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Preparación

```
User@DESKTOP-U73I4LB MINGW64 ~ (master)
$ cd Documents/Bioinformatica

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica (master)
$ mkdir tc2_BenalcazarAndres

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica (master)
$ ls
CSB-master/  CSB-master.zip  tc2_BenalcazarAndres/

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica (master)
$ cd tc2_BenalcazarAndres

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (ma
ster)
$ ls
AgGCN1.0_properties.csv
```

Selección

```
User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ cut -d "," -f "1,4,6" AgGCN1.0_properties.csv > EigenBetw.tsv
```

Bash scrpt 1

```
User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ nano tc2_BenalcazarAndres.sh

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ cat tc2_BenalcazarAndres.sh
#! Bin Bash

echo "Primeras 7 filas"

head -n 7 EigenBetw.tsv

echo "Ultimas 5 filas"

tail -n 5 EigenBetw.tsv

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ bash tc2_BenalcazarAndres.sh
Primeras 7 filas
id,eigenvector,betweenness
AGAP000002,0.008787135,2.91E-05
AGAP000005,0.013750498,0.000171241
AGAP000007,7.90E-06,0
AGAP000008,0.000383447,1.22E-06
AGAP000009,0.013802427,0.000654142
AGAP000010,0.000101576,0
Ultimas 5 filas
AGAP029781,0.000987921,1.49E-05
AGAP029784,3.45E-05,0.000155039
AGAP029786,0.000146935,5.04E-05
AGAP029787,9.99E-06,1.22E-07
AGAP029789,0.001757408,0.001160083
```

Bash scrip 2


```
User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ nano tc2_BenalcazarAndres2.sh

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ cat tc2_BenalcazarAndres2.sh
# ! bin bash


grep AGAP[0-9]*[5], EigenBetw.tsv | sort -k 3 > EigenBetw5.csv

User@DESKTOP-U73I4LB MINGW64 ~/Documents/Bioinformatica/tc2_BenalcazarAndres (master)
$ bash tc2_BenalcazarAndres2.sh
```