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#List of useful functions from course 2

factor(), as.factor()

tapply()

matrix(), as.matrix()
data.frame(), as.data.frame()
cbind()
rbind()

t()
class()

data()
apply()

write.table()
read.table()


rowMeans()
rowSums()
colSums()
colMeans()
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```

A.

1.Have a look on a text file "expression.txt". Read it in as a dataframe geneExpression.

2.Change column names for short "s1","s2" etc.

3.Compute average/max/min expression value for each gene.

4. Compute average signal for each sample.

5. Samples 1:3 are cancer samples before treatment, 4:6 after treatment, 7:9 are control samples. Obtain average expression for each group separately, for the first gene.

6. As above, for all genes.

B.

1.Prepare a dataframe "Trial"with 44 rows and 2 columns. First column is "PatientAge", with numbers 2-8 (assign them as you want), as numeric, another is "TesterName", with two names ("Koval","Schmidt").

2. Load dataset bacteria, from library mass.

3. Take only results from 11 week of trial from bacteria.

4. Add your dataframe "Trial" as additional columns.

5. What is average age of a patient with high/low response to a drug?
Age range of dr Kovacs and dr Schmidt patients?
Average (median) age of placebo/drug/drug+ patients?

6. Write your dataframe to a file.