less`**

WORK

- Write a pipeline that counts the lines of the result of an ls –lR command

Linux text processing tools

Read a text file to modify its contents

- sort
- uniq
- cut
- grep

Sorting text

sort

-n: sort numerically

-f: case insensitive

-r: reverse sort order

-ts: use s as field separator (instead of space)

-kn: sort on the n-th field (1 being the first field)

- `cat months.txt`
- `sort months.txt`

WORK!

- Sort months by the second column.
- Is it working? How can you sort numerically?
- Sort months by the second column largest values first

Columns work with cut

Try these commands and understand their output

- `cut –f1 months.txt`
- `cut -d ' ' -f1 months.txt`
- `cut -d ' ' -f1,2 months.txt`
- `cut -d ' ' -f1-3 months.txt`

WORK!

- Create a file called seasons.txt where you write the result of extracting the third column
- Sort this new seasons.txt file
- now use sort –u option to sort the file. What difference you see in the output?
- Now extract 3rd column and sort the file using a pipeline

WORK!

- Check the result of adding these commands to the previous cut pipelines
- sort -u
- sort | uniq
- sort | uniq -c

Grep: search and you shall find

- **grep** extracts lines that match a string

```
grep [options] regular-expression [file]
```

- The input file is read line by line
- If the line matches the criteria defined by regular expression the line is written to the standard output
- Example: `grep winter months.txt`

Linux tools: grep

Try these grep operations:

- `grep “december” months.txt`
- `grep “12 winter” months.*`
- `grep “7 winter” months.*`
- `grep –n “12 winter” months.*`

Filtering and processing input with bash scripts

Welcome to scripting

- Make sure you understand the process before you start: where are the input files, the results?
- Which operations you need to do: design
- Which tools are you going to use: find the right options
- Work with each tool individually and then join inputs and outputs: prototype and test!
- Write and document your script for the next user after you
- There is more than one way to do it!

Grep example

- A GFF file contains genome annotation info
- http://www.sequenceontology.org/gff3.shtml
- Objective: get all lines form locus Os01g01070 from all.gff3

Example GFF

seqId	source	type	Start	End				Attributes (ID of feature)
Chr1	MSU_osa1rt	gene	2903	10817	.	+	.	ID=LOC_OS01g01010
Chr1	MSU_osa1rt	exon	2903	3268	.	+	.	ID=LOC_OS01g01010

```
grep LOC_Os01g01070 all.gff3
```

Grep options

−i: ignore case

−v: inverse, shows lines that do not match

−l: list, show the name of the files that contain a match

−n: shows line number of the match

Grep example

- Use article-large.csv to answer the question:
- How many of those articles are about Linux?

```
grep –i ”Linux” articles-large.csv
```

Regular expressions

- Formal way of describing sets of strings

  . = any character

  ^= beginning of the line

  $= end of the line

  += any string

  []= set of characters

  [1-9]= any number between 1 and 9

  Example, chromosome 1 to chromosome5 data:

```
grep chr[1-5] all.gff3
```

Regular expressions

Example, find chromosome 1 to chromosome5 data:

```
grep chr[1-5] all.gff3
```

- `chr1: OK`
- `chr2: OK`
- `chr9: NO MATCH`
- `chr20: NO MATCH`

Filter mRNA structures from chr1 and only on the + strand

- From TAIR9_mRNA.bed

```
egrep ’^chr1’ mRNA.bed

All lines that…
^    : Start at the beginning of the line
chr1: then have “chr1” string
```

Filter mRNA structures from chr1 and only on the + strand

- From TAIR9_mRNA.bed

```
egrep '^chr1' mRNA.bed
egrep '^chr1.+' mRNA.bed
```

```
.  :matches any character
.+: matches any positive number of characters
->Any features in chr1
```

Filter mRNA structures from chr1 and only on the + strand

```
egrep ‘^chr1.+\+’ mRNA.bed
```

`\+ : Match only those lines that contain a “+” symbol`

`->only structures on the + strand`

Filter mRNA structures from chr1 and only on the + strand

```
egrep '^chr1.+\+' mRNA.bed >/tmp/chr1-test.txt
```

```
Output file in chr1-test.txt
```

Linux tool: word count

- wc [options] file

```
-c: show number of characters
-w: show number of words
-l: show number of lines
```

```
wc –l months.txt
```

How many mRNA entries on chr1?

- First, filter chr1 lines from input

```
grep chr1 mRNA.bed
```

- Then, count the number of lines

```
grep chr1 mRNA.bed | wc -l
```

WORK

- How many articles about Linux in articles-large.csv?

GFF WORK example

seqId	source	type	Start	End				Attributes (ID of feature)
Chr1	MSU_osa1rt	gene	2903	10817	.	+	.	ID=LOC_OS01g01010
Chr1	MSU_osa1rt	exon	2903	3268	.	+	.	ID=LOC_OS01g01010

```
grep LOC_Os01g01070 all.gff3
```

WORK!

1. How would you change the last grep so that you match all lines except those at chromosome 1?
2. How many genes are in the gff file format? Use a pipeline to solve this question
3. How many different genes?
4. Sort gff file by chromosome and by source
5. Sort mRNA by chromosome number and then by starting position

WORK!

1. How would you change the last grep so that you match all lines except those at chromosome 1?

```
grep –v chr1 mRNA.bed | wc -l
```

WORK!

2. How many genes are in the gff file format?
   Use a pipeline to solve this question

```
cat file.gff | wc –l

cut –f3 –d ‘ ‘ file.gff | wc -l
```

WORK!

3. How many different genes?

```
cut –f9 file.gff|sort|uniq|wc -l
```

WORK!

4. Sort gff file by chromosome and by source

```
sort –k1 –k2 file.gff
```

Sort gff file by chromosome number and then by starting position

```
cut –f1 –f4 file.gff|sort –k1 –k2 >/tmp/chr_test.txt
```

Awk: filter and modify

- Use awk to extract specific fields from a file
- Then, do manipulations or calculations on the extracted fields

```
awk –F delimiter '{ print $X }'
```

delimiter is the field separator (default is space)

$X is the field number

$0: complete line

$1, $2, $3, : first, second, third field

$NF: last field

http://www.grymoire.com/Unix/Awk.html

Get gene positions from gff example

- Get first 10 gene positions from example
  - Get starting position from example:
    ```
    awk '{print $4}' file.gff
    ```
  - Get only first line
    ```
    awk '{print $4}' file.gff | head -1
    ```
  - Get first 15 lines for genes in chr1
    ```
    awk '{if($1="chr1") print $4;}' file.gff | head –15
    ```

GFF WORK example

seqId	source	type	Start	End				Attributes (ID of feature)
Chr1	MSU_osa1rt	gene	2903	10817	.	+	.	ID=LOC_OS01g01010
Chr1	MSU_osa1rt	exon	2903	3268	.	+	.	ID=LOC_OS01g01010

Use awk to convert formats

- Convert GFF format to a personalized: chr, gene id, positions

Input:

```
Chr1 source type pos1 pos2 aux strand aux gene_id
Chr1 MSU_osa1rt gene 2903 10817 . + . ID=LOC_OS01g01010
```

Output:

```
Chromosome geneid pos1 pos2
Chr1 ID=LOC_OS01g01010 2903 10817
```

Use awk to convert formats

- Convert GFF format to personalized output

Input:

```
Chr1 MSU_osa1rt gene 2903 10817 . + . ID=LOC_OS01g01010
```

Output:

```
Chr1 ID=LOC_OS01g01010 2903 10817
```

```
awk '{print $1"\t"$9"\t"$4"\t"$5}' file.gff
```

Use awk to convert formats

```
awk ’BEGIN {print ”chromosome\tgeneid\tpos1\tpos2” }
     {print $1”\t”$9”\t”$4”\t”$5}
     {END print ”End of report----”} ’
file.gff
```

WORK!

- How many unique authors are on that list?
- How many articles did each author write?

Sed: changing text on the fly

- Sed (stream editor) can be used to make changes in lines of text
- http://www.grymoire.com/Unix/Sed.html
- Substitution tool is very used

```
sed –e ‘s/r1/s1/’ file
```

  - s: substitute command
  - /: separator
  - r1: regular expression to be replaced
  - s1: text that will replace regular expression match

Example

- Write a file with text editor with the lines

```
Hello,hello,hello
Hello,hello,hello
```

- Now let’s apply sed to translate commas into semi-colons

```
sed –e ‘s/,/;/’ hello.txt >hello-sed.txt
```

- Now try this:

```
    sed –e ‘s/,/;/g’ hello.txt >hello-sed.txt
```

More cut options

- Use cut to extract fields from text files
  - By extracting fixed text sizes

    ```
    cut –c <fields> file
    ```

  - <fields> can be
    - N: n-th element
    - N-M: from N to M
    - N- : from N element on
    - -M: until the M element

Example: cutting text columns

- Create a acgt.txt file with the text

```
ACGTACGTacgtACGTACGT
```

- To extract a range of characters:

```
cut –c 9-12 acgt.txt
cut –c 9- acgt.txt
cut –c -12 acgt.txt
```

uniq to find the needle in the haystack

Use uniq to:

- Eliminate duplicate lines
- Display unique lines
- Show and count duplicate lines
- INPUT MUST BE SORTED!

Duplicate example

- `ls –l /tmp`
- `ls –l /tmp | awk ‘{print $3}’ | sort | uniq`

Display unique or duplicate lines

- Get lines that appear only once: -u
- Get lines that appear more than once: -d
- Get the count of the lines: -c
- Example

```
ls –l /tmp | awk ‘{print $3}’ | sort | uniq -d
```

WORK!

- Create a new list of january 20 articles
- Extract the authors of those articles with the number of words each author wrote

Taking decisions with *if*

```
if [expresion1];
then
   expresion2
fi
```

```
V1="foo"
V2="foo2"
if [ "$V1" = "$V2" ]; then
    echo ”TRUE!"
else
    echo "FALSE!"
fi
```

if conditions

Operator	**Description**
! EXPRESSION	The EXPRESSION is false.
-n STRING	The length of STRING is greater than zero.
-z STRING	The lengh of STRING is zero (ie it is empty).
STRING1 = STRING2	STRING1 is equal to STRING2
STRING1 != STRING2	STRING1 is not equal to STRING2
INTEGER1 -eq INTEGER2	INTEGER1 is numerically equal to INTEGER2
INTEGER1 -gt INTEGER2	INTEGER1 is numerically greater than INTEGER2
INTEGER1 -lt INTEGER2	INTEGER1 is numerically less than INTEGER2
-d FILE	FILE exists and is a directory.
-e FILE	FILE exists.
-r FILE	FILE exists and the read permission is granted.
-s FILE	FILE exists and it's size is greater than zero
-w FILE	FILE exists and the write permission is granted.
-x FILE	FILE exists and the execute permission is granted

WORK!

Open your hello_script.bash

check that the user name parameter is not empty using *if*

```
#!/bin/bash
firstArg=$1
secondArg=$2
echo “You have entered \”$firstArg\” and
\”$secondArg\””
```

Doing repetitive work with *for*

```
for i in 1 2 3;
do
   echo "$i ”
done
```

Repetitive work with *for*

listing files from a folder

```
files = `ls *.txt`
for file in $files
do
   cat $file >> Output.txt
done
```

repetitive work with *for*

```
for filename in `ls *.gz`
   do echo $filename
```

Decompressing on the fly!

WORK!

```
for filename in `ls *.gz`
   do echo $filename
```

Now modify the script to print the first 10 lines of each file in the compressed tarball

WORK!

- Plant gene data set
  - What plants systems contain a Smell gene?
  - How many plant systems contain a Color gene?
  - What genes are in common between apple and pear? Which are specific to each of them?
  - How many genes are in common to all three plant systems?