

Scientific programming in 

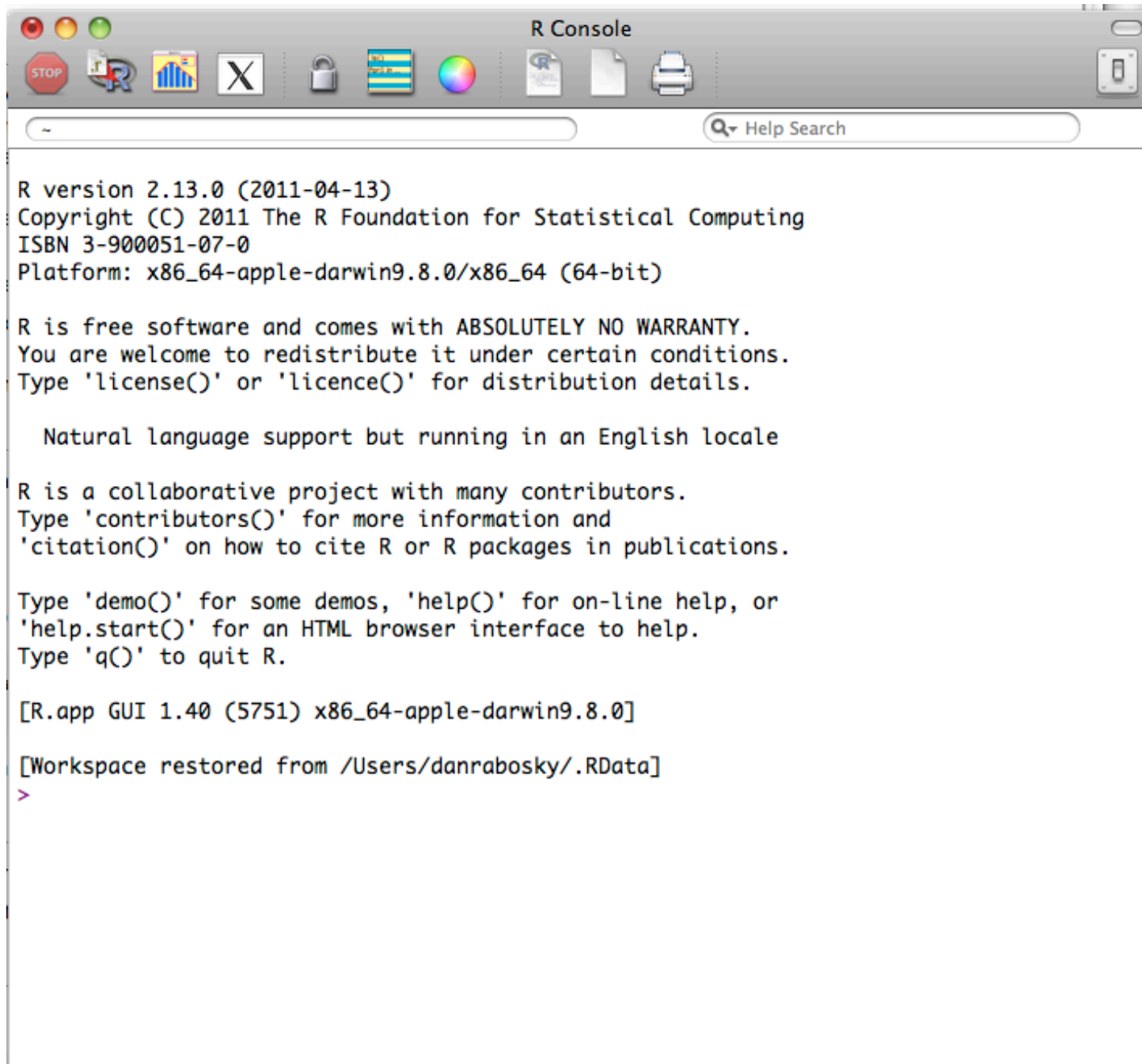
# **R: a multipurpose scientific programming environment for 95% of ecology & evolution**

- Data manipulation
- Basic statistics
- Advanced statistics
- **Programming: simulation and modeling of data**
- Scripting: save and/or repeat your analyses exactly.
- Scientific graphics
- Speed: from **idea** to **results** in *hours* or less!

## Limitations on R

- Learning curve
- Memory: limits on virtual memory
- Computational speed:
  - *some problems are not R friendly*

# Getting started with R



```
R version 2.13.0 (2011-04-13)
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

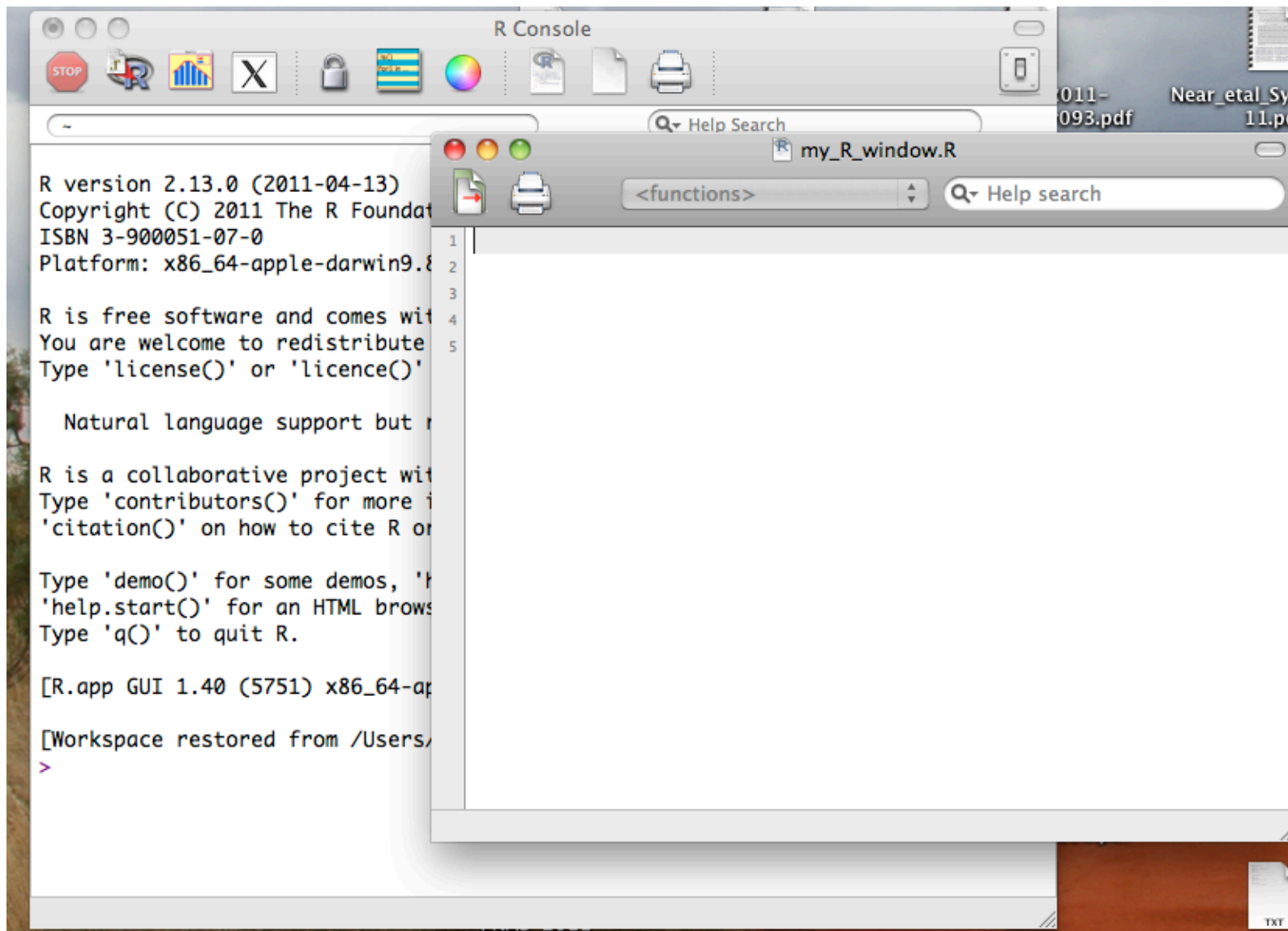
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

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.

[R.app GUI 1.40 (5751) x86_64-apple-darwin9.8.0]

[Workspace restored from /Users/danrabosky/.RData]
>
```

**This is the R editor. Launch with CMD+N [mac]**



# Structure of your R environment



**Preloaded base stuff**

# Structure of your R environment



## Preloaded base stuff

### **Datatypes & structures:**

`numeric, character, factor, data.frame`

**Functions:** `dnorm(), lm(), list(), rm()`

### **Programming keywords:**

`for, function, while, in`

# Structure of your R environment



Preloaded base stuff

**Stuff you create**



# Structure of your R environment



## Preloaded base stuff

Variables you create:

```
x <- runif(10)
```

Data you load:

```
myData <- scan('mydata.txt')
```

**Stuff you create**

# Structure of your R environment



Preloaded base stuff

**Other people's stuff:**

- packages and data
- “libraries”

# Structure of your R environment



Preloaded base stuff

**Other people's stuff:**

- packages and data
- “libraries”

```
>library(ape)  
>data(bird.orders)  
>plot.phylo(bird.orders)
```

# Structure of your R environment



## Preloaded base stuff

### Other people's stuff:

- packages and data
- “libraries”

**Stuff you create**

# Basic data types

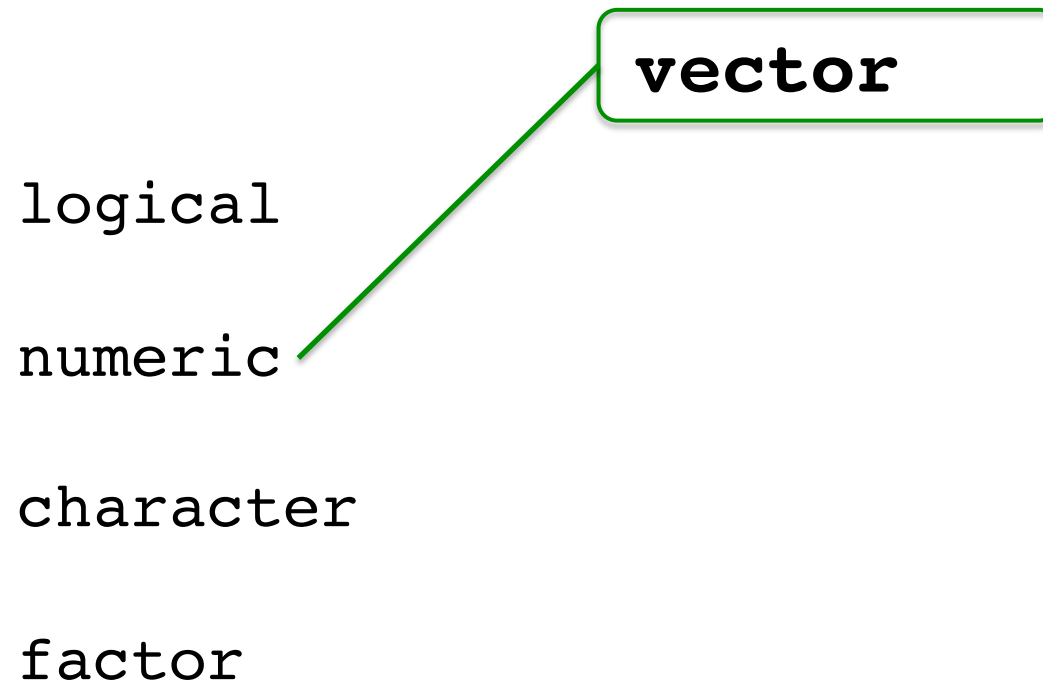
logical

numeric

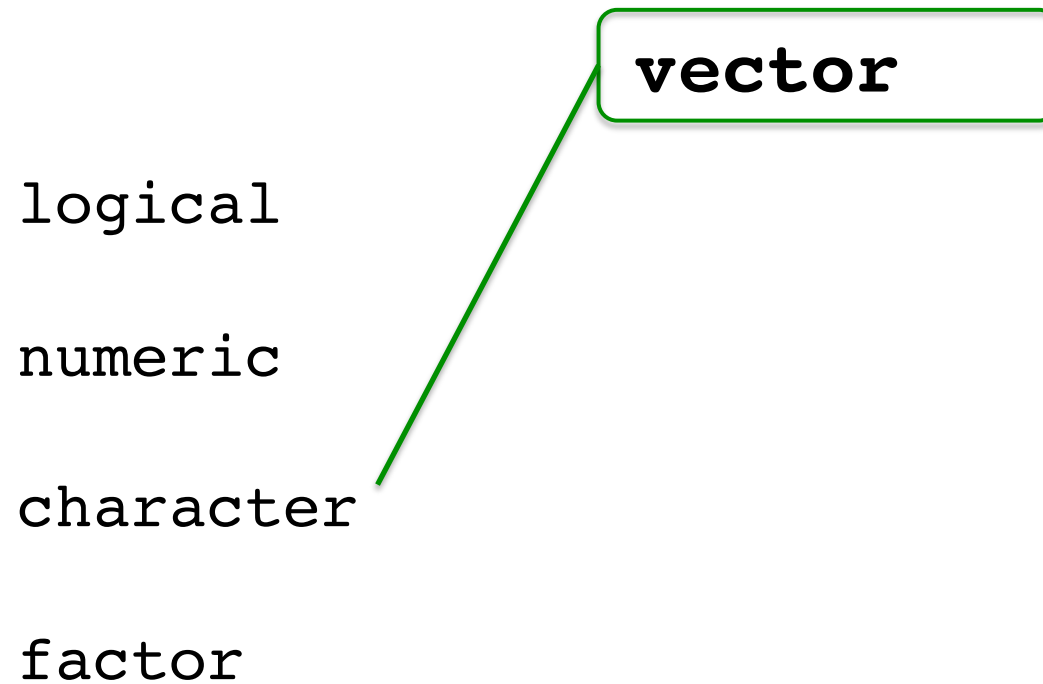
character

factor

# Basic data structures



# Basic data structures



# Data structures

**vector**

logical

numeric

character

factor

**matrix**  
**array**



# Data structures

**vector**

logical

**matrix**

numeric

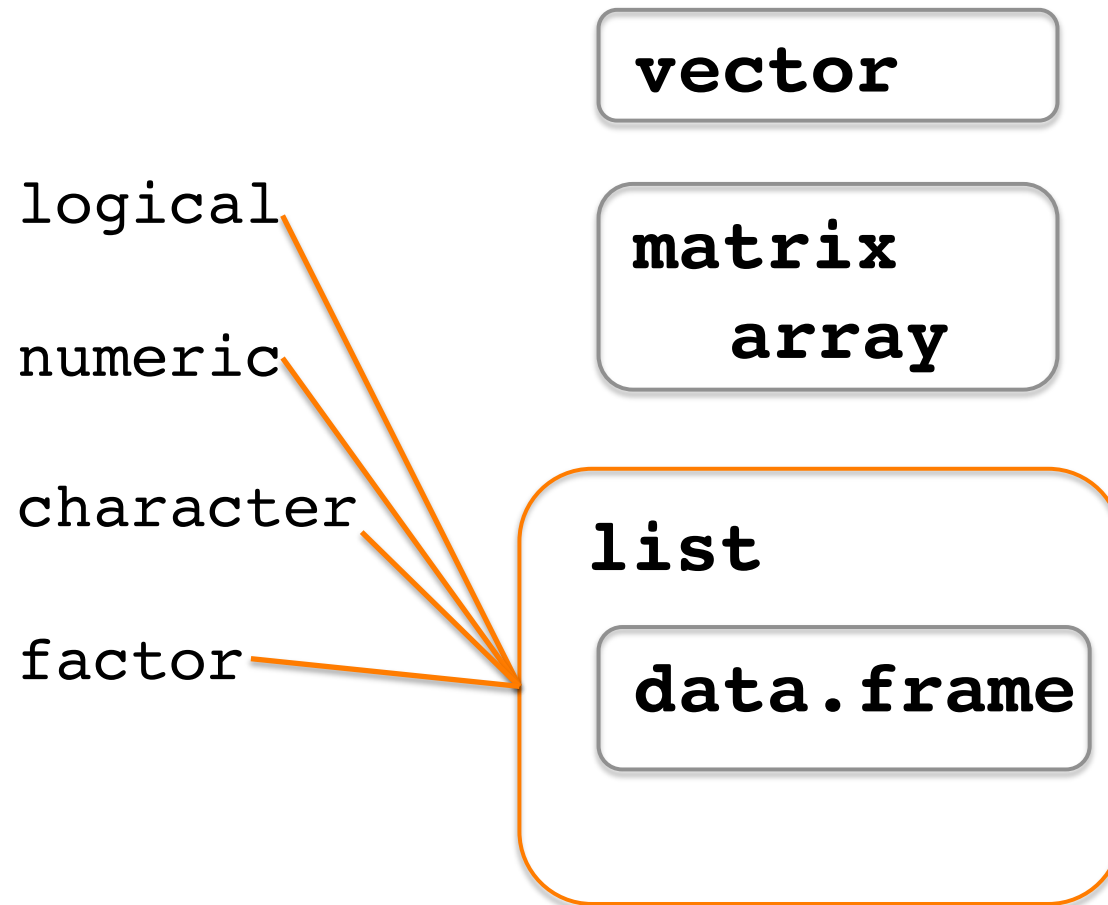
**array**

character

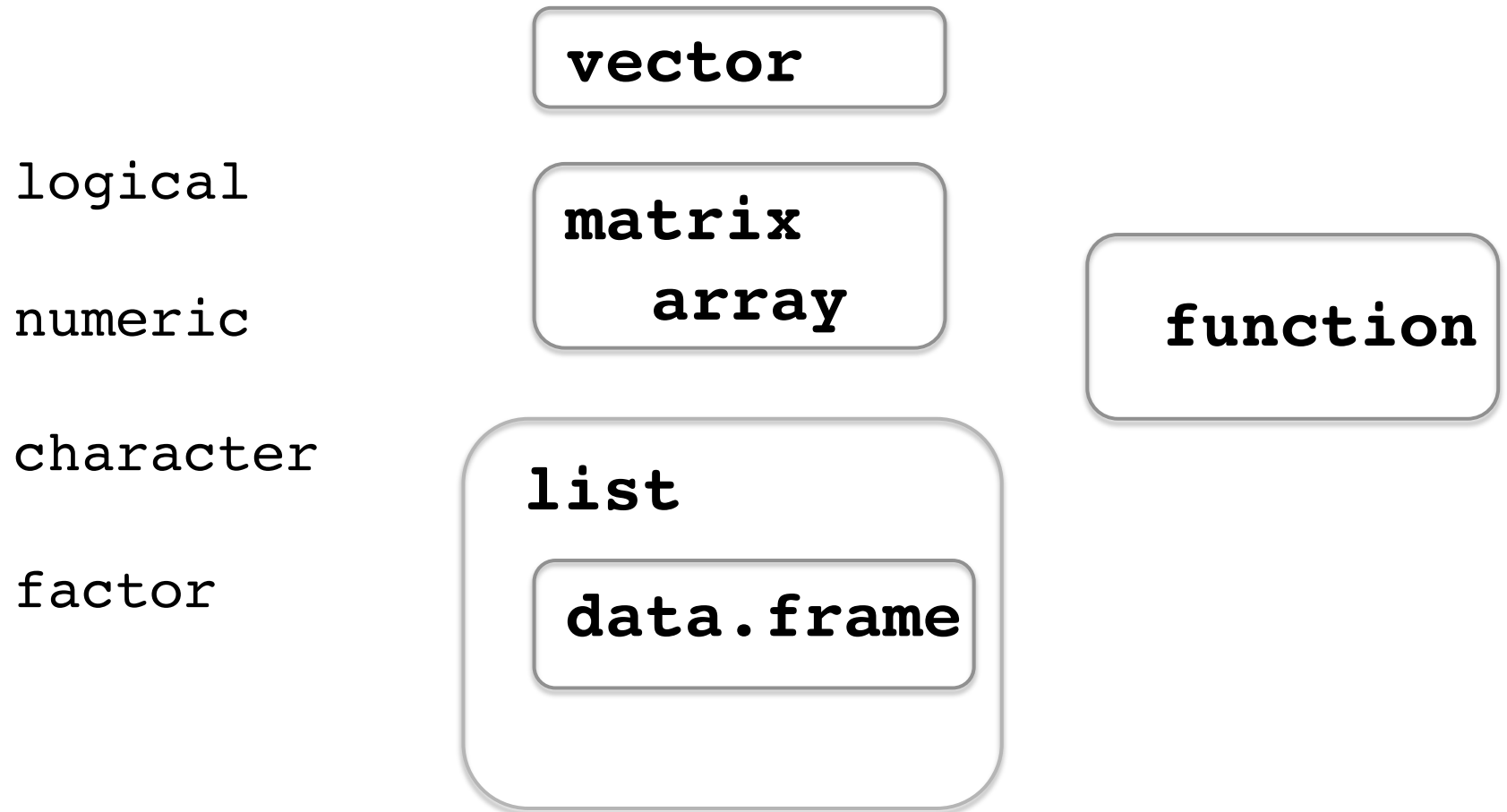
factor

**data.frame**

# Data structures



# Perform operations on data



## ***Data types***

logical

numeric

character

factor

## ***Data “containers”***

**vector**

**matrix**  
**array**

**list**

**data.frame**

## ***Operations***

**function**

# **R commandments**

## Be aware of thy directory

- `dir()`
- `getwd()`
- `setwd(...)`
- `file.choose()`

## Keep a clean workspace and working directory

- Remove all objects from workspace:

```
rm(list = ls())
```

When quitting R:

- DO NOT save your workspace.
- DO save your script files

## Keep $R$ updated

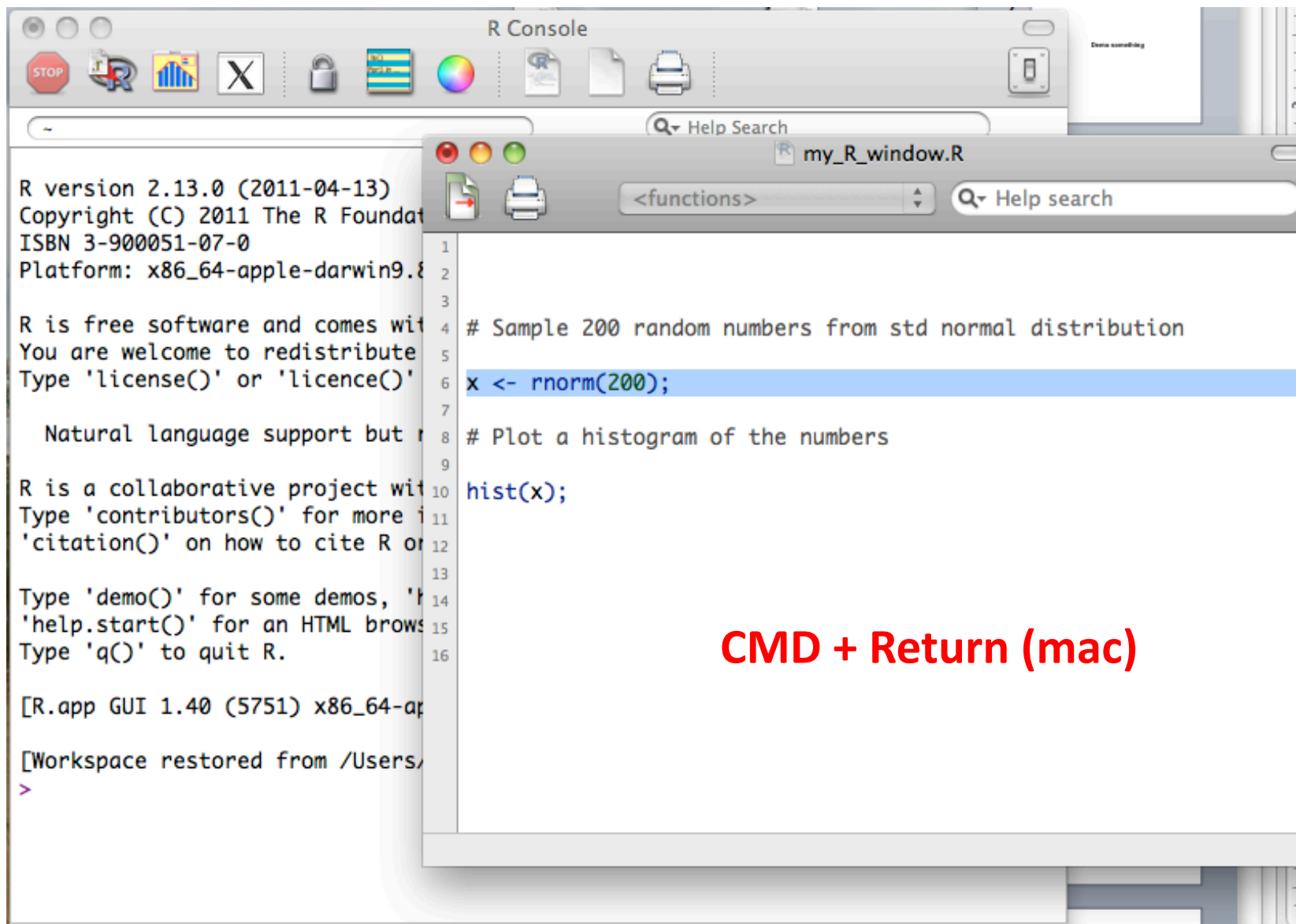
- *Failing to update  $R$  will lead to many cryptic problems.*



## Use the Editor

- *Never, ever execute more than a single line of code at a time in the R console window*
- *Except for “quick looks” at data and results, almost all your work should be done in the Editor*
- *Save everything frequently*

# Sourcing and executing code



## Getting help

*Type `?myFunction` for help on `myFunction`*

- *Numerous online resources*
- *<http://www.r-project.org/mail.html>*
- *R-help*
- *R-sig-phylo*
- *R-sig-ecology*
- *R-sig-mixed-models*

## Parentheses, brackets, braces

- *These are very different: [ ] , { } , ( )*
- *Brackets [ ] access data from matrices, vectors, and dataframes*
- *Braces { } are strictly used in programming*
- *Parentheses ( ) are required for function calls and to specify “order of operations” for calculations*

# Semicolon

- Strongly recommended to end statements with a semicolon;

## The “arrow operator” versus “equals sign”

- Assignments in R are made with `<-`  
`x <- 10;`
- Never use arrow in right-to-left direction, e.g.,  
`10 -> x`
- equals sign:
  - 1. Function arguments:  
`myData <- read.table(file = 'my_datafile.txt');`
  - 2. Logical comparisons

## Commenting your code

# Commented code looks like this

# This line will not be executed

# Put lots of comments in your code

**The end**