

## LAB5

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(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.

Ans) To look for pattern Meningioma in the data file and redirect it to the new file we use the command:

- `grep "Meningioma" BrainCancer.csv > LinesWithMeningioma.out`

Then to see the content of the new file use the command:

- `cat LinesWithMeningioma`

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep "Meningioma" BrainCancer.csv > LinesWithMeningioma.out
```

```
ibab@IBAB-RA-Comp201:~/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
```

```
87,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-Comp201:~/LAB5$ echo "Command used: grep /"Meningioma/" BrainCancer.csv > LinesWithMeningioma.out
```

```
Command used: grep /Meningioma/ BrainCancer.csv > LinesWithMeningioma.out
```

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

Ans) To count the number of male in the study we use the command:

- `grep -c "Male" BrainCancer.csv`

To count the number of female in the study use the command:

- `grep -c "Female" BrainCancer.csv`

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -c "Male" BrainCancer.csv
43
ibab@IBAB-RA-Comp201:~/LAB5$ grep -c "Female" BrainCancer.csv
45
```

There were total of 43 male and 45 female in this study.

(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.

Ans) Meningioma

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep Supratentorial BrainCancer.csv > Supratentorialsorted.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep -c Male Supratentorialsorted.out
34
ibab@IBAB-RA-Comp201:~/LAB5$
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -i Infratentorial BrainCancer.csv > Infratentorial BrainCancer.csv > Infratentorialsorted.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep -ci Female Infratentorialsorted.out
20
ibab@IBAB-RA-Comp201:~/LAB5$
```

(4) Find out which patient has the lowest ki value.

Ans) To find out the patient with lowest ki value use command:

- `sort -n -t ',' -k5,5 BrainCancer.csv`

```
ibab@IBAB-RA-Comp201:~/LAB5$ sort -n -t ',' -k5,5 BrainCancer.csv
,sex,diagnosis,loc,ki,gtv,sterео,status,time
63,Female,HG glioma,Supratentorial,40,22.87,SRT,1,3.38
```

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

Ans) First we created an output file for SRS after sorting it using the command:

- `grep -e 'SRS' BrainCancer.csv > Srsbraincancer.csv`

Then we use command:

- `grep 'Infratentorial' Srsbraincancer.csv`

It gives us the list

- `grep 'Infratentorial' -c Srsbraincancer.csv`

This command is used to list the number of entries.

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -e 'SRS' BrainCancer.csv > Srsbraincancer.csv
ibab@IBAB-RA-Comp201:~/LAB5$ ls
BrainCancer.csv LinesWithMeningioma.out Srsbraincancer.csv
ibab@IBAB-RA-Comp201:~/LAB5$ cat srsbraincancer.csv
cat: srsbraincancer.csv: No such file or directory
ibab@IBAB-RA-Comp201:~/LAB5$ cat Srsbraincancer.csv
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
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep 'Infratentorial' Srsbraincancer.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-Comp201:~/LAB5$ grep 'Infratentorial' -c Srsbraincancer.csv
11
```

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

```
ibab@IBAB-RA-Comp201:~/LAB5$ sort -t "," -k 9 -n -r BrainCancer.csv
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
```



```

ibab@IBAB-RA-Comp201:~/LAB5$ sort -t "," -k 9 -n -r BrainCancer.csv -o months.out
ibab@IBAB-RA-Comp201:~/LAB5$ head -n14 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
ibab@IBAB-RA-Comp201:~/LAB5$

```

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

Ans)

```

ibab@IBAB-RA-Comp201:~/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

```

In order to get patients with HG glioma we used the command:

- `grep "HG glioma" months.out`

As we get the list, we will count the patients with survival time more than 50 months.

- There was only one patient with HG glioma and survival time 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?

Ans)

```
ibab@IBAB-RA-Comp201:~/LAB5$ sort -t "," -k 9 -n BrainCancer.csv -o Lesst30months.out
ibab@IBAB-RA-Comp201:~/LAB5$ head -50 Lesst30months.out
,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
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ head -50 Lesst30months.out > 30months.out
ibab@IBAB-RA-Comp201:~/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
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -i Supratentorial 30months.out > Supratentorial30months.out
```

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep -i "LG glioma" Supratentorial30months.out
31,Female,LG glioma,Supratentorial,80,0.85,SRS,1,6.1
50,Female,LG glioma,Supratentorial,80,0.19,SRS,0,11.51
73,Male,LG glioma,Supratentorial,90,2.64,SRT,0,20.13
26,Male,LG glioma,Supratentorial,90,4.23,SRT,1,25.02
ibab@IBAB-RA-Comp201:~/LAB5$ grep -ci "LG glioma" Supratentorial30months.out
4
ibab@IBAB-RA-Comp201:~/LAB5$
```



(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.

Ans) By default grep does not ignore case but it does perform case sensitive searches.

```
ibab@IBAB-RA-Comp201:~/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
```

(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)

Ans) In order to see the number of patients dead at the end of the study, as we know that 0=alive and 1=dead, we use the command

- `grep "1," BrainCancer.csv`

This will list all the patients that are dead at the end of the study

```
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
61, Female, HG glioma, Supratentorial, 80, 12.08, SRT, 1, 7.25
62, Male, Meningioma, Supratentorial, 80, 11.51, SRT, 1, 14.62
```

In order to get the number of the dead patients by the end of the study we will use the command:

- `grep -c ",1," BrainCancer.csv`

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

This will give us the number of dead patients i.e 35

(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?

Ans) In order to get the list of patients that have cancer in their infratentorial region we will use the command:

- `grep "Infratentorial" BrainCancer.csv`

This will list all the patients with cancer in infratentorial region.

To get the count of these patients we use the command:

- `grep -c "Infratentorial" BrainCancer.csv`



There were total 19 such patients

```
ibab@IBAB-RA-Comp201:~/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-Comp201:~/LAB5$ grep -c "Infratentorial" BrainCancer.csv
19
```

Now in order to restrict the output to first 10 patients we will first make a folder for the patients with cancer in infratentorial region, we will use the command:

- `grep "Infratentorial" BrainCancer.csv > Infratentorialsorted.out`

This command will make a separate folder, now in order to restrict the output to first 10 patients we'll use the command:

- `head -n10 Infratentorialsorted.out`

We will get the list

```
ibab@IBAB-RA-Comp201:~/LAB5$ grep "Infratentorial" BrainCancer.csv > Infratentorialsorted.out
ibab@IBAB-RA-Comp201:~/LAB5$ Head -n10 Infratentorialsorted.out
Command 'Head' not found, did you mean:
  command 'head' from deb coreutils (9.4-2ubuntu2)
Try: sudo apt install <deb name>
ibab@IBAB-RA-Comp201:~/LAB5$ head -n10 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,1,51.02
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
ibab@IBAB-RA-Comp201:~/LAB5$
```



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

Ans) In order to create an archive file by combining the outputs of question 1 to 5, first we have to create separate files for each output.

Then in order to create the output file we will give command:

- `tar -cvf outputs.tar LinesWithMeningioma.out Maleesorted.out Femaleesorted.out Supratentorialsorted.out Infratentorialsorted.out Ki.out lowestki.out`

This command creates an archive file of all the files created of outputs of 1-5.

```
ibab@IBAB-RA-Comp201:~/LAB5$ sort -n -t ',' -k5,5 BrainCancer.csv > Ki.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep 'Infratentorial Srsbraincancer.csv > lowestki.out
> ^C
ibab@IBAB-RA-Comp201:~/LAB5$ grep 'Infratentorial' Srsbraincancer.csv > lowestki.out
ibab@IBAB-RA-Comp201:~/LAB5$ ls
BrainCancer.csv      Infratentorialsorted.out  lowestki.out          Srsbraincancer.csv
Femaleesorted.out    Ki.out                    Maleesorted.out       Supratentorialsorted.out
Infratentorial       LinesWithMeningioma.out  months.out
ibab@IBAB-RA-Comp201:~/LAB5$ tar -cvf outputs.tar LinesWithMeningioma.out Maleesorted.out Fema
leesorted.out Supratentorialsorted.out Infratentorialsorted.out Ki.out lowestki.out
LinesWithMeningioma.out
Maleesorted.out
Femaleesorted.out
Supratentorialsorted.out
Infratentorialsorted.out
Ki.out
lowestki.out
ibab@IBAB-RA-Comp201:~/LAB5$ cat outputs.tar
LinesWithMeningioma.out0000664000175100017510000000446315043113037014105 0ustar  ibabibab1,Fem
Trash ngingioma,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) Create a zipped and archived file by combining the outputs of questions 6-11.

Ans)

First we need to create separate files for each output from question 6 to 11 using the command below:

```
ibab@IBAB-RA-Comp201:~/LAB5$ head -n14 months.out > 14monthss.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep "HG glioma" months.out > HGgliomaa.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep -i "LG glioma" Supratentorial30months.out > LGglioma.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep -i SuprATenToriAL BrainCancer.csv > i.out
ibab@IBAB-RA-Comp201:~/LAB5$ grep ",1," BrainCancer.csv > 1.out
ibab@IBAB-RA-Comp201:~/LAB5$ head -n10 Infratentorialsorted.out > n10infra.out
ibab@IBAB-RA-Comp201:~/LAB5$ ls
14monthss.out      Infratentorialsorted.out  Maleesorted.out
1.out              i.out                     months.out
30months.out       Ki.out                    n10infra.out
BrainCancer.csv    Lesst30months.out        outputs.tar
Femaleesorted.out  LGglioma.out              Srsbraincancer.csv
HGgliomaa.out      LinesWithMeningioma.out  Supratentorial30months.out
Infratentorial     lowestki.out              Supratentorialsorted.out
```

Then in order to create a zipped and archived file of the combined output of 6-11 we used the command:

- `tar -cvzf outputs2.tar 14monthss.out HGgliomaa.out LGglioma.out i.out n10infra.out`

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

(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.

Ans)

In order to list and extract the contents of the archive file created in 12 to a new directory we first use the command:

- `tar -xvf outputs.tar`

```
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
```

To check whether the contents of archive file has been transferred to a new directory we do this step.

```
ibab@IBAB-RA-Comp201:~/LAB5$ cd out1extract
ibab@IBAB-RA-Comp201:~/LAB5/out1extract$ cat outputs.tar
LinesWithMeningioma.out0000664000175100017510000000446315043113037014105 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.

Ans)

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



