

Lecture 02  
2020 Spring Data-622  
Review of Statistics and Probability with R  
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Acknowledgements:  
Generous support from IBM Power Systems Academic Initiative  
IBM PSAI provides computing infrastructure for free

# Refresher

In the next two weeks we will set a goal to achieve:

working proficiency in R and

introduce essential concepts from Statistical/Probability/Linear Algebra

R is a comprehensive mature language, 35 years in the running.

We will introduce capabilities limited to what is required for this course.

If R is an ocean, [Statistics/Probability/Linear Algebra] are an universe.

Therefore, the next two lectures, are limited review of topics, on need-only basis

Loading datasets into data.frames

Partitioning datasets

Apply/lapply vector operations

EDA:descriptive/summary statistics

EDA:correlation,Cov,std,var

Normalizing/scaling

Loading datasets into data.frames

Partitioning datasets

Apply/lapply vector operations

EDA:descriptive/summary statistics

EDA:correlation,Cov,std,var

Normalizing/scaling

# Loading data

Source:

- preloaded,  
text,

- Files on disk:

  - Tab

  - comma seperated values,

- From the internet:

  - dataset using URLs

Visualizing

- Pairs

Data Preparation

- Coding

- Scaling

- sampling

- randomizing

- Training

- Test

For R, you can use Rstudio or Rgui or any other tool you prefer.

# Working Environment: R on IBM Cloud

```
rkannan@F4Linux1: ~  
rkannan@F4Linux1:~$ R  
  
R version 3.2.3 (2015-12-10) -- "Wooden Christmas-Tree"  
Copyright (C) 2015 The R Foundation for Statistical Computing  
Platform: powerpc64le-unknown-linux-gnu (64-bit)  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
> alldsets<-data()  
> str(alldsets)  
List of 4  
 $ title   : chr "Data sets"  
 $ header  : NULL  
 $ results: chr [1:105, 1:4] "datasets" "datasets" "datasets" "  
 ..- attr(*, "dimnames")=List of 2  
 .. ..$ : NULL  
 .. ..$ : chr [1:4] "Package" "LibPath" "Item" "Title"  
 $ footer  : chr "Use `data(package = .packages(all.available =  
available* packages.)"
```

preloaded data  
str function

For R, you can use Rstudio or Rgui. Or on IBM Cloud as shown above. On IBM, enter R to start R.

# Working Environment: R on IBM Cloud

```
> head(alldsets$results)
  Package LibPath Item
[1,] "datasets" "/usr/lib/R/library" "AirPassengers"
[2,] "datasets" "/usr/lib/R/library" "BJsales"
[3,] "datasets" "/usr/lib/R/library" "BJsales.lead (BJsales)"
[4,] "datasets" "/usr/lib/R/library" "BOD"
[5,] "datasets" "/usr/lib/R/library" "CO2"
[6,] "datasets" "/usr/lib/R/library" "ChickWeight"
Title
[1,] "Monthly Airline Passenger Numbers 1949-1960"
[2,] "Sales Data with Leading Indicator"
[3,] "Sales Data with Leading Indicator"
[4,] "Biochemical Oxygen Demand"
[5,] "Carbon Dioxide Uptake in Grass Plants"
[6,] "Weight versus age of chicks on different diets"
> dim(alldsets$results)
[1] 105 4
```

*str* function reveals the inner structure of any R Object  
head – is like Unix *head* cmd reveals 6/8 lines  
We find alldsets\$results is a data.frame of 105 rows  
each with 4 columns, using *dim* function

For R, you can use Rstudio or Rgui. Or on IBM Cloud as shown above.

# R comes with many datasets

```
7 6 6 6 WWWusage Internet Usage per Minute
8 4 4 4 WorldPhones The World's Telephones
9 12 12 12 ability.cov Ability and Intelligence Tests
10 7 7 7 airmiles Passenger Miles on Commercial US Airlines, 1937-1960
11 5 5 5 airquality New York Air Quality Measurements
> data() anscombe Anscombe's Quartet of 'Identical' Simple Linear Regressions
> | attenu The Joyner-Boore Attenuation Data
< attitude The Chatterjee-Price Attitude Data
austres Quarterly Time Series of the Number of Australian Residents
heaver1 (heavers) Body Temperature Series of Two Beavers
```

```
> anscombe
  x1 x2 x3 x4    y1    y2    y3    y4
1 10 10 10 8  8.04 9.14  7.46  6.58
2  8  8  8 8  6.95 8.14  6.77  5.76
3 13 13 13 8  7.58 8.74 12.74  7.71
4  9  9  9 8  8.81 8.77  7.11  8.84
5 11 11 11 8  8.33 9.26  7.81  8.47
6 14 14 14 8  9.96 8.10  8.84  7.04
7  6  6  6 8  7.24 6.13  6.08  5.25
8  4  4  4 19 4.26 3.10  5.39 12.50
9 12 12 12 8 10.84 9.13  8.15  5.56
10 7  7  7 8  4.82 7.26  6.42  7.91
11 5  5  5 8  5.68 4.74  5.73  6.89
```

Anscombe, is one of the 105 pre-loaded datasets

Anscombe is an instructive dataset in that it reminds us the importance of visual review of data and relationships.

Quantitative review alone could be misleading – a simple chart reveals lot more

John Snow stopped Cholera in London merely With visualization.

# Anscombe quartets in R

```
> summ1<-lm(anscombe$y1~anscombe$x1)
> summ2<-lm(anscombe$y2~anscombe$x2)
> summ3<-lm(anscombe$y3~anscombe$x3)
> summ4<-lm(anscombe$y4~anscombe$x4)
> summ1
```

```
Call:
lm(formula = anscombe$y1 ~ anscombe$x1)
```

```
Coefficients:
(Intercept)  anscombe$x1
      3.0001         0.5001
```

```
> summ2
```

```
Call:
lm(formula = anscombe$y2 ~ anscombe$x2)
```

```
Coefficients:
(Intercept)  anscombe$x2
      3.001         0.500
```

```
> summ3
```

```
Call:
lm(formula = anscombe$y3 ~ anscombe$x3)
```

```
Coefficients:
(Intercept)  anscombe$x3
      3.0025         0.4997
```

```
> summ4
```

```
Call:
lm(formula = anscombe$y4 ~ anscombe$x4)
```

```
Coefficients:
(Intercept)  anscombe$x4
      3.0017         0.4999
```

Note that

```
> apply(anscombe,2,sd)
      x1      x2      x3      x4      y1      y2      y3      y4
3.316625 3.316625 3.316625 3.316625 2.031568 2.031657 2.030424 2.030579
> apply(anscombe,2,mean)
      x1      x2      x3      x4      y1      y2      y3      y4
9.000000 9.000000 9.000000 9.000000 7.500909 7.500909 7.500000 7.500909
> |
```

Continuing, on with Anscombe, the Central tendencies and dispersion are identical. A regression yields over them near identical results. We can iterate over the columns of a df using *apply* func.

So are they identical?

Let us seek some guidance with charts.

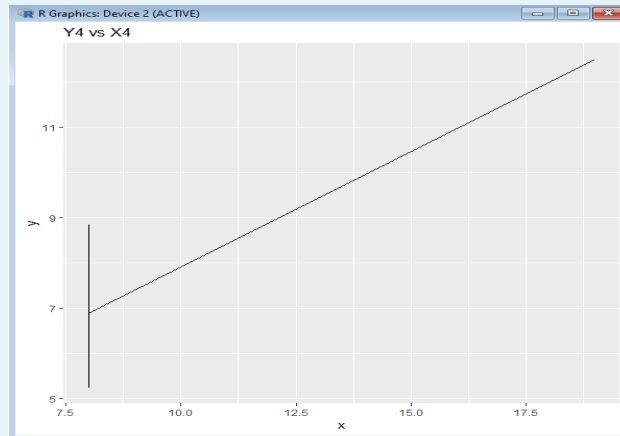
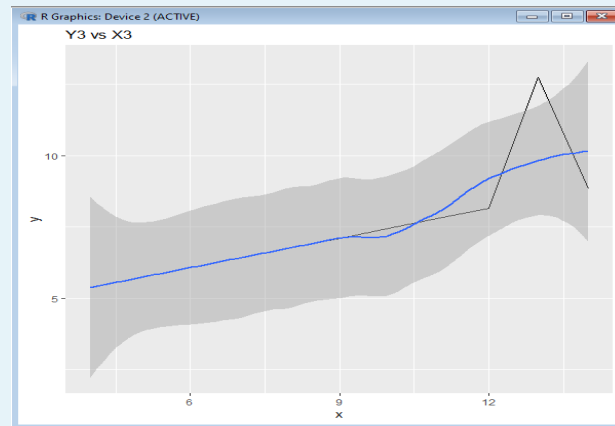
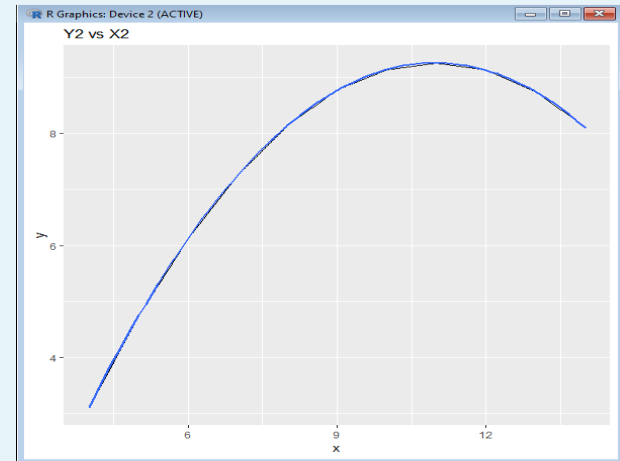
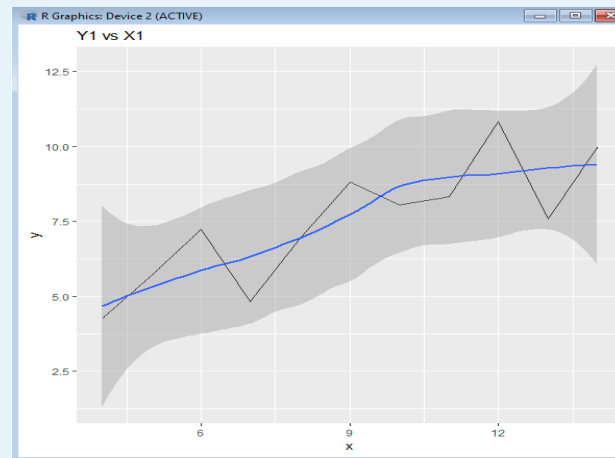


# Anscombe Charts!

*Wow!  
Anscombe  
vectors are  
anything but  
same.*

*A picture is  
Worth a  
Thousand  
Words.*

*EDA is important  
to get to know  
your data.*



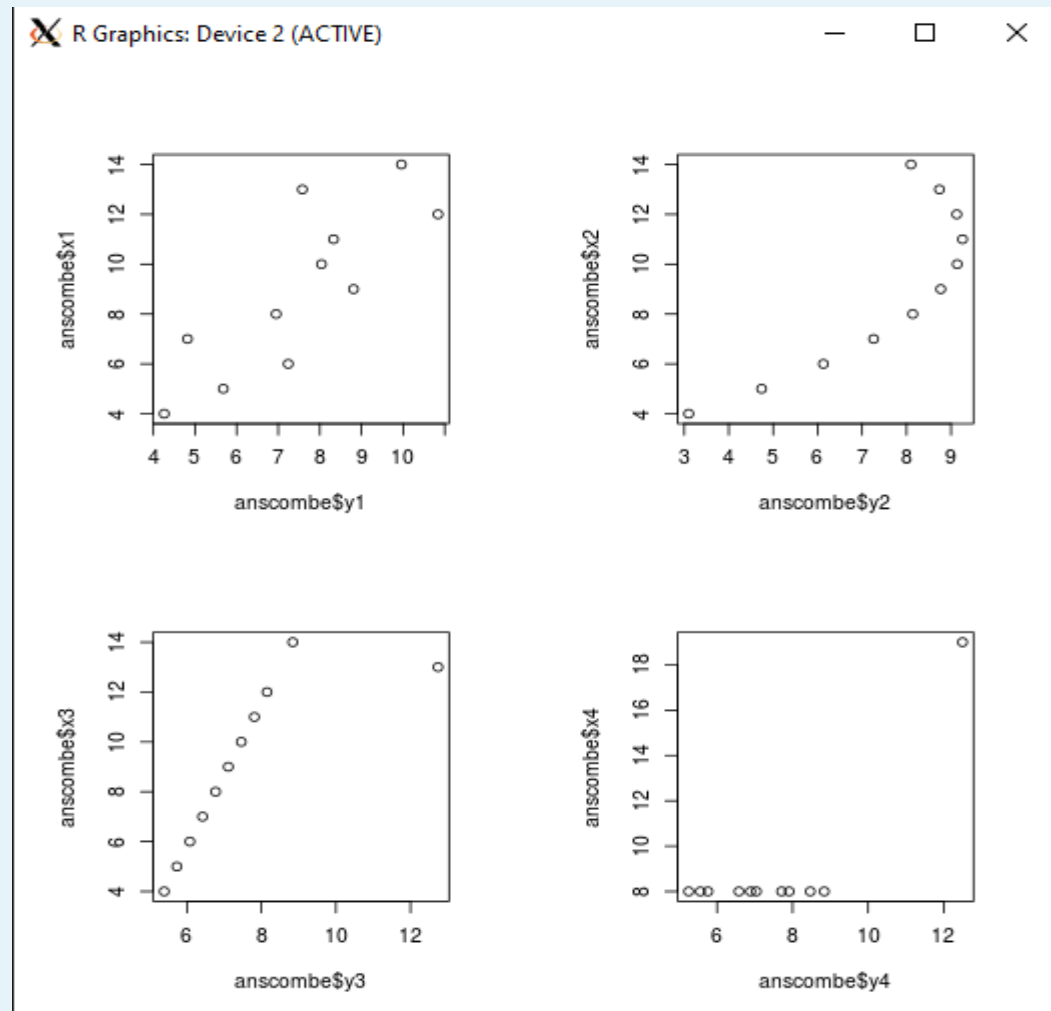
```
ggplot(data.frame(x=anscombe$x2,y=anscombe$y2),aes(x=x,y=y))+ggtitle("Y2 vs X2")+geom_line()+geom_smooth()
ggplot(data.frame(x=anscombe$x1,y=anscombe$y1),aes(x=x,y=y))+ggtitle("Y1 vs X1")+geom_line()+geom_smooth()
ggplot(data.frame(x=anscombe$x3,y=anscombe$y3),aes(x=x,y=y))+ggtitle("Y3 vs X3")+geom_line()+geom_smooth()
ggplot(data.frame(x=anscombe$x4,y=anscombe$y4),aes(x=x,y=y))+ggtitle("Y4 vs X4")+geom_line()+geom_smooth()
```



# Base R comes with plot

*Plot anscombe data side by side*

```
old<-par(mfrow=c(2,2),pty="s")  
plot(anscombe$y1,anscombe$x1)  
plot(anscombe$y2,anscombe$x2)  
plot(anscombe$y3,anscombe$x3)  
plot(anscombe$y4,anscombe$x4)
```



# Vector processing with R

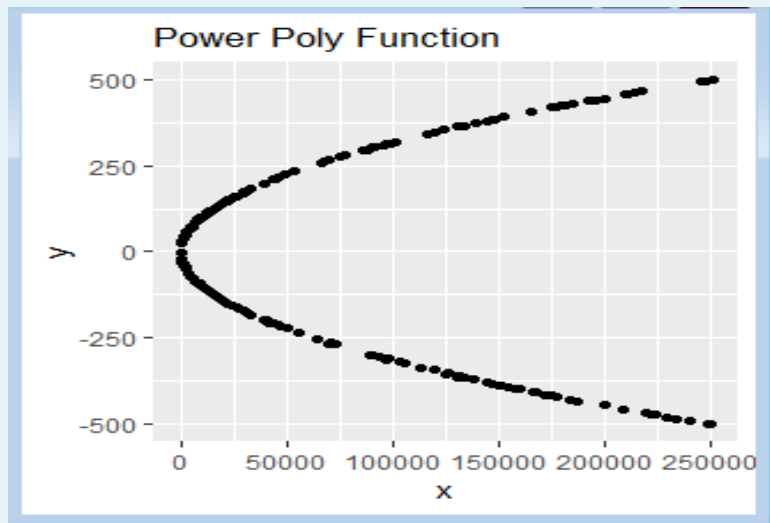
```
set.seed(13); # so it can be repeated and reproduced
base_x<-sample(-500:500,200,replace=T);
# base_x is a vector of 200 numbers between -500, 500
delta_x<-rnorm(200) # vector of 200 random normal !
# numbers with 0 mean and a variance of 1
delta_2_13<-rnorm(200,2,13)# 200 random normal
# numbers with mean 2 and variance 13
expt_x<-base_x+delta_x ; # expt is vector of perturbations
# #  $y=x+2*\sin(1.5*x)+N(0,0.2)$ 
Y<-rnorm(200,0,0.2)+expt_x+2*sin(1.5*expt_x)
dfyx<-data.frame(y=Y,x=expt_x)# linear rel

dfyxsq<-data.frame(y=Y,x=expt_x*expt_x)#power fun, poly

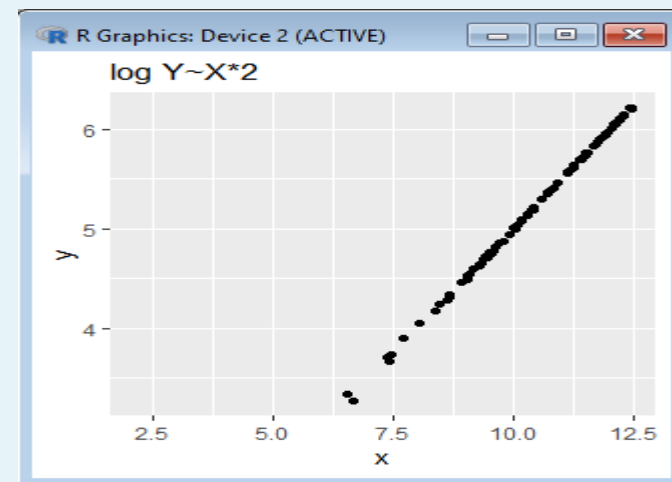
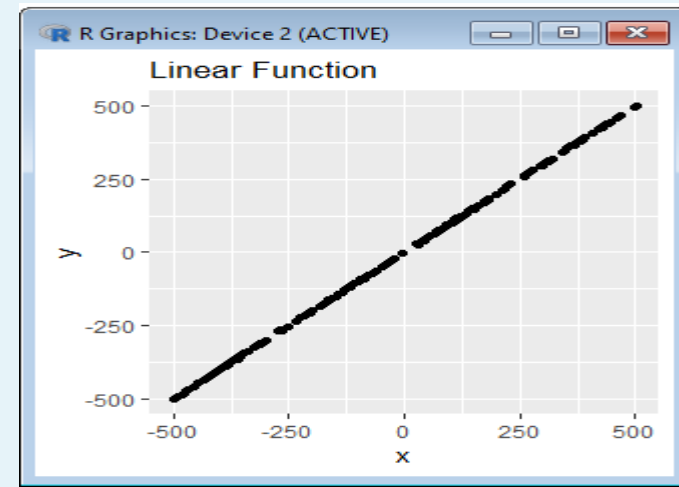
logdfyxsq<-log(dfyxsq)#log transformation
```

# Trivial plots with ggplot

```
if (!require(ggplot2)) require(ggplot2)
ggplot(dfyx,aes(y=y,x=x))+geom_point()
+ggtitle("Linear Function")
ggplot(dfyxsq,aes(y=y,x=x))+geom_point()
+ggtitle("Power Poly Function")
```



```
ggplot(log(dfyxsq),aes(y=y,x=x))+geom_point()+ggtitle("log Y~X*2")
```



# Let us take stock

*We have examined anscombe one of many preloaded datasets in R*

*We used str, dim and head – certain helper functions to examine data.frames.*

*We used apply to compute sd and mean columnwise*

*We plotted some trivial charts*

*We generated data using the formula*

$$y = x + 2 \cdot \sin(1.5 \cdot x) + N(0, 0.2)$$

*Squared x to make it a polynomial*

*And then took the log to make a linear equation*

*We plotted each case*

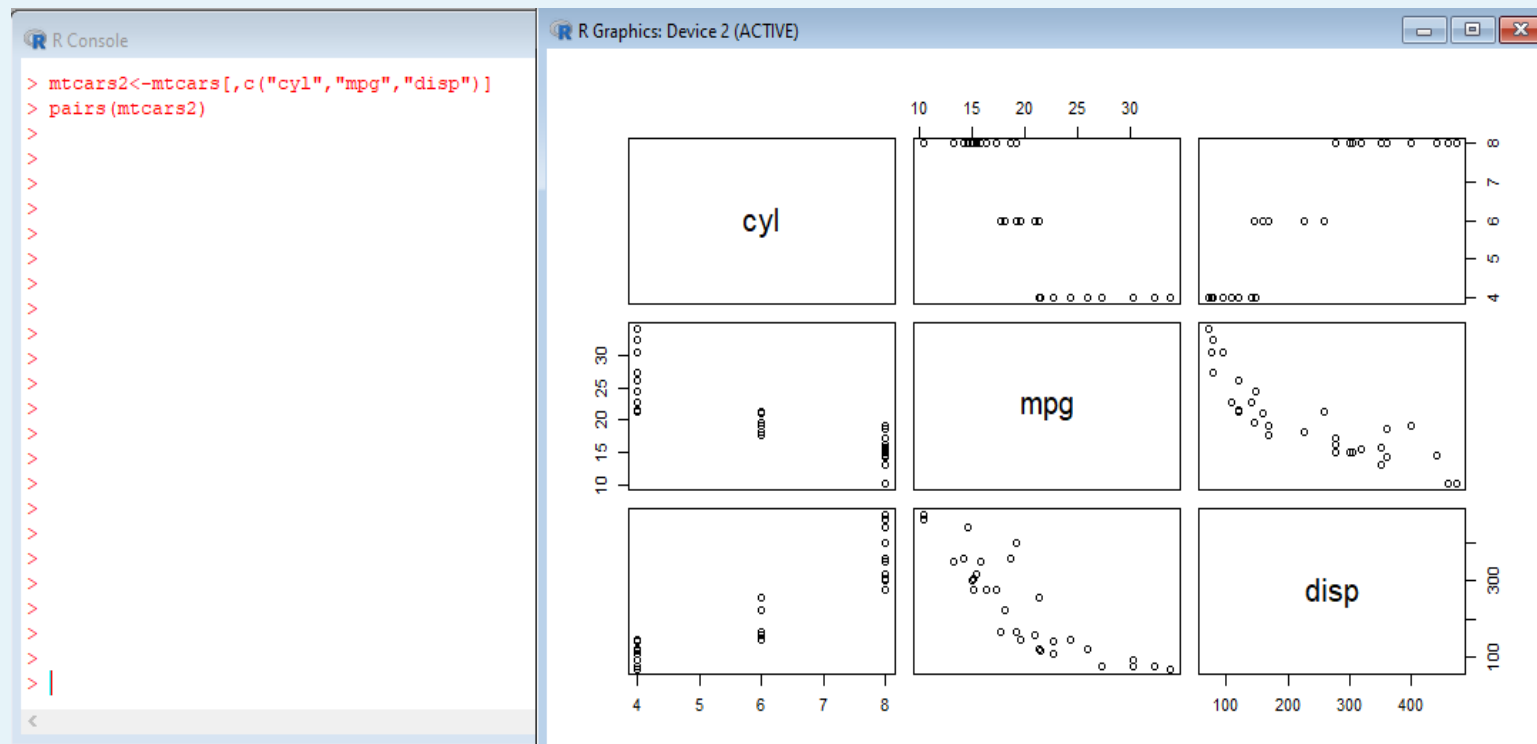
*Now we move on to loading data from URLs, external files*

*Along the way we will learn to use preliminary data cleaning*

*Tasks*

# EDA:pairs

```
mtcars2<-mtcars[,c("cyl","mpg","disp")]
pairs(mtcars2)
```



# Sourcing data from the net

```
wine<-read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/wine/wine.data",sep=";",head=F)
head(wine)
```

```
> wine<-read.csv("http://archive.ics.uci.edu/ml/machine-learning-databases/wine/
wine.data",sep=";",head=F)
> head(wine)
  V1  V2  V3  V4  V5  V6  V7  V8  V9  V10 V11 V12 V13 V14
1  1 14.23 1.71 2.43 15.6 127 2.80 3.06 0.28 2.29 5.64 1.04 3.92 1065
2  1 13.20 1.78 2.14 11.2 100 2.65 2.76 0.26 1.28 4.38 1.05 3.40 1050
3  1 13.16 2.36 2.67 18.6 101 2.80 3.24 0.30 2.81 5.68 1.03 3.17 1185
4  1 14.37 1.95 2.50 16.8 113 3.85 3.49 0.24 2.18 7.80 0.86 3.45 1480
5  1 13.24 2.59 2.87 21.0 118 2.80 2.69 0.39 1.82 4.32 1.04 2.93 735
6  1 14.20 1.76 2.45 15.2 112 3.27 3.39 0.34 1.97 6.75 1.05 2.85 1450
```

```
plot(wine$V4, wine$V5)
text(wine$V4, wine$V5,wine$V1)
dfx<-data.frame(avg=unlist(apply(wine,2,mean)),sd=unlist(apply(wine,2,sd)),
xx=names(wine))
```

```
dfx2<-
cbind(dfx,high=unlist(apply(wine,2,max)),low=unlist(apply(wine,2,min)))
```

As we can see the features are not comparable...

# More operation on data.frames twh

*TheWorkHorse of data science in R*

```
> dfx2<-cbind(dfx,high=unlist(apply(wine,2,max)),low=unlist(apply(wine,2,min)))
> dfx2
```

	avg	sd	x	high	low
V1	1.9382022	0.7750350	V1	3.00	1.00
V2	13.0006180	0.8118265	V2	14.83	11.03
V3	2.3363483	1.1171461	V3	5.80	0.74
V4	2.3665169	0.2743440	V4	3.23	1.36
V5	19.4949438	3.3395638	V5	30.00	10.60
V6	99.7415730	14.2824835	V6	162.00	70.00
V7	2.2951124	0.6258510	V7	3.88	0.98
V8	2.0292697	0.9988587	V8	5.08	0.34
V9	0.3618539	0.1244533	V9	0.66	0.13
V10	1.5908989	0.5723589	V10	3.58	0.41
V11	5.0580899	2.3182859	V11	13.00	1.28
V12	0.9574494	0.2285716	V12	1.71	0.48
V13	2.6116854	0.7099904	V13	4.00	1.27
V14	746.8932584	314.9074743	V14	1680.00	278.00

*sd is the standard deviation and V2,V5,V6,V11,V14 are much different than the others. Range has defined by high/low is wildly varying.*

*The effect due to changes in V1 is very likely to be masked by changes in these variables. We must normalize them – aka scaling.*



# scaling

```
> scaled<-apply(wine,2,FUN=function(v) {(v-mean(v))/sd(v)})  
> dim(scaled)==dim(wine)
```

```
scaleddfx<-data.frame(max=unlist(apply(scaled,2,max)),  
min=unlist(apply(scaled,2,min)))
```

```
> scaleddfx  
      max      min  
V1  1.370000 -1.210529  
V2  2.253415 -2.427388  
V3  3.100446 -1.428952  
V4  3.147447 -3.668813  
V5  3.145637 -2.663505  
V6  4.359076 -2.082381  
V7  2.532372 -2.101318  
V8  3.054216 -1.691200  
V9  2.395645 -1.862979  
V10 3.475269 -2.063214  
V11 3.425768 -1.629691  
V12 3.292407 -2.088840  
V13 1.955399 -1.889723  
V14 2.963114 -1.488987
```

```
> dfx2[,c("high","low")]  
      high  low  
V1      3.00  1.00  
V2     14.83 11.03  
V3      5.80  0.74  
V4      3.23  1.36  
V5     30.00 10.60  
V6    162.00 70.00  
V7      3.88  0.98  
V8      5.08  0.34  
V9      0.66  0.13  
V10     3.58  0.41  
V11    13.00  1.28  
V12     1.71  0.48  
V13     4.00  1.27  
V14   1680.00 278.00
```

*Range is  
comparable.*

# Effect of Scaling

```
scaleddfx<-data.frame(max=unlist(apply(scaled,2,max)),
min=unlist(apply(scaled,2,min)))
scaledsd<-apply(scaled,2,sd)
(scaledavg<-apply(scaled,2,mean))
round((scaledavg<-apply(scaled,2,mean)),1)
```

```
> scaledsd<-apply(scaled,2,sd)
> scaledsd
V1 V2 V3 V4 V5 V6 V7 V8 V9 V10 V11 V12 V13 V14
1 1 1 1 1 1 1 1 1 1 1 1 1 1
> (scaledavg<-apply(scaled,2,mean))
      V1      V2      V3      V4      V5
8.194132e-17 -8.594093e-16 -6.734236e-17 8.046486e-16 -7.683704e-17
      V6      V7      V8      V9      V10
-4.095117e-17 -1.391677e-17 6.947239e-17 -1.041614e-16 -1.287594e-16
      V11      V12      V13      V14
3.675080e-17 2.100477e-16 3.009648e-16 -1.037131e-16
> round((scaledavg<-apply(scaled,2,mean)),1)
V1 V2 V3 V4 V5 V6 V7 V8 V9 V10 V11 V12 V13 V14
0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

*Every variable has equal influence*

# Sourcing data from console

```
df <- read.table(header=TRUE, text='  
cond yval  
A 2  
B 2.5  
C 1.6  
)
```

*# Three variables*

```
df2 <- read.table(header=TRUE, text='  
cond1 cond2 yval  
A I 2  
A J 2.5  
A K 1.6  
B I 2.2  
B J 2.4  
B K 1.2  
C I 1.7  
C J 2.3  
C K 1.9  
)
```

# Preparing data for Analysis

Iris – another preloaded dataset

```
> iris[20:30,]  
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species  
20           5.1         3.8          1.5          0.3  setosa  
21           5.4         3.4          1.7          0.2  setosa  
22           5.1         3.7          1.5          0.4  setosa  
23           4.6         3.6          1.0          0.2  setosa  
24           5.1         3.3          1.7          0.5  setosa  
25           4.8         3.4          1.9          0.2  setosa  
26           5.0         3.0          1.6          0.2  setosa  
27           5.0         3.4          1.6          0.4  setosa  
28           5.2         3.5          1.5          0.2  setosa  
29           5.2         3.4          1.4          0.2  setosa  
30           4.7         3.2          1.6          0.2  setosa  
  
> dim(iris)  
[1] 150  5  
  
> iris[50:55,]  
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species  
50           5.0         3.3          1.4          0.2  setosa  
51           7.0         3.2          4.7          1.4 versicolor  
52           6.4         3.2          4.5          1.5 versicolor  
53           6.9         3.1          4.9          1.5 versicolor  
54           5.5         2.3          4.0          1.3 versicolor  
55           6.5         2.8          4.6          1.5 versicolor  
> |
```

```
> table(iris$Species)  
  
  setosa versicolor virginica  
    50      50      50
```

# Generating representative sample

```
> iris[20:30,]
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
20          5.1         3.8          1.5         0.3  setosa
21          5.4         3.4          1.7         0.2  setosa
22          5.1         3.7          1.5         0.4  setosa
23          4.6         3.6          1.0         0.2  setosa
24          5.1         3.3          1.7         0.5  setosa
25          4.8         3.4          1.9         0.2  setosa
```

Is not representative

```
iris[sample(1:nrow(iris),5,replace=F),]
```

```
> iris[sample(1:nrow(iris),5,replace=F),]
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
65          5.6         2.9         3.6         1.3 versicolor
123         7.7         2.8         6.7         2.0  virginica
110         7.2         3.6         6.1         2.5  virginica
80          5.7         2.6         3.5         1.0 versicolor
71          5.9         3.2         4.8         1.8 versicolor
> tridx<-sample(nrow(iris),110,replace=F)
> tridx
 [1] 81 79 140 106 116 45 103 78 71 100 25 23 26 136 27 119 130 11 51 8 87
[22] 68 149 93 113 19 145 53 111 1 62 142 34 59 132 92 108 24 35 98 74 77
[43] 70 99 95 44 56 9 66 75 30 28 144 148 67 128 76 21 146 64 141 43 125
[64] 32 52 20 69 96 124 60 82 61 150 4 88 2 139 73 14 122 16 126 3 49
[85] 29 115 114 137 134 133 138 38 46 37 58 84 22 15 97 135 13 121 118 104 50
[106] 131 83 101 105 63
> trainset<-iris[tridx,]
> testset<-iris[-tridx,]
```

# Iris into train/test set

```
> trainset<-iris[tridx,]
> testset<-iris[-tridx,]
> dim(testset)
[1] 40  5
> dim(trainset)
[1] 110  5
> head(trainset)
      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
81           5.5         2.4         3.8         1.1 versicolor
79           6.0         2.9         4.5         1.5 versicolor
140          6.9         3.1         5.4         2.1  virginica
106          7.6         3.0         6.6         2.1  virginica
116          6.4         3.2         5.3         2.3  virginica
45           5.1         3.8         1.9         0.4   setosa
> head(testset)
      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
5           5.0         3.6         1.4         0.2   setosa
6           5.4         3.9         1.7         0.4   setosa
7           4.6         3.4         1.4         0.3   setosa
10          4.9         3.1         1.5         0.1   setosa
12          4.8         3.4         1.6         0.2   setosa
17          5.4         3.9         1.3         0.4   setosa
```

# We can now split datasets

```
> tridx<-sample(nrow(iris),110,replace=F)
> tridx
 [1] 81 79 140 106 116 45 103 78 71 100 25 23 26 136 27 119 130 11 51 8 87
[22] 68 149 93 113 19 145 53 111 1 62 142 34 59 132 92 108 24 35 98 74 77
[43] 70 99 95 44 56 9 66 75 30 28 144 148 67 128 76 21 146 64 141 43 125
[64] 32 52 20 69 96 124 60 82 61 150 4 88 2 139 73 14 122 16 126 3 49
[85] 29 115 114 137 134 133 138 38 46 37 58 84 22 15 97 135 13 121 118 104 50
[106] 131 83 101 105 63
> trainset<-iris[tridx,]
> testset<-iris[-tridx,]
> dim(testset)
[1] 40 5
> dim(trainset)
[1] 110 5
> head(trainset)
   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
81           5.5         2.4         3.8         1.1 versicolor
79           6.0         2.9         4.5         1.5 versicolor
140          6.9         3.1         5.4         2.1 virginica
106          7.6         3.0         6.6         2.1 virginica
116          6.4         3.2         5.3         2.3 virginica
45           5.1         3.8         1.9         0.4 setosa
> head(testset)
   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
5             5.0         3.6         1.4         0.2 setosa
6             5.4         3.9         1.7         0.4 setosa
7             4.6         3.4         1.4         0.3 setosa
10            4.9         3.1         1.5         0.1 setosa
12            4.8         3.4         1.6         0.2 setosa
17            5.4         3.9         1.3         0.4 setosa
> |
```



# Splitting into 10 Folds

```
> seq(1,nrow(iris),15)
[1] 1 16 31 46 61 76 91 106 121 136
> starts<-seq(1,nrow(iris),15)
> ends<-seq(15,nrow(iris),15)
> ends
[1] 15 30 45 60 75 90 105 120 135 150
> sample3<-iris[starts[3]:ends[3],]
> sample3
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
31	4.8	3.1	1.6	0.2	setosa
32	5.4	3.4	1.5	0.4	setosa
33	5.2	4.1	1.5	0.1	setosa
34	5.5	4.2	1.4	0.2	setosa
35	4.9	3.1	1.5	0.2	setosa
36	5.0	3.2	1.2	0.2	setosa
37	5.5	3.5	1.3	0.2	setosa
38	4.9	3.6	1.4	0.1	setosa
39	4.4	3.0	1.3	0.2	setosa
40	5.1	3.4	1.5	0.2	setosa
41	5.0	3.5	1.3	0.3	setosa
42	4.5	2.3	1.3	0.3	setosa
43	4.4	3.2	1.3	0.2	setosa
44	5.0	3.5	1.6	0.6	setosa
45	5.1	3.8	1.9	0.4	setosa

But this is not random

# 3<sup>rd</sup> Fold

```
> iris2<-sample(nrow(iris),nrow(iris),replace=F)
> iris2
 [1] 63 57 27 30 136 43 76 75 94 3 114 91 46 89 93 141 36 77 64 106 90
[22] 29 132 12 1 81 21 17 72 37 124 120 50 74 109 134 13 118 148 73 24 62
[43] 42 40 69 110 60 116 19 11 49 2 97 38 65 18 102 7 95 15 80 140 34
[64] 84 68 103 33 41 135 127 9 99 39 96 20 101 44 126 147 82 131 139 53 115
[85] 137 31 92 125 112 59 66 16 108 5 56 23 32 78 111 28 129 4 149 123 88
[106] 87 52 105 83 45 128 146 71 86 133 14 26 6 100 98 67 10 55 8 35 144
[127] 122 117 107 47 145 61 121 130 70 51 143 79 138 104 150 113 48 54 58 85 142
[148] 119 22 25
```

```
> iris2
 [1] 63 57 27 30 136 43 76 75 94 3 114 91 46 89 93 141 36 77 64 106 90
[22] 29 132 12 1 81 21 17 72 37 124 120 50 74 109 134 13 118 148 73 24 62
[43] 42 40 69 110 60 116 19 11 49 2 97 38 65 18 102 7 95 15 80 140 34
[64] 84 68 103 33 41 135 127 9 99 39 96 20 101 44 126 147 82 131 139 53 115
[85] 137 31 92 125 112 59 66 16 108 5 56 23 32 78 111 28 129 4 149 123 88
[106] 87 52 105 83 45 128 146 71 86 133 14 26 6 100 98 67 10 55 8 35 144
[127] 122 117 107 47 145 61 121 130 70 51 143 79 138 104 150 113 48 54 58 85 142
[148] 119 22 25
> random_sample3<-iris2[starts[3]:ends[3]]
> iris_random_sample3<-iris[random_sample3,]
> iris_random_sample3
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
124          6.3         2.7          4.9         1.8 virginica
120          6.0         2.2          5.0         1.5 virginica
50           5.0         3.3          1.4         0.2 setosa
74           6.1         2.8          4.7         1.2 versicolor
109          6.7         2.5          5.8         1.8 virginica
134          6.3         2.8          5.1         1.5 virginica
13          4.8         3.0          1.4         0.1 setosa
118          7.7         3.8          6.7         2.2 virginica
148          6.5         3.0          5.2         2.0 virginica
73           6.3         2.5          4.9         1.5 versicolor
24           5.1         3.3          1.7         0.5 setosa
62           5.9         3.0          4.2         1.5 versicolor
42           4.5         2.3          1.3         0.3 setosa
40           5.1         3.4          1.5         0.2 setosa
69           6.2         2.2          4.5         1.5 versicolor
```

# What have we learned?

We can load data  
from network  
from file  
from console

We can plot

We can scale

We can split dataset

<http://www.endmemo.com/program/R/>

<http://www.r-tutor.com/>

<http://www.r-bloggers.com/>

<https://stackoverflow.com/questions>