

1. Import and check the type of the normalExp and tumorExp data sets (what can you tell about this type?) (6 points)

code	Solution
<pre>normaldata = read.csv("normalExp.csv") normaldata class(normaldata)  tumordata = read.csv("tumorExp.csv") tumordata class(tumordata)</pre>	<pre>&gt; normaldata = read.csv("normalExp.csv") &gt; normaldata       TCGA.01.0630 TCGA.01.0631 TCGA.01.0633 TCGA.01.0636 TCGA.01.0637 TCGA.01.0628 EGFR      8.886259      7.348632      8.148822      8.198942      8.259905      7.764373 KLF6      7.307082      9.200284      7.562461      6.936270      8.837477      6.712114 FOXO1     8.291179      7.144513      8.012996      7.752654      8.031862      7.944712 KRAS      7.361094      7.736765      7.650435      7.463626      7.681267      7.670060 JAK2      4.326798      4.000098      4.331242      4.654296      3.448365      3.472066 BRCA1     4.370355      3.895343      3.817901      4.499409      4.421144      4.388495 BRCA2     3.220345      3.079436      3.364516      3.294702      3.474015      3.584013 PPM1D     6.560268      6.824938      6.723147      6.484294      6.818931      6.439352        TCGA.01.0639 TCGA.01.0642 EGFR      7.856745      7.811012 KLF6      7.143543      7.236533 FOXO1     7.507472      8.146701 KRAS      7.573284      8.208569 JAK2      3.956650      3.981076 BRCA1     4.532583      4.268729 BRCA2     3.334245      3.376060 PPM1D     6.607215      6.150508  &gt; class(normaldata) [1] "data.frame" &gt; &gt; tumordata = read.csv("tumorExp.csv") &gt; tumordata       TCGA.04.1369 TCGA.24.1418 TCGA.24.1563 TCGA.29.1771 TCGA.04.1655 TCGA.29.1777 EGFR      5.060003      7.383045      5.931034      7.207645      8.407892      5.974618 KLF6      7.377910      8.766834      9.486722      7.974520      8.182600      7.411823 FOXO1     5.625710      6.775382      5.362052      5.964881      6.454333      5.184914 KRAS      8.421762      8.794266      8.517094      8.246681      8.738823      7.875965 JAK2      3.386156      3.438309      3.607809      3.481014      2.917321      3.291126 BRCA1     4.141160      5.328484      3.612883      4.122214      4.282340      3.967829 BRCA2     3.632617      3.511651      3.323840      3.395268      3.329490      3.335866 PPM1D     6.980356      6.216540      6.085997      5.357830      5.499110      5.066974        TCGA.24.1471 TCGA.24.1416 TCGA.57.1994 TCGA.13.2057 TCGA.29.1703 TCGA.61.1917 EGFR      7.657310      6.463173      7.181912      7.445510      5.870279      5.270615 KLF6      8.648110      8.364860      7.937576      8.735051      8.676373      7.103598 FOXO1     7.939452      7.303630      7.165856      6.402323      7.295114      5.743263 KRAS      7.157274      8.483690      8.945927      8.128096      8.238454      7.993623 JAK2      3.963698      3.983162      3.797457      3.959677      3.395853      4.450674 BRCA1     4.903775      4.996964      5.124529      4.154705      5.373137      4.388181 BRCA2     3.483512      3.367925      3.576835      3.367691      3.553240      3.392990 PPM1D     5.422997      6.479176      6.209645      5.939055      6.718564      5.546955        TCGA.24.1413 TCGA.13.0913 TCGA.29.1761 TCGA.23.1021 TCGA.24.0982 TCGA.24.0966 EGFR      6.570493      5.383341      4.470363      5.624689      6.485947      5.754661 KLF6      7.019943      6.293020      6.152085      7.750143      6.874055      6.269402 FOXO1     5.842737      6.484341      6.495431      6.099960      6.820046      4.917277 KRAS      8.130629      7.970974      10.403139      8.486648      8.882275      7.548257 JAK2      3.982605      4.513809      3.409040      3.606931      3.457588      4.283048 BRCA1     4.054316      5.775366      5.528097      4.696397      5.185307      4.197093 BRCA2     3.472658      3.182368      3.465528      3.236769      3.430962      3.830006 PPM1D     5.748525      6.042188      5.532423      4.666394      5.988788      5.046822        TCGA.09.1674 TCGA.36.1577 TCGA.61.1910 TCGA.36.2549 TCGA.24.1551 TCGA.04.1530 EGFR      7.417657      5.583338      6.295938      6.393803      8.455510      7.203857 KLF6      7.078536      7.930765      7.010922      6.933679      7.456075      8.401772 FOXO1     5.205596      5.096611      6.607509      5.818956      5.276104      6.394195 KRAS      9.571163      8.150551      6.916884      8.423704      8.074850      8.817448 JAK2      2.951450      4.212052      3.173352      3.670467      4.099102      3.521188 BRCA1     6.517016      3.584344      3.929980      5.139534      4.671936      6.066134 BRCA2     4.189611      5.555121      3.562476      3.152375      3.379381      3.242516 PPM1D     7.230765      5.182415      7.086274      5.341389      5.706639      6.325948        TCGA.61.2098 TCGA.61.2094 TCGA.23.1124 TCGA.24.2290 TCGA.13.1409 TCGA.25.2400 EGFR      8.504935      7.376611      8.519813      6.844420      6.835626      8.177517 KLF6      6.264148      7.830504      8.294090      8.270891      6.380965      8.256739 FOXO1     6.305705      6.577306      6.605281      7.650190      7.302064      5.605641 KRAS      8.230691      8.251794      7.926829      8.708903      8.132808      9.150722 JAK2      3.303488      4.306267      4.328727      3.828836      3.221592      3.958849 BRCA1     5.706437      3.748930      4.341102      3.550883      3.686756      4.596487 BRCA2     3.311406      3.236709      3.162059      3.238795      3.228089      3.643608 PPM1D     7.298528      6.165728      5.183895      5.979889      5.090294      5.708432        TCGA.13.0919 TCGA.13.0904 TCGA.30.1855 TCGA.24.1930 TCGA.13.0768 TCGA.24.1845 EGFR      5.897047      4.024547      8.025283      7.405110      7.859898      7.192806 KLF6      8.776524      6.281318      6.175444      7.208022      8.612784      5.768561 FOXO1     6.373851      6.372266      7.351887      7.266947      6.962750      4.496813 KRAS      8.440605      7.323903      9.101963      8.088363      8.434468      8.096015 JAK2      3.788200      3.174112      3.633150      4.742378      5.086697      3.723721 BRCA1     5.129867      3.523312      4.654339      4.067981      4.054344      4.267927 BRCA2     3.189119      3.401729      4.030419      3.820492      3.365173      3.330569 PPM1D     4.771009      5.016151      6.324593      5.743286      5.182118      6.211173        TCGA.23.1113 TCGA.61.2102 TCGA.13.0765 TCGA.24.1430 TCGA.09.1669 TCGA.30.1862 EGFR      7.166182      7.908679      8.825793      6.545420      4.665497      7.418400 KLF6      7.382572      6.079434      7.166549      6.175040      6.950743      6.984289 FOXO1     8.532079      6.108450      6.509030      7.233574      6.076317      6.795477 KRAS      8.804615      11.150979      9.236091      8.251407      7.845321      6.694549 JAK2      3.915334      3.679756      3.421799      3.196269      4.164194      4.514230 BRCA1     5.252385      5.461139      3.677874      3.307945      4.018949      4.214578 BRCA2     3.511039      3.546889      3.884753      3.698259      3.859160      3.283301 PPM1D     5.244137      7.401416      5.918347      5.124145      6.347931      6.060255        TCGA.24.1557 TCGA.61.2003 TCGA.25.1319 TCGA.57.1586 TCGA.23.1116 TCGA.09.1670 EGFR      6.502309      8.414512      4.194467      6.556381      7.025319      7.534319 KLF6      6.906516      7.755758      6.807017      5.978730      8.516755      7.704951 FOXO1     6.560688      6.549668      5.184747      6.629846      6.523719      5.541329 KRAS      8.805088      7.782150      8.018011      8.226098      11.265863      8.152662 JAK2      3.703985      3.993708      3.624039      3.409648      3.439970      3.394533 BRCA1     3.164340      4.169041      4.766858      4.385461      4.855328      5.209944 BRCA2     4.127839      3.449947      3.273529      3.264562      3.304455      3.029466 PPM1D     5.790422      5.955922      6.519775      8.404009      5.926534      5.224780</pre>

	TCGA.13.1477	TCGA.24.1562
EGFR	8.510289	6.826002
KLF6	6.669788	7.581904
FOXO1	6.236546	7.740928
KRAS	8.167551	7.619080
JAK2	3.359313	3.191245
BRCA1	4.890973	4.164284
BRCA2	3.542452	3.248926
PPM1D	6.793148	5.416121
> class(tumordata)		
[1] "data.frame"		

2. Select only the columns of BRCA1 in two data sets and assign them to two different vector variables (6 points)

code	Solution
c<-unname(unlist(normaldata[6,])) c d<-unname(unlist(tumordata[6,])) d	> c<-unname(unlist(normaldata[6,])) > c [1] 4.370355 3.895343 3.817901 4.499409 4.421144 4.388495 4.532583 4.268729 > d<-unname(unlist(tumordata[6,])) > d [1] 4.141160 5.328484 3.612883 4.122214 4.282340 3.967829 4.903775 4.996964 5.124529 [10] 4.154705 5.373137 4.388181 4.054316 5.775366 5.528097 4.696397 5.185307 4.197093 [19] 6.517016 3.584344 3.929980 5.139534 4.671936 6.066134 5.706437 3.748930 4.341102 [28] 3.550883 3.686756 4.596487 5.129867 3.523312 4.654339 4.067981 4.054344 4.267927 [37] 5.252385 5.461139 3.677874 3.307945 4.018949 4.214578 3.164340 4.169041 4.766858 [46] 4.385461 4.855328 5.209944 4.890973 4.164284

3. Calculate the mean, median, variance and standard deviation of vector variables from problem2 using built-in functions such as mean(), median(),var(),sqrt(var()) (6 points)

code	solution
mean(c) median(c) var(c) sqrt(var(c))  mean(d) median(d) var(d) sqrt(var(d))	> mean(c) [1] 4.274245 > median(c) [1] 4.379425 > var(c) [1] 0.07330763 > sqrt(var(c)) [1] 0.2707538 > > mean(d) [1] 4.532184 > median(d) [1] 4.363282 > var(d) [1] 0.5617598 > sqrt(var(d)) [1] 0.7495064

4. (7 points)

1. Calculate the means of all genes of two data sets and generate one new matrix or data frame containing the results.
2. Save new results into a csv file.

code	solution
<b>1.</b> normalMeans<-rowMeans(normaldata, na.rm = FALSE, dims = 1) normalMeans tumorMeans<-rowMeans(tumordata, na.rm = FALSE, dims = 1) tumorMeans  df1<-data.frame(normalMeans) df1  df2<-data.frame(tumorMeans) df2 dfcom<-cbind(df1, df2) dfcom  <b>2.</b> write.csv(dfcom, "C:\\Users\\Mostafiz\\Desktop\\mydata2.csv")	<pre> &gt; normalMeans&lt;-rowMeans(normaldata, na.rm = FALSE, dims = 1) &gt; normalMeans       EGFR      KLF6      FOXO1      KRAS      JAK2      BRCA 1  8.034336  7.616971  7.854011  7.668138  4.021324  4.27424 5  3.340916  6.576082 &gt; tumorMeans&lt;-rowMeans(tumordata, na.rm = FALSE, dims = 1) &gt; tumorMeans       EGFR      KLF6      FOXO1      KRAS      JAK2      BRCA 1  6.804996  7.412328  6.387375  8.416494  3.733139  4.53218 4  3.499069  5.924476 &gt; &gt; df1&lt;-data.frame(normalMeans) &gt; df1       normalMeans EGFR      8.034336 KLF6      7.616971 FOXO1      7.854011 KRAS      7.668138 JAK2      4.021324 BRCA1      4.274245 BRCA2      3.340916 PPM1D      6.576082 &gt; &gt; df2&lt;-data.frame(tumorMeans) &gt; df2       tumorMeans EGFR      6.804996 KLF6      7.412328 FOXO1      6.387375 KRAS      8.416494 JAK2      3.733139 BRCA1      4.532184 BRCA2      3.499069 PPM1D      5.924476 &gt; dfcom&lt;-cbind(df1, df2) &gt; dfcom       normalMeans tumorMeans EGFR      8.034336      6.804996 KLF6      7.616971      7.412328 FOXO1      7.854011      6.387375 KRAS      7.668138      8.416494 JAK2      4.021324      3.733139 BRCA1      4.274245      4.532184 BRCA2      3.340916      3.499069 PPM1D      6.576082      5.924476 </pre>