```
sus@LAPTOP-4S1EJHL9 MINGW64 ~
 #ejercicio 1.10.1
asus@LAPTOP-4S1EJHL9 MINGW64 ~
$ #literal 1
usus@LAPTOP-4S1EJHL9 MINGW64 ~
#ir de csb sandbox
asus@LAPTOP-4S1EJHL9 MINGW64 ~
scd Documents/univercidad/BIOINFO3/CSB-master\ \(1\)/CSB-master/unix/sandbox/
ter/unix/sandbox
$ #literal 2
master/unix/sandbox
Marra2014_data.fasta
                 my_file.tmp
                              tarea4/
                 my_files.fasta
Papers and reviews'/
usus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
 wc Marra2014_data.fasta
 9515 13335 566026 Marra2014_data.fasta
wc -n ../data/Marra2014_data.fasta
wc: unknown option -- n
Try 'wc --help' for more information.
-master/unix/sandbox
$ wc -l ../data/Marra2014_data.fasta
9515 ../data/Marra2014_data.fasta
master/unix/sandbox
wc ../data/Marra2014_data.fasta
9515 13335 566026 ../data/Marra2014_data.fasta
sus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
master/unix/sandbox
$ #literal 3
cp ../data/Marra2014_data.fasta my_filefasta2.fasta
```

```
$ #literal 3
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
-master/unix/sandbox
$ cp ../data/Marra2014_data.fasta my_filefasta2.fasta
aster/unix/sandbox
$ 1s
               my_file.tmp
my_filefasta2.fasta
                               my_files.fasta
Marra2014_data.fasta
Papers and reviews'/
                               tarea4/
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
-master/unix/sandbox
$ #literal 4
master/unix/sand
$ grep -c isgroup0036 my_filefasta2.fasta
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
$ grep -c isgroup0036 Marra2014_data.fasta
aster/unix/sandbox
$ 1s
               Marra2014_data.fasta
                              my_files.fasta
Papers and reviews'/
$ ls my_filefasta2.fasta
my_filefasta2.fasta
-master/unix/sandbox
$ grep -c isogroup00001 Marra2014_data.fasta
master/unix/san
$ #nota otra palabra si busca pero la del ejercicio me encuentra O coincidencias
```

```
MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
     ter/unix/sandbox
$ #literal 5
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
$ cat my_filefasta2.fasta | tr ' ' ',' > my_filefasta3.tmp
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
 master/unix/sandbox
$ 1s
Marra2014_data.fasta my_file.tmp my_filefasta3.tmp
'Papers and reviews'/ my_filefasta2.fasta my_files.fasta
                                                                         tarea4/
-master/unix/sandbox
$ rm my_filefasta3.tmp
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
 master/unix/sandbox
$ 1s
Marra2014_data.fasta my_file.tmp
'Papers and reviews'/ my_filefasta2.fasta
                                                   my_files.fasta
                                                  tarea4/
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
-master/unix/sandbox
$ rm my_file.tmp
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
 master/unix/sandbox
$ 1s
Marra2014_data.fasta my_filefasta2.fasta tarea4/
'Papers and reviews'/ my_files.fasta
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
-master/unix/sandbo
$ rm my_file.fasta
rm: cannot remove 'my_file.fasta': No such file or directory
$ cat my_filefasta2.fasta | tr -s ' ' ',' > my filefasta3_tmp tr: extra operand 'filefasta3_tmp'
Try 'tr --help' for more information.
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
-master/unix/sandbox
$ cat my_filefasta2.fasta | tr -' ' ',' > my filefasta3_tmp
tr: unknown option --
Try 'tr --help' for more information.
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
```

```
$ cat my_filefasta2.fasta | tr ' ' ',' > my filefasta3_tmp
tr: extra operand 'filefasta3_tmp'
 Try 'tr --help' for more information.
  -master/unix/sandbox

$ cat my_filefasta2.fasta | tr ' ' ',' > my filefasta3_tmp

tr: extra operand 'filefasta3_tmp'

Try 'tr --help' for more information.
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
 $ cat my_filefasta2.fasta | tr ' ' ',' > my_filefasta3.tmp
  master/unix/sandbox
 $ 1s
  Marra2014_data.fasta
                                                                                                                   my_filefasta3.tmp
                                                                                                                                                                     tarea4/
                                                            mγ
                                                            my_filefasta2.fasta
                                                                                                                   my_files.fasta
  'Papers and reviews'/
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
   -master/unix/sandbo>
 $ grep isogroups my_filefasta3.tmp
  asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
           ter/unix/sandbox
 $ #literal 6
 asus@LArtor

-master/unix/sandbox

$ grep '>' my_filefasta2.fasta

-contig00001 length=527 numre
>contig00001
>contig00002
>contig00003
>contig00004
                                                            numreads=2
                                                                                           gene=isogroup00001 status=it_thresh
                                                                                           gene=isogroup00001 status=it_thresh
gene=isogroup00001 status=it_thresh
gene=isogroup00001 status=it_thresh
                                  length=551
                                                               numreads=8
                                  length=541
                                                               numreads=2
                                  length=291
                                                               numreads=3
>contig00004
>contig00005
>contig00008
>contig00010
>contig00011
                                  length=580
                                                              numreads=12 gene=isogroup00001 status=it_thresh
numreads=35 gene=isogroup00001 status=it_thresh
                                  length=3288
                                  length=1119 numreads=10 gene=isogroup00001 status=it_thresh
length=202 numreads=4 gene=isogroup00001 status=it_thresh
length=5563 numreads=61 gene=isogroup00001 status=it_thresh
length=824 numreads=10 gene=isogroup00001 status=it_thresh
 >contig00012
                                  length=707
length=568
                                                              numreads=6 gene=isogroup00001 status=it_thresh
numreads=2 gene=isogroup00001 status=it_thresh
numreads=4 gene=isogroup00001 status=it_thresh
 >contig00013
>contig00014
                                  length=123 numreads=4 gene=isogroup00001 status=it_thresh length=1721 numreads=22 gene=isogroup00001 status=it_thresh length=788 numreads=15 gene=isogroup00001 status=it_thresh
>contig00015
>contig00016
>contig00017
                                  length=1886 numreads=12 gene=isogroup00001 status=it_thresh length=802 numreads=3 gene=isogroup00001 status=it_thresh length=885 numreads=10 gene=isogroup00001 status=it_thresh length=142 numreads=3 gene=isogroup00001 status=it_thresh length=130 numreads=4 gene=isogroup00001 status=it_thresh length=178 numreads=7 gene=isogroup00001 status=it_thresh length=178 numreads=178 numreads=1
 >contig00018
 >contig00022
>contig00023
>contig00025
>contig00026
>contig00027
                                                                                                                                           status=it_thresh
status=it_thresh
 >contig00028
>contig00029
                                                                                            gene=isogroup00001
gene=isogroup00001
                                  length=135
                                                               numreads=2
                                  length=465
                                                               numreads=5
                                  length=121
 >contig00030
                                                               numreads=3
                                                                                            gene=isogroup00001
                                                                                                                                            status=it_thresh
                                  length=595
length=1202
                                                                                            gene=isogroup00001 status=it_thresh
  gene=isogroup00001 status=it_thresh
 >contig00031
>contig00032
                                                               numreads=9
                                                               numreads=5
                                                                                                                                              status=it_thresh
                                  length=540 numreads=27
                                                                                               gene=isogroup00001
 >contig00033
                                  length=1004 numreads=6 gene=isogroup00001 status=it_thresh length=566 numreads=8 gene=isogroup00001 status=it_thresh length=3571 numreads=8 gene=isogroup00001 status=it_thresh
 >contig00034
>contig00035
                                  length=3571
length=1168
                                                                numreads=8 gene=isogroup00001
 >contig00036
                                  length=1168 numreads=10 gene=isogroup00001 status=it_thresh length=371 numreads=94 gene=isogroup00001 status=it_thresh length=2505 numreads=15 gene=isogroup00001 status=it_thresh length=620 numreads=11 gene=isogroup00001 status=it_thresh
 >contig00037
>contig00039
 >contig00040
 >contig00042
>contig00044
                                  length=1301 numreads=4 gene=isogroup00001 status=it_thresh
 >contig00045
>contig00046
                                  length=563 numreads=6 gene=isogroup00001 status=it_thresh length=1046 numreads=44 gene=isogroup00001 status=it_thresh
```

```
>contigo1373
                                numreads=10 gene=isogroup00042 status=isotig
                  length=509
                 length=522 numreads=5 g
length=575 numreads=57
length=124 numreads=56
>contig01375
                                numreads=5 gene=isogroup00042 status=isotig
                 length=575 numreads=57 gene=isogroup00042 status=isotig
length=124 numreads=56 gene=isogroup00042 status=isotig
length=1545 numreads=10 gene=isogroup00043 status=isotig
length=3094 numreads=71 gene=isogroup00043 status=isotig
>contig01378
>contig01379
>contig01380
>contig01384
>contig01385
                 length=1965 numreads=7
                                                 gene=isogroup00043 status=isotig
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
-master/unix/sandbox
$ grep '>' my_filefasta2.fasta | head -n2
>contig00001 length=527 numreads=2 gene=isogroup00001 status=it_thresh
>contig00002 length=551 numreads=8 gene=isogroup00001 status=it_thresh
-master/unix/sandbox
$ grep '>' my_filefasta2.fasta | cut -d ',' -f 4 | sort | uniq | wc -l
          -master/unix/sandbox
$ #literal 7
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
$ grep '>' my_filefasta2.fasta | cut -d ',' -f 1,3 | sort '=' -k 2 -n -r | head
-n 1
sort: cannot read: '=': No such file or directory
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
-master/unix/sandbox
$ grep '>' my_filefasta2.fasta | cut -d ',' -f 1,3 | sort -t '=' -k 2 -n -r | he
ad -n 1
contig01115 length=6087 numreads=185 gene=isogroup00030 status=isotig>
```

ejercicio 1.10.2

```
$ # ejercicio 1.10.2
$ head -n 3 ../data/Gesquiere2011_data.csv |
usus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
-master/unix/sandbox
$ head -n 3 ../data/Gesquiere2011_data.csv
      GC
66.9
maleID
             64.57
      51.09
             35.57
usus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
$ cut -f 1 ../data/Gesquiere2011_data.csv |head -n 3
maleID
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
$ cut -f 1 ../data/Gesquiere2011_data.csv | grep -c -w 3
$ cut -f 1 ../data/Gesquiere2011_data.csv | grep -c -w 27
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB
master/unix/sandbox
```

```
ejercicio 1.10.2
head |-n 3 ../data/Gesquiere2011_data.csv
ut -f 1 ../data/Gesquiere2011_data.csv
ut -f 1 ../data/Gesquiere2011_data.csv
ut -f 1 ../data/Gesquiere2011_data.csv
                                                                                                                                                              head -n 3
grep -c -w 3
grep -c -w 27
```

```
ejercicio 1.10.3
                       MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB-master/unix/sar
  #ejercicio 1.10.4
 lsus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/san
 #literal 1
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB
-master/unix/sandbox
$ cd ../data/
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
 ter/unix/data
$ cd Saavedra2013
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ster/unix/data/Saavedra2013
$ echo "El numero de columnas es:" ; head -n1 n1.txt | grep -o " " | wc -l ; echo El numero de filas es:" ; wc -l n1.txt
El numero de columnas es:
80
El numero de filas es:
97 n1.txt
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data/Saavedra2013
$ #literal 2
 asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
$ for f in $(ls*.txt); do echo "El numero de columnas es:" ; head -n 1 $f | awk `{p rint NF}` ; echo "El numero de filas es:"; cat $f | wc -l; done bash: ls*.txt: command not found
 $ for f in $(ls *.txt); do echo "El numero de columnas es:"; head -n 1 $f | awk `{ print NF}`; echo "El numero de filas es:"; cat $f | wc -l; done El numero de columnas es:
GNU long options: (extensions)
Short options:
                                     --characters-as-bytes
         -с
                                     --traditional
                                    --copyright
--dump-variables[=file]
--debug[=file]
--source='program-text'
         -C
         -d[file]
-D[file]
-e 'program-text'
```

:c 🥹

```
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ster/unix/data/Saavedra2013
$ nano ejercicio3.sh

asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ster/unix/data/Saavedra2013
$ bash ejercicio3.sh
El numero de columna es:
80
el numero de filas es:
97
El numero de folumna es:
20
el numero de filas es:
14
Inumero de filas es:
91
el numero de filas es:
270
El numero de filas es:
270
El numero de filas es:
270
El numero de filas es:
```

ejercicio 1.10.4

```
sus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ter/unix/data/Saavedra2013
ster/unix/data/
$ #ejercicio 4
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data/Saavedra2013
$ #literal 1
ster/unix/data/Saavedra2013
$ cd ../
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINF03/CSB-master (1)/CSB-ma
ster/unix/data
$ cut -d ',' -f 7 ../data/Buzzard2015_data.csv | head -n 1
biomass
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data
$ #punto 2
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
$ cut -d ',' -f 7 ../data/Buzzard2015_data.csv | tail -n +2 | sort |uniq | wc -l
285
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data
$ #punto 3
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ster/unix/data
$ cut -d ',' -f 7 ../data/Buzzard2015_data.csv | tail -n +2 | sort -n | head -n 1
1.048466198
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data $ #punto 4
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-ma
ster/unix/data

$ cut -d ',' -f 7 ../data/Buzzard2015_data.csv | tail -n +2 | sort -n | tail -n 1

14897.29471
asus@LAPTOP-4S1EJHL9 MINGW64 ~/Documents/univercidad/BIOINFO3/CSB-master (1)/CSB-master/unix/data
```