1) I created a new directory Lab4 under which the file Heart.csv is stored.

- To create symbolic link we use ***ln -s.*** whereas to create hardlink we simply use ***ln.***
- If we use the same name for the links it gives a message saying FILE ALREADY EXISTS, therefore not letting us create another file of same name.
- To prove the links were created correctly, we use **ls -l** command. It shows that the size of the hard link and soft link are different to each other , whereas hardlink file is of the same size as the orignal file.

```
ibab@IBAB-RA-Comp203:~$ cd Lab4
ibab@IBAB-RA-Comp203:~/Lab4$ ln heart.csv heart_hlink
ln: failed to access 'heart.csv': No such file or directory
ibab@IBAB-RA-Comp203:~/Lab4$ ln Heart heart_hlink
ln: failed to access 'Heart': No such file or directory
ibab@IBAB-RA-Comp203:~/Lab4$ ln Heart.csv heart_hlink
ibab@IBAB-RA-Comp203:~/Lab4$ ln -s Heart.csv heart_slink
ibab@IBAB-RA-Comp203:~/Lab4$ ls -l
total 40
-rw-rw-r-- 2 ibab ibab 19925 Jul 31 14:06 Heart.csv
-rw-rw-r-- 2 ibab ibab 19925 Jul 31 14:06 heart_hlink
lrwxrwxrwx 1 ibab ibab     9 Jul 31 14:21 heart_slink -> Heart.csv
ibab@IBAB-RA-Comp203:~/Lab4$
```

```
ibab@IBAB-RA-Comp203:~/Lab4$ ls -l
total 40
-rw-rw-r-- 2 ibab ibab 19925 Jul 31 14:06 Heart.csv
-rw-rw-r-- 2 ibab ibab 19925 Jul 31 14:06 heart_hlink
lrwxrwxrwx 1 ibab ibab     9 Jul 31 14:21 heart_slink -> Heart.csv
ibab@IBAB-RA-Comp203:~/Lab4$ ln -s Heart.csv heart_hlink
ln: failed to create symbolic link 'heart_hlink': File exists
ibab@IBAB-RA-Comp203:~/Lab4$
```

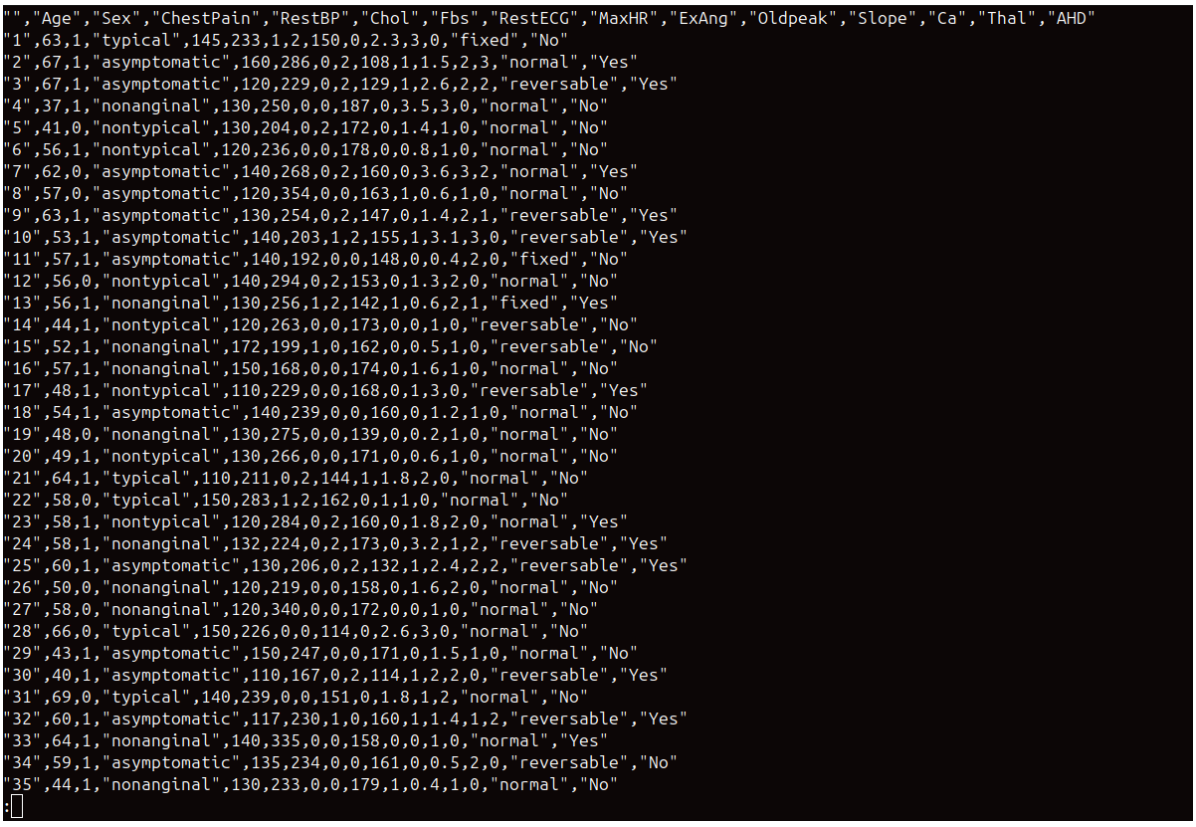
2) To check the filetype of the file Heart.csv, we use the command ***file <filename>***, which shows the filetype as ASCII text or in UTF.

```
ibab@IBAB-RA-Comp203:~/Lab4$ file Heart.csv
Heart.csv: CSV ASCII text
ibab@IBAB-RA-Comp203:~/Lab4$
```

3)

- ***more*** command reads the entire file before displaying the contents. It reads the file and prints it in an understandable manner.
- ***less*** command prints the entire file in a detailed manner. It prints all the contents of the file with better utility.
- The number of pages can simply be determined by the number of times we press the spacebar which in this case is ***7*** times.

```
ibab@IBAB-RA-Comp203:~/Lab4$ more Heart.csv
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Ol
dpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
"10",53,1,"asymptomatic",140,203,1,2,155,1,3.1,3,0,"reversable","Yes"
"11",57,1,"asymptomatic",140,192,0,0,148,0,0.4,2,0,"fixed","No"
"12",56,0,"nontypical",140,294,0,2,153,0,1.3,2,0,"normal","No"
"13",56,1,"nonanginal",130,256,1,2,142,1,0.6,2,1,"fixed","Yes"
"14",44,1,"nontypical",120,263,0,0,173,0,0,1,0,"reversable","No"
"15",52,1,"nonanginal",172,199,1,0,162,0,0.5,1,0,"reversable","No"
"16",57,1,"nonanginal",150,168,0,0,174,0,1.6,1,0,"normal","No"
"17",48,1,"nontypical",110,229,0,0,168,0,1,3,0,"reversable","Yes"
"18",54,1,"asymptomatic",140,239,0,0,160,0,1.2,1,0,"normal","No"
"19",48,0,"nonanginal",130,275,0,0,139,0,0.2,1,0,"normal","No"
"20",49,1,"nontypical",130,266,0,0,171,0,0.6,1,0,"normal","No"
"21",64,1,"typical",110,211,0,2,144,1,1.8,2,0,"normal","No"
"22",58,0,"typical",150,283,1,2,162,0,1,1,0,"normal","No"
```



```
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Oldpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
"10",53,1,"asymptomatic",140,203,1,2,155,1,3.1,3,0,"reversable","Yes"
"11",57,1,"asymptomatic",140,192,0,0,148,0,0.4,2,0,"fixed","No"
"12",56,0,"nontypical",140,294,0,2,153,0,1.3,2,0,"normal","No"
"13",56,1,"nonanginal",130,256,1,2,142,1,0.6,2,1,"fixed","Yes"
"14",44,1,"nontypical",120,263,0,0,173,0,0,1,0,"reversable","No"
"15",52,1,"nonanginal",172,199,1,0,162,0,0.5,1,0,"reversable","No"
"16",57,1,"nonanginal",150,168,0,0,174,0,1.6,1,0,"normal","No"
"17",48,1,"nontypical",110,229,0,0,168,0,1,3,0,"reversable","Yes"
"18",54,1,"asymptomatic",140,239,0,0,160,0,1.2,1,0,"normal","No"
"19",48,0,"nonanginal",130,275,0,0,139,0,0.2,1,0,"normal","No"
"20",49,1,"nontypical",130,266,0,0,171,0,0.6,1,0,"normal","No"
"21",64,1,"typical",110,211,0,2,144,1,1.8,2,0,"normal","No"
"22",58,0,"typical",150,283,1,2,162,0,1,1,0,"normal","No"
"23",58,1,"nontypical",120,284,0,2,160,0,1.8,2,0,"normal","Yes"
"24",58,1,"nonanginal",132,224,0,2,173,0,3.2,1,2,"reversable","Yes"
"25",60,1,"asymptomatic",130,206,0,2,132,1,2.4,2,2,"reversable","Yes"
"26",50,0,"nonanginal",120,219,0,0,158,0,1.6,2,0,"normal","No"
"27",58,0,"nonanginal",120,340,0,0,172,0,0,1,0,"normal","No"
"28",66,0,"typical",150,226,0,0,114,0,2.6,3,0,"normal","No"
"29",43,1,"asymptomatic",150,247,0,0,171,0,1.5,1,0,"normal","No"
"30",40,1,"asymptomatic",110,167,0,2,114,1,2,2,0,"reversable","Yes"
"31",69,0,"typical",140,239,0,0,151,0,1.8,1,2,"normal","No"
"32",60,1,"asymptomatic",117,230,1,0,160,1,1.4,1,2,"reversable","Yes"
"33",64,1,"nonanginal",140,335,0,0,158,0,0,1,0,"normal","Yes"
"34",59,1,"asymptomatic",135,234,0,0,161,0,0.5,2,0,"reversable","No"
"35",44,1,"nonanginal",130,233,0,0,179,1,0.4,1,0,"normal","No"
:
```

4) To get the first 35 lines of the given file we use ***head*** command and mention the number of lines we want to print with ***-n.***

```
ibab@IBAB-RA-Comp203:~/Lab4$ head -n 35 Heart.csv
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Oldpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
"10",53,1,"asymptomatic",140,203,1,2,155,1,3.1,3,0,"reversable","Yes"
"11",57,1,"asymptomatic",140,192,0,0,148,0,0.4,2,0,"fixed","No"
"12",56,0,"nontypical",140,294,0,2,153,0,1.3,2,0,"normal","No"
"13",56,1,"nonanginal",130,256,1,2,142,1,0.6,2,1,"fixed","Yes"
"14",44,1,"nontypical",120,263,0,0,173,0,0,1,0,"reversable","No"
"15",52,1,"nonanginal",172,199,1,0,162,0,0.5,1,0,"reversable","No"
"16",57,1,"nonanginal",150,168,0,0,174,0,1.6,1,0,"normal","No"
"17",48,1,"nontypical",110,229,0,0,168,0,1,3,0,"reversable","Yes"
"18",54,1,"asymptomatic",140,239,0,0,160,0,1.2,1,0,"normal","No"
"19",48,0,"nonanginal",130,275,0,0,139,0,0.2,1,0,"normal","No"
"20",49,1,"nontypical",130,266,0,0,171,0,0.6,1,0,"normal","No"
"21",64,1,"typical",110,211,0,2,144,1,1.8,2,0,"normal","No"
"22",58,0,"typical",150,283,1,2,162,0,1,1,0,"normal","No"
"23",58,1,"nontypical",120,284,0,2,160,0,1.8,2,0,"normal","Yes"
"24",58,1,"nonanginal",132,224,0,2,173,0,3.2,1,2,"reversable","Yes"
"25",60,1,"asymptomatic",130,206,0,2,132,1,2.4,2,2,"reversable","Yes"
"26",50,0,"nonanginal",120,219,0,0,158,0,1.6,2,0,"normal","No"
"27",58,0,"nonanginal",120,340,0,0,172,0,0,1,0,"normal","No"
"28",66,0,"typical",150,226,0,0,114,0,2.6,3,0,"normal","No"
"29",43,1,"asymptomatic",150,247,0,0,171,0,1.5,1,0,"normal","No"
"30",40,1,"asymptomatic",110,167,0,2,114,1,2,2,0,"reversable","Yes"
"31",69,0,"typical",140,239,0,0,151,0,1.8,1,2,"normal","No"
"32",60,1,"asymptomatic",117,230,1,0,160,1,1.4,1,2,"reversable","Yes"
"33",64,1,"nonanginal",140,335,0,0,158,0,0,1,0,"normal","Yes"
"34",59,1,"asymptomatic",135,234,0,0,161,0,0.5,2,0,"reversable","No"
ibab@IBAB-RA-Comp203:~/Lab4$
```

5) To get the last 15 lines of the data files, we use the command ***tail -n***, the -n allowing us to enter the number of lines we want to be printed.

```
ibab@IBAB-RA-Comp203:~/Lab4$ tail -n 15 Heart.csv
"289",56,1,"nontypical",130,221,0,2,163,0,0,1,0,"reversable","No"
"290",56,1,"nontypical",120,240,0,0,169,0,0,3,0,"normal","No"
"291",67,1,"nonanginal",152,212,0,2,150,0,0.8,2,0,"reversable","Yes"
"292",55,0,"nontypical",132,342,0,0,166,0,1.2,1,0,"normal","No"
"293",44,1,"asymptomatic",120,169,0,0,144,1,2.8,3,0,"fixed","Yes"
"294",63,1,"asymptomatic",140,187,0,2,144,1,4,1,2,"reversable","Yes"
"295",63,0,"asymptomatic",124,197,0,0,136,1,0,2,0,"normal","Yes"
"296",41,1,"nontypical",120,157,0,0,182,0,0,1,0,"normal","No"
"297",59,1,"asymptomatic",164,176,1,2,90,0,1,2,2,"fixed","Yes"
"298",57,0,"asymptomatic",140,241,0,0,123,1,0.2,2,0,"reversable","Yes"
"299",45,1,"typical",110,264,0,0,132,0,1.2,2,0,"reversable","Yes"
"300",68,1,"asymptomatic",144,193,1,0,141,0,3.4,2,2,"reversable","Yes"
"301",57,1,"asymptomatic",130,131,0,0,115,1,1.2,2,1,"reversable","Yes"
"302",57,0,"nontypical",130,236,0,2,174,0,0,2,1,"normal","Yes"
"303",38,1,"nonanginal",138,175,0,0,173,0,0,1,NA,"normal","No"
ibab@IBAB-RA-Comp203:~/Lab4$
```

6) The ***History*** command gives us last few commands that were entered by the user.

```
ibab@IBAB-RA-Comp203:~/Lab4$ history
 1035  ./pycharm.sh
 1036  clear
 1037  cd Vindhya/pycharm_Vindhya/pycharm-community-2024.2.1/bin
 1038  ./pycharm.sh
 1039  cd Vibn
 1040  cd Vindhya/
 1041  cd pycharm_Vindhya/
 1042  ls
 1043  cd ..
 1044  cd pycharm
 1045  ls
 1046  cd pyt
 1047  cd pythonProject/
```

The history command also gives the command code along with the command name. Here the second last command is tail -n of the code 2032.

```
 2026  clear
 2027  head -n 35 Heart.csv
 2028  clear
 2029  ls -l
 2030  ln -s Heart.csv heart_hlink
 2031  clear
 2032  tail -n 15 Heart.csv
 2033  clear
 2034  history
ibab@IBAB-RA-Comp203:~/Lab4$
```

To print the second last command we use both the process ID and the first letter of the command.

```
/home/ibab/Lab4
ibab@IBAB-RA-Comp203:~/Lab4$ !t 2032
tail -n 15 Heart.csv 2032
==> Heart.csv <==
"289",56,1,"nontypical",130,221,0,2,163,0,0,1,0,"reversable","No"
"290",56,1,"nontypical",120,240,0,0,169,0,0,3,0,"normal","No"
"291",67,1,"nonanginal",152,212,0,2,150,0,0.8,2,0,"reversable","Ye
s"
"292",55,0,"nontypical",132,342,0,0,166,0,1.2,1,0,"normal","No"
"293",44,1,"asymptomatic",120,169,0,0,144,1,2.8,3,0,"fixed","Yes"
"294",63,1,"asymptomatic",140,187,0,2,144,1,4,1,2,"reversable","Ye
s"
"295",63,0,"asymptomatic",124,197,0,0,136,1,0,2,0,"normal","Yes"
"296",41,1,"nontypical",120,157,0,0,182,0,0,1,0,"normal","No"
"297",59,1,"asymptomatic",164,176,1,2,90,0,1,2,2,"fixed","Yes"
"298",57,0,"asymptomatic",140,241,0,0,123,1,0.2,2,0,"reversable","
Yes"
"299",45,1,"typical",110,264,0,0,132,0,1.2,2,0,"reversable","Yes"
```

7)

I. Here, we Sort the data according to the first column, and save the output in a new file called col1_sorted.out.

```
ibab@IBAB-RA-Comp203:~/Lab4$ head Heart.csv
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Oldpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
ibab@IBAB-RA-Comp203:~/Lab4$ sort -t ',' -k 1 -n Heart.csv > col1_sorted.out
ibab@IBAB-RA-Comp203:~/Lab4$ head col1_sorted.out
"100",48,1,"asymptomatic",122,222,0,2,186,0,0,1,0,"normal","No"
"101",45,1,"asymptomatic",115,260,0,2,185,0,0,1,0,"normal","No"
"102",34,1,"typical",118,182,0,2,174,0,0,1,0,"normal","No"
"103",57,0,"asymptomatic",128,303,0,2,159,0,0,1,1,"normal","No"
"104",71,0,"nonanginal",110,265,1,2,130,0,0,1,1,"normal","No"
"10",53,1,"asymptomatic",140,203,1,2,155,1,3.1,3,0,"reversable","Yes"
"105",49,1,"nonanginal",120,188,0,0,139,0,2,2,3,"reversable","Yes"
"106",54,1,"nontypical",108,309,0,0,156,0,0,1,0,"reversable","No"
"107",59,1,"asymptomatic",140,177,0,0,162,1,0,1,1,"reversable","Yes"
"108",57,1,"nonanginal",128,229,0,2,150,0,0.4,2,1,"reversable","Yes"
ibab@IBAB-RA-Comp203:~/Lab4$
```

ii. Here, we sort the data according to the 'Age' column and save the the output in a new file called age_sorted.out.

We use sort -c along with the filename to see if the new file was sorted or not.

```
ibab@IBAB-RA-Comp203:~/Lab4$ sort -t ',' -k 2 -n Heart.csv > age_sorted.out
ibab@IBAB-RA-Comp203:~/Lab4$ ls age_sorted.out
age_sorted.out
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c

age_sorted.out
>
^C
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c age_sorted.out
sort: age_sorted.out:2: disorder: "133",29,1,"nontypical",130,204,0,2,202,0,0,
1,0,"normal","No"
ibab@IBAB-RA-Comp203:~/Lab4$
```

iii. Here, we sort in a reverse manner according to the 'RestBP' column, and save output in a new file called restbp_revsort.out. We check if the file is sorted using sort -c <filename>

```
ibab@IBAB-RA-Comp203:~/Lab4$ head Heart.csv
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Ol
dpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
ibab@IBAB-RA-Comp203:~/Lab4$ sort -t ',' -k 5 -nr Heart.csv > restbp_revsort.o
ut
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c restbp_revsort.out
sort: restbp_revsort.out:5: disorder: "173",59,0,"asymptomatic",174,249,0,0,14
3,1,0,2,0,"normal","Yes"
ibab@IBAB-RA-Comp203:~/Lab4$
```

iv. Here we use the man command to help us learn which commands we must place instead. We use keywords of GNU to print the given functions.

```
ibab@IBAB-RA-Comp203:~$ cd Lab4
ibab@IBAB-RA-Comp203:~/Lab4$ sort --field-separator=',' --key=1 --numeric-sort H
eart.csv > col1_sorted_gnu.out
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c col1_sorted_gnu.out
ibab@IBAB-RA-Comp203:~/Lab4$ sort --field-separator=',' --key=2 --numeric-sort -
-reverse Heart.csv > age_sorted_gnu.out
ibab@IBAB-RA-Comp203:~/Lab4$
```

v & vi.

```
ibab@IBAB-RA-Comp203:~/Lab4$ head Heart.csv
"","Age","Sex","ChestPain","RestBP","Chol","Fbs","RestECG","MaxHR","ExAng","Ol
dpeak","Slope","Ca","Thal","AHD"
"1",63,1,"typical",145,233,1,2,150,0,2.3,3,0,"fixed","No"
"2",67,1,"asymptomatic",160,286,0,2,108,1,1.5,2,3,"normal","Yes"
"3",67,1,"asymptomatic",120,229,0,2,129,1,2.6,2,2,"reversable","Yes"
"4",37,1,"nonanginal",130,250,0,0,187,0,3.5,3,0,"normal","No"
"5",41,0,"nontypical",130,204,0,2,172,0,1.4,1,0,"normal","No"
"6",56,1,"nontypical",120,236,0,0,178,0,0.8,1,0,"normal","No"
"7",62,0,"asymptomatic",140,268,0,2,160,0,3.6,3,2,"normal","Yes"
"8",57,0,"asymptomatic",120,354,0,0,163,1,0.6,1,0,"normal","No"
"9",63,1,"asymptomatic",130,254,0,2,147,0,1.4,2,1,"reversable","Yes"
ibab@IBAB-RA-Comp203:~/Lab4$ sort -t ',' -k 2 -n -k 5 -n Heart.csv > age_restb
p_sort.out
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c age_restbp_sort.out
sort: age_restbp_sort.out:2: disorder: "133",29,1,"nontypical",130,204,0,2,202
,0,0,1,0,"normal","No"
ibab@IBAB-RA-Comp203:~/Lab4$ sort -t ',' -k 3 -n -k 2 -n -k 4 -n Heart.csv > s
ex_age_chpain_sort.out
ibab@IBAB-RA-Comp203:~/Lab4$ sort -c sex_age_chpain_sort.out
sort: sex_age_chpain_sort.out:2: disorder: "226",34,0,"nontypical",118,210,0,0
,192,0,0.7,1,0,"normal","No"
ibab@IBAB-RA-Comp203:~/Lab4$
```

We sort the data 1) according to age, and then according to RestBP.

2) according to sex, then according to age, then according to ChestPain.

To do this, wesimply use the -k and -n command, which allows us to sort multiple things at once.