1.10.2 Hormone Levels in Baboons

Gesquiere et al. (2011) studied hormone levels in the blood of baboons. Every individual was sampled several times.

- 1. How many times were the levels of individuals 3 and 27 recorded?
- 2. Write a script taking as input the file name and the ID of the individual, and returning the number of records for that ID.
- 3. [Advanced]¹⁷ Write a script that returns the number of times each individual was sampled.

LIT 1

```
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ nano script.sh
_ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
Buzzard2015_about.txt
                          Gesquiere2011_data.csv Pacifici2013_data.csv
                                                                              miRNA/
Buzzard2015_data.csv
                          Marra2014_about.txt
                                                    Saavedra2013/
                                                                              sandbox
Gesquiere2011_about.txt Pacifici2013_about.txt Saavedra2013_about.txt
                                                                              script.sh
_ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ cat script.sh
cut -f 1 $1.csv | grep -c -w $2
LENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main) $ bash script.sh Gesquiere2011_data.scv 1
cut: Gesquiere2011_data.scv.csv: No such file or directory
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
 bash script.sh Gesquiere2011_data 1
10
 .ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ bash script.sh Gesquiere2011_data 2
_ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ bash script.sh Gesquiere2011_data 3
61
LENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main) $ bash script.sh Gesquiere2011_data 4
 ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ bash script.sh Gesquiere2011_data 5
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ bash script.sh Gesquiere2011_data 6
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
 bash script.sh Gesquiere2011_data 7
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main) bash script.sh Gesquiere2011_data 8
17
ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
 bash script.sh Gesquiere2011_data 9
_ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
$ bash script.sh Gesquiere2011_data 10
 .ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (main)
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MINGW64:/c/Users/LENOVO/Videos/BIOINFOR/CSB-master/unix/data (master)
$ nano script2.sh

LENOVO@allan MINGW64 ~/Videos/BIOINFOR/CSB-master/unix/data (master)
$ 1s
$ Buzzard2015_about.txt Gesquiere2011_about.txt Marra2014_about.txt Pacifici2013_data.csv Saavedra2013_about.txt sandbox script2.sh
Buzzard2015_data.csv Gesquiere2011_data.csv Pacifici2013_about.txt Saavedra2013/ miRNA/ script.sh

LENOVO@allan MINGW64 ~/Videos/BIOINFOR/CSB-master/unix/data (master)
$ cat script2.sh
cut -f 1 $1.csv | sort | uniq -c

LENOVO@allan MINGW64 ~/Videos/BIOINFOR/CSB-master/unix/data (master)
$ bash script2.sh Gesquiere2011_data|
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ENOVO@allan MINGW64 ~/videos/BIOINFOR/CSB-master/unix/data (master) bash script2.sh Gesquiere2011_data
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          42 120
          12 121
          9 122
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13 127
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          ENOVO@allan MINGW64 ~/Videos/BIOINFOR/CSB-master/unix/data (master)
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