

BIOINFORMÁTICA

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Nivel: Sexto

TAREA EN CLASES 3

```
MINGW32/c/Users/HP/Documents/CSB-master/unix/sandbox
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ touch condicional.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ nano condicional.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ cp while.sh condicional.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ nano condicional.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ cat condicional.sh
#!/bin/bash
edad=20
if [ $edad -lt 18]
then
    echo "no ingresa a la gallera"
else
    echo "libre ingreso"
fi
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ |
```

- While
- For

```
MINGW32/c/Users/HP/Documents/CSB-master/unix/sandbox
$ cp while.sh for.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ nano for.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ cat for.sh
#!/bin/bash
for i in 2 4 6 8
do
    x=$((i*3))
    echo "valor $i. triple $x"
done
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ nano for.sh
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ cat for.sh
#!/bin/bash
for i in 2 4 6 8
do
    x=$((i*3))
    echo "valor $i. triple $x"
done
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ ./for.sh
valor 2. triple 6
valor 4. triple 12
valor 6. triple 18
valor 8. triple 24
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ for i in 2 3 4 ; do echo "hola $1"; done
hola
hola
hola
```

```
MINGW32/c/Users/HP/Documents/CSB-master/unix/sandbox
GNU nano 5.8 for.sh
#!/bin/bash
echo "primera forma"
for i in 2 4 6 8
do
    x=$(( i**3 ))
    echo "valor $i, cubo $x"
done

echo "segunda forma"
for i in {5..100..20}
do
    x=$(( i**3 ))
    echo "valor $i, cubo $x"
done

echo "tercera forma"
for ((i=10; i<101; i+3 ))
do
    x=$(( i**3 ))
    echo "valor $i, cubo $x"
done
```

- miRNA

```
MINGW32/c/Users/HP/Documents/CSB-master/unix/data/miRNA
$ cd ../data/
bash: cd: ../data/: No such file or directory

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/sandbox
$ cd ../data/

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ls
Buzzard2015_about.txt  Gesquiere2011_data.csv  Pacifici2013_about.txt  Saavedra2013_about.txt  contadoresecuencias.sh*
Buzzard2015_data.csv  Marra2014_about.txt    Pacifici2013_data.csv  bodym.sh                 miRNA/
Gesquiere2011_about.txt  Marra2014_data.fasta  Saavedra2013/         contadoresecuencias.csv*

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ls miRNA/
contadoresecuencias.csv  ggo_miR.fasta  miRNA_about.txt  ppa_miR.fasta  ptr_miR.fasta
contadoresecuencias.sh*  hsa_miR.fasta  miR_about.txt   ppy_miR.fasta  ssy_miR.fasta

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cd miRNA/

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ for file in *.fasta; do head -n 2 $file; done
>ggo-miR-31 MIMAT0002381
GGCAAGAUGCUGGCAUAGCUG
>hsa-miR-576-3p MIMAT0004796
AAGAUGUGGAAAAUUGGAUUC
>ppa-miR-15a MIMAT0002646
UAGCAGCACAUAAUGGUUUGUG
>ppy-miR-569 MIMAT0016013
AGUUAAGAAUCCUGGAAAGU
>ptr-miR-224 MIMAT0002595
CAAAGUCACUAGUGGUCCGUUUA
>ssy-miR-514 MIMAT0005761
AUUGACACUUCUGUGAGUAG
```

Activar Windows

MINGW32/c/Users/HP/Documents/CSB-master/unix/data/miRNA

```
$ cd ../data/

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ls
Buzzard2015_about.txt      Gesquiere2011_data.csv    Pacifici2013_about.txt    Saavedra2013_about.txt    contadorsecuencias.sh*
Buzzard2015_data.csv       Marra2014_about.txt      Pacifici2013_data.csv     bodym.sh                  miRNA/
Gesquiere2011_about.txt    Marra2014_data.fasta     Saavedra2013/            contadorsecuencias.csv*

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ls miRNA/
contadorsecuencias.csv     ggo_miR.fasta            miRNA_about.txt          ppa_miR.fasta            ptr_miR.fasta
contadorsecuencias.sh*     hsa_miR.fasta            miR_about.txt            ppy_miR.fasta            ssy_miR.fasta

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cd miRNA/

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ for file in *.fasta; do head -n 2 $file; done
>ggo-miR-31 MIMAT0002381
GGCAAGUUGGCAUAGCUG
>hsa-miR-576-3p MIMAT0004796
AAGAUGUGGAAAAUUGGAAUC
>ppa-miR-15a MIMAT0002646
UAGCAGCACAUAAUGGUUUGUG
>ppy-miR-569 MIMAT0016013
AGUUAAGAAUCCUGGAAAGU
>ptr-miR-224 MIMAT0002595
CAAGUCACUAGUGGUCCGUUUA
>ssy-miR-514 MIMAT0005761
AUUGACACUUCUGAGUAG

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ for file in *.fasta; do head -n 2 $file | wc; done
 2      3      47
 2      3      52
 2      3      49
 2      3      48
 2      3      50
 2      3      47

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Ve a Con
```

MINGW32/c/Users/HP/Documents/CSB-master/unix/data

```
CAAGUCACUAGUGGUCCGUUUA
AUAGGCACCAAAAGCAACAA

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ for file in p*.fasta; do head -n 5 $file | cut -d ">" -f 1 | tr "U" "" | wc; done
tr: when not truncating set1, string2 must be non-empty
 0      0      0
tr: when not truncating set1, string2 must be non-empty
 0      0      0
tr: when not truncating set1, string2 must be non-empty
 0      0      0

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ cd ../&/
[1] 2029
bash: /: Is a directory
[1]+  Done                  cd ..

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ cd ../

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ for file in miRNA/p*.fasta; do head -n 5 $file | cut -d ">" -f 1 | tr "U" "" | wc; done
tr: when not truncating set1, string2 must be non-empty
 0      0      0
tr: when not truncating set1, string2 must be non-empty
 0      0      0
tr: when not truncating set1, string2 must be non-empty
 0      0      0

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ for file in miRNA/p*.fasta; do head -n 5 $file | cut -d ">" -f 1 | tr "U" " " | wc; done
 5      11      49
 5      12      49
 5       8      49
```

```
MINGW32/c/Users/HP/Documents/CSB-master/unix/data
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ cd ../
[1] 2029
bash: /: Is a directory
[1]+  Done                  cd ../

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data/miRNA
$ cd ../

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ for file in miRNA/p*.fasta; do head -n 5 $file | cut -d ">" -f 1 | tr "U" " " | wc; done
tr: when not truncating set1, string2 must be non-empty
0      0      0
tr: when not truncating set1, string2 must be non-empty
0      0      0
tr: when not truncating set1, string2 must be non-empty
0      0      0

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ for file in miRNA/p*.fasta; do head -n 5 $file | cut -d ">" -f 1 | tr "U" " " | wc; done
5      11     49
5      12     49
5      8      49

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ touch enzymertest.sh

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymertest.sh

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cat enzymertest.sh
#!/bin/bash
for file in miRNA/p*.fasta
do
    head -n 5 $file | cut -d ">" -f 1 | tr "U" " " >> enzymeresult.text
done
```

- Enzima

```
5      8      49
HP@DESKTOP-IAK9CAK MINGW32 ~/documents/CSB-master/unix/data
$ touch enzymertest.sh

HP@DESKTOP-IAK9CAK MINGW32 ~/documents/CSB-master/unix/data
$ nano enzymertest.sh

HP@DESKTOP-IAK9CAK MINGW32 ~/documents/CSB-master/unix/data
$ cat enzymertest.sh
#!/bin/bash
for file in miRNA/p*.fasta
do
    head -n 5 $file | cut -d ">" -f 1 | tr "U" " " >> enzymeresult.text
done

HP@DESKTOP-IAK9CAK MINGW32 ~/documents/CSB-master/unix/data
$ ./enzymertest.sh

HP@DESKTOP-IAK9CAK MINGW32 ~/documents/CSB-master/unix/data
$ ls
buzzard2015_about.txt  Gesquiere2011_data.csv  Pacifici2013_about.txt  Saavedra2013_about.txt  contadorsecuencias.sh*  miRNA/
buzzard2015_data.csv  Marraz2014_about.txt   Pacifici2013_data.csv  bodym.sh                enzymertest.sh*
Gesquiere2011_about.txt  Marraz2014_data.fasta  Saavedra2013/         contadorsecuencias.csv*  enzymeresult.text

HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cat enzymeresult.text

AGCAGCACAA  AA  GG      G  G
AAAG  GC  G  CG  GCAGG  AG

AG  AA  GAA  CC  GGAAAG
G  GCC  AC  GAGC  GA  A  CAG

CAAG  CAC  AG  GG  CCG      A
A  AGGCACCAAAAGCAACAA
```

MINGW32/c/Users/HP/Documents/CSB-master/unix/data

```
AAAG GC G CG GCAGG AG
```

```
AG AA GAA CC GAAAG
```

```
G GCC AC GAGC GA A CAG
```

```
CAAG CAC AG GG CCG A
```

```
A AGGCACAAAAGCAACAA
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymeres
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymerest.sh
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymerest.sh
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cat enzymerest.sh
#!/bin/bash
for file in $1
do
    head -n 5 $file | cut -d ">" -f 1 | tr "U" " " >> $2
done
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ./enzymerest.sh miRNA/*.fasta otros.txt
```

MINGW32/c/Users/HP/Documents/CSB-master/unix/data

```
$ nano enzymerest.sh
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cat enzymerest.sh
#!/bin/bash
for file in $1
do
    head -n 5 $file | cut -d ">" -f 1 | tr "U" " " >> $2
done
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ./enzymerest.sh miRNA/*.fasta otros.txt
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymerest.sh
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ nano enzymerest.sh
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ cat enzymerest.sh
#!/bin/bash
```

```
for file in $1
do
    head -n 5 $file | cut -d ">" -f 1 | tr "U" " " >> out.csv
done
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ./enzymerest.sh miRNA/*.fasta out.csv
```

```
HP@DESKTOP-IAK9CAK MINGW32 ~/Documents/CSB-master/unix/data
$ ls
```

Buzzard2015_about.txt	Gesquiere2011_data.csv	Pacifici2013_about.txt	Saavedra2013_about.txt	contadorsecuencias.sh*	miRNA/
Buzzard2015_data.csv	Marra2014_about.txt	Pacifici2013_data.csv	bodym.sh	enzymerest.sh*	out.csv
Gesquiere2011_about.txt	Marra2014_data.fasta	Saavedra2013/	contadorsecuencias.csv*	enzymeresult.txt	Activar Windows