```
> #1.(a) read text file which creates a data frame called Su
> Su <- read.delim("G:/My Drive/Personal/Grad Program/CSC 587 - Adv Data Mining/Scripts/datamining-main/Rscripts/data/Su_raw_matrix.txt")
> #1.(b)
> mean(Su$Liver_2.CEL)  #mean of Liver_2.CEL column
[1] 241.8246
> sd(Su$Liver_2.CEL)   #standard deviation of Liver_2.CEL column
[1] 1133.352
> #1.(c)
> colMeans(Su)  #mean or average of each column
      Brain_1.CEL      Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL Fetal_liver_1.CEL Fetal_liver_2.CEL       Liver_1.CEL
         204.9763         315.0924          198.3439          267.6551          209.8722          399.1482          160.8558
      Liver_2.CEL
         241.825
> colSums(Su)  #sum of each column
      Brain_1.CEL      Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL Fetal_liver_1.CEL Fetal_liver_2.CEL       Liver_1.CEL
         2588031          3978357          2504290          3379413          2649846          5039645          2030966
      Liver_2.CEL
         3053278


>
```