(1) We use grep command for looking for the pattern "Meningioma" in the file BrainCancer.csv, and save it to the file "LineswithMeningioma.out"

To see the contents of the new file we use cat command.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep "Meningioma" BrainCancer.csv > LineswithMeningioma.out
ibab@IBAB-RA-Comp203:~/Lab5$ cat LineswithMeningioma.out
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
9,Female,Meningioma,Supratentorial,70,12.16,SRT,0,34.66
12,Female,Meningioma,Infratentorial,90,6.54,SRS,0,34.26
13,Female,Meningioma,Infratentorial,90,0.63,SRS,0,32.98
15,Female,Meningioma,Supratentorial,60,9.18,SRT,0,41.44
19,Male,Meningioma,Supratentorial,80,13.49,SRS,1,6.92
20,Female,Meningioma,Supratentorial,90,2.5,SRT,0,30.16
21,Female,Meningioma,Supratentorial,80,2.82,SRS,0,24.39
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
25,Female,Meningioma,Supratentorial,70,6.48,SRT,1,33.41
29,Male,Meningioma,Supratentorial,60,3.81,SRT,0,36.1
30,Female,Meningioma,Supratentorial,90,4.72,SRS,0,65.02
32,Male,Meningioma,Supratentorial,90,2.56,SRS,0,44.39
35,Female,Meningioma,Supratentorial,90,7.3,SRT,0,5.51
37,Female,Meningioma,Supratentorial,80,6.6,SRT,0,14.75
40,Female,Meningioma,Supratentorial,90,2.54,SRT,0,45.74
41,Female,Meningioma,Supratentorial,80,1.57,SRT,0,2.03
43,Female,Meningioma,Supratentorial,70,6.7,SRT,0,14.56
44,Male,Meningioma,Supratentorial,80,12.63,SRT,1,4.16
46,Male,Meningioma,Supratentorial,60,7.09,SRS,1,31.25
48,Female,Meningioma,Supratentorial,80,26.31,SRT,1,39.54
49,Male,Meningioma,Supratentorial,70,0.97,SRT,1,1.41
52,Female,Meningioma,Infratentorial,90,9.24,SRT,0,26.85
54,Male,Meningioma,Infratentorial,80,24.41,SRT,0,39.54
60,Female,Meningioma,Supratentorial,90,2.47,SRT,0,17.57
62,Male,Meningioma,Supratentorial,80,11.51,SRT,1,14.62
64,Male,Meningioma,Supratentorial,80,4.77,SRT,0,67.38
66,Female,Meningioma,Supratentorial,100,4,SRT,0,52.23
69,Female,Meningioma,Supratentorial,80,6.93,SRS,0,10.1
70,Female,Meningioma,Supratentorial,70,3.63,SRT,0,32.82
71,Male,Meningioma,Supratentorial,70,8.45,SRT,0,19.41
72,Male,Meningioma,Supratentorial,80,20.93,SRT,1,31.15
76,Female,Meningioma,Supratentorial,80,31.74,SRT,0,57.25
77,Female,Meningioma,Supratentorial,80,2.39,SRS,0,73.74
78,Female,Meningioma,Supratentorial,90,7.26,SRT,0,49.05
79,Female,Meningioma,Supratentorial,100,9.66,SRT,0,39.25
80,Female,Meningioma,Infratentorial,70,2.94,SRS,0,1.54
86,Male,Meningioma,Supratentorial,90,2.5,SRT,0,32.82
87,Male,Meningioma,Supratentorial,90,2.02,SRS,0,42.07
ibab@IBAB-RA-Comp203:~/Lab5$ echo "Command used: grep \"Meningioma\" BrainCancer.csv > LineswithMeningioma.out"
Command used: grep "Meningioma" BrainCancer.csv > LineswithMeningioma.out
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

(2) We use the grep -c for counting the number of males and females in the given file.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep -c 'Male' BrainCancer.csv
43
ibab@IBAB-RA-Comp203:~/Lab5$ grep -c 'Female' BrainCancer.csv
45
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

(3) We use the command grep and grep -v=c for getting the number of Supratentorials in the given file.
To ignore the case we use the command grep -i.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep Supratentorial BrainCancer.csv > Supratentorial_sorted.out
ibab@IBAB-RA-Comp203:~/Lab5$ grep -c Male Supratentorial_sorted.out
34
ibab@IBAB-RA-Comp203:~/Lab5$ grep -i Infratentorial BrainCancer.csv > Infratentorial_sorted.out

ibab@IBAB-RA-Comp203:~/Lab5$ grep -ri female infratentorial_sorted.out
grep: infratentorial_sorted.out: No such file or directory
ibab@IBAB-RA-Comp203:~/Lab5$ grep -ri female Infratentorial_sorted.out
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
12,Female,Meningioma,Infratentorial,90,6.54,SRS,0,34.26
13,Female,Meningioma,Infratentorial,90,0.63,SRS,0,32.98
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
33,Female,Other,Infratentorial,70,13.45,SRT,1,10.82
52,Female,Meningioma,Infratentorial,90,9.24,SRT,0,26.85
80,Female,Meningioma,Infratentorial,70,2.94,SRS,0,1.54
ibab@IBAB-RA-Comp203:~/Lab5$ grep -Ci female Infratentorial_sorted.out
grep: i: invalid context length argument
ibab@IBAB-RA-Comp203:~/Lab5$ grep -ci female Infratentorial_sorted.out
10
ibab@IBAB-RA-Comp203:~/Lab5$
```

(4) Using sort -n -t ',' -k here allows us to get the information on a specific column, which here is the lowest Ki value.

```
ibab@IBAB-RA-Comp203:~/Lab5$ head BrainCancer.csv
,sex,diagnosis,loc,ki,gtv,stereo,status,time
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
2,Male,HG glioma,Supratentorial,90,19.35,SRT,1,8.98
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
5,Male,HG glioma,Supratentorial,90,5.06,SRT,1,6.3
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
9,Female,Meningioma,Supratentorial,70,12.16,SRT,0,34.66
ibab@IBAB-RA-Comp203:~/Lab5$ sort -t ',' -k 5 -n BrainCancer.csv
 > ki_sorted.out
ibab@IBAB-RA-Comp203:~/Lab5$ sort -c ki_sorted.out
sort: ki_sorted.out:2: disorder: 29,Male,Meningioma,Supratentori
al,60,3.81,SRT,0,36.1
ibab@IBAB-RA-Comp203:~/Lab5$
```

(5)This is done by a series of commands. We make the use of grep, followed by cat command to save the contents in a new file and also view the file created.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep -e 'SRS' BrainCancer.csv > srsbrain.csv
ibab@IBAB-RA-Comp203:~/Lab5$ ls
BrainCancer.csv  ki_sorted.out  LineswithMeningioma.out  srsbrain.csv
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'Infratentorial' srsbrain.csv
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
12,Female,Meningioma,Infratentorial,90,6.54,SRS,0,34.26
13,Female,Meningioma,Infratentorial,90,0.63,SRS,0,32.98
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
34,Male,Other,Infratentorial,80,6.81,SRS,0,57.11
56,Male,Other,Infratentorial,90,0.48,SRS,0,54.43
57,Male,HG glioma,Infratentorial,80,0.22,SRS,0,33.67
68,Male,Other,Infratentorial,70,0.01,SRS,0,23.67
80,Female,Meningioma,Infratentorial,70,2.94,SRS,0,1.54
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'Infratentorial' -c srsbrain.csv
11
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

(6) sort command helps us list the patients who have a survival of more than 50 months

```
ibab@IBAB-RA-Comp203:~/Lab5$ sort -t ',' -k 9 -n -r BrainCancer.csv -o mon
ths.out
ibab@IBAB-RA-Comp203:~/Lab5$ head -n 15 months.out
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
77,Female,Meningioma,Supratentorial,80,2.39,SRS,0,73.74
64,Male,Meningioma,Supratentorial,80,4.77,SRT,0,67.38
30,Female,Meningioma,Supratentorial,90,4.72,SRS,0,65.02
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
76,Female,Meningioma,Supratentorial,80,31.74,SRT,0,57.25
34,Male,Other,Infratentorial,80,6.81,SRS,0,57.11
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
56,Male,Other,Infratentorial,90,0.48,SRS,0,54.43
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
66,Female,Meningioma,Supratentorial,100,4,SRT,0,52.23
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
14,Male,NA,Supratentorial,90,6.38,SRT,0,50.85
78,Female,Meningioma,Supratentorial,90,7.26,SRT,0,49.05
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

(7) Through the grep command, we are able to sort the patients with HG Glioma into afile. Only one patient with HG glioma has a survival of more than 50 months.

```
ibab@IBAB-RA-Comp203:~/Lab5$ head months.out
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
77,Female,Meningioma,Supratentorial,80,2.39,SRS,0,73.74
64,Male,Meningioma,Supratentorial,80,4.77,SRT,0,67.38
30,Female,Meningioma,Supratentorial,90,4.72,SRS,0,65.02
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
76,Female,Meningioma,Supratentorial,80,31.74,SRT,0,57.25
34,Male,Other,Infratentorial,80,6.81,SRS,0,57.11
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
56,Male,Other,Infratentorial,90,0.48,SRS,0,54.43
ibab@IBAB-RA-Comp203:~/Lab5$ grep "HG glioma" months.out
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
81,Female,HG glioma,Supratentorial,80,15.45,SRT,1,46.16
57,Male,HG glioma,Infratentorial,80,0.22,SRS,0,33.67
51,Female,HG glioma,Supratentorial,90,0.04,SRT,0,31.67
84,Male,HG glioma,Supratentorial,80,0.16,SRT,1,20.69
58,Male,HG glioma,Supratentorial,80,3.75,SRT,1,19.9
55,Female,HG glioma,Supratentorial,80,0.63,SRT,1,16.92
42,Male,HG glioma,Supratentorial,90,0.28,SRT,1,16.43
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
10,Male,HG glioma,Supratentorial,100,2.53,SRT,0,11.48
74,Female,HG glioma,Supratentorial,80,0.19,SRT,1,11.02
53,Male,HG glioma,Supratentorial,90,2.5,SRT,1,9.77
2,Male,HG glioma,Supratentorial,90,19.35,SRT,1,8.98
61,Female,HG glioma,Supratentorial,80,12.08,SRT,1,7.25
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
85,Male,HG glioma,Supratentorial,80,19.81,SRT,1,6.39
5,Male,HG glioma,Supratentorial,90,5.06,SRT,1,6.3
38,Male,HG glioma,Supratentorial,90,9.95,SRT,1,6.23
47,Male,HG glioma,Supratentorial,80,29.27,SRT,0,5.15
67,Female,HG glioma,Supratentorial,80,7.59,SRT,1,4.56
63,Female,HG glioma,Supratentorial,40,22.87,SRT,1,3.38
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
```

(8) We use a series pf commands sort, head, grep . There are 4 patients with LG glioma.

```
ibab@IBAB-RA-Comp203:~$ cd Lab5
ibab@IBAB-RA-Comp203:~/Lab5$ sort -t ',' -k 9 -n BrainCancer.csv -o Less30_mths.out
ibab@IBAB-RA-Comp203:~/Lab5$ head -50 Less30_mths.out > 30months.out
ibab@IBAB-RA-Comp203:~/Lab5$ grep -i Supratentorial 30months.out
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
49,Male,Meningioma,Supratentorial,70,0.97,SRT,1,1.41
41,Female,Meningioma,Supratentorial,80,1.57,SRT,0,2.03
63,Female,HG glioma,Supratentorial,40,22.87,SRT,1,3.38
44,Male,Meningioma,Supratentorial,80,12.63,SRT,1,4.16
67,Female,HG glioma,Supratentorial,80,7.59,SRT,1,4.56
47,Male,HG glioma,Supratentorial,80,29.27,SRT,0,5.15
35,Female,Meningioma,Supratentorial,90,7.3,SRT,0,5.51
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
38,Male,HG glioma,Supratentorial,90,9.95,SRT,1,6.23
5,Male,HG glioma,Supratentorial,90,5.06,SRT,1,6.3
85,Male,HG glioma,Supratentorial,80,19.81,SRT,1,6.39
19,Male,Meningioma,Supratentorial,80,13.49,SRS,1,6.92
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
36,Female,Other,Supratentorial,70,14.26,SRT,0,7.18
61,Female,HG glioma,Supratentorial,80,12.08,SRT,1,7.25
2,Male,HG glioma,Supratentorial,90,19.35,SRT,1,8.98
53,Male,HG glioma,Supratentorial,90,2.5,SRT,1,9.77
69,Female,Meningioma,Supratentorial,80,6.93,SRS,0,10.1
74,Female,HG glioma,Supratentorial,80,0.19,SRT,1,11.02
10,Male,HG glioma,Supratentorial,100,2.53,SRT,0,11.48
50,Female,LG glioma,Supratentorial,80,0.19,SRS,0,11.51
27,Male,Other,Supratentorial,60,34.64,SRT,1,11.57
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
43,Female,Meningioma,Supratentorial,70,6.7,SRT,0,14.56
62,Male,Meningioma,Supratentorial,80,11.51,SRT,1,14.62
37,Female,Meningioma,Supratentorial,80,6.6,SRT,0,14.75
42,Male,HG glioma,Supratentorial,90,0.28,SRT,1,16.43
55,Female,HG glioma,Supratentorial,80,0.63,SRT,1,16.92
60,Female,Meningioma,Supratentorial,90,2.47,SRT,0,17.57
71,Male,Meningioma,Supratentorial,70,8.45,SRT,0,19.41
75,Male,Other,Supratentorial,100,24.91,SRT,0,19.74
58,Male,HG glioma,Supratentorial,80,3.75,SRT,1,19.9
```

(9) By default grep does not ignore the case. We use grep -i to ignore the case.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep -i SUpraTentORial BrainCancer.csv
2,Male,HG glioma,Supratentorial,90,19.35,SRT,1,8.98
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
5,Male,HG glioma,Supratentorial,90,5.06,SRT,1,6.3
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
9,Female,Meningioma,Supratentorial,70,12.16,SRT,0,34.66
10,Male,HG glioma,Supratentorial,100,2.53,SRT,0,11.48
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93
14,Male,NA,Supratentorial,90,6.38,SRT,0,50.85
15,Female,Meningioma,Supratentorial,60,9.18,SRT,0,41.44
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
19,Male,Meningioma,Supratentorial,80,13.49,SRS,1,6.92
20,Female,Meningioma,Supratentorial,90,2.5,SRT,0,30.16
21,Female,Meningioma,Supratentorial,80,2.82,SRS,0,24.39
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
25,Female,Meningioma,Supratentorial,70,6.48,SRT,1,33.41
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
27,Male,Other,Supratentorial,60,34.64,SRT,1,11.57
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
29,Male,Meningioma,Supratentorial,60,3.81,SRT,0,36.1
30,Female,Meningioma,Supratentorial,90,4.72,SRS,0,65.02
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
32,Male,Meningioma,Supratentorial,90,2.56,SRS,0,44.39
35,Female,Meningioma,Supratentorial,90,7.3,SRT,0,5.51
36,Female,Other,Supratentorial,70,14.26,SRT,0,7.18
37,Female,Meningioma,Supratentorial,80,6.6,SRT,0,14.75
38,Male,HG glioma,Supratentorial,90,9.95,SRT,1,6.23
40,Female,Meningioma,Supratentorial,90,2.54,SRT,0,45.74
41,Female,Meningioma,Supratentorial,80,1.57,SRT,0,2.03
42,Male,HG glioma,Supratentorial,90,0.28,SRT,1,16.43
43,Female,Meningioma,Supratentorial,70,6.7,SRT,0,14.56
44,Male,Meningioma,Supratentorial,80,12.63,SRT,1,4.16
46,Male,Meningioma,Supratentorial,60,7.09,SRS,1,31.25
47,Male,HG glioma,Supratentorial,80,29.27,SRT,0,5.15
```

(10) Here once again, we use the grep -c command to get everything inorder. We get a total of 35 dead patients.

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep ",1," BrainCancer.csv
2,Male,HG glioma,Supratentorial,90,19.35,SRT,1,8.98
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
5,Male,HG glioma,Supratentorial,90,5.06,SRT,1,6.3
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
19,Male,Meningioma,Supratentorial,80,13.49,SRS,1,6.92
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
25,Female,Meningioma,Supratentorial,70,6.48,SRT,1,33.41
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
27,Male,Other,Supratentorial,60,34.64,SRT,1,11.57
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
33,Female,Other,Infratentorial,70,13.45,SRT,1,10.82
38,Male,HG glioma,Supratentorial,90,9.95,SRT,1,6.23
39,Male,Other,Infratentorial,80,12.51,SRT,1,29.7
42,Male,HG glioma,Supratentorial,90,0.28,SRT,1,16.43
44,Male,Meningioma,Supratentorial,80,12.63,SRT,1,4.16
46,Male,Meningioma,Supratentorial,60,7.09,SRS,1,31.25
48,Female,Meningioma,Supratentorial,80,26.31,SRT,1,39.54
49,Male,Meningioma,Supratentorial,70,0.97,SRT,1,1.41
53,Male,HG glioma,Supratentorial,90,2.5,SRT,1,9.77
55,Female,HG glioma,Supratentorial,80,0.63,SRT,1,16.92
58,Male,HG glioma,Supratentorial,80,3.75,SRT,1,19.9
59,Female,Other,Supratentorial,80,11.83,SRT,1,22.03
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -c ",1," BrainCancer.csv
35
ibab@IBAB-RA-Comp201:~/LAB5$
```

(11) grep -c allows us to get the count of the infratentorial patients. We use head command to restrict the total to 10 people. We get a total of 19 people.

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'Infratentorial' BrainCancer.csv
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
12,Female,Meningioma,Infratentorial,90,6.54,SRS,0,34.26
13,Female,Meningioma,Infratentorial,90,0.63,SRS,0,32.98
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.02
33,Female,Other,Infratentorial,70,13.45,SRT,1,10.82
34,Male,Other,Infratentorial,80,6.81,SRS,0,57.11
39,Male,Other,Infratentorial,80,12.51,SRT,1,29.7
45,Male,Other,Infratentorial,90,3.12,SRT,0,18.95
52,Female,Meningioma,Infratentorial,90,9.24,SRT,0,26.85
54,Male,Meningioma,Infratentorial,80,24.41,SRT,0,39.54
56,Male,Other,Infratentorial,90,0.48,SRS,0,54.43
57,Male,HG glioma,Infratentorial,80,0.22,SRS,0,33.67
68,Male,Other,Infratentorial,70,0.01,SRS,0,23.67
80,Female,Meningioma,Infratentorial,70,2.94,SRS,0,1.54
83,Male,LG glioma,Infratentorial,90,30.41,SRT,0,1.18
88,Male,Other,Infratentorial,80,0.11,SRT,0,13.9
ibab@IBAB-RA-Comp203:~/Lab5$ grep -c 'Infratentorial' BrainCancer.csv
19
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

```
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'Infratentorial' Brai
nCancer.csv > Infratentorialsorted.out
ibab@IBAB-RA-Comp203:~/Lab5$ head Infratentorialsorted.
out
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
12,Female,Meningioma,Infratentorial,90,6.54,SRS,0,34.26
13,Female,Meningioma,Infratentorial,90,0.63,SRS,0,32.98
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
24,Female,Meningioma,Infratentorial,100,2.13,SRS,1,51.0
2
33,Female,Other,Infratentorial,70,13.45,SRT,1,10.82
34,Male,Other,Infratentorial,80,6.81,SRS,0,57.11
39,Male,Other,Infratentorial,80,12.51,SRT,1,29.7
ibab@IBAB-RA-Comp203:~/Lab5$ 
```

(12) tar helps us create an archived file.

```
ibab@IBAB-RA-Comp203:~/Lab5$ sort -n -l ',' -k 5 , 5 -n BrainCancer.csv > Ki.out
sort: invalid option -- 'l'
Try 'sort --help' for more information.
ibab@IBAB-RA-Comp203:~/Lab5$ sort -n -l ',' -k 5,5  BrainCancer.csv > Ki.out
sort: invalid option -- 'l'
Try 'sort --help' for more information.
ibab@IBAB-RA-Comp203:~/Lab5$ sort -n -t ',' -k 5,5  BrainCancer.csv > Ki.out
ibab@IBAB-RA-Comp203:~/Lab5$ ls BrainCancer.csv
BrainCancer.csv
ibab@IBAB-RA-Comp203:~/Lab5$ ls Lab5
ls: cannot access 'Lab5': No such file or directory
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'Infratentorial' srsbrain.csv > lowestki.out
ibab@IBAB-RA-Comp203:~/Lab5$ ls
30months.out            LineswithMeningioma.out
BrainCancer.csv         lowestki.out
Infratentorial_sorted.out  months.out
Infratentorialsorted.out   srsbrain.csv
Ki.out                  Supratentorial_30.out
ki_sorted.out           Supratentorial_sorted.out
Less30_mths.out
ibab@IBAB-RA-Comp203:~/Lab5$ tar -cvf outputs.tar LineswithMenigioma.out Supratentorial.sorted.out Infratentorialsorted.out Ki.out lowestki.out
tar: LineswithMenigioma.out: Cannot stat: No such file or directory
tar: Supratentorial.sorted.out: Cannot stat: No such file or directory
Infratentorialsorted.out
Ki.out
lowestki.out
tar: Exiting with failure status due to previous errors
ibab@IBAB-RA-Comp203:~/Lab5$ tar -cvf outputs.tar LineswithMeningioma.out Supratentorial_sorted.out Infratentorialsorted.out Ki.out lowestki.out
LineswithMeningioma.out
Supratentorial_sorted.out
Infratentorialsorted.out
Ki.out
lowestki.out
ibab@IBAB-RA-Comp203:~/Lab5$ cat outputs.tar
LineswithMeningioma.out000066400017510001751000000044631505635376701417  0ustar  ibabibab1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
```

(13)

```
months.out:28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
grep: .: Is a directory
grep: HGglioma.out: No such file or directory
ibab@IBAB-RA-Comp203:~/Lab5$ grep 'HG glioma' months.out > HGglioma.out
ibab@IBAB-RA-Comp203:~/Lab5$ grep -i 'LG glioma' Supratentorial_30.out > LGglioma.out
ibab@IBAB-RA-Comp203:~/Lab5$ grep -i SUPratenTORial BrainCancer.csv > i.out
ibab@IBAB-RA-Comp203:~/Lab5$ grep -,l,' BrainCancer.csv > l.out
> ^C
ibab@IBAB-RA-Comp203:~/Lab5$ head -n Infratentorial_sorted.out > nInfra.out
head: invalid number of lines: 'Infratentorial_sorted.out'
ibab@IBAB-RA-Comp203:~/Lab5$ ls
14months.out
30months.out
BrainCancer.csv
HGglioma.out
Infratentorial_sorted.out
Infratentorialsorted.out
i.out
Ki.out
ki_sorted.out
Less30_mths.out
LGglioma.out
LineswithMeningioma.out
lowestki.out
months.out
nInfra.out
outputs.tar
srsbrain.csv
Supratentorial_30.out
Supratentorial_sorted.out
ibab@IBAB-RA-Comp203:~/Lab5$
```

```
ibab@IBAB-RA-Comp203:~$ cd Lab5
ibab@IBAB-RA-Comp203:~/Lab5$ tar -cvzf outputs2.tar 14months.out HGglioma
.out LGglioma.out i.out n10infra.out
14months.out
HGglioma.out
LGglioma.out
i.out
```

(14)

```
ibab@IBAB-RA-Comp201:~/LAB5$ tar -xvf outputs.tar
LinesWithMeningioma.out
Maleesorted.out
Femaleesorted.out
Supratentorialsorted.out
Infratentorialsorted.out
Ki.out
lowestki.out
ibab@IBAB-RA-Comp201:~/LAB5$
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ mv outputs.tar out1extract
ibab@IBAB-RA-Comp201:~/LAB5$ cd out1extract
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ cd out1extract
ibab@IBAB-RA-Comp201:~/LAB5/out1extract$ cat outputs.tar
LinesWithMeningioma.out0000664000175100017510000000044631504311303701410 5 0ustar  ibabibab1,Fem
ale,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
7,Male,Meningioma,Supratentorial,80,3.19,SRT,0,55.8
```

(15) List and extract the contents of the archived-zipped file
in (13) to a new directory and list the contents of the new directory.

```
ibab@IBAB-RA-Comp201:~/LAB5$ tar -xvf outputs2.tar
14monthss.out
HGgliomaa.out
LGglioma.out
i.out
n10infra.out
```