

Week2: Getting started with R

Overview

What is R?

- R is a programming environment
 - uses a well-developed but simple programming language
 - allows for rapid development of new tools according to user demand
 - these tools are distributed as packages, which any user can download to customize the R environment

Why using R?

- Complete statistical environment and programming language
- Efficient functions and data structures for data analysis
- Powerful graphics
- Access to fast growing number of analysis packages
- Most widely used language in applied statistics
- Is standard for data mining and statistical analysis
- Technical advantages: free, open-source, available for all OSs

R Working Environments

Some R working environments with support for syntax highlighting and utilities to send code to the R console:

- RStudio: excellent choice for beginners (Cheat Sheet)
- Basic R code editors provided by Rguis
- gedit, Rgedit, RKWard, Eclipse, Tinn-R, Notepad++, NppToR
- Vim-R-Tmux: R working environment based on vim and tmux
- Emacs (ESS add-on package)

Example: RStudio

New integrated development environment (IDE) for R. Highly functional for both beginners and advanced.

RStudio IDE

Some useful shortcuts: **Ctrl+Enter** (send code), **Ctrl+Shift+C** (comment/uncomment), **Ctrl+1/2** (switch window focus)

Getting Started with R

Installation of R and packages

1. Base R and most R packages are available for download from the Comprehensive R Archive Network (CRAN)
 - <http://www.r-project.org/>
 - base R comes with a number of basic data management, analysis, and graphical tools

- R's power and flexibility, however, lie in its array of packages (currently more 8,000!)
2. Install RStudio from RStudio.
 3. Install CRAN Packages from R console like this:

```
install.packages(c("pkg1", "pkg2"))
install.packages("pkg.zip", repos=NULL)
```

Startup and Closing R

- *Starting R*: The R GUI versions, including RStudio, under Windows and Mac OS X can be opened by double-clicking their icons. Alternatively, one can start it by typing R in a terminal (default under Linux).
- *Startup/Closing Behavior*: The R environment is controlled by hidden files in the startup directory: `.RData`, `.Rhistory` and `.Rprofile` (optional).
- *Closing R*:

```
q()
```

Save workspace image? [y/n/c]:

- *Note*: When responding with y, then the entire R workspace will be written to the `.RData` file which can become very large. Often it is sufficient to just save an analysis protocol in an R source file. This way one can quickly regenerate all data sets and objects.

Navigating directories

- Create an object with the assignment operator `<-` or `=`

```
object <- ...
```

- List objects in current R session

```
ls()
```

- Return content of current working directory

```
dir()
```

- Return path of current working directory

```
getwd()
```

- Change current working directory

```
setwd("/home/user")
```

Basic Syntax

- General R command syntax

```
object <- function_name(arguments)
object <- object[arguments]
```

- Finding help

```
?function_name
```

- Load a library/package

```
library("my_library")
```

- List functions defined by a library

```
library(help="my_library")
```

- Load library manual (PDF or HTML file)

```
vignette("my_library")
```

- Execute an R script from within R

```
source("my_script.R")
```

- Execute an R script from command-line (the first of the three options is preferred)

```
$ Rscript my_script.R  
$ R CMD BATCH my_script.R  
$ R --slave < my_script.R
```

Data Types

- Numeric data

Example: 1, 2, 3, ...

```
x <- c(1, 2, 3)  
x
```

```
## [1] 1 2 3
```

```
is.numeric(x)
```

```
## [1] TRUE
```

```
as.character(x)
```

```
## [1] "1" "2" "3"
```

- Character data

Example: "a", "b", "c", ...

```
x <- c("1", "2", "3")  
x
```

```
## [1] "1" "2" "3"
```

```
is.character(x)
```

```
## [1] TRUE
```

```
as.numeric(x)
```

```
## [1] 1 2 3
```

- Complex data

Example: mix of both

```
c(1, "b", 3)
```

```
## [1] "1" "b" "3"
```

- Logical data

Example: TRUE of FALSE

```
x <- 1:10 < 5
```

```
x
```

```
## [1] TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE
```

```
!x
```

```
## [1] FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE
```

```
which(x) # Returns index for the 'TRUE' values in logical vector
```

```
## [1] 1 2 3 4
```

Data objects

Object types

- Vectors (1D)

Definition: numeric or character

```
myVec <- 1:10; names(myVec) <- letters[1:10]
```

```
myVec[1:5]
```

```
## a b c d e
```

```
## 1 2 3 4 5
```

```
myVec[c(2,4,6,8)]
```

```
## b d f h
```

```
## 2 4 6 8
```

```
myVec[c("b", "d", "f")]
```

```
## b d f
```

```
## 2 4 6
```

- Factors (1D)

Definition: vectors with grouping information

```
factor(c("dog", "cat", "mouse", "dog", "dog", "cat"))
```

```
## [1] dog cat mouse dog dog cat
```

```
## Levels: cat dog mouse
```

- Matrices (2D)

Definition: two dimensional structures with data of same type

```
myMA <- matrix(1:30, 3, 10, byrow = TRUE)
```

```
class(myMA)
```

```
## [1] "matrix"
```

```
myMA[1:2,]
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]    1    2    3    4    5    6    7    8    9    10
## [2,]   11   12   13   14   15   16   17   18   19   20
```

```
myMA[1, , drop=FALSE]
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## [1,]    1    2    3    4    5    6    7    8    9    10
```

- Data Frames (2D)

Definition: two dimensional objects with data of variable types

```
myDF <- data.frame(Col1=1:10, Col2=10:1)
myDF[1:2, ]
```

```
##   Col1 Col2
## 1     1   10
## 2     2    9
```

- Arrays

Definition: data structure with one, two or more dimensions

- Lists

Definition: containers for any object type

```
myL <- list(name="Fred", wife="Mary", no.children=3, child.ages=c(4,7,9))
myL
```

```
## $name
## [1] "Fred"
##
## $wife
## [1] "Mary"
##
## $no.children
## [1] 3
##
## $child.ages
## [1] 4 7 9
```

```
myL[[4]][1:2]
```

```
## [1] 4 7
```

- Functions

Definition: piece of code

```
myfct <- function(arg1, arg2, ...) {
  function_body
}
```

Subsetting of data objects

- Subsetting by positive or negative index/position numbers

```
myVec <- 1:26; names(myVec) <- LETTERS
myVec[1:4]
```

```
## A B C D
## 1 2 3 4
```

- Subsetting by same length logical vectors

```
myLog <- myVec > 10
myVec[myLog]
```

```
## K L M N O P Q R S T U V W X Y Z
## 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
```

- Subsetting by field names

```
myVec[c("B", "K", "M")]
```

```
## B K M
## 2 11 13
```

- Subset with \$ sign: references a single column or list component by its name

```
iris$Species[1:8]
```

```
## [1] setosa setosa setosa setosa setosa setosa setosa setosa
## Levels: setosa versicolor virginica
```

Important Utilities

- Combining Objects

The c function combines vectors and lists

```
c(1, 2, 3)
```

```
## [1] 1 2 3
```

```
x <- 1:3; y <- 101:103
c(x, y)
```

```
## [1] 1 2 3 101 102 103
```

```
iris$Species[1:8]
```

```
## [1] setosa setosa setosa setosa setosa setosa setosa setosa
## Levels: setosa versicolor virginica
```

The cbind and rbind functions can be used to append columns and rows, respectively.

```
ma <- cbind(x, y)
ma
```

```
##      x    y
## [1,] 1 101
## [2,] 2 102
## [3,] 3 103
```

```
rbind(ma, ma)
```

```
##      x    y
## [1,] 1 101
```

```
## [2,] 2 102
## [3,] 3 103
## [4,] 1 101
## [5,] 2 102
## [6,] 3 103
```

- Accessing Dimensions of Objects

Length and dimension information of objects

```
length(iris$Species)
```

```
## [1] 150
```

```
dim(iris)
```

```
## [1] 150 5
```

- Accessing Name Slots of Objects

Accessing row and column names of 2D objects

```
rownames(iris)[1:8]
```

```
## [1] "1" "2" "3" "4" "5" "6" "7" "8"
```

```
colnames(iris)
```

```
## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width"
```

```
## [5] "Species"
```

- Return name field of vectors and lists

```
names(myVec)
```

```
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q"
```

```
## [18] "R" "S" "T" "U" "V" "W" "X" "Y" "Z"
```

```
names(myL)
```

```
## [1] "name" "wife" "no.children" "child.ages"
```

- Sorting Objects

The function `sort` returns a vector in ascending or descending order

```
sort(10:1)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10
```

The function `order` returns a sorting index for sorting an object

```
sortindex <- order(iris[,1], decreasing = FALSE)
```

```
sortindex[1:12]
```

```
## [1] 14 9 39 43 42 4 7 23 48 3 30 12
```

```
iris[sortindex,][1:2,]
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
```

```
## 14 4.3 3.0 1.1 0.1 setosa
```

```
## 9 4.4 2.9 1.4 0.2 setosa
```

```
sortindex <- order(-iris[,1]) # Same as decreasing=TRUE
```

Sorting multiple columns

```
iris[order(iris$Sepal.Length, iris$Sepal.Width),][1:2,]

##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 14              4.3         3.0          1.1         0.1  setosa
## 9               4.4         2.9          1.4         0.2  setosa
```

Operators and Calculations

- Comparison Operators

Comparison operators: ==, !=, <, >, <=, >=

```
1==1
```

```
## [1] TRUE
```

Logical operators: AND: &, OR: |, NOT: !

```
x <- 1:10; y <- 10:1
x > y & x > 5
```

```
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE
```

- Basic Calculations

To look up math functions, see [Function Index](#) here

```
x + y
```

```
## [1] 11 11 11 11 11 11 11 11 11 11 11
```

```
sum(x)
```

```
## [1] 55
```

```
mean(x)
```

```
## [1] 5.5
```

```
apply(iris[1:6,1:3], 1, mean)
```

```
##           1           2           3           4           5           6
## 3.333333 3.100000 3.066667 3.066667 3.333333 3.666667
```

Reading and Writing External Data

- Import of tabular data

Import of a tab-delimited tabular file

```
myDF <- read.delim("myData.xls", sep="\t")
```

Import of Excel file. Note: working with tab- or comma-delimited files is more flexible and preferred.

```
library(gdata)
```

```
myDF <- read.xls("myData.xls")
```

- Export of tabular data

```
write.table(myDF, file="myfile.xls", sep="\t", quote=FALSE, col.names=NA)
```


- Line-wise import

```
myDF <- readLines("myData.txt")
```

- Line-wise export

```
writeLines(month.name, "myData.txt")
```

- Copy and paste into R

On Windows/Linux systems

```
read.delim("clipboard")
```

On Mac OS X systems

```
read.delim(pipe("pbpaste"))
```

- Copy and paste from R

On Windows/Linux systems

```
write.table(iris, "clipboard", sep="\t", col.names=NA, quote=F)
```

On Mac OS X systems

```
zz <- pipe('pbcopy', 'w')
write.table(iris, zz, sep="\t", col.names=NA, quote=F)
close(zz)
```

Useful R Functions

- Unique entries

Make vector entries unique with `unique`

```
length(iris$Sepal.Length)
```

```
## [1] 150
```

```
length(unique(iris$Sepal.Length))
```

```
## [1] 35
```

- Count occurrences

Count occurrences of entries with `table`

```
table(iris$Species)
```

```
##
```

```
##      setosa versicolor  virginica
```

```
##      50         50         50
```

- Aggregate data

Compute aggregate statistics with `aggregate`

```
aggregate(iris[,1:4], by=list(iris$Species), FUN=mean, na.rm=TRUE)
```

```
##      Group.1 Sepal.Length Sepal.Width Petal.Length Petal.Width
```

```
## 1      setosa      5.006      3.428      1.462      0.246
```

```
## 2 versicolor      5.936      2.770      4.260      1.326
```

```
## 3  virginica      6.588      2.974      5.552      2.026
```

- Intersect data

Compute intersect between two vectors with `%in%`

```
month.name %in% c("May", "July")
```

```
## [1] FALSE FALSE FALSE FALSE TRUE FALSE TRUE FALSE FALSE FALSE FALSE
## [12] FALSE
```

- Merge data frames

Join two data frames by common field entries with `merge` (here row names by `x=0`). To obtain only the common rows, change `all=TRUE` to `all=FALSE`. To merge on specific columns, refer to them by their position numbers or their column names.

```
frame1 <- iris[sample(1:length(iris[,1]), 30), ]
frame1[1:2,]
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 125           6.7         3.3         5.7         2.1 virginica
## 55           6.5         2.8         4.6         1.5 versicolor
```

```
dim(frame1)
```

```
## [1] 30  5
```

```
my_result <- merge(frame1, iris, by.x = 0, by.y = 0, all = TRUE)
dim(my_result)
```

```
## [1] 150 11
```

Graphics in R

Advantages

- Powerful environment for visualizing scientific data
- Integrated graphics and statistics infrastructure
- Publication quality graphics
- Fully programmable
- Highly reproducible
- Full LaTeX and Markdown support via `knitr` and R `markdown`
- Vast number of R packages with graphics utilities

Documentation for R Graphics

**** General ****

- Graphics Task Page - URL
- R Graph Gallery - URL
- R Graphical Manual - URL
- Paul Murrell's book R (Grid) Graphics - URL

Interactive graphics

- `rggobi` (GGobi) - URL
- `iplots` - URL
- Open GL (`rgl`) - URL

Graphics Environments

Viewing and saving graphics in R

- On-screen graphics
- postscript, pdf, svg
- jpeg, png, wmf, tiff, ...

Four major graphic environments

- (a) Low-level infrastructure
 - R Base Graphics (low- and high-level)
 - `grid`: Manual
- (b) High-level infrastructure `\begin{itemize}`
 - `lattice`: Manual, Intro, Book
 - `ggplot2`: Manual, Intro, Book

Base Graphics: Overview

Important high-level plotting functions

- `plot`: generic x-y plotting
- `barplot`: bar plots
- `boxplot`: box-and-whisker plot
- `hist`: histograms
- `pie`: pie charts
- `dotchart`: cleveland dot plots
- `image`, `heatmap`, `contour`, `persp`: functions to generate image-like plots
- `qqnorm`, `qqline`, `qqplot`: distribution comparison plots
- `pairs`, `coplot`: display of multivariate data

Help on graphics functions

- `?myfct`
- `?plot`
- `?par`

Preferred Object Types

- Matrices and data frames
- Vectors
- Named vectors

Scatter Plots

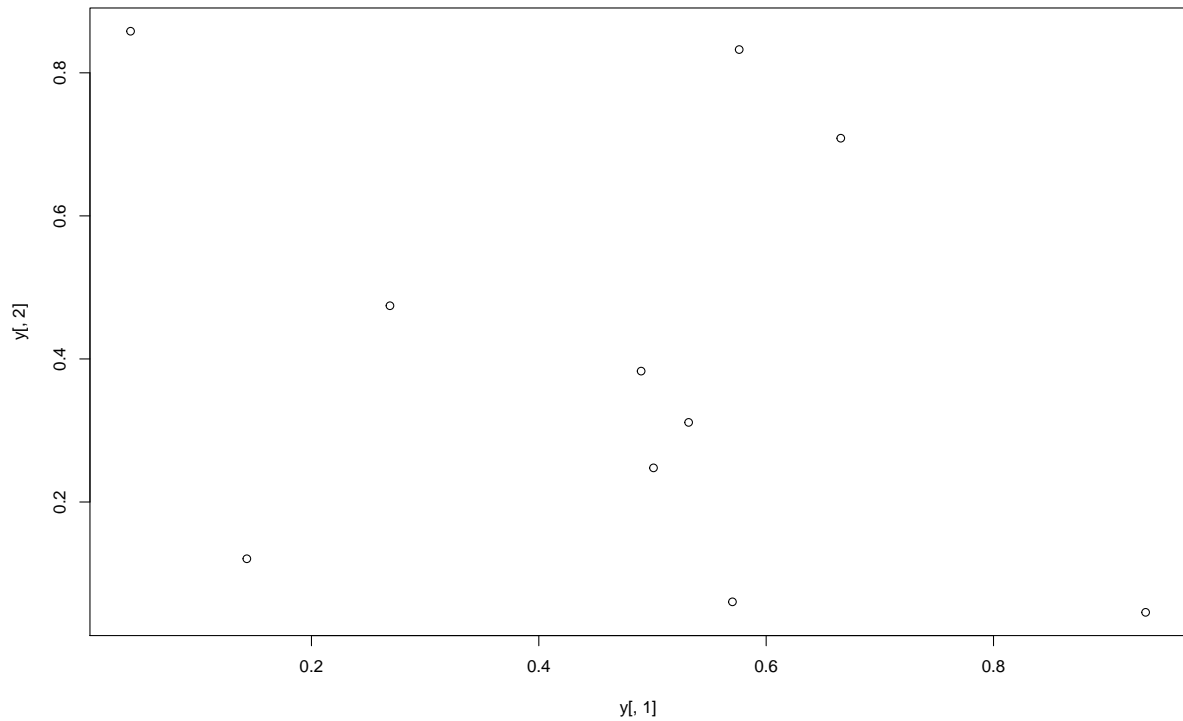
Basic Scatter Plot

- Sample data set for subsequent plots

```
set.seed(1410)
y <- matrix(runif(30), ncol=3, dimnames=list(letters[1:10], LETTERS[1:3]))
```

- Plot data

```
plot(y[,1], y[,2])
```



All pairs

```
```r
pairs(y)
```
```

```
![] (Figs/pairs_scatter_plot-1.pdf)<!-- -->
```

With labels

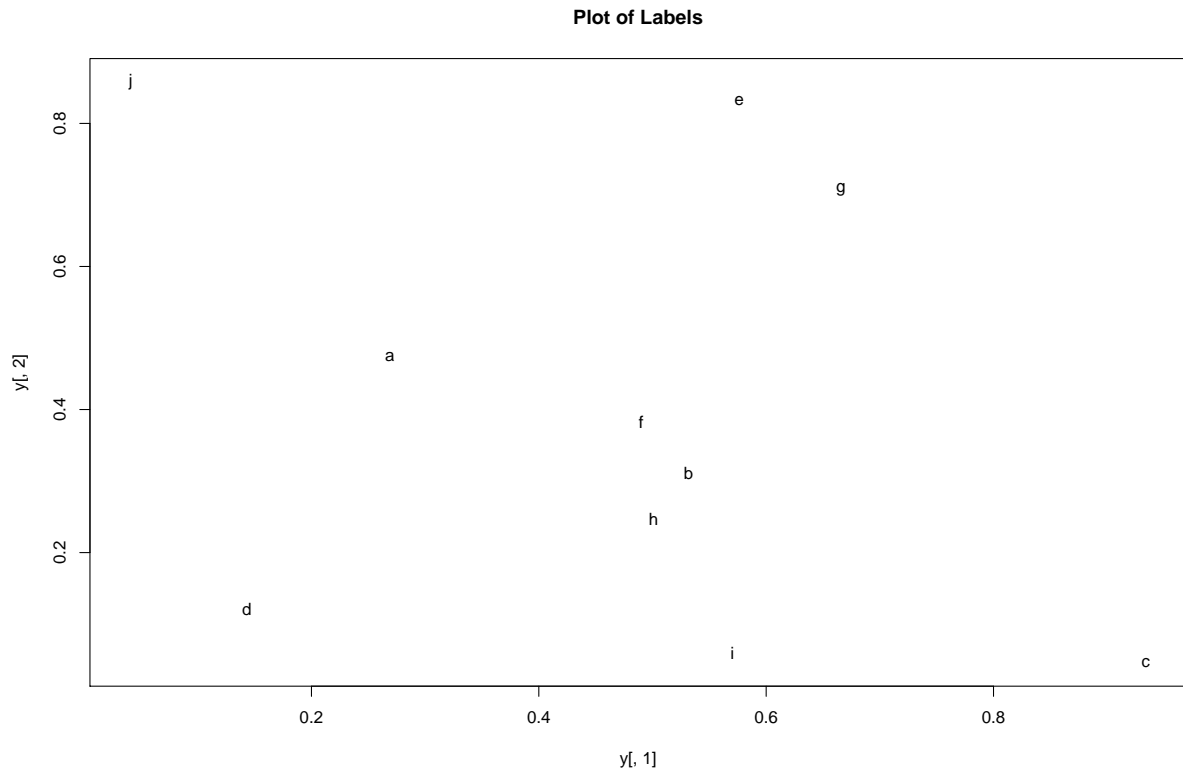
```
```r
plot(y[,1], y[,2], pch=20, col="red", main="Symbols and Labels")
text(y[,1]+0.03, y[,2], rownames(y))
```
```

```
![] (Figs/labels_scatter_plot-1.pdf)<!-- -->
```

More examples

- Print instead of symbols the row names

```
plot(y[,1], y[,2], type="n", main="Plot of Labels")
text(y[,1], y[,2], rownames(y))
```



- Usage of important plotting parameters

```
grid(5, 5, lwd = 2)
op <- par(mar=c(8,8,8,8), bg="lightblue")
plot(y[,1], y[,2], type="p", col="red", cex.lab=1.2, cex.axis=1.2,
      cex.main=1.2, cex.sub=1, lwd=4, pch=20, xlab="x label",
      ylab="y label", main="My Main", sub="My Sub")
par(op)
```

- Important arguments

- `mar`: specifies the margin sizes around the plotting area in order: `c(bottom, left, top, right)`
- `col`: color of symbols
- `pch`: type of symbols, samples: `example(points)`
- `lwd`: size of symbols
- `cex`: control font sizes
- For details see `?par`

Add regression line

```
```r
plot(y[,1], y[,2])
myline <- lm(y[,2]~y[,1]); abline(myline, lwd=2)
```
```

```
![] (Figs/plot_regression-1.pdf)<!-- -->
```

```
```r
summary(myline)
```
```

```

```
##
Call:
lm(formula = y[, 2] ~ y[, 1])
##
Residuals:
Min 1Q Median 3Q Max
-0.40357 -0.17912 -0.04299 0.22147 0.46623
##
Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.5764 0.2110 2.732 0.0258 *
y[, 1] -0.3647 0.3959 -0.921 0.3839

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
Residual standard error: 0.3095 on 8 degrees of freedom
Multiple R-squared: 0.09589, Adjusted R-squared: -0.01712
F-statistic: 0.8485 on 1 and 8 DF, p-value: 0.3839
```

```

Log scale

- Same plot as above, but on log scale

```

```r
plot(y[,1], y[,2], log="xy")
```

<!-- -->

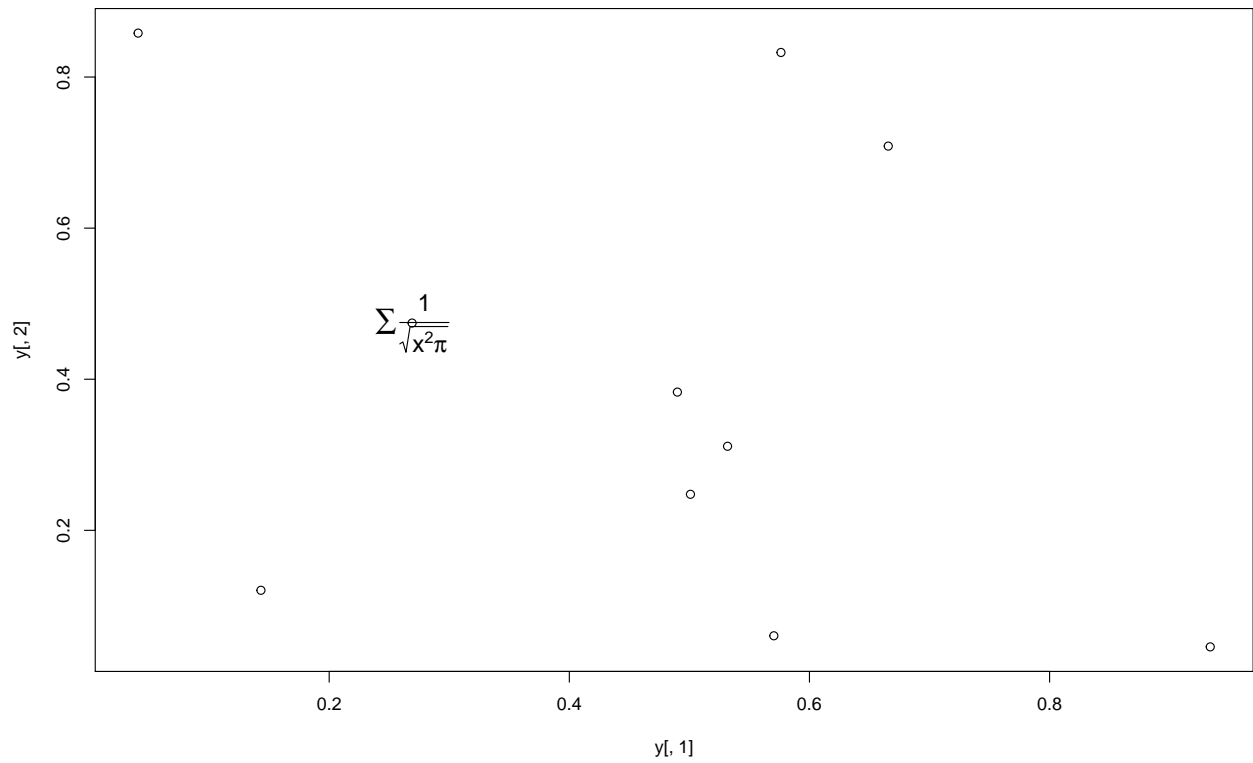
```

Add a mathematical expression

```

plot(y[,1], y[,2]); text(y[1,1], y[1,2], expression(sum(frac(1,sqrt(x^2*pi)))), cex=1.3)

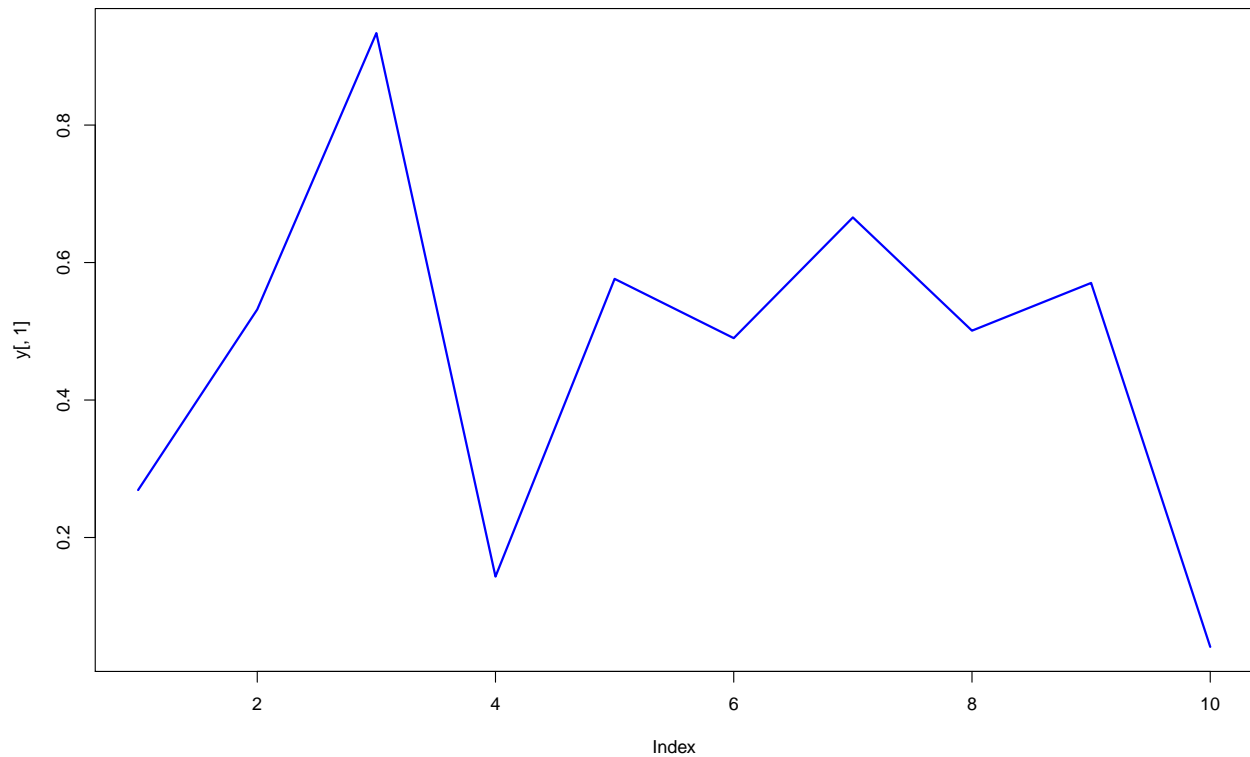
```



Line Plots

Single data set

```
plot(y[,1], type="l", lwd=2, col="blue")
```



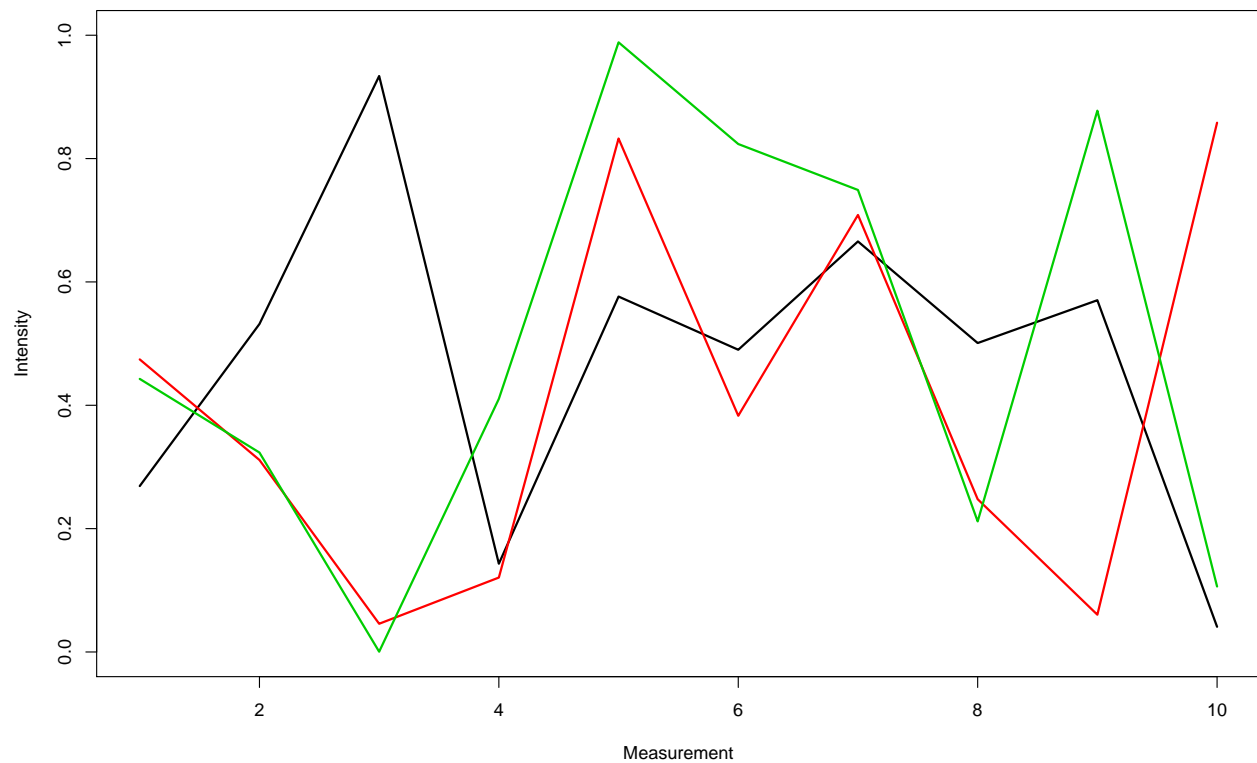
Many Data Sets

Plots line graph for all columns in data frame `y`. The `split.screen` function is used in this example in a for loop to overlay several line graphs in the same plot.

```
split.screen(c(1,1))
```

```
## [1] 1
```

```
plot(y[,1], ylim=c(0,1), xlab="Measurement", ylab="Intensity", type="l", lwd=2, col=1)
for(i in 2:length(y[,1])) {
  screen(1, new=FALSE)
  plot(y[,i], ylim=c(0,1), type="l", lwd=2, col=i, xaxt="n", yaxt="n", ylab="", xlab="", main="", bty="n")
}
```

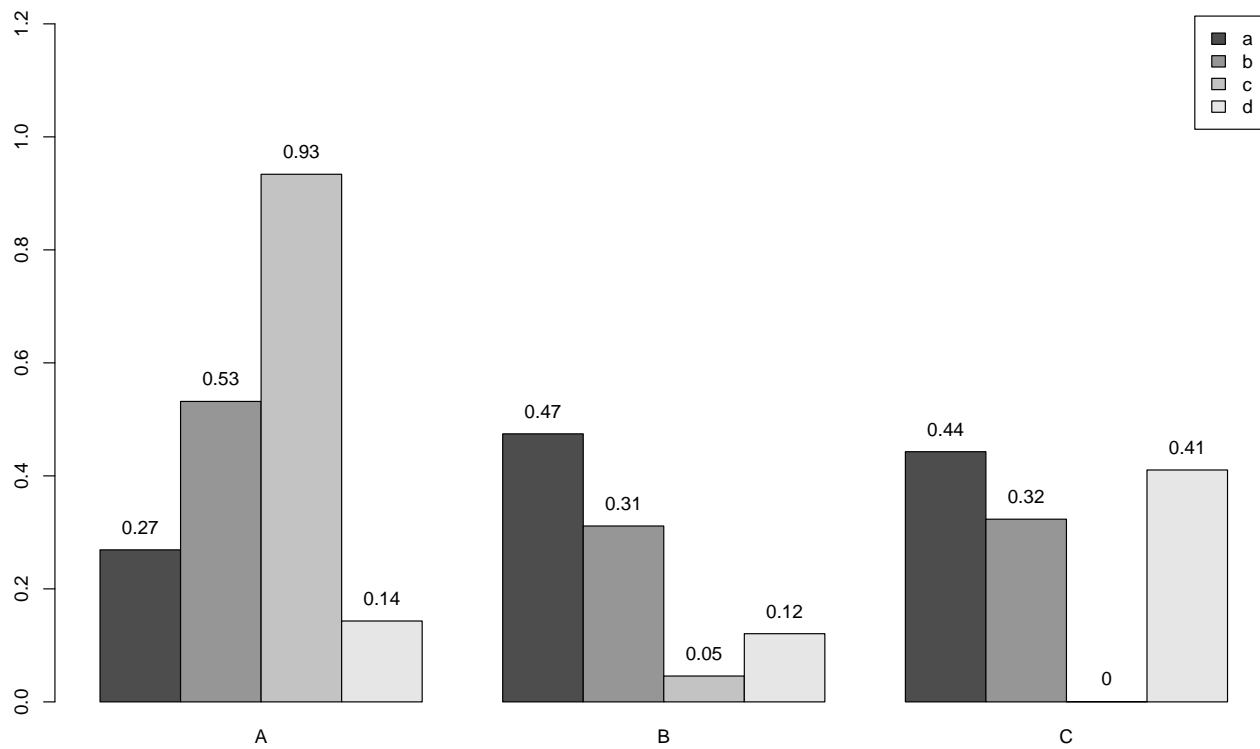



```
close.screen(all=TRUE)
```

Bar Plots

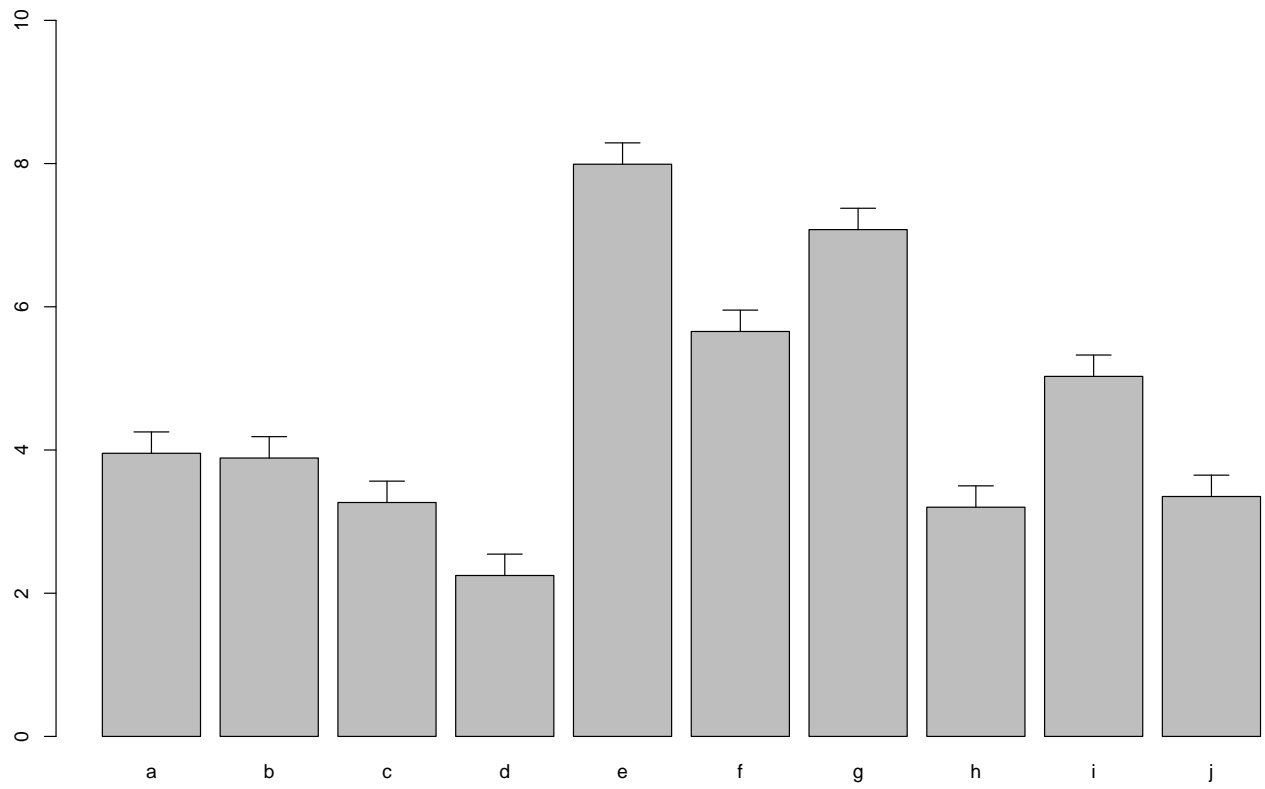
Basics

```
barplot(y[1:4,], ylim=c(0, max(y[1:4,])+0.3), beside=TRUE, legend=letters[1:4])
text(labels=round(as.vector(as.matrix(y[1:4,])),2), x=seq(1.5, 13, by=1) + sort(rep(c(0,1,2), 4)), y=as
```



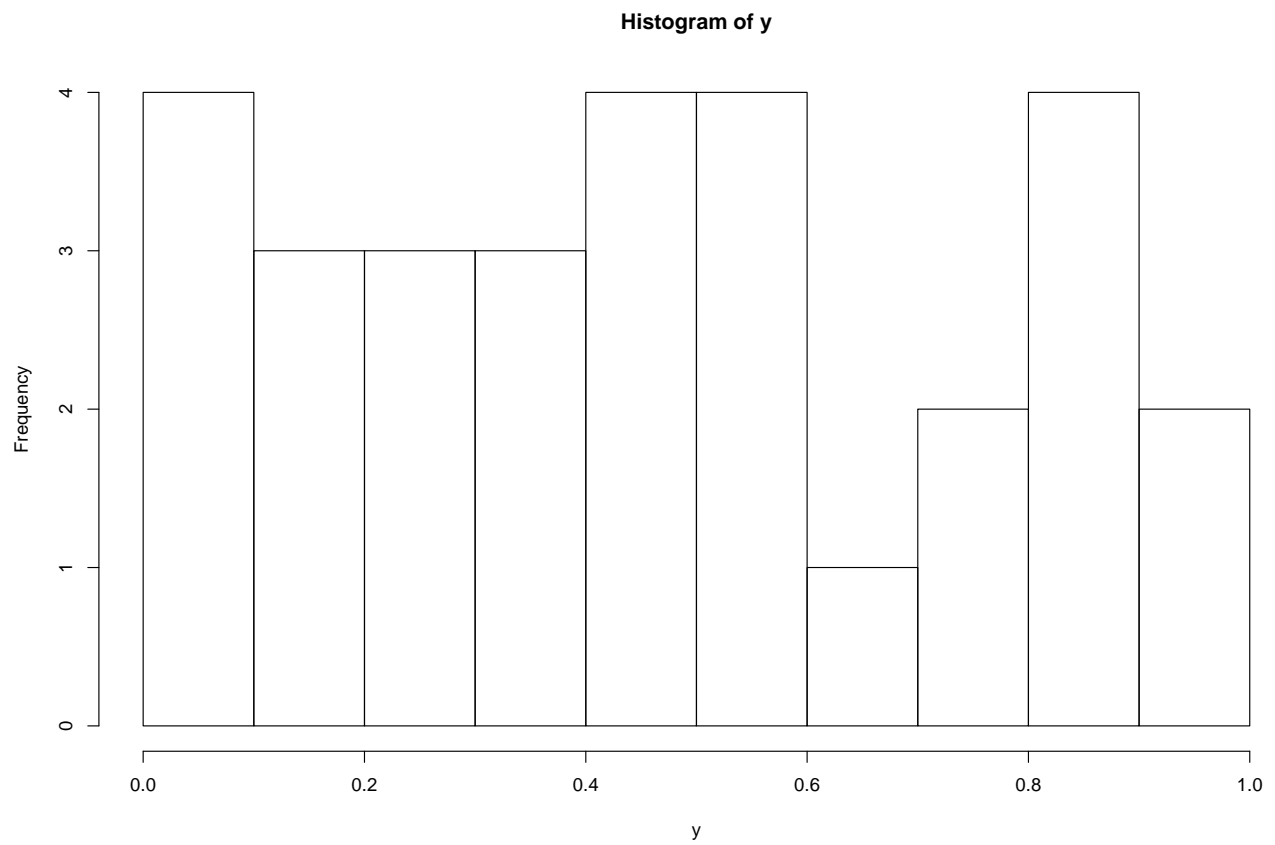
Error Bars

```
bar <- barplot(m <- rowMeans(y) * 10, ylim=c(0, 10))
stdev <- sd(t(y))
arrows(bar, m, bar, m + stdev, length=0.15, angle = 90)
```



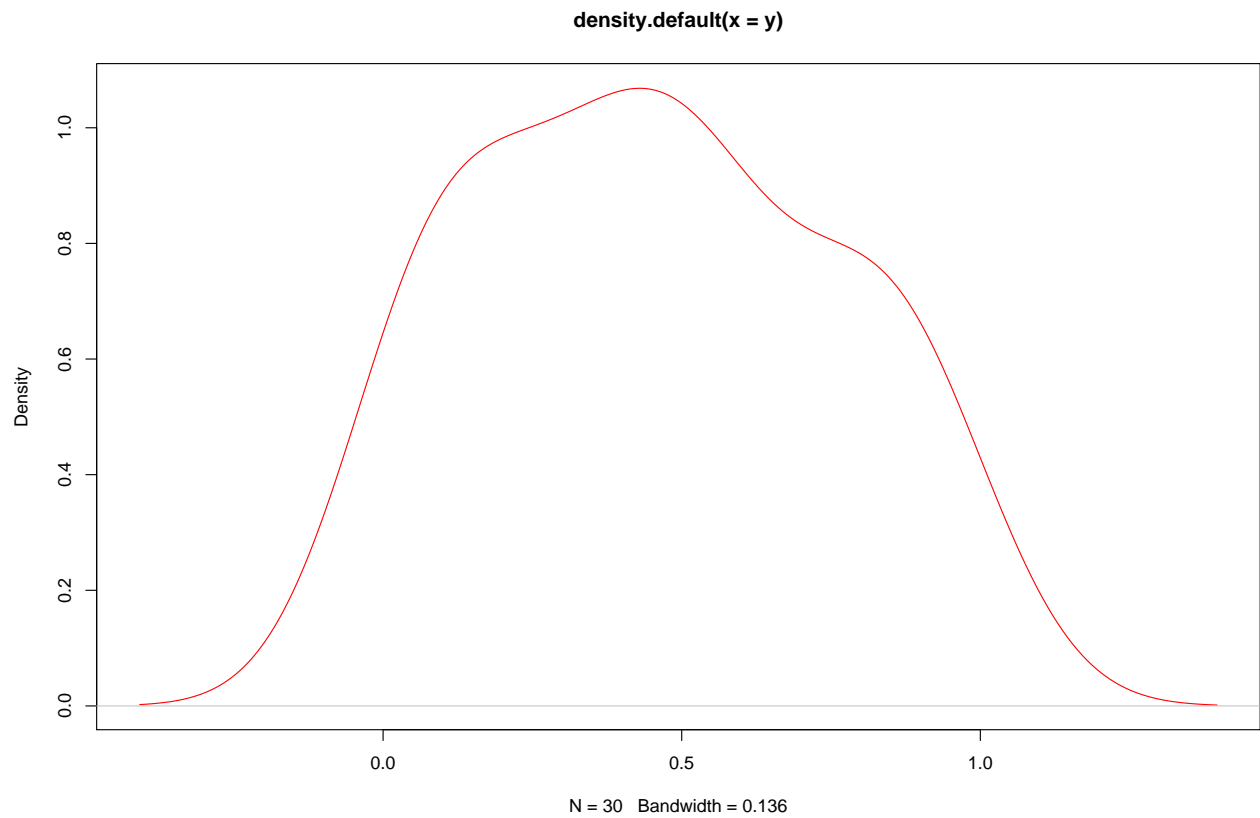
Histograms

```
hist(y, freq=TRUE, breaks=10)
```



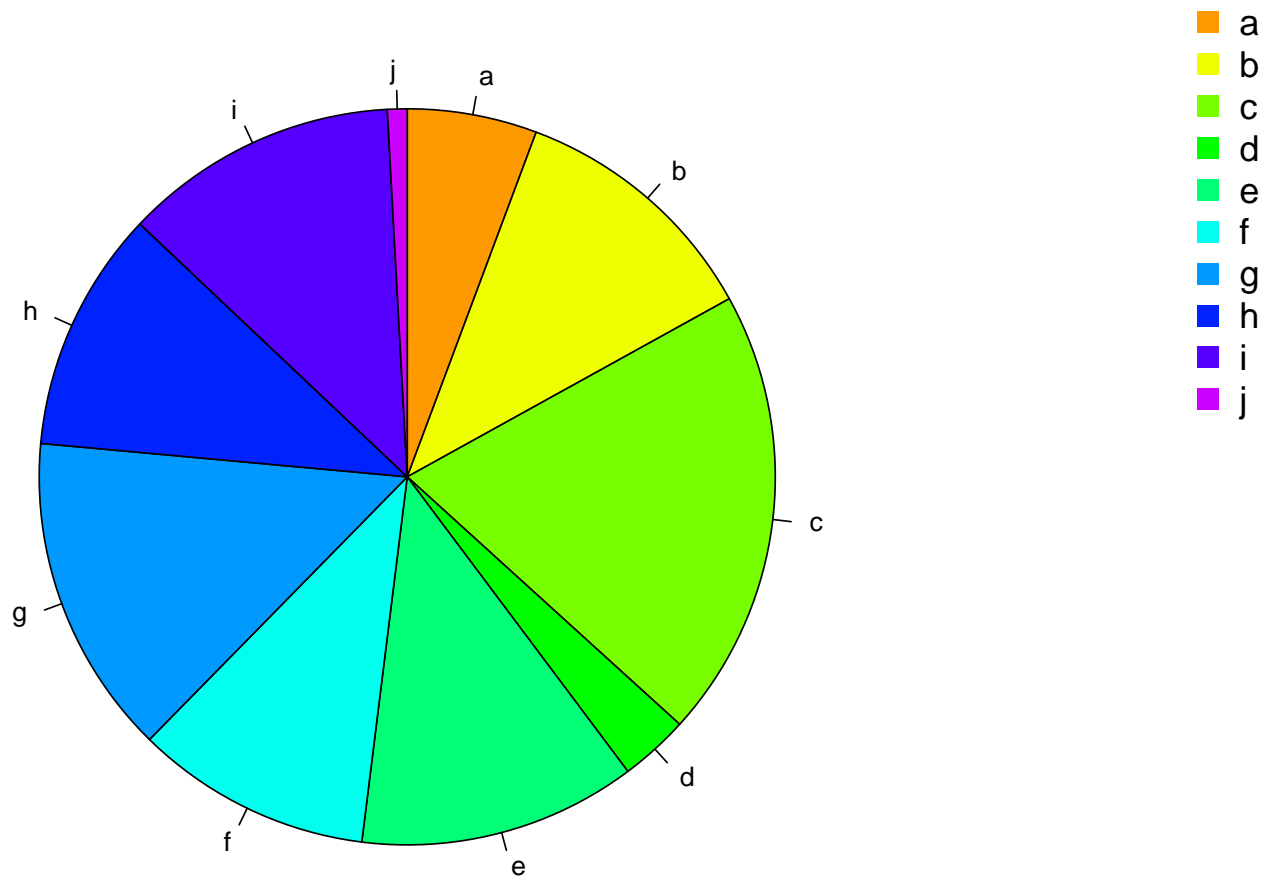
Density Plots

```
plot(density(y), col="red")
```



Pie Charts

```
pie(y[,1], col=rainbow(length(y[,1]), start=0.1, end=0.8), clockwise=TRUE)
legend("topright", legend=row.names(y), cex=1.3, bty="n", pch=15, pt.cex=1.8,
col=rainbow(length(y[,1]), start=0.1, end=0.8), ncol=1)
```



Color Selection Utilities

- Default color palette and how to change it

```
palette()

## [1] "black" "red" "green3" "blue" "cyan" "magenta" "yellow"
## [8] "gray"

palette(rainbow(5, start=0.1, end=0.2))
palette()

## [1] "#FF9900" "#FFBF00" "#FFE600" "#F2FF00" "#CCFF00"

palette("default")
```

- The gray function allows to select any type of gray shades by providing values from 0 to 1

```
gray(seq(0.1, 1, by= 0.2))

## [1] "#1A1A1A" "#4D4D4D" "#808080" "#B3B3B3" "#E6E6E6"
```

- Color gradients with colorpanel function from gplots library

```
library(gplots)
colorpanel(5, "darkblue", "yellow", "white")

## [1] "#00008B" "#808046" "#FFFF00" "#FFFF80" "#FFFFFF"
```

Much more on colors in R see Earl Glynn's color chart [here](#)

Saving Graphics to File

- After the `pdf()` command all graphs are redirected to file `test.pdf`. Works for all common formats similarly: jpeg, png, ps, tiff, ...

```
pdf("test.pdf")
plot(1:10, 1:10)
dev.off()
```

- Generates Scalable Vector Graphics (SVG) files that can be edited in vector graphics programs, such as Inkscape.

```
library("RSvgDevice")
devSVG("test.svg")
plot(1:10, 1:10)
dev.off()
```

Basic Statistics

- `summary` is a generic function to summarize many types of R objects, including datasets.

```
summary(iris)
```

| ## | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|----|---------------|---------------|---------------|---------------|
| ## | Min. :4.300 | Min. :2.000 | Min. :1.000 | Min. :0.100 |
| ## | 1st Qu.:5.100 | 1st Qu.:2.800 | 1st Qu.:1.600 | 1st Qu.:0.300 |
| ## | Median :5.800 | Median :3.000 | Median :4.350 | Median :1.300 |
| ## | Mean :5.843 | Mean :3.057 | Mean :3.758 | Mean :1.199 |
| ## | 3rd Qu.:6.400 | 3rd Qu.:3.300 | 3rd Qu.:5.100 | 3rd Qu.:1.800 |
| ## | Max. :7.900 | Max. :4.400 | Max. :6.900 | Max. :2.500 |
| ## | Species | | | |
| ## | setosa :50 | | | |
| ## | versicolor:50 | | | |
| ## | virginica :50 | | | |
| ## | | | | |
| ## | | | | |
| ## | | | | |

- Compare the mean of two groups

```
s=iris[which(iris$Species=='setosa'), 1];
v=iris[which(iris$Species=='virginica'), 1];
t.test(s,v, paired=T)
```

```
##
## Paired t-test
##
## data: s and v
## t = -16.344, df = 49, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.776513 -1.387487
## sample estimates:
```

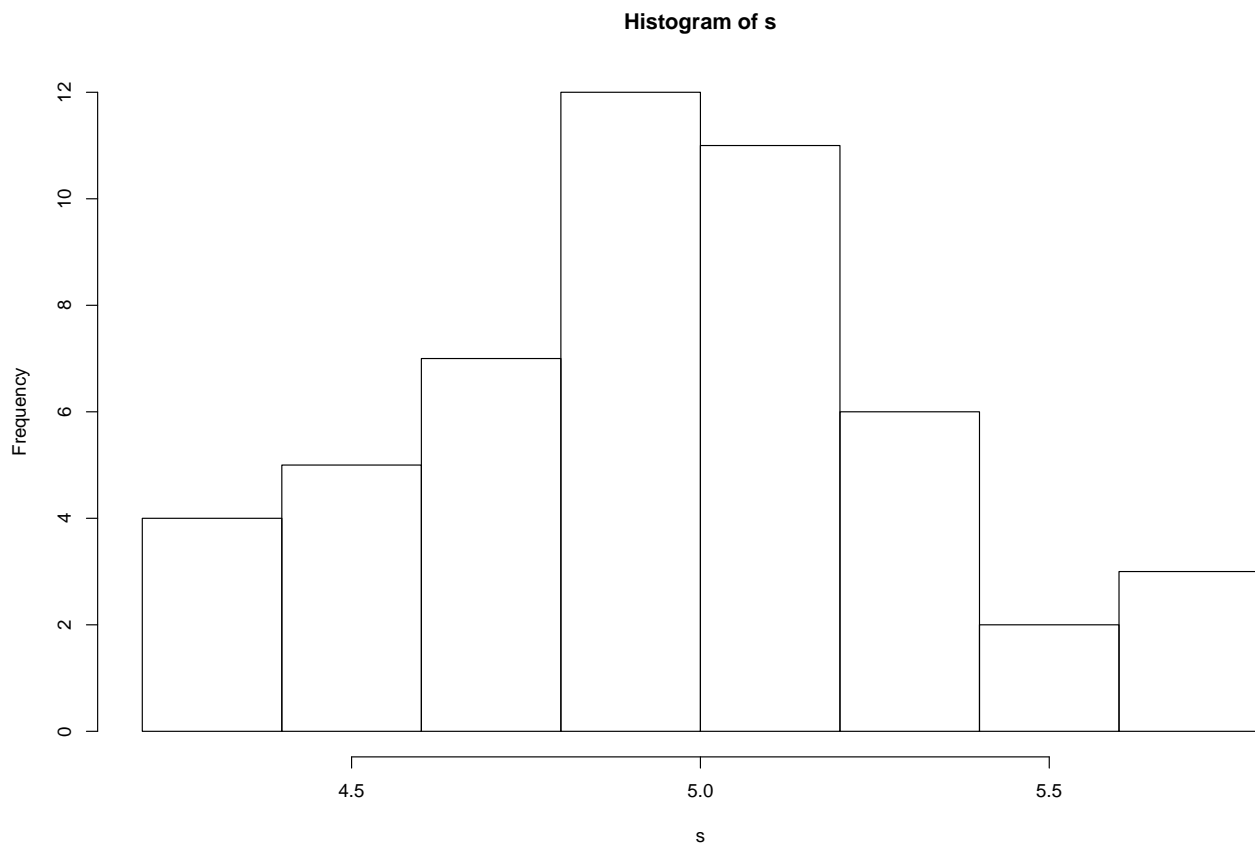
```
## mean of the differences
## -1.582
```

- Check the normality of my data

```
s=iris[which(iris$Species=='setosa'), 1];
shapiro.test(s);
```

```
##
## Shapiro-Wilk normality test
##
## data: s
## W = 0.9777, p-value = 0.4595
```

```
hist(s, breaks=10);
```



- Test correlation between two data sets

```
s=iris[which(iris$Species=='setosa'), 1];
v=iris[which(iris$Species=='setosa'), 2];
cor.test(s,v)
```

```
##
## Pearson's product-moment correlation
##
## data: s and v
## t = 7.6807, df = 48, p-value = 6.71e-10
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.5851391 0.8460314
```



```
## sample estimates:
##      cor
## 0.7425467

• Build a linear model

myModel = lm(iris[,1] ~ iris[, 2] + iris[, 3] + iris[, 4])
summary(myModel)

##
## Call:
## lm(formula = iris[, 1] ~ iris[, 2] + iris[, 3] + iris[, 4])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82816 -0.21989  0.01875  0.19709  0.84570
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.85600    0.25078   7.401 9.85e-12 ***
## iris[, 2]      0.65084    0.06665   9.765 < 2e-16 ***
## iris[, 3]      0.70913    0.05672  12.502 < 2e-16 ***
## iris[, 4]     -0.55648    0.12755  -4.363 2.41e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3145 on 146 degrees of freedom
## Multiple R-squared:  0.8586, Adjusted R-squared:  0.8557
## F-statistic: 295.5 on 3 and 146 DF,  p-value: < 2.2e-16

step(myModel, direction="backward")

## Start:  AIC=-343.04
## iris[, 1] ~ iris[, 2] + iris[, 3] + iris[, 4]
##
##              Df Sum of Sq    RSS    AIC
## <none>                 14.445 -343.04
## - iris[, 4]    1     1.8834 16.329 -326.66
## - iris[, 2]    1     9.4353 23.881 -269.63
## - iris[, 3]    1    15.4657 29.911 -235.86
##
## Call:
## lm(formula = iris[, 1] ~ iris[, 2] + iris[, 3] + iris[, 4])
##
## Coefficients:
## (Intercept)  iris[, 2]  iris[, 3]  iris[, 4]
##      1.8560      0.6508      0.7091     -0.5565

• ANOVA

myAnova<-aov(iris[,1] ~ iris[, 5])
summary(myAnova)

##              Df Sum Sq Mean Sq F value Pr(>F)
## iris[, 5]      2  63.21  31.606  119.3 <2e-16 ***
## Residuals    147  38.96   0.265
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```