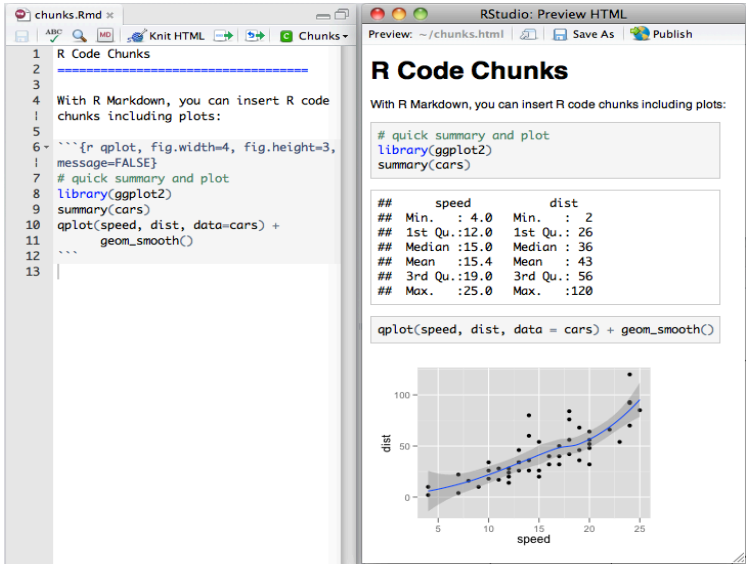
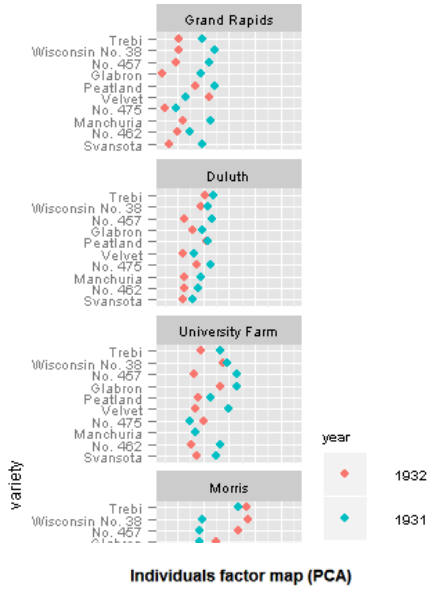
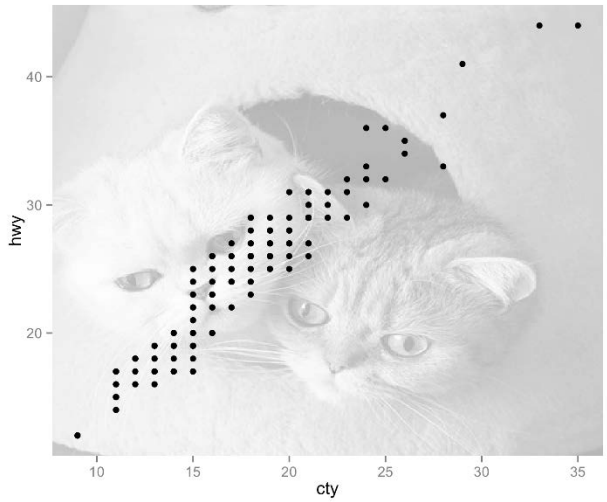
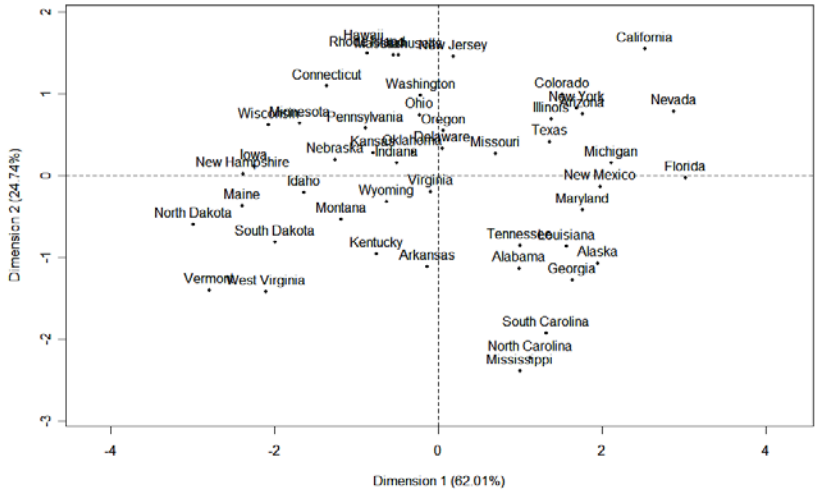
An Introduction to R







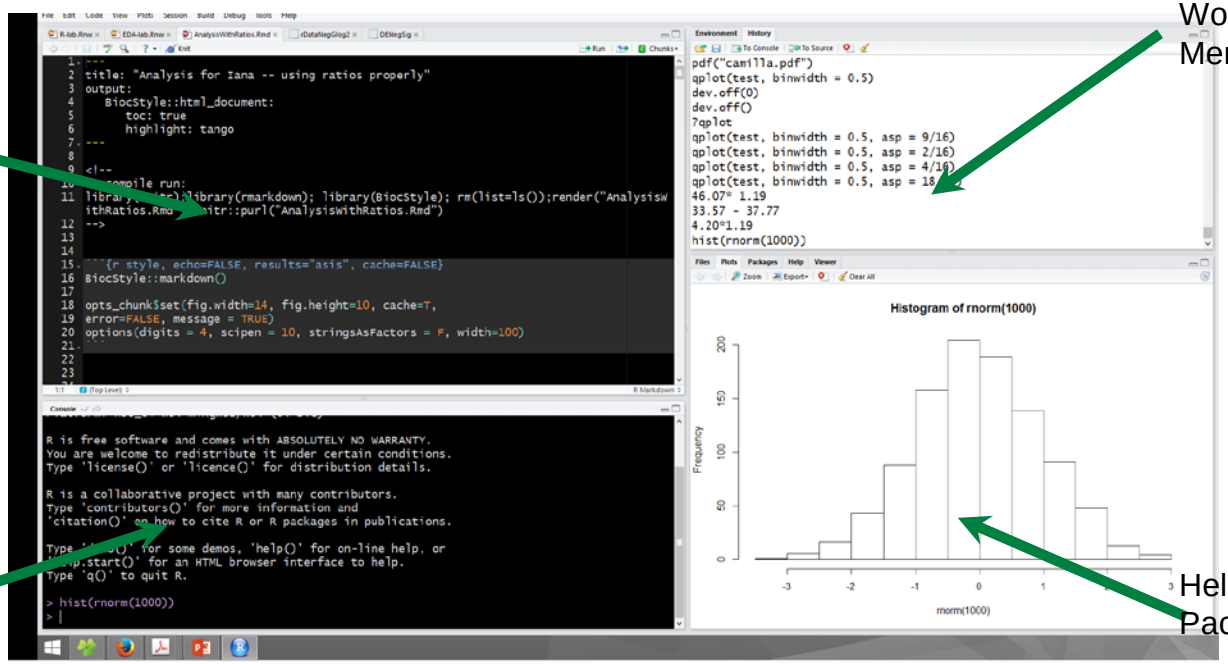


Bernd Klaus, EMBL

R Studio window layout

Script Window: Collection of your commands

Console: Execute commands and see R's output



Workspace: Data in Memory and History

Help, Plots and Packages Window

R packages, getting help

CRAN repository: http://cran.r-project.org

Biostatistics / Bioinformatics: http://bioconductor.org

- install via `install.packages(packagename)`
- ... or use `biocLite` from Bioconductor
- load via `library(packagename)`
- overview `sessionInfo()`

- RStudio: Tools --> Install packages
- activate packages using the packages tab in the plot window!
- Help: `?packagename / functionname, browseVignettes("packages")`
- Rseek: http://www.rseek.org/
- Working directory: `setwd(), getwd()`

Rationale of learning R

The syntax of R is simple and logical

Allows to quickly allow for a basic understanding of simple R programs

The best, and in a sense the only, way to learn R is through trial-and- error on simple and then more complex examples

<u>Essential books</u>

Dalgaard (2002) - Introductory Statistics with R

Venables and Ripley (2002) - Modern Applied Statistics with S.

Wickham Advanced R

R as a calculator

- Assigments are done with `<-` , or alternatively with `=`
- Ex. `a <- 5` => Variable a has value `5`
- R has basic calculator capabilities:
- `a+b, a-b, a*b, a^b (a**b), a %% b (a MOD b)`
- additionally functions like `sqrt(a), sin(a) ...`
- and some simple statistics:
  - `mean(a,b)`
  - `summary(a,b)`
  - Variance `var(a,b)`
  - `min(a,b), max(a,b)`

Objects in R

- R is an object-oriented language
- Object = all data Items in R
- Objects are instances of “blue-prints” called classes:

- Elementary Types:

`numeric`: real number

`string`: chain of characters, Text

`factor`: String or numbers, describing certain categories

`logical`: TRUE, FALSE

`NA`: missing value

- Data Storage Types:

`Vectors, Matrices, Data Frames`

Some simple commands ...

assign value “9” to an object `a`: `a<-9`

- Is a a string?

`is.character(a) =>  FALSE`

- Is a number?

`is.numeric(a) => TRUE`

- Now turn it into a factor

`a<-as.factor(a)`

- Is it a factor?

`is.factor(a) => TRUE`

- Assign an string to `a`: `a<- “NAME”;`
- What’s a?

`summary(a) => Length 1 Class character`

Vectors = collection of simple obj.

- `a <- c(5,6,7)`; a now is a vector with elements 5, 6, 7
- How long is a? `length(a)`
- Access: `a[Position]`

`=> a[2]` gives `6`

Arithmetic works on vectors just as it does on single numbers

- `3*a` gives `(15,18,21)`
- `a[2] = a[2]*3` gives `(5,18,7)`
- Sorting and related: `sort(a), order(a), rank(a)`
- Useful functions for vector creation:

  Sequence: `seq(from=1,to=10)`

  Repetition: `rep(x = 1, times = 10)`

Matrices = 2-dim. vectors

```
mat <- matrix(c(1,0,0,0,1,0,0,0,1), nrow = 3 )
```

creates unit matrix and saves it in `mat`

- Access with [Row, Column], i.e. `mat[1,1]` gives `1`

`mat[,1]` - first column

- Select single rows/cols can be done accordingly:
  `mat[rows,] mat[,cols]`

- consecutive rows / cols via `mat[from:to,]`

- Exclude via minus sign `mat[-lines,]`

Matrix access: example

```
A <- matrix(seq(1,9), nrow = 3,
  byrow=T)
```

$$A = \begin{pmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \\ 7 & 8 & 9 \end{pmatrix}$$

- `A[1,3]`=3
- `A[3,1]`=7
- `A[1,]`=1,2,3
- `A[,1]`=1,4,7
- `A[,-1]`= $\begin{pmatrix} 2 & 3 \\ 5 & 6 \\ 8 & 9 \end{pmatrix}$ = `A[,2:3]`

Lists = Collections of arbitrary obj.

Lists can contain “columns” of arbitrary objects of arb. length; Access with `list[[entrynumber]]/list[[“name”]]`

```
L = list(one=1, two=c(1,2), five=seq(1, 4, length=5))
L

#> $one
#> [1] 1
#>
#> $two
#> [1] 1 2
#>
#> $five
#> [1] 1.00 1.75 2.50 3.25 4.00

names(L)

#> [1] "one"  "two"  "five"

 L$five + 10

#> [1] 11.0 11.8 12.5 13.2 14.0

## equivalent
L[[3]] + 10

#> [1] 11.0 11.8 12.5 13.2 14.0
```

`L[[2]]` would also give `1 2` as output!

Importing data to data frames

Easy with RStudio: Tools -> Import

Example file: Patients.csv (NA is a marker for a quantity that is not available)

	Height,	Weight
P1,	1.65,	80.0
P2,	1.30,	NA
P3,	1.20,	50.0

R-Code: `patients <- read.csv(file = /path/to/filename/Patients.csv, header = TRUE)`

Excel read/write via the package `xlsx, read.xlsx / write.xlsx`

data.frame: tables in R

data.frame = Class representing tables in R

(a dataframe is a list of columns)

- Columns are variables; Rows are observations
- `head()` gives first entries
- `names()` gives column names
- Access to variables (columns):
  - `dataframe$colname (just like a named list)`
  - `dataframe[,"colname"]`
  - `dataframe[["colname"]] (just like a named list)`

```
#>   Patient Height Weight Gender
#> 1      P1   1.65     80      f
#> 2      P2   1.30             m
#> 3      P3   1.20     50      f
```

```
str(pat.xls)
```

```
#> 'data.frame': 3 obs. of  4 variables:
#>  $ Patient: chr  "P1" "P2" "P3"
#>  $ Height : num  1.65 1.3 1.2
#>  $ Weight : chr  "80" "  " "50"
#>  $ Gender : chr  "f" "m" "f"
```

Looking at pat

It has weight, height and gender of three people.

Gender is a factor => special type for vectors that represent categories

```
pat

#>    Height Weight Gender
#> P1   1.65     80      f
#> P2   1.30     NA      m
#> P3   1.20     50      f

str(pat)

#> 'data.frame': 3 obs. of  3 variables:
#>  $ Height: num  1.65 1.3 1.2
#>  $ Weight: num  80 NA 50
#>  $ Gender: chr  " f" " m" " f"
```

Since data frames are just special lists, they can be accessed in the same way

```
pat$Height

#> [1] 1.65 1.30 1.20
```

```
#equivalent
pat[[1]]

#> [1] 1.65 1.30 1.20
```

Looking at pat: Subsetting

- `Variable == value`: equal
- `Variable != value`: un–equal
- `Variable < value`: less
- `Variable > value`: greater
- &: *and*
- |: *or*
- !: negation
- %*in*%: is element?

```
### access via subset
subset(pat, Height<1.5)

#>    Height Weight Gender
#> P2    1.3     NA      m
#> P3    1.2     50      f
```

Using R functions

Using `?matrix,` you will find the following information on the matrix function:

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
   dimnames = NULL)
```

- Variables for which values can be given are in the round brackets
- Otherwise, R will use the standard values indicated by "=" if there are any

- `matrix(c(1,0), nrow = 2 )` creates a matrix with 2 rows and 1 column
- `matrix(c(1,0,3,4), nrow = 2, ncol = 2 )` creates a 2 x 2 matrix
- Equivalent but not recommended: `matrix(c(1,0,3,4), 2, 2)`

"Apply" commands

Apply commands allows to apply a function to every row or column of a data matrix

```
apply(X, MARGIN, FUN, ...)
```

`MARGIN: 1` (row-wise) or `2` (column-wise)

`FUN:` The function to apply

Additional apply functions: `lapply` (lists), `sapply` (lapply wrapper trying to convert the result into a matrix), `tapply`, `aggregate` (apply according to factor groups),

`mapply` (apply to corresponding elements of multiple inputs)

...

apply for patients

* Calculate mean for each of the first two columns

```
# Calculate mean for each of the first two columns
sapply(X = pat[,1:2], FUN = mean, na.rm = TRUE)

#> Height Weight
#>   1.38  65.00
```

* Mean height separately for each gender

```
# Mean height separately for each gender
tapply(X = pat$Height, FUN = mean, INDEX = pat$Ge)

#>    f    m
#> 1.42 1.30
```

Irises

Iris virginica

Iris setosa

Iris versicolor

Apply example for irisis

the iris data gives measurements in centimeters of 5 variables for 3 plant species.

```
> iris[1:3,1:3]
Sepal.Length Sepal.Width Petal.Length
1          5.1         3.5          1.4
2          4.9         3.0          1.4
3          4.7         3.2          1.3

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

       1        2        3
3.333333 3.100000 3.066667
```

Graphics in R

base graphics and ggplot2 (grammar of graphics) are commonly used to produce plots in R; in a nutshell:

base R: “canvas” model you start with a white space and add graphical elements step by step

ggplot2: “grammar” of graphics model. You start by organizing your data in the right way, then a plot is a mapping from data to aesthetics

aesthetics = things that you can visually perceive:

color, shape or geometric objects like points, lines, bars

Nice lectures by Roger Pen:

http://www.youtube.com/watch?v=HeqHMM4ziXA

http://www.youtube.com/watch?v=n8kYa9vu1l8

Graphics in base R

Default command: `plot()` , there are other specialized commands like `hist()` or `pie()`

```
plot(x, y, type, main, par (...) )
```

`x`: x-axis data

`y:` y-axis data (may be missing)

`type=l,p,h,b:` display lines / points / horizontal lines ...

`main:` plot heading

`par (...):` additional graphical parameters, see `?par` for more Info ...

Changing graphical parameters

`par(cex, col, lty, mfrow, pch, x/yaxs)`

- `cex` Scaling of graphical elements
- `col` Color (`colors()` shows predefined colors, see also http://research.stowers-institute.org/efg/R/Color/Chart/)
- `lty:` Line type
- `mfrow / mfcol:` positioning of multiple plots
- `pch:` use different plotting symbols
- `x/yaxs:` y / x-axis style

`A parameter can be obtained with ?par`

Graphical Elements in R

`plot()`: opens a new graphics window

Additional elements can then be added, e.g.

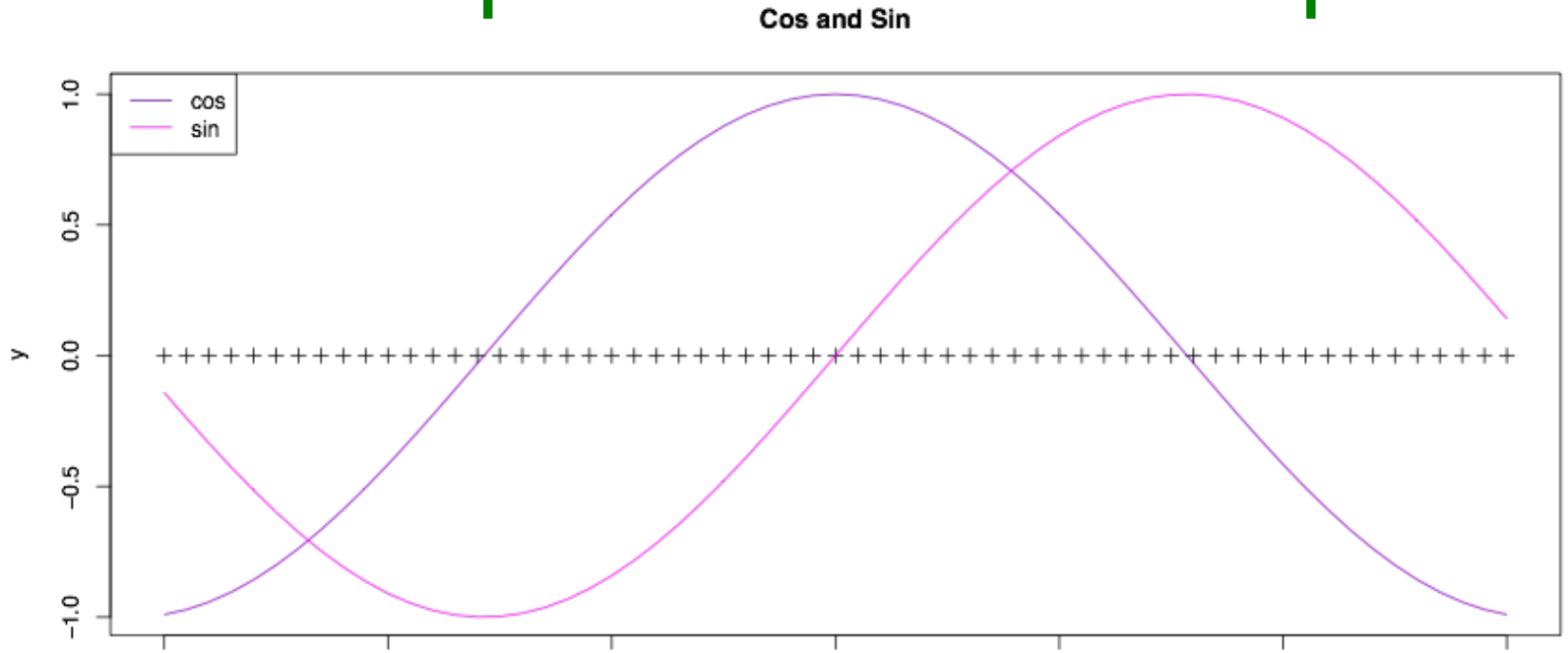
- `lines()`, `points()`, `legend()`, `text()` ...

Plots can be plotted into files using graphical devices like `pdf()`, `ps()` and `jpg()`

`dev.off()` shuts down the graphical device and saves the file

help can be obtained by calling e.g. `?legend`.

Graphics in R - Example




```
pdf(file="plot-example.pdf", width=12, height=6)x = seq(-3,3, by
  = 0.1); y  <- cos(x); z  <- sin(x)plot(x,y, type="l",
  col="darkviolet", main="Cos and Sin")points(x, rep(0,
  length(x)), pch=3)lines(x,z, type="l",
  col="magenta")legend("topleft", c("cos","sin"),
  col=c("darkviolet", "magenta"), lty=1)dev.off()
```

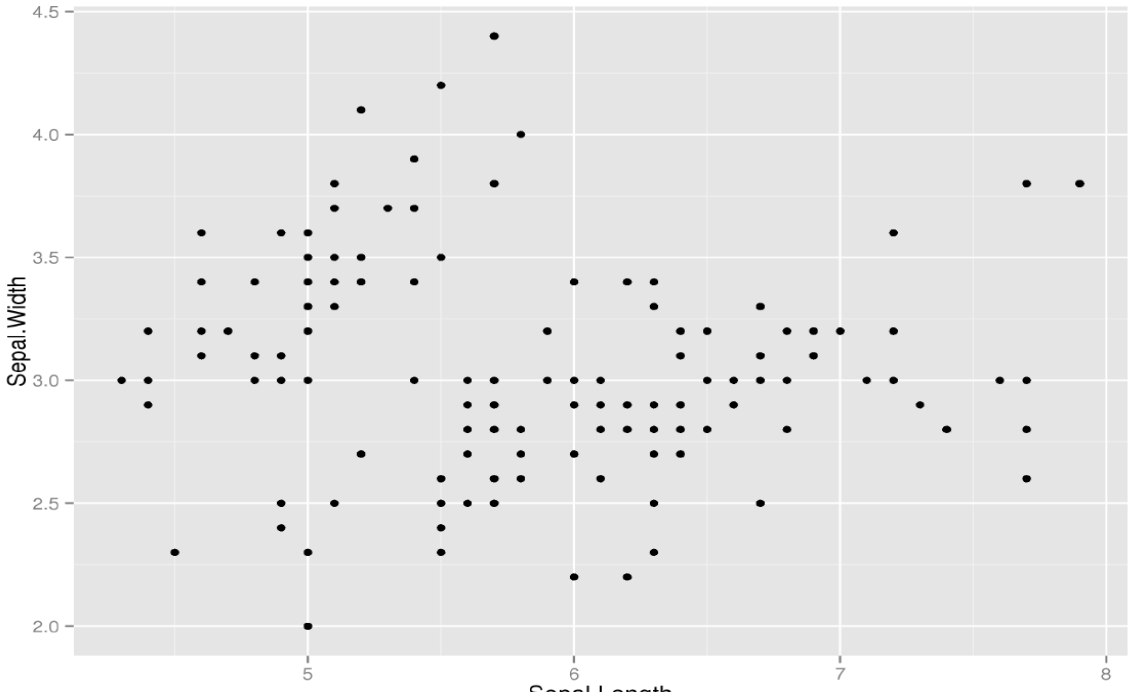
ggplot2 example

We use the iris data set: to produce a simple scatterplot of Sepal.Length and Sepal.Width one can map Sepal.Length to the x and Sepal.Width to y axis

```
p <- ggplot(iris, aes(Sepal.Length, Sepal.Width) )
```

Then we can a point geometry to produce a scatterplot

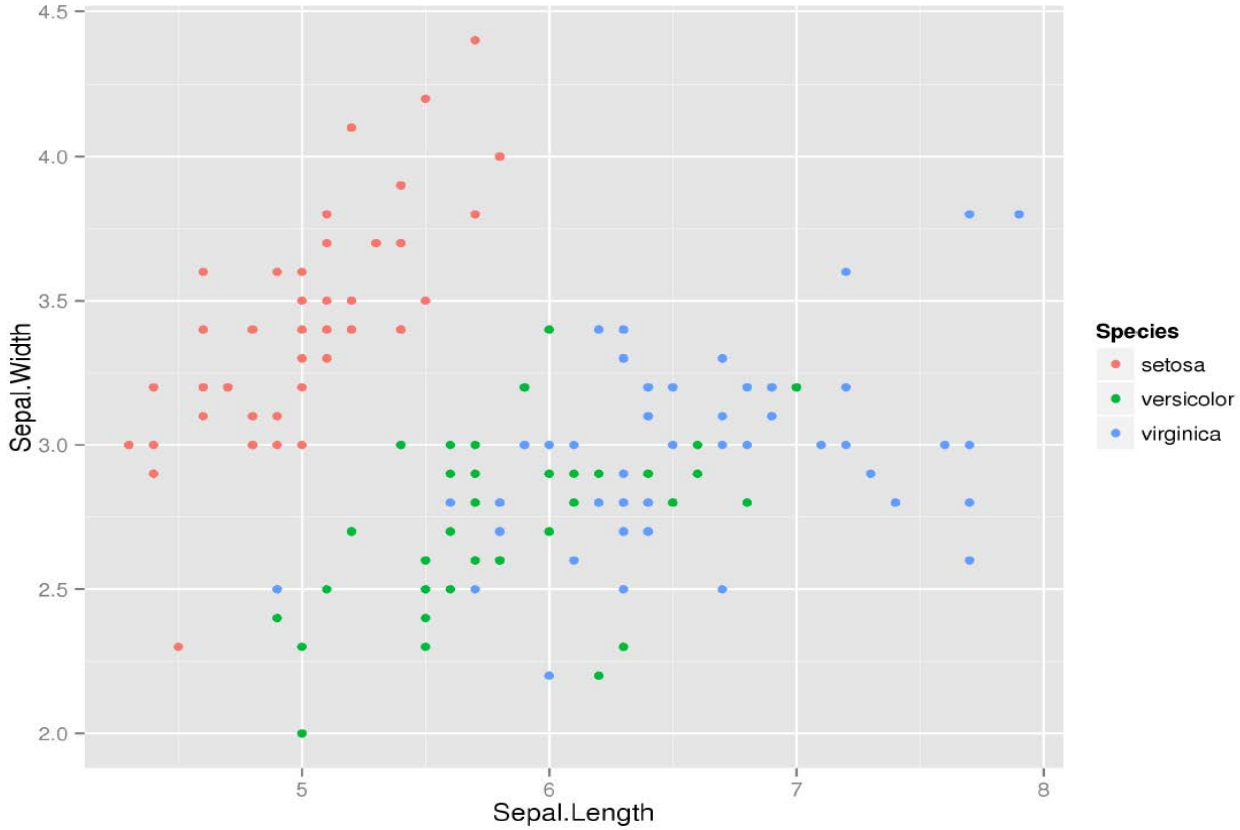
```
p + geom_point()
```



Example continued

we can further map the species to color, here using the qplot() command, the ggplot 2 version of plot()

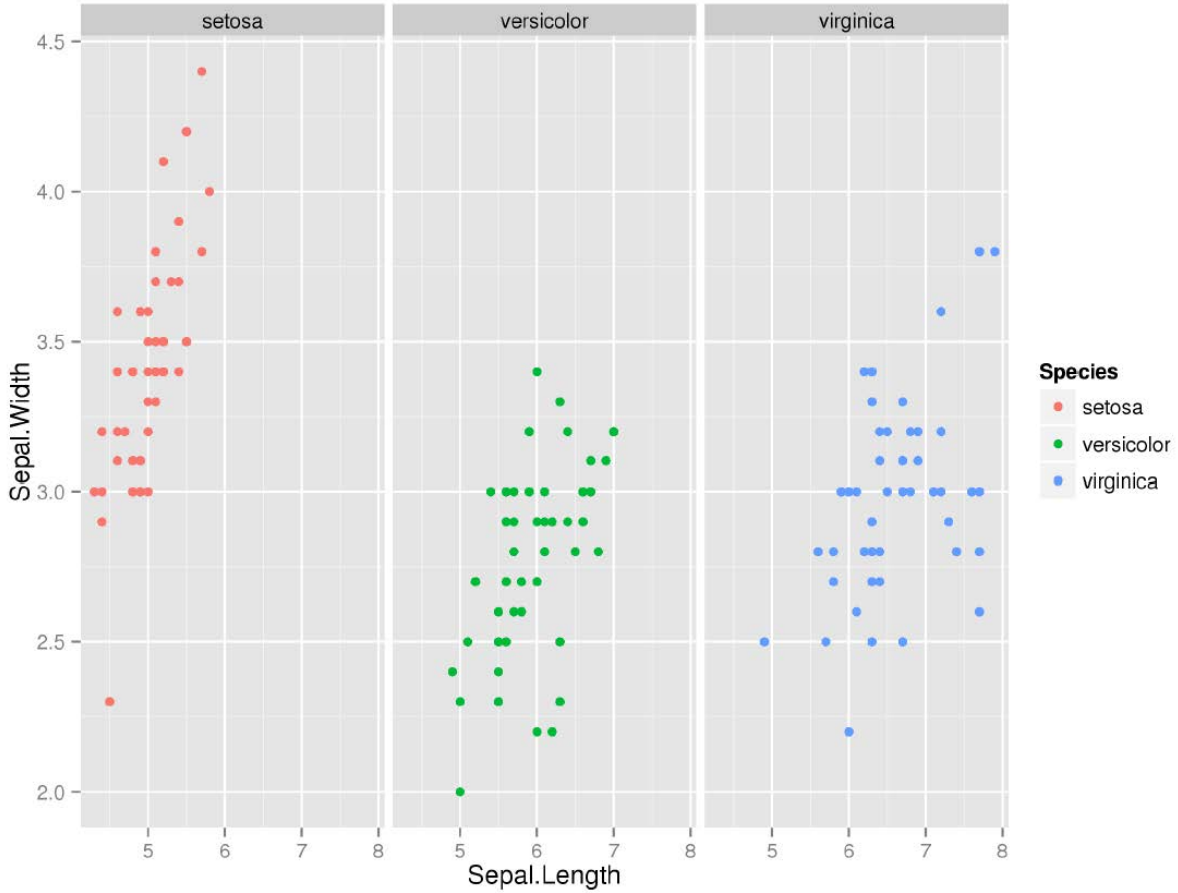
qplot(Sepal.Length, Sepal.Width, data = iris, color = Species)



Panels in ggplot2

you can easily split the plots into panels using factors

(qplot(Sepal.Length, Sepal.Width, data = iris,
color = Species, facets = . ~ Species))



qplot summary

- can be used much like plot, but has nice additional options

```
qplot(x, y = NULL, ..., data, facets = NULL, NA), ylim =
c(NA, NA), log = "", main = NULL, xlab =
deparse(substitute(x)), ylab = deparse(substitute(y)))
```

- `facets:` split the plot into facets
- `main:` title of the plot
- `color, fill:` set to factor/string in the data set in order to color the plot depending on that factor. Use `I("colorname")` to use a specific color
- geom: specify a “geometry” to be used in the plots, examples include point, line, boxplot, histogram etc.

Programming in R

You can create your own function by using the following template

```
function.name<-function(arguments, options) {
  ...
  ...
  return()
}
```

`arguments:` compulsory arguments

`options:` optional arguments with default values

`{ }:` the function code is in curly brackets

`return():` return value of the function, if omitted, R returns the result of the last computation performed

Example: mean value function

```
my.mean <-function(data) {
my.sum<-sum(data, na.rm=TRUE)
my.length<-length(!is.na(data))
my.sum/my.length
}
```

`my.mean` function name

`data` input data

`my.sum, my.length` local variables, only visible within the function

`return value:` last statement, i.e. calculated mean value

Example: Currency converter

Example: Currency Converter

```
euro.calc<-function(x) {
  # convert euro to us dollars
 x*1.13
}
```

x: formal argument, necessary to execute the functionreturn(...): specifies return value of the function

indicate comments, ALWAYS COMMENT EXTENSIVELY!

Programming Statements

If-Statement: Computation is only performed if a certain condition is met

```
w= 3
        if( w < 5 ){
        d=2
        }else{
        d=10
        }
d

#> [1] 2
```

For-Loop: Computation is done a specified number of times

```
h <- seq(from = 1, to = 8)
s <- integer() # create empty integer vector
        for(i in 2:10)
        {
        s[i] <- h[i] * 10
        }
s

#>  [1] NA 20 30 40 50 60 70 80 NA NA
```

Log. operators: ==(=), !=(≠),<=(≤) and >=(≥), combine with & (“and”) and | (“or”)

```
> a = c(1,2,3,4)
> b = c(5,6,7,8)
> f = a[b==5 | b==8]
> f
[1] 1 4
```

Currency converter including an If statement

```
euro.calc<-function(x, currency="US") {
  ## currency has a default argrument "US"
  if(currency=="US") return(x*1.13)
  if(currency=="Pounds") return(x*0.65)
}
```

`x:` formal argument, necessary to execute the function`currency:` optional argument, set to "US" by default

`return(...):` specifies return value of the function

ifelse statement

```
ifelse(vec, assignmentTRUE, assignmentFALSE)
```

operates on a logical vector `vec` and performs assignment based on its evaluation

very useful to replace values of a vector

Example:

```
s <- seq(from = 1, to = 10)
binary.s <- ifelse(s > 5, "high", "low")
binary.s

#>  [1] "low"  "low"  "low"  "low"  "low"  "high" "h
```