

Statistical Models in Computational Biology

Tutorial: A Primer for programming in R

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Overview

- Introduction
- R Basics
 - R Objects: Vector, Matrix, Data Frame and List
 - Function Definition
 - File I/O
- Conditional and Repetitive Execution
 - `if` and `else`
 - Loops and subsetting
 - `*apply()` functions
- Graphical Procedures
- External Packages and Misc. Functions
- Resources



Introduction: What is R?



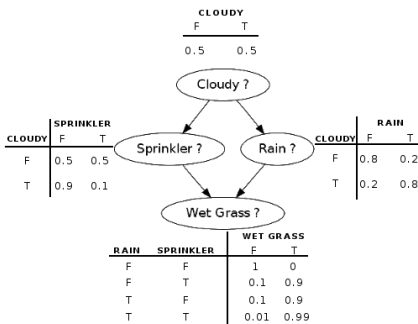
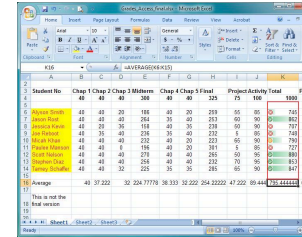
The Swiss Army Knife for Data Analysis

Introduction: What is R?

- Interpreted programming language based on S
 - Individual statements compiled to machine code
 - PRO: high flexibility; CON: slow
 - Interface to C, C++, FORTRAN
- Open source
 - Freely available for Linux, OSX, Win (<http://r-project.org>)
 - Large and active community
- Wide variety of statistical and graphical analysis tools
 - Modeling, statistical tests, classification, clustering, ...
 - Easy creation of publication-ready plots
 - > 3500 packages providing additional functionality

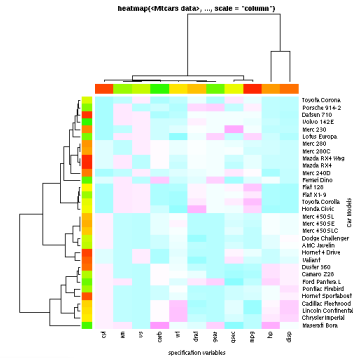
Introduction: Typical Workflow

Data Manipulation
parse, edit, reshape

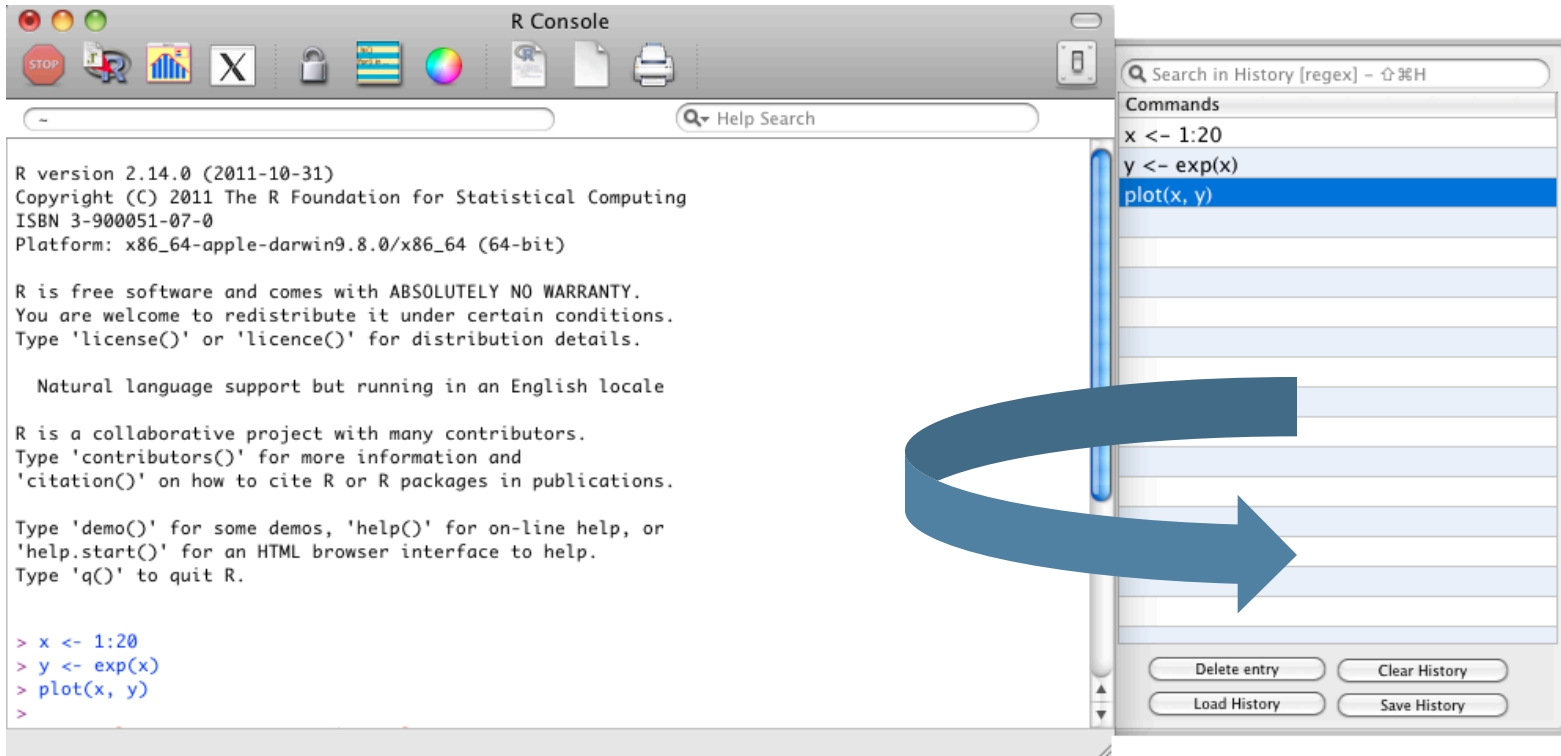


Data Modeling
model, analyse

Data Visualisation
plot



Introduction: Your First R Session



R Console

R version 2.14.0 (2011-10-31)
Copyright (C) 2011 The R Foundation for Statistical Computing
ISBN 3-900051-07-0
Platform: x86_64-apple-darwin9.8.0/x86_64 (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.

```
> x <- 1:20  
> y <- exp(x)  
> plot(x, y)  
>
```

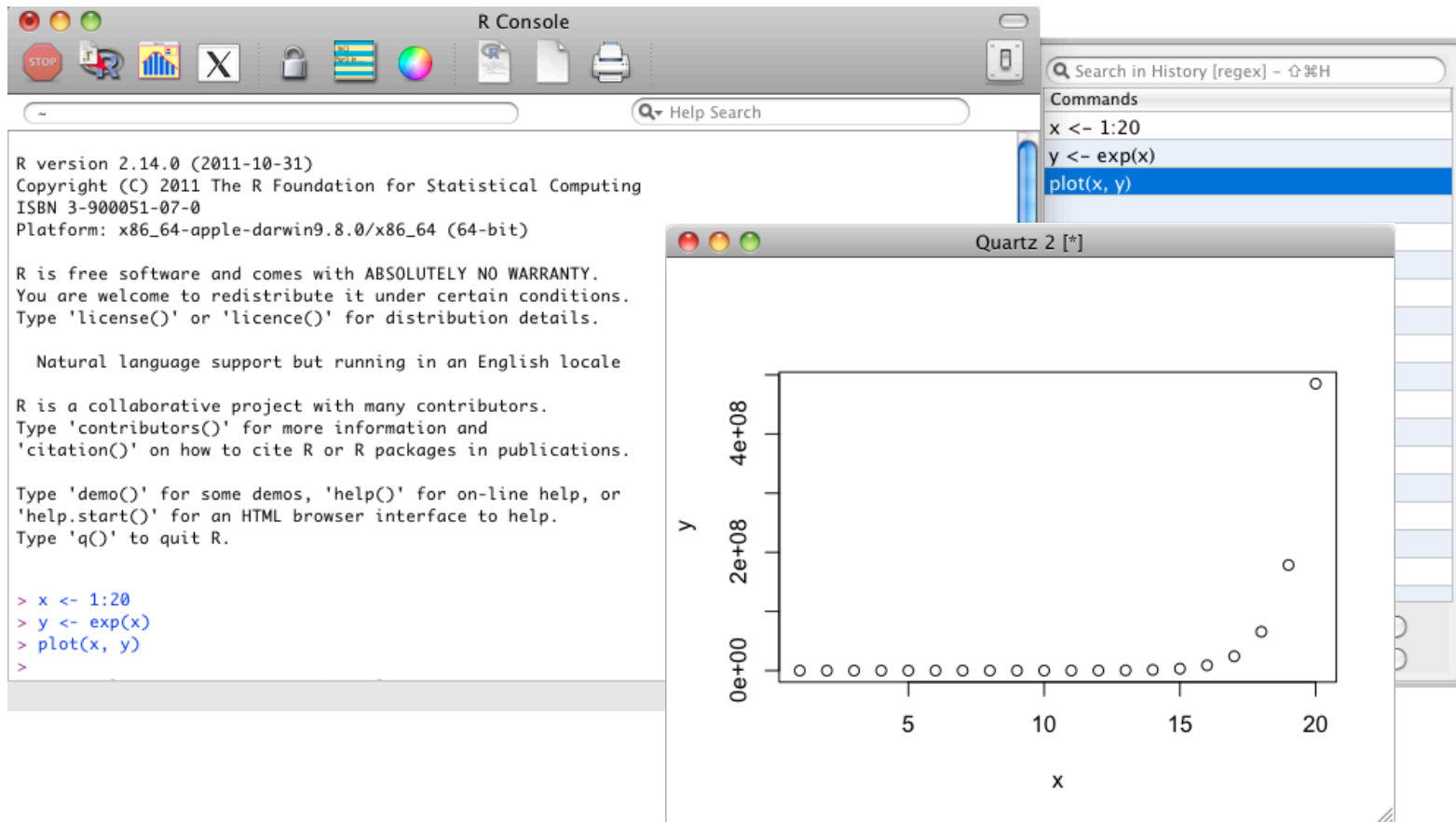
Search in History [regex] - ⌘H

Commands

- x <- 1:20
- y <- exp(x)
- plot(x, y)

Delete entry Clear History
Load History Save History

Introduction: Your First R Session



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```
> x <- 1:20  
> y <- exp(x)  
> plot(x, y)  
>
```

Quartz 2 [*]

Search in History [regex] - ⌘H

Commands

```
x <- 1:20  
y <- exp(x)  
plot(x, y)
```

Y

4e+08
2e+08
0e+00

x

5 10 15 20

R Basics: Getting Started

- Hello World

```
> print("Hello World!")
```
- Help on operators, functions etc. available internally

```
> help("*")  
> help(exp)
```
- Assignment operator

```
> e <- m*c^2
```
- Display defined objects

```
> ls()
```
- Remove object e

```
> rm(e)
```
- `# This is a comment`

R Basics: Vector

- Ordered collection of items of same type/mode (logical, integer, double, complex, character, factor, raw)
- Create using combine function

```
> vec <- c(0, 1, 1, 2, 3, 5, 8)
```
- Create using sequence and repetition

```
> vec <- seq(1, 5, by = 1) # short: 1:5
> vec <- rep(1, length = 17)
```
- Operators $+$, $-$, $*$, $/$, and $^$ are applied *element wise*

```
> c(2, 5, 10) * c(1, 5, -1.7)
[1] 2 25 -17
```
- Recycling

```
> c(1, 2, 3, 4) * c(1, 2)
[1] 1 4 3 8
```

R Basics: Vector

- Indexing (R is *one-indexed!*)

```
> vec <- c(0, 1, 2, 3, 4)
```

```
> vec[c(2,4)]
```

```
[1] 1 3
```

- Basic functions

- Number of elements

```
length(vec)
```

- Sum of elements

```
sum(vec)
```

- Arithmetic mean

```
mean(vec)
```

- Empirical variance

```
var(vec)
```

- Smallest and largest element

```
range(vec)
```

R Basics: Character Vector

- Character vectors

```
> names <- c("Einstein", "Curie")
```

- Length of strings

```
> nchar(names)
```

```
[1] 8 5
```

- String manipulations

```
> substring(names[1], 4, 8)
```

```
[1] "stein"
```

```
> paste(c("A.", "M."), names)
```

```
[1] "A. Einstein" "M. Curie"
```

```
> strsplit("String with spaces", " ")
```

```
[1] "String" "with" "spaces"
```

R Basics: Logical Vector

- Logical vectors
 - `> logi <- c(TRUE, TRUE, FALSE)`
- Often result from comparison `<`, `<=`, `>`, `>=`, `==`, and `!=`
- Can be used for indexing
 - `> vec <- c(5, 19, 2, 7)`
 - `> ind <- vec > 3 #c(TRUE, TRUE, FALSE, TRUE)`
 - `> vec[ind]`
 - `[1] 5 19 7`
- Operators on logical vectors `x` and `y` (lazy: `&&`, `||`)
 - NOT `! x`
 - AND `x & y`
 - OR `x | y`
 - XOR `xor(x, y)`

R Basics: Matrix

- 2D extension of vector (n-dimensional: use `array()`)

- Create matrix (default: by column)

```
> m.test <- matrix(seq(1, 10), nrow=2, ncol=5)
```

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

- Indexing

```
> m.test[1, 1:3]
```

```
[1] 1 3 5
```

- All standard matrix operators available, e.g.

- Transposition `t()`
- Matrix mult. `%*%` #without "`%`": element wise
- Inversion `solve()`

R Basics: Data Frame

- Extension of matrix: columns of *different* type
- Frequently used data structure (resembles spreadsheet)

- Create data frame

```
> fname <- c("Rebecca", "Peter", "Jessica")  
> age <- c(27, 58, 28)  
> people <- data.frame(first.names = fname, age = age)
```

	first.names	age
1	Rebecca	27
2	Peter	58
3	Jessica	28

- Indexing by column/row number or name
 - `> people$age # or: people[, "age"]; or: people[, 2]`
 - `[1] 27 58 28`
- Concatenate using `cbind()` and `rbind()`

R Basics: List

- Ordered collection of (named) objects of *different* types

```
> lst <- list(7, name="John", child.ages=c(3, 5))
```
- Indexing by `[[position]]` and `$name`

```
> lst[[3]] # or: lst$child.ages
[1] 3 5
```
- Concatenation using `combine`
 - ```
> lst2 = c(lst, list(wife="Mary"))
```

## R Basics: File I/O

- Std. method to read (write) data frames from (to) *text files*
  - `read.table(file, header=FALSE, sep="", skip=0, ...)`
  - `write.table(x, file="", append=FALSE, sep=" ", ...)`
- Similar methods:
  - `read.delim()`
  - `read.csv()`
  - `read.xls()`
  - `scan()`
- Check `help()` for a complete list of parameters and their defaults (eg. `colClasses`, `stringsAsFactors`, ...)
- Read and write data as R object: `load()` and `save()`



# R Basics: File I/O (Text File Example)

- Tab separated file `mydata.txt`

| Id          | Name     | Expressed | FoldChange |
|-------------|----------|-----------|------------|
| FBgn0000463 | Delta    | YES       | 2.3        |
| FBgn0000524 | deltex   | NO        | NA         |
| FBgn0000547 | echinoid | YES       | 5.1        |
| FBgn0017550 | Regena   | YES       | 2.2        |

- Read `mydata.txt`

```
> md <- read.table("mydata.txt", header=T, sep="\t")
> md$FoldChange
[1] 2.3 NA 5.1 2.2
```

- Write `Id` and `FoldChange` columns to `md_procd.txt`

```
> write.table(md[, c(1,4)], file="md_procd.txt",
sep="\t", row.names=F)
```

# R Basics: Defining Functions

- Syntax

```
add <- function(a, b) {
 s = a + b
 return(s)
}
```

- `return()` missing: result of last computation is returned

- Named arguments and defaults

```
foo <- function(x1, x2, x3=2) {
 x1 / x2 * x3
}
```

```
> foo(x2=7, x1=21) # x1, x2: reversed, x3: default
[1] 6
```

# Conditional and Repetitive Execution

- if/else statement

```
if (expr) {
 ...
} else {
 ...
}
```

- For Loop

```
for (i in expr) {
 ...
}
```

- While Loop

```
while (expr) {
 ...
}
```

- WARNING:

- Loops are not very efficient in R
- ... and not very elegant
- Use *subsetting* or `*apply()` functions

# Subsetting

- Assume we have data frame `df` with gene IDs and an expression value. Task: Remove rows with neg. expr value
- Using a for loop (complicated...)

```
> result = c()
> for (i in 1:nrow(df)) {
+ if (df$expr[i] > 0) {
+ result = rbind(result, df[i,])
+ }
+ }
```

- Using *subsetting*

```
> result = df[which(df$expr > 0),]
> result = df[-which(df$expr <= 0),] #minus indexing
```

## Family of `*apply()` functions

- Syntax (other: `lapply()`, `sapply()`, ...)  
`apply(X, MARGIN, FUN, ...)`
- Given a matrix  

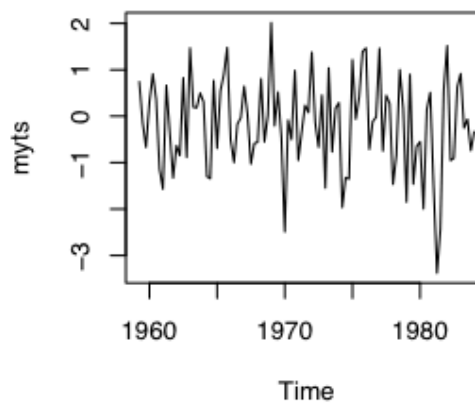
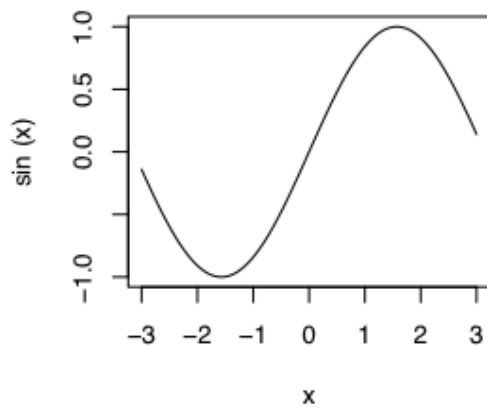
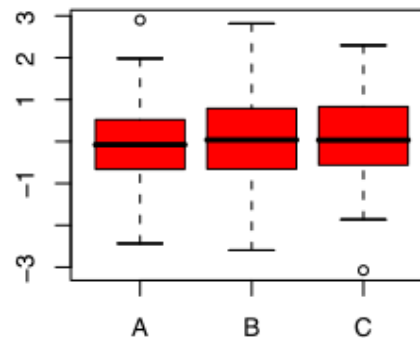
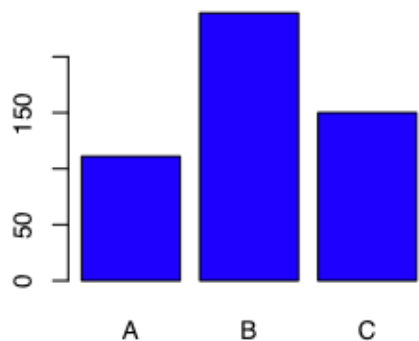
```
> m <- matrix(1:10, nrow=2, ncol=5)
```
- Compute the sum of each **column**  

```
> apply(m, 2, sum)
```
- Applying a custom function  

```
> check <- function(row, dist, C) {
+ avg.to.dist <- mean(row[1:dist])
+ return(if(avg.to.dist > C) TRUE else FALSE)
+ }
```

```
> apply(m, 1, check, dist=3, C=3)
[1] FALSE TRUE
```

# Graphical Procedures



# Graphical Procedures

- Generic function for plotting: `plot(x, y, ...)`
- Frequently used arguments

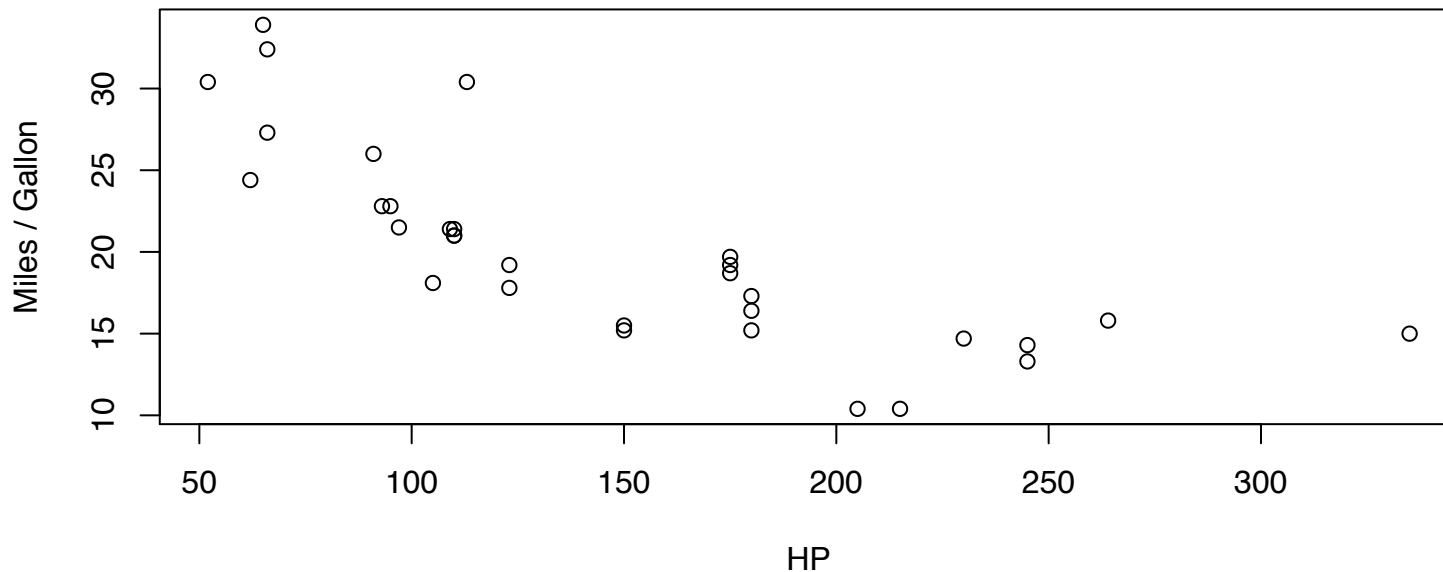
| Description                        | Argument                                            |
|------------------------------------|-----------------------------------------------------|
| Style of plot (points, lines, ...) | <code>type=""</code>                                |
| Plot title                         | <code>main=""</code>                                |
| Axis labels                        | <code>xlab=""</code> , <code>ylab=""</code>         |
| Axis limits                        | <code>xlim=c(a,b)</code> , <code>ylim=c(c,d)</code> |
| Colour                             | <code>col="green"</code>                            |
| Legend                             | <code>legend()</code>                               |

- Selection of *high*-level plotting functions  
`boxplot()`, `barplot()`, `hist()`, `pie()`, ...
- Selection of *low*-level plotting functions  
`lines()`, `points()`, `text()`, `abline()`, ...

# Graphical Procedures (Example)

```
Attach built in mtcars data set, ?mtcars for info
> data(mtcars)
```

```
Plot horse power against miles per gallon
> plot(mtcars$hp, mtcars$mpg, xlab="HP", ylab="Miles / Gallon")
```





# Graphical Procedures (Example)

```
Fit a simple linear regression
> lsr = lm(mtcars$mpg ~ mtcars$hp) # mpg = a * hp + b
```

```
Show coefficients
```

```
> lsr
```

```
Call:
```

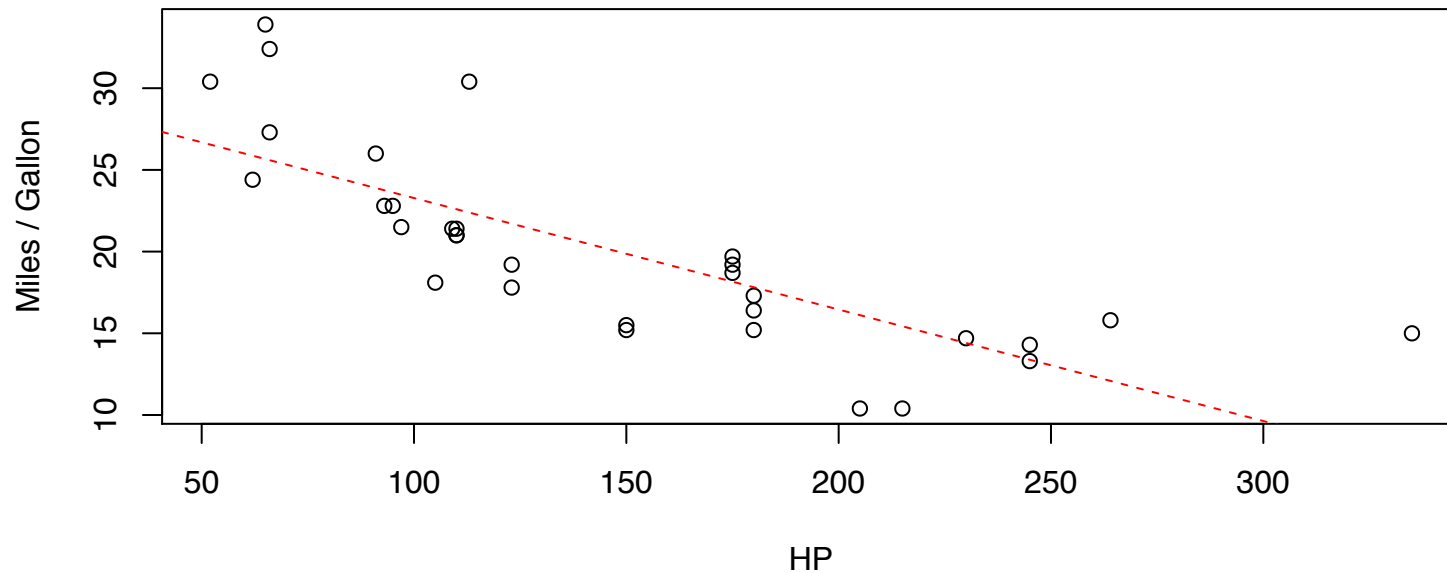
```
lm(formula = mtcars$mpg ~ mtcars$hp)
```

```
Coefficients:
```

```
(Intercept) mtcars$hp
 30.09886 -0.06823
```

# Graphical Procedures (Example)

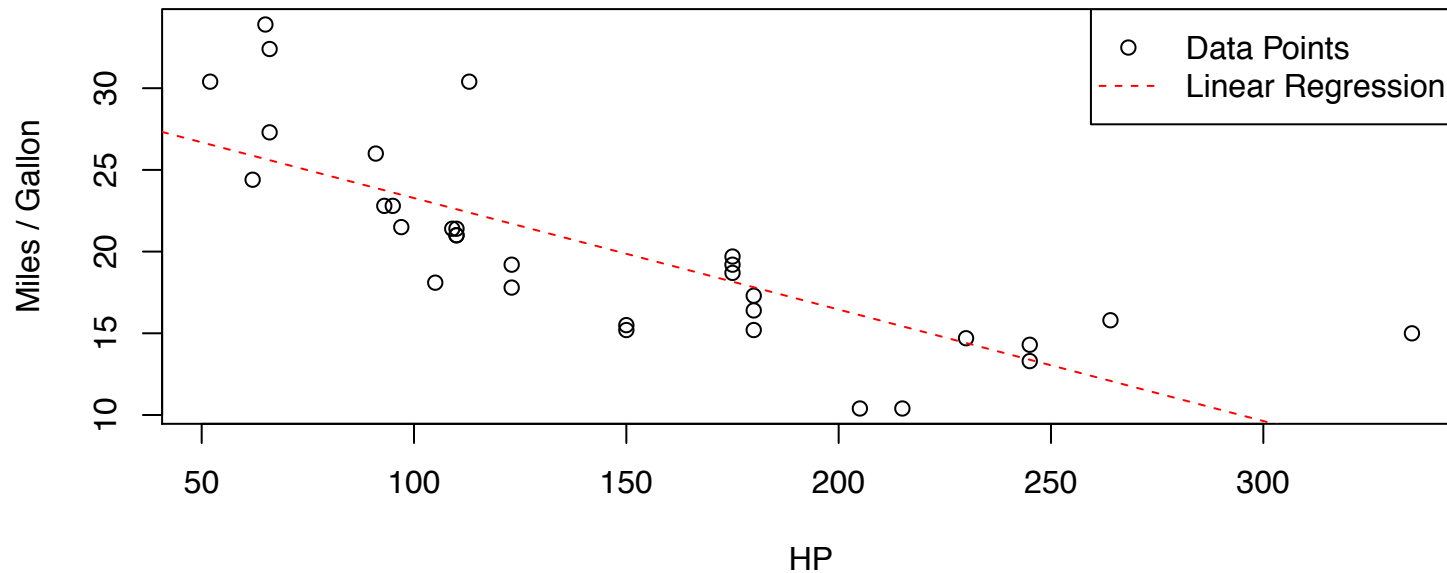
```
Add the model to the plot using low-level plotting function
> abline(lsr$coefficients, lty=2, col="red")
```



# Graphical Procedures (Example)

```
Add a legend
```

```
> legend("topright", c("Data Points", "Linear Regression"), pch=c(1,
NA), lty=c(0, 2), col=c("black", "red"))
```



# Using External Packages

- Main sources for packages
  - <http://cran.r-project.org/web/packages/>
  - <http://www.bioconductor.org/packages/release/bioc/>
- Installing downloaded packages from command line  
R CMD INSTALL [-l lib\_path] package\_name.tar.gz
- Downloading and installing packages from bioconductor
  - > `source("http://bioconductor.org/biocLite.R")`
  - > `biocLite("package_name")`
- Loading packages in R
  - > `library(package_name)`
  - > `help(package=package_name)`
  - Á

# Misc. Useful Functions

| Purpose                            | Function Name                     |
|------------------------------------|-----------------------------------|
| Generic object summary statistics  | <code>summary(obj)</code>         |
| Show first and last part of object | <code>head(obj), tail(obj)</code> |
| Cast objects                       | <code>as.&lt;type&gt;(obj)</code> |
| Show object structure              | <code>str(obj)</code>             |
| Show list of attached packages     | <code>search()</code>             |
| Show list of attached objects      | <code>ls()</code>                 |
| Clear workspace                    | <code>rm(list=ls())</code>        |
| Identify masked objects            | <code>conflicts()</code>          |
| Include code from external script  | <code>source(file)</code>         |
| Run system command                 | <code>system("cmd")</code>        |

# Resources

- R Manuals and Tutorials

<http://cran.r-project.org/manuals.html>

<http://www.statmethods.net/>

- R/Matlab Reference

<http://www.math.umaine.edu/~hiebler/comp/matlabR.html>

- R-Help Mailing List

<https://stat.ethz.ch/mailman/listinfo/r-help>

- StatET plugin for Eclipse IDE

<http://www.walware.de/goto/statet>

# Bayes Example Output (fair coin, $n=20$ )

