

Learning goals: Linux OS commands grep, tar, gzip

NOTE: Save screenshots of each exercise, and upload your work to your github account as Lab5.pdf by end of Friday Aug 1.

For this lab, download 'BrainCancer.csv' to a folder called 'Lab5'. If the file download to the "Downloads" folder by default, move the file to the folder 'Lab5'.

The data file contains the following columns for the survival times of patients diagnosed with brain cancer.

- Sex Male or Female patients
- diagnosis Meningoma, LG glioma, HG glioma and Other
- loc Location of the cancer- infratentorial or supratentorial
- ki Karnofsky index is a scale to assess the functional impairment of a patient with cancer. 100 is normal and 0 is dead.
- gtv gross tumor volume in cc
- stereo stereotactic methods 'SRS' and 'SRT'
- status whether the patient is alive at the end of the study 0=Yes, 1=No
- time survival time in months

EXERCISES Start a fresh terminal for this Lab.

- (1) Look for the pattern 'Meningioma' in the data file. Redirect the output to a new file called 'LinesWithMeningioma.out'. Show the command used and the contents of this new file in your screenshot.

```
keshavaa@Keshavaa:~/lab5$ grep -w Meningioma BrainCancer.csv > LinesWithMeningioma.out
keshavaa@Keshavaa:~/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
```

- (2) How many males and females were present in this study? How will you create a grep filter to find this out?

```
keshavaa@Keshavaa:~/lab5$ grep -c "Male" BrainCancer.csv
43
keshavaa@Keshavaa:~/lab5$ grep -c "Female" BrainCancer.csv
45
keshavaa@Keshavaa:~/lab5$
```

- (3) How many males have supratentorial brain cancer and how many females have infratentorial cancer? Which option in grep makes you ignore the case while searching? Make use of this in this exercise.

```
keshavaa@Keshavaa:~/lab5$ grep ',Female,' BrainCancer.csv > female.txt
keshavaa@Keshavaa:~/lab5$ grep 'Infratentorial' female.txt
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
keshavaa@Keshavaa:~/lab5$ grep -c 'Infratentorial' female.txt
10
keshavaa@Keshavaa:~/lab5$
```

```

keshavaa@Keshavaa:~/lab5$ grep 'Supratentorial' male.txt
2, Male, HG glioma, Supratentorial, 90, 19.35, SRT, 1, 8.98
5, Male, HG glioma, Supratentorial, 90, 5.06, SRT, 1, 6.3
7, Male, Meningioma, Supratentorial, 80, 3.19, SRT, 0, 55.8
8, Male, LG glioma, Supratentorial, 80, 12.37, SRT, 0, 42.1
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
18, Male, HG glioma, Supratentorial, 90, 10.8, SRT, 0, 82.56
19, Male, Meningioma, Supratentorial, 80, 13.49, SRS, 1, 6.92
22, Male, HG glioma, Supratentorial, 70, 14.44, SRT, 1, 14
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
32, Male, Meningioma, Supratentorial, 90, 2.56, SRS, 0, 44.39
38, Male, HG glioma, Supratentorial, 90, 9.95, SRT, 1, 6.23
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
47, Male, HG glioma, Supratentorial, 80, 29.27, SRT, 0, 5.15
49, Male, Meningioma, Supratentorial, 70, 0.97, SRT, 1, 1.41
53, Male, HG glioma, Supratentorial, 90, 2.5, SRT, 1, 9.77
58, Male, HG glioma, Supratentorial, 80, 3.75, SRT, 1, 19.9
62, Male, Meningioma, Supratentorial, 80, 11.51, SRT, 1, 14.62
64, Male, Meningioma, Supratentorial, 80, 4.77, SRT, 0, 67.38
65, Male, LG glioma, Supratentorial, 80, 9.58, SRT, 0, 78.75
71, Male, Meningioma, Supratentorial, 70, 8.45, SRT, 0, 19.41
72, Male, Meningioma, Supratentorial, 80, 20.93, SRT, 1, 31.15
73, Male, LG glioma, Supratentorial, 90, 2.64, SRT, 0, 20.13
75, Male, Other, Supratentorial, 100, 24.91, SRT, 0, 19.74
84, Male, HG glioma, Supratentorial, 80, 0.16, SRT, 1, 20.69
85, Male, HG glioma, Supratentorial, 80, 19.81, SRT, 1, 6.39
86, Male, Meningioma, Supratentorial, 90, 2.5, SRT, 0, 32.82
87, Male, Meningioma, Supratentorial, 90, 2.02, SRS, 0, 42.07
keshavaa@Keshavaa:~/lab5$ grep -c 'Supratentorial' male.txt
34

```

(4) Find out which patient has the lowest ki value. (Hint: Use sort for this, it's easier)

```

keshavaa@Keshavaa:~/lab5$ sort -t ',' -k4 -n BrainCancer.csv
10, Male, HG glioma, Supratentorial, 100, 2.53, SRT, 0, 11.48
11, Male, LG glioma, Supratentorial, 80, 0.14, SRT, 1, 35.93
12, Female, Meningioma, Infratentorial, 90, 6.54, SRS, 0, 34.26
13, Female, Meningioma, Infratentorial, 90, 0.63, SRS, 0, 32.98
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
17, Female, Other, Infratentorial, 60, 24, SRT, 1, 6.82
18, Male, HG glioma, Supratentorial, 90, 10.8, SRT, 0, 82.56
19, Male, Meningioma, Supratentorial, 80, 13.49, SRS, 1, 6.92
1, Female, Meningioma, Infratentorial, 90, 6.11, SRS, 0, 57.64
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
23, Female, Other, Infratentorial, 80, 2.11, SRS, 0, 10.49
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
29, Male, Meningioma, Supratentorial, 60, 3.81, SRT, 0, 36.1
2, Male, HG glioma, Supratentorial, 90, 19.35, SRT, 1, 8.98
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
33, Female, Other, Infratentorial, 70, 13.45, SRT, 1, 10.82

```


- (5) Print out the output by searching for the patterns 'SRS' as well as 'infratentorial'. How many such entries are there?

```
keshavaa@Keshavaa:~/lab5$ grep 'SRS' BrainCancer.csv > SRS.csv
keshavaa@Keshavaa:~/lab5$ grep 'Infratentorial' SRS.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
```

- (6) List the patients who have survival times more than 50 months.

```
keshavaa@Keshavaa:~/lab5$ sort -t ',' -k9 -n BrainCancer.csv > Sorted50.csv
keshavaa@Keshavaa:~/lab5$ ls
BrainCancer.csv female.txt lab5.pdf LinesWithMeningioma.out male.txt Sorted50.csv Sorted50.out Sorted.out sorted_time.csv
keshavaa@Keshavaa:~/lab5$ head -14n Sorted50.csv
head: invalid trailing option -- n
Try 'head --help' for more information.
keshavaa@Keshavaa:~/lab5$ head -n14 Sorted50.csv
,sex,diagnosis,loc,ki,gtv,stereo,status,time
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
83,Male,LG glioma,Infratentorial,90,30.41,SRT,0,1.18
49,Male,Meningioma,Supratentorial,70,0.97,SRT,1,1.41
80,Female,Meningioma,Infratentorial,70,2.94,SRS,0,1.54
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
```

- (7) List the patients who have HG glioma and ave survival times more than 50 months. How many are there?

```
keshavaa@Keshavaa:~/lab5$ sort -t ',' -k8 -n hg.csv > hg_sorted.csv
sort: cannot read hg.csv: No such file or directory
keshavaa@Keshavaa:~/lab5$ sort -t ',' -k8 -n HG.csv > hg_sorted.csv
keshavaa@Keshavaa:~/lab5$ ls
BrainCancer.csv female.txt HG.csv hg_sorted.csv lab5.pdf LinesWithMeningioma.out male.txt Sorted50.csv Sorted50.out Sorted.out sorted_time.csv SRS.csv
keshavaa@Keshavaa:~/lab5$ cat hg_sorted.csv
47,Male,HG glioma,Supratentorial,80,29.27,SRT,0,5.15
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
10,Male,HG glioma,Supratentorial,100,2.53,SRT,0,11.48
63,Female,HG glioma,Supratentorial,40,22.87,SRT,1,3.38
67,Female,HG glioma,Supratentorial,80,7.59,SRT,1,4.56
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
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
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
51,Female,HG glioma,Supratentorial,90,0.04,SRT,0,31.67
57,Male,HG glioma,Infratentorial,80,0.22,SRS,0,33.67
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
74,Female,HG glioma,Supratentorial,80,0.19,SRT,1,11.02
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
42,Male,HG glioma,Supratentorial,90,0.28,SRT,1,16.43
55,Female,HG glioma,Supratentorial,80,0.63,SRT,1,16.92
58,Male,HG glioma,Supratentorial,80,3.75,SRT,1,19.9
84,Male,HG glioma,Supratentorial,80,0.16,SRT,1,20.69
81,Female,HG glioma,Supratentorial,80,15.45,SRT,1,46.16
```

```

keshavaa@Keshavaa:~/lab5$ sort -t',' -k8 -n -r HG.csv > hg_sorted.csv
keshavaa@Keshavaa:~/lab5$ cat hg_sorted.csv
81,Female,HG glioma,Supratentorial,80,15.45,SRT,1,46.16
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
74,Female,HG glioma,Supratentorial,80,0.19,SRT,1,11.02
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
57,Male,HG glioma,Infratentorial,80,0.22,SRS,0,33.67
51,Female,HG glioma,Supratentorial,90,0.04,SRT,0,31.67
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
67,Female,HG glioma,Supratentorial,80,7.59,SRT,1,4.56
63,Female,HG glioma,Supratentorial,40,22.87,SRT,1,3.38
10,Male,HG glioma,Supratentorial,100,2.53,SRT,0,11.48
28,Male,HG glioma,Supratentorial,70,33.69,SRT,1,0.07
47,Male,HG glioma,Supratentorial,80,29.27,SRT,0,5.15
keshavaa@Keshavaa:~/lab5$ head -n 1 hg_sorted.csv
81,Female,HG glioma,Supratentorial,80,15.45,SRT,1,46.16

```

There is only one Patient who has HG glioma and average survival times more than 50 months

- (8) List the patients who have LG glioma with location supratentorial and survival times less than 30 months. How many are there?

```

keshavaa@Keshavaa:~/lab5$ grep "LG glioma" BrainCancer.csv > Lg.csv
keshavaa@Keshavaa:~/lab5$ cat Lg.csv
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
50,Female,LG glioma,Supratentorial,80,0.19,SRS,0,11.51
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
73,Male,LG glioma,Supratentorial,90,2.64,SRT,0,20.13
83,Male,LG glioma,Infratentorial,90,30.41,SRT,0,1.18
keshavaa@Keshavaa:~/lab5$ grep -w "Supratentorial" Lg.csv
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
50,Female,LG glioma,Supratentorial,80,0.19,SRS,0,11.51
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
73,Male,LG glioma,Supratentorial,90,2.64,SRT,0,20.13
keshavaa@Keshavaa:~/lab5$ grep -w "Supratentorial" Lg.csv > Lg_sorted.csv
keshavaa@Keshavaa:~/lab5$ cat Lg_sorted.csv
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
50,Female,LG glioma,Supratentorial,80,0.19,SRS,0,11.51
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
73,Male,LG glioma,Supratentorial,90,2.64,SRT,0,20.13
keshavaa@Keshavaa:~/lab5$ sort -t',' -k9 -n -r Lg_sorted.csv > lg_final
keshavaa@Keshavaa:~/lab5$ head -n4 lg_final
65,Male,LG glioma,Supratentorial,80,9.58,SRT,0,78.75
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
8,Male,LG glioma,Supratentorial,80,12.37,SRT,0,42.1
11,Male,LG glioma,Supratentorial,80,0.14,SRT,1,35.93

```

There are 4 patients who have LG glioma with location supratentorial and survival time less than 30 months.

- (9) By default does grep ignore or not ignore case? Demonstrate this by using the appropriate option and by running the grep command without this option.

Normal :- Case-sensitive (default)

```
keshavaa@Keshavaa:~/lab5$ grep "Female" BrainCancer.csv
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
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
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
20,Female,Meningioma,Supratentorial,90,2.5,SRT,0,30.16
21,Female,Meningioma,Supratentorial,80,2.82,SRS,0,24.39
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
```

Modify :- Case-insensitive (-i option)

```
keshavaa@Keshavaa:~/lab5$ grep -i 'female' BrainCancer.csv
1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
3,Female,Meningioma,Infratentorial,70,7.95,SRS,0,26.46
4,Female,LG glioma,Supratentorial,80,7.61,SRT,1,47.8
6,Female,Meningioma,Supratentorial,80,4.82,SRS,0,52.75
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
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
20,Female,Meningioma,Supratentorial,90,2.5,SRT,0,30.16
21,Female,Meningioma,Supratentorial,80,2.82,SRS,0,24.39
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
```

- (10) List the patients who are dead at the end of the study. How many are there? Find another way to listing this set of patients (look up grep man pages to look for a specific option to select non-matching lines)

```
keshavaa@Keshavaa:~/lab5$ grep ',1' BrainCancer.csv > dead.txt
keshavaa@Keshavaa:~/lab5$ cat dead.txt
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
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
16,Female,HG glioma,Supratentorial,70,11.38,SRS,1,7.05
17,Female,Other,Infratentorial,60,24,SRT,1,6.82
18,Male,HG glioma,Supratentorial,90,10.8,SRT,0,82.56
19,Male,Meningioma,Supratentorial,80,13.49,SRS,1,6.92
22,Male,HG glioma,Supratentorial,70,14.44,SRT,1,14
23,Female,Other,Infratentorial,80,2.11,SRS,0,10.49
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
```

```
keshavaa@Keshavaa:~/lab5$ wc -l dead.txt
56 dead.txt
keshavaa@Keshavaa:~/lab5$
```

56 pateints are dead .

(11) Let's list the patients who have their cancer in infratentorial location. How many are there?

How do I restrict the output to first ten patients?

```
keshavaa@Keshavaa:~/lab5$ head -n 10 infra.txt
keshavaa@Keshavaa:~/lab5$ grep "Infratentorial" BrainCancer.csv > infra.txt
keshavaa@Keshavaa:~/lab5$ ls
BrainCancer.csv  female.txt  hg_sorted.csv  lab5.pdf  lg_final  LinesWithMeningoma.out  Sorted50.csv  Sorted.out  SRS.csv
dead.txt         HG.csv     infra.txt      Lg.csv    Lg_sorted.csv  male.txt      Sorted50.out  sorted_time.csv
keshavaa@Keshavaa:~/lab5$ cat infra.txt
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
keshavaa@Keshavaa:~/lab5$ cat -w infra.txt
cat: invalid option -- 'w'
Try 'cat --help' for more information.
keshavaa@Keshavaa:~/lab5$ head -n 10 infra.txt
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
keshavaa@Keshavaa:~/lab5$ wc -l infra.txt
19 infra.txt
keshavaa@Keshavaa:~/lab5$
```

(12) Create an archive file by combining the outputs of questions 1-5.

```
keshavaa@Keshavaa:~/lab5$ tar -cvf Q1_to_Q5.tar LinesWithMeningoma.out male.txt female.txt SRS.csv
LinesWithMeningoma.out
male.txt
female.txt
SRS.csv
keshavaa@Keshavaa:~/lab5$ cat Q1_to_Q5.tar
LinesWithMeningoma.out0000664000175000017500000000446315044443431015513 0ustar  keshavaaKeshavaa1,Female,Meningioma,Infratentorial,90,6.11,SRS,0,57.64
```

(13) Create a zipped and archived file by combining the outputs of questions 6-11.

```
keshavaa@Keshavaa:~/lab5$ tar -cvf Q6_to_Q11.tar sorted_time.csv hg_sorted.csv lg_final dead.txt infra.txt
sorted_time.csv
hg_sorted.csv
lg_final
dead.txt
infra.txt
keshavaa@Keshavaa:~/lab5$
```

(14) List and extract the contents of the archive file created in (12) to a new directory and list the contents of the new directory.

```
keshavaa@Keshavaa: ~/lab1$ mkdir extracted_Q1_Q5
mkdir: cannot create directory 'extracted_Q1_Q5': File exists
keshavaa@Keshavaa: ~/lab1$ tar -xvf Q1_to_Q5.tar -C extracted_Q1_Q5
LinesWithMeningoma.out
male.txt
female.txt
SRS.csv
keshavaa@Keshavaa: ~/lab1$ ls extracted_Q1_Q5
female.txt  LinesWithMeningoma.out  male.txt  SRS.csv
keshavaa@Keshavaa: ~/lab1$
```

(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.

```
keshavaa@Keshavaa: ~/lab1$ mkdir extracted_Q6_Q11
keshavaa@Keshavaa: ~/lab1$
New Volume
keshavaa@Keshavaa: ~/lab1$
tar -xvf Q6_to_Q11.tar.gz -C extracted_Q6_Q11
sorted_time.csv
hg_sorted.csv
lg_final
lg_final
dead.txt
infra.txt
keshavaa@Keshavaa: ~/lab1$
ls extracted_Q6_Q11
dead.txt  hg_sorted.csv  infra.txt  lg_final  sorted_time.csv
keshavaa@Keshavaa: ~/lab1$
```