Introduction to R
A Short Overview

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Introduction

- Look and Feel of the R Environment
- R Library Repositories
- Installation
- Getting Around
- Basic Syntax
- Data Types and Subsetting
- Important Utilities
- Basic Calculations
- Reading and Writing External Data
- Some Great R Functions
- Graphics Utilities

Graphics Environments
- Base Graphics

Exercise: Analysis Routine
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
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 bioinformatics
- Is standard for data mining and biostatistical analysis
- Technical advantages: free, open-source, available for all OSs

Books & Documentation

- simpleR - Using R for Introductory Statistics (John Verzani, 2004) [Link]
- Bioinformatics and Computational Biology Solutions Using R and Bioconductor (Gentleman et al., 2005) [Link]
- More on this see “Finding Help” section in UCR Manual [Link]
What You’ll Get?

R Gui: OS X

Command-line R: Linux/OS X

R Gui: Windows

Introduction to R

Introduction

Look and Feel of the R Environment

Slide 6/70
RStudio: Alternative Working Environment for R

New integrated development environment (IDE) for R that works well for beginners and developers.

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

Introduction

Look and Feel of the R Environment

R Library Depositories

Installation

Getting Around

Basic Syntax

Data Types and Subsetting

Important Utilities

Basic Calculations

Reading and Writing External Data

Some Great R Functions

Graphics Utilities

Graphics Environments

Base Graphics

Exercise: Analysis Routine
Package Depositories

- CRAN (>3500 packages) general data analysis
- Bioconductor (>700 packages) bioscience data analysis
- Omegahat (>30 packages) programming interfaces
Outline

**Introduction**
- Look and Feel of the R Environment
- R Library Depositories

**Installation**
- Getting Around
- Basic Syntax
- Data Types and Subsetting
- Important Utilities
- Basic Calculations
- Reading and Writing External Data
- Some Great R Functions
- Graphics Utilities

**Graphics Environments**
- Base Graphics

**Exercise: Analysis Routine**
Installation of R and Add-on Packages

Install R for your operating system from:

http://cran.at.r-project.org

Install RStudio from:

http://www.rstudio.com/ide/download

Installation of CRAN Packages

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

Installation of Bioconductor Packages

> source("http://www.bioconductor.org/biocLite.R")
> library(BiocInstaller)
> BiocVersion()
> biocLite()
> biocLite(c("pkg1", "pkg2"))

For more details see Bioc Install page and BiocInstaller
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation

Getting Around

Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
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).

```r
## 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.
Getting Around

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")
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around

Basic Syntax

Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments

Base Graphics

Exercise: Analysis Routine
Basic R Syntax

General R command syntax

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

Finding help

> ?function_name

Load a library

> library("my_library")

Lists all functions defined by a library

> library(help="my_library")

Load library manual (PDF file)

> vignette("my_library")
Executing R Scripts

Execute an R script from within R

> source("my_script.R")

Execute an R script from command-line

Rscript my_script.R
R CMD BATCH my_script.R
R --slave < my_script.R
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax

Data Types and Subsetting

Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Data Types I

**Numeric data: 1, 2, 3**

```r
> x <- c(1, 2, 3); x
[1] 1 2 3
> is.numeric(x)
[1] TRUE
> as.character(x)
[1] "1" "2" "3"
```

**Character data: "a", "b", "c"**

```r
> x <- c("1", "2", "3"); x
[1] "1" "2" "3"
> is.character(x)
[1] TRUE
> as.numeric(x)
[1] 1 2 3
```
Complex data
> c(1, "b", 3)
[1] "1" "b" "3"

Logical data
> x <- 1:10 < 5
> x

[1] TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

> !x

[1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE

> which(x) # Returns index for the 'TRUE' values in logical vector
[1] 1 2 3 4
Data Objects: Vectors and Factors

Vectors (1D)

```r
> 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): vectors with grouping information

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

[1] dog cat mouse dog dog cat
Levels: cat dog mouse
Data Objects: Matrices, Data Frames and Arrays

Matrices (2D): two dimensional structures with data of same type

```r
> myMA <- matrix(1:30, 3, 10, byrow = TRUE)
> class(myMA)
[1] "matrix"

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

```r
> myMA[1, , drop=FALSE]
[1,]  1  2  3  4  5  6  7  8  9  10
```

Data Frames (2D): two dimensional structures with variable data types

```r
> myDF <- data.frame(Col1=1:10, Col2=10:1)
> myDF[1:2,]
     Col1 Col2
 1     1   10
 2     2    9
```

Arrays: data structure with one, two or more dimensions
Lists: containers for any object type

\[
\text{myL} <- \text{list(name="Fred", wife="Mary", no.children=3, child.ages=c(4,7,9))}
\]

\[
\text{myL}
\]

$\text{name}$

[1] "Fred"

$\text{wife}$

[1] "Mary"

$\text{no.children}$

[1] 3

$\text{child.ages}$

[1] 4 7 9

\[
\text{myL}[4][1:2]
\]

[1] 4 7

Functions: piece of code

\[
\text{myfct} <- \text{function(arg1, arg2, \ldots) \{}
+ \text{function\_body}
+ \text{\}}
\]
General Subsetting Rules

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

Calling a single column or list component by its name with the $ sign
> iris$Species[1:8]

[1] setosa setosa setosa setosa setosa setosa setosa setosa
Levels: setosa versicolor virginica
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting

Important Utilities

Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Combining Objects

The `c` function combines vectors and lists

```r
> c(1, 2, 3)
[1] 1 2 3
> x <- 1:3; y <- 101:103
> c(x, y)
[1]  1  2  3 101 102 103
```

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

```r
> 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 Name Slots and Dimensions of Objects

Length and dimension information of objects

> `length(iris$Species)`

[1] 150

> `dim(iris)`

[1] 150 5

Accessing row and column names of 2D objects

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

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

> `colnames(iris)`


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" "R" "S"

> `names(myL)`

[1] "name" "wife" "no.children" "child.ages"
Sorting Objects

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

```r
> 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

```r
> 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,]

<table>
<thead>
<tr>
<th></th>
<th>Sepal.Length</th>
<th>Sepal.Width</th>
<th>Petal.Length</th>
<th>Petal.Width</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>4.3</td>
<td>3.0</td>
<td>1.1</td>
<td>0.1</td>
<td>setosa</td>
</tr>
<tr>
<td>9</td>
<td>4.4</td>
<td>2.9</td>
<td>1.4</td>
<td>0.2</td>
<td>setosa</td>
</tr>
</tbody>
</table>

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

Sorting on multiple columns

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

<table>
<thead>
<tr>
<th></th>
<th>Sepal.Length</th>
<th>Sepal.Width</th>
<th>Petal.Length</th>
<th>Petal.Width</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>4.3</td>
<td>3.0</td>
<td>1.1</td>
<td>0.1</td>
<td>setosa</td>
</tr>
<tr>
<td>9</td>
<td>4.4</td>
<td>2.9</td>
<td>1.4</td>
<td>0.2</td>
<td>setosa</td>
</tr>
</tbody>
</table>
```
Outline

Introduction
- Look and Feel of the R Environment
- R Library Depositories
- Installation
- Getting Around
- Basic Syntax
- Data Types and Subsetting
- Important Utilities

Basic Calculations
- Reading and Writing External Data
- Some Great R Functions
- Graphics Utilities

Graphics Environments
- Base Graphics

Exercise: Analysis Routine
Basic Operators and Calculations

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 TRUE TRUE

Calculations: to look up math functions, see Function Index

> x + y


> sum(x)

[1] 55

> mean(x)

[1] 5.5

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

          1        2        3        4        5        6
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations

Reading and Writing External Data

Some Great R Functions
Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Import data from tabular files into R
> myDF <- read.delim("myData.xls", sep="\t")

Export data from R to tabular files
> write.table(myDF, file="myfile.xls", sep="\t", quote=FALSE, col.names=NA)

Copy and paste (e.g. from Excel) into R
> ## On Windows/Linux systems:
> read.delim("clipboard")
> ## On Mac OS X systems:
> read.delim(pipe("pbpaste"))

Copy and paste from R into Excel or other programs
> ## 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)
Exercise 1: Object Subsetting Routines and Import/Export

Task 1  Sort the rows of the iris data frame by its first column and sort its columns alphabetically by column names.

Task 2  Subset the first 12 rows, export the result to a text file and view it in Excel.

Task 3  Change some column titles in Excel and import the result into R.

Structure of iris data set:

```r
class(iris)
[1] "data.frame"
dim(iris)
[1] 150  5
colnames(iris)
```
Outline

Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data

Some Great R Functions

Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Some Great R Functions I

**The `unique()` function to make vector entries unique**

```r
> length(iris$Sepal.Length)
[1] 150
> length(unique(iris$Sepal.Length))
[1] 35
```

**The `table()` function counts the occurrences of entries**

```r
> table(iris$Species)

    setosa versicolor virginica
     50      50       50
```

**The `aggregate()` function computes statistics of data aggregates**

```r
> 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
```
The `%in%` function returns the intersect between two vectors

```r
> month.name %in% c("May", "July")
[1] FALSE FALSE FALSE FALSE TRUE FALSE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

The `merge()` function joins two data frames by common field entries, 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.

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

Sepal.Length Sepal.Width Petal.Length Petal.Width Species
36 5.0 3.2 1.2 0.2 setosa
   
4  4.6 3.1 1.5 0.2 setosa

> dim(frame1)
[1] 30 5

> my_result <- merge(frame1, iris, by.x = 0, by.y = 0, all = TRUE)
> dim(my_result)
[1] 150 11
```
Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions

Graphics Utilities

Graphics Environments
Base Graphics

Exercise: Analysis Routine
Graphics in R

- Powerful environment for visualizing scientific data
- Integrated graphics and statistics infrastructure
- Publication quality graphics
- Fully programmable
- Highly reproducible
- Full \LaTeX \textsuperscript{Link} & Sweave \textsuperscript{Link} support
- Vast number of R packages with graphics utilities
Documentation on Graphics in R

General

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

Interactive graphics

- rggobi (GGobi)
- iplots
- Open GL (rgl)
Graphics Environments

Viewing and saving graphics in R

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

Four major graphic environments

- Low-level infrastructure
  - R Base Graphics (low- and high-level)
  - grid: Manual Link, Book Link

- High-level infrastructure
  - lattice: Manual Link, Intro Link, Book Link
  - ggplot2: Manual Link, Intro Link, Book Link
Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments

Base Graphics

Exercise: Analysis Routine
Introduction

Look and Feel of the R Environment
R Library Depositories
Installation
Getting Around
Basic Syntax
Data Types and Subsetting
Important Utilities
Basic Calculations
Reading and Writing External Data
Some Great R Functions
Graphics Utilities

Graphics Environments

Base Graphics

Exercise: Analysis Routine
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 multivariant data

Help on these functions

- ?myfct
- ?plot
- ?par
Matrices and data frames
Vectors
Named vectors
Scatter Plot: very basic

Sample data set for subsequent plots

\[
\text{set.seed(1410)}
\]
\[
\text{y <- matrix(runif(30), ncol=3, dimnames=list(letters[1:10], LETTERS[1:3]))}
\]
\[
\text{plot(y[,1], y[,2])}
\]
Scatter Plot: all pairs

\[ \text{pairs}(y) \]
Scatter Plot: 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))
```

![Scatter Plot](attachment:image.png)

Symbols and Labels

y[, 1] y[, 2] a b c d e f g h i j
Scatter Plots: more examples

Print instead of symbols the row names

\begin{verbatim}
> plot(y[,1], y[,2], type="n", main="Plot of Labels")
> text(y[,1], y[,2], rownames(y))
\end{verbatim}

Usage of important plotting parameters

\begin{verbatim}
> 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)
\end{verbatim}

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.\ast**: control font sizes
- For details see ?par
Add a regression line to a plot

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

Same plot as above, but on log scale

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

Add a mathematical expression to a plot

```r
> plot(y[,1], y[,2]); text(y[1,1], y[1,2],
> expression(sum(frac(1,sqrt(x^2*pi)))), cex=1.3)
```
Task 1 Generate scatter plot for first two columns in iris data frame and color dots by its Species column.

Task 2 Use the xlim/ylim arguments to set limits on the x- and y-axes so that all data points are restricted to the left bottom quadrant of the plot.

Structure of iris data set:

> class(iris)

[1] "data.frame"

> iris[1:4,]

<table>
<thead>
<tr>
<th></th>
<th>Sepal.Length</th>
<th>Sepal.Width</th>
<th>Petal.Length</th>
<th>Petal.Width</th>
<th>Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5.1</td>
<td>3.5</td>
<td>1.4</td>
<td>0.2</td>
<td>setosa</td>
</tr>
<tr>
<td>2</td>
<td>4.9</td>
<td>3.0</td>
<td>1.4</td>
<td>0.2</td>
<td>setosa</td>
</tr>
<tr>
<td>3</td>
<td>4.7</td>
<td>3.2</td>
<td>1.3</td>
<td>0.2</td>
<td>setosa</td>
</tr>
<tr>
<td>4</td>
<td>4.6</td>
<td>3.1</td>
<td>1.5</td>
<td>0.2</td>
<td>setosa</td>
</tr>
</tbody>
</table>

> table(iris$Species)

<table>
<thead>
<tr>
<th></th>
<th>setosa</th>
<th>versicolor</th>
<th>virginica</th>
</tr>
</thead>
<tbody>
<tr>
<td>count</td>
<td>50</td>
<td>50</td>
<td>50</td>
</tr>
</tbody>
</table>
Line Plot: Single Data Set

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

![Graph showing a line plot with y values indexed from 2 to 10 and ranges for y from 0.2 to 0.8. The x-axis is labeled as Index with values 2 to 10.]
Line Plots: Many Data Sets

```r
> 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)
```

![Line Plot Example](image-url)
Bar Plot Basics

```r
> 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.vector(as.matrix(y[1:4,]))+0.04)
```

- **A**: 0.27, 0.93
- **B**: 0.14, 0.31, 0.12, 0.05
- **C**: 0.41, 0.44, 0.32, 0.0
Bar Plots with 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")

density.default(x = y)

N = 30   Bandwidth = 0.136

Density

0.0 0.5 1.0
0.0 0.2 0.4 0.6 0.8 1.0
density.default(x = y)
N = 30   Bandwidth = 0.136

N = 30   Bandwidth = 0.136
Pie Charts

```r
> 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" "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")

Much more on colors in R see Earl Glynn’s color chart [Link]
After the `pdf()` command all graphs are redirected to file `test.pdf`. Works for all common formats similarly: jpeg, png, ps, tiff, ...

```r
> 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.

```r
> svg("test.svg"); plot(1:10, 1:10); dev.off()
```
Exercise 3: Bar Plots

**Task 1** Calculate the mean values for the Species components of the first four columns in the iris data set. Organize the results in a matrix where the row names are the unique values from the iris Species column and the column names are the same as in the first four iris columns.

**Task 2** Generate two bar plots: one with stacked bars and one with horizontally arranged bars.

Structure of iris data set:

```r
> class(iris)
[1] "data.frame"

> iris[1:4,]

Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1  5.1        3.5      1.4   0.2   setosa
2  4.9        3.0      1.4   0.2   setosa
3  4.7        3.2      1.3   0.2   setosa
4  4.6        3.1      1.5   0.2   setosa

> table(iris$Species)

    setosa versicolor virginica
 50      50       50
```
Outline

Introduction
- Look and Feel of the R Environment
- R Library Depositories
- Installation
- Getting Around
- Basic Syntax
- Data Types and Subsetting
- Important Utilities
- Basic Calculations
- Reading and Writing External Data
- Some Great R Functions
- Graphics Utilities

Graphics Environments
- Base Graphics

Exercise: Analysis Routine
The following exercise introduces a variety of useful data analysis utilities in R.
Step 1 To get started with this exercise, direct your R session to a dedicated workshop directory and download into this directory the following sample tables. Then import the files into Excel and save them as tab delimited text files.

- MolecularWeight_tair7.xls
- TargetP_analysis_tair7.xls

Import the tables into R

```r
> ## Import molecular weight table
> my_mw <- read.delim(file="MolecularWeight_tair7.xls", header=T, sep="\t")
> my_mw[1:2,]

   Sequence.id Molecular.Weight.Da Residues
 1    AT1G08520.1          83285      760
 2    AT1G08530.1          27015      257

> ## Import subcellular targeting table
> my_target <- read.delim(file="TargetP_analysis_tair7.xls", header=T, sep="\t")
> my_target[1:2,]

   GeneName Loc   cTP   mTP   SP   other
 1    AT1G08520.1  C 0.822 0.137 0.029 0.039
 2    AT1G08530.1  C 0.817 0.058 0.010 0.100
```
Analysis Routine: Merging Data Frames

Step 2 Assign uniform gene ID column titles

```r
> colnames(my_target)[1] <- "ID"
> colnames(my_mw)[1] <- "ID"
```

Step 3 Merge the two tables based on common ID field

```r
> my_mw_target <- merge(my_mw, my_target, by.x="ID", by.y="ID", all.x=T)
```

Step 4 Shorten one table before the merge and then remove the non-matching rows (NAs) in the merged file

```r
> my_mw_target2a <- merge(my_mw, my_target[1:40,], by.x="ID", by.y="ID", all.x=T)
> # To remove non-matching rows, use the argument setting 'all=F'.
> my_mw_target2 <- na.omit(my_mw_target2a)
> # Removes rows containing "NAs" (non-matching rows).
```

**Problem 1:** How can the merge function in the previous step be executed so that only the common rows among the two data frames are returned? Prove that both methods - the two step version with `na.omit` and your method - return identical results.

**Problem 2:** Replace all NAs in the data frame `my_mw_target2a` with zeros.
Step 5  Retrieve all records with a value of greater than 100,000 in 'MW' column and 'C' value in 'Loc' column (targeted to chloroplast).

```r
> query[1:4, ]

<table>
<thead>
<tr>
<th>ID</th>
<th>ID</th>
<th>Molecular.Weight.Da.</th>
<th>Residues</th>
<th>Loc</th>
<th>cTP</th>
<th>mTP</th>
<th>SP</th>
<th>other</th>
</tr>
</thead>
<tbody>
<tr>
<td>219</td>
<td>AT1G02730.1</td>
<td>132588</td>
<td>1181</td>
<td>C</td>
<td>0.972</td>
<td>0.038</td>
<td>0.008</td>
<td>0.045</td>
</tr>
<tr>
<td>243</td>
<td>AT1G02890.1</td>
<td>136825</td>
<td>1252</td>
<td>C</td>
<td>0.748</td>
<td>0.529</td>
<td>0.011</td>
<td>0.013</td>
</tr>
<tr>
<td>281</td>
<td>AT1G03160.1</td>
<td>100732</td>
<td>912</td>
<td>C</td>
<td>0.871</td>
<td>0.235</td>
<td>0.011</td>
<td>0.007</td>
</tr>
<tr>
<td>547</td>
<td>AT1G05380.1</td>
<td>126360</td>
<td>1138</td>
<td>C</td>
<td>0.740</td>
<td>0.099</td>
<td>0.016</td>
<td>0.358</td>
</tr>
</tbody>
</table>
```

> dim(query)

```
[1] 170 8
```

Problem 3: How many protein entries in the my_mw_target data frame have a MW of greater then 4,000 and less then 5,000. Subset the data frame accordingly and sort it by MW to check that your result is correct.
Step 6  Use a regular expression in a substitute function to generate a separate ID column that lacks the gene model extensions.

```r
> my_mw_target3 <- data.frame(loci=gsub("\..*", "",
+ as.character(my_mw_target[,1]), perl = TRUE),
+ my_mw_target)
> my_mw_target3[1:3,1:8]

<table>
<thead>
<tr>
<th>loci</th>
<th>ID</th>
<th>Molecular.Weight.Da.</th>
<th>Residues</th>
<th>Loc</th>
<th>cTP</th>
<th>mTP</th>
<th>SP</th>
</tr>
</thead>
<tbody>
<tr>
<td>AT1G01010</td>
<td>AT1G01010.1</td>
<td>49426</td>
<td>429</td>
<td>_</td>
<td>0.10</td>
<td>0.090</td>
<td>0.075</td>
</tr>
<tr>
<td>AT1G01020</td>
<td>AT1G01020.1</td>
<td>28092</td>
<td>245</td>
<td>*</td>
<td>0.01</td>
<td>0.636</td>
<td>0.158</td>
</tr>
<tr>
<td>AT1G01020</td>
<td>AT1G01020.2</td>
<td>21711</td>
<td>191</td>
<td>*</td>
<td>0.01</td>
<td>0.636</td>
<td>0.158</td>
</tr>
</tbody>
</table>
```

Problem 4: Retrieve those rows in `my_mw_target3` where the second column contains the following identifiers: `c("AT5G52930.1", "AT4G18950.1", "AT1G15385.1", "AT4G36500.1", "AT1G67530.1")`. Use the `%in%` function for this query. As an alternative approach, assign the second column to the row index of the data frame and then perform the same query again using the row index. Explain the difference of the two methods.
Step 7  Count the number of duplicates in the loci column with the table function and append the result to the data frame with the cbind function.

> mycounts <- table(my_mw_target3[,1])[my_mw_target3[,1]]
> my_mw_target4 <- cbind(my_mw_target3, Freq=mycounts[as.character(my_mw_target3[,1])])

Step 8  Perform a vectorized division of columns 3 and 4 (average AA weight per protein)

> data.frame(my_mw_target4, avg_AA_WT=(my_mw_target4[,3] / my_mw_target4[,4]))[1:2,5:11]

<table>
<thead>
<tr>
<th>Loc</th>
<th>cTP</th>
<th>mTP</th>
<th>SP</th>
<th>other</th>
<th>Freq</th>
<th>avg_AA_WT</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>_</td>
<td>0.10</td>
<td>0.090</td>
<td>0.075</td>
<td>0.925</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>*</td>
<td>0.01</td>
<td>0.636</td>
<td>0.158</td>
<td>0.448</td>
<td>2</td>
</tr>
</tbody>
</table>

Step 9  Calculate for each row the mean and standard deviation across several columns

> mymean <- apply(my_mw_target4[,6:9], 1, mean)
> mystdev <- apply(my_mw_target4[,6:9], 1, sd, na.rm=TRUE)
> data.frame(my_mw_target4, mean=mymean, stdev=mystdev)[1:2,5:12]

<table>
<thead>
<tr>
<th>Loc</th>
<th>cTP</th>
<th>mTP</th>
<th>SP</th>
<th>other</th>
<th>Freq</th>
<th>mean</th>
<th>stdev</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>_</td>
<td>0.10</td>
<td>0.090</td>
<td>0.075</td>
<td>0.925</td>
<td>1</td>
<td>0.2975</td>
</tr>
<tr>
<td>2</td>
<td>*</td>
<td>0.01</td>
<td>0.636</td>
<td>0.158</td>
<td>0.448</td>
<td>2</td>
<td>0.3130</td>
</tr>
</tbody>
</table>
Step 10 Generate scatter plot columns: 'MW' and 'Residues'

```r
> plot(my_mw_target4[1:500,3:4], col="red")
```
Step 11 Write the data frame `my_mw_target4` into a tab-delimited text file and inspect it in Excel.

```r
> write.table(my_mw_target4, file="my_file.xls", quote=F, sep="\t",
+  col.names = NA)
```

**Problem 5:** Write all commands from this exercise into an R script named `exerciseRbasics.R`, or download it from here [Link](#). Then execute the script with the `source` function like this: `source("exerciseRbasics.R")`. This will run all commands of this exercise and generate the corresponding output files in the current working directory.
> sessionInfo()

R version 3.0.2 (2013-09-25)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
[1] C

attached base packages:
[1] stats  graphics  utils  datasets  grDevices  methods  base

loaded via a namespace (and not attached):
[1] tools_3.0.2