R

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Outline

1. Object-Oriented Programming
2. Data Visualization
3. R Package
4. Bioconductor
5. Reproducible Research in R

Next

1. Object-Oriented Programming
   - History
     - S3
     - S4
2. Data Visualization
3. R Package
4. Bioconductor
5. Reproducible Research in R

S4 Classes and methods

History

- 1976, Rick Becker and John Chambers, S on Honeywell OS
- Ported to UNIX, S2
- Around 1986, functional programming and object self-description, S3
- 1992, concept of classes and methods, S4
- 2010, Reference Classes (RC), R 2.12

appendix in Software for Data Analysis by Chambers

S4 Classes and methods

OO Systems in R

- S3
- S4
- RC
- Base Types

Best Reference: http://adv-r.had.co.nz/OO-essentials.html

S3

S4 Classes and methods

S4 in R

```
library(stats4)
library(pryr)
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
nLL <- function(lambda) -sum(dpois(y, lambda, log = TRUE))
fit <- mle(nLL, start = list(lambda = 5), nobs = length(y))
isS4(fit)
```

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

```
otype(fit)
```

```
## [1] "S4"
```

```
isS4(nobs)
```

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

```
ftype(nobs)
```

S4 Classes and methods

Defining classes and creating objects

```
setClass("Person",
 slots = list(name = "character", age = "numeric"))
setClass("Employee",
 slots = list(boss = "Person"),
 contains = "Person")

alice <- new("Person", name = "Alice", age = 40)
john <- new("Employee", name = "John", age = 20, boss = alice)
```

S4 Classes and methods

access slots of an S4 object

```
alice@age
slot(john, "boss")
```

S4 Classes and methods

Creating new methods and generics

```
setGeneric("union")
setMethod("union",
 c(x = "data.frame", y = "data.frame"),
 function(x, y) {
   unique(rbind(x, y))
 }
)
setGeneric("myGeneric", function(x) {
 standardGeneric("myGeneric")
})
```

Next

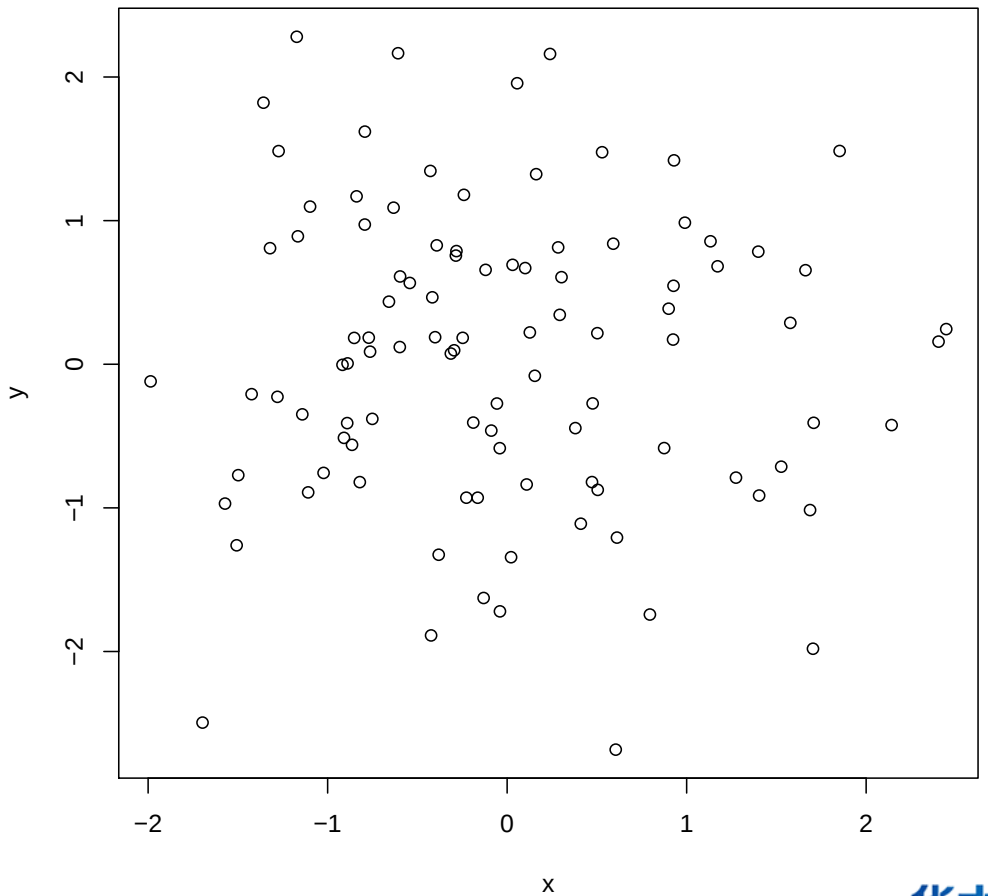
1 Object-Oriented Programming

2 Data Visualization
- Scatter Plot
- 时间序列
- 柱状图
- 饼图
- 分类数据绘图
- 绘制分布
- 箱线图

3 R Package

4 Bioconductor

plot



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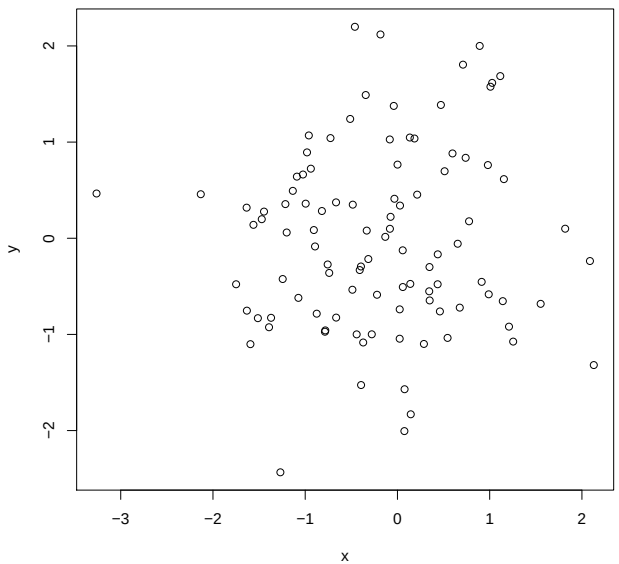
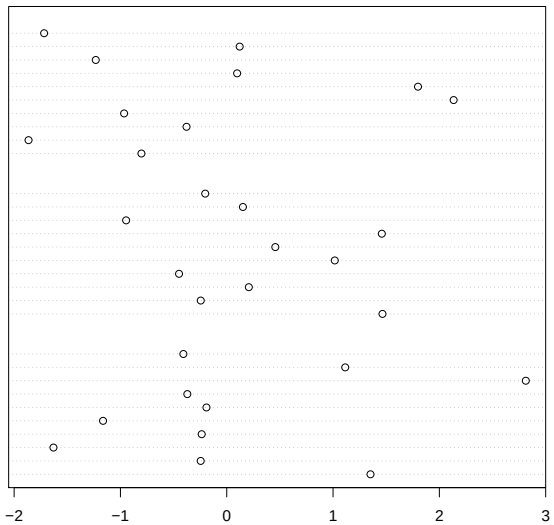
plot

```
x = rnorm(100)
y = rnorm(100)
plot(x, y)
```



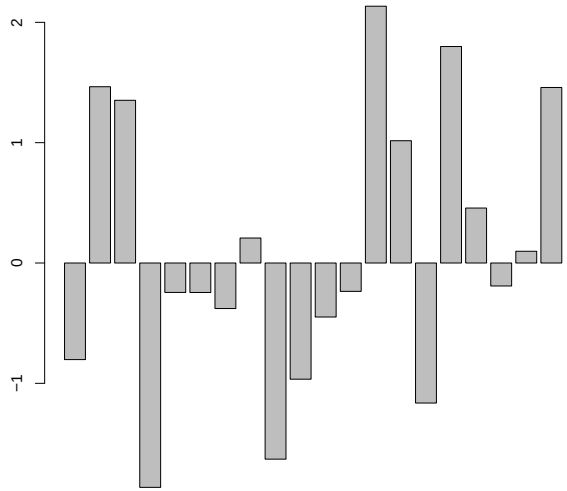
dotchart

```
x = rnorm(30)
dotchart(x, groups = rep(1:3,10))
```



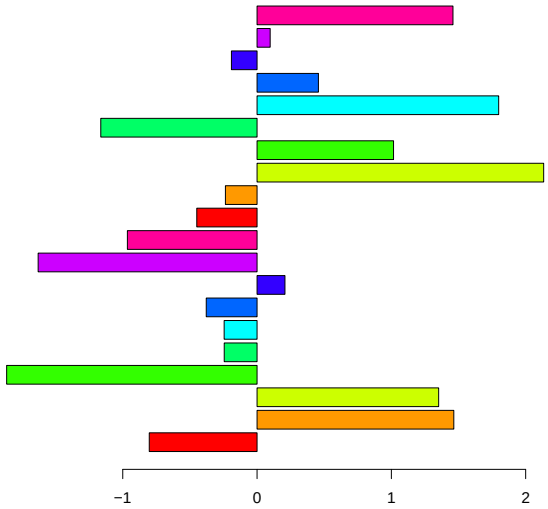
barplot

```
barplot(x[1:20])
```



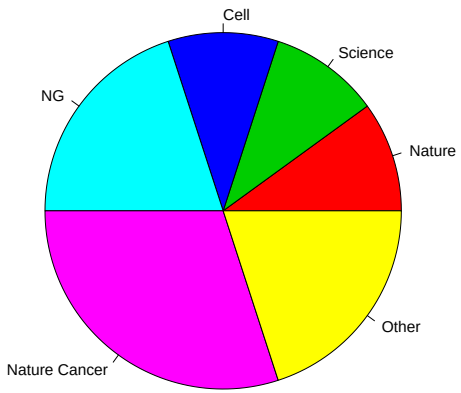
barplot

```
barplot(x[1:20], width=2, horiz=T, col=rainbow(10))
```



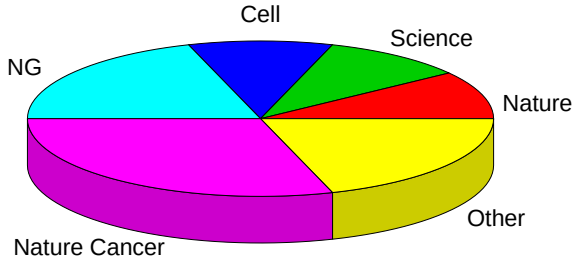
pie

```
pie(c(10,10,10,20,30,20), c("Nature","Science","Cell","NG",
Cancer","Other"),col=2:7)
```



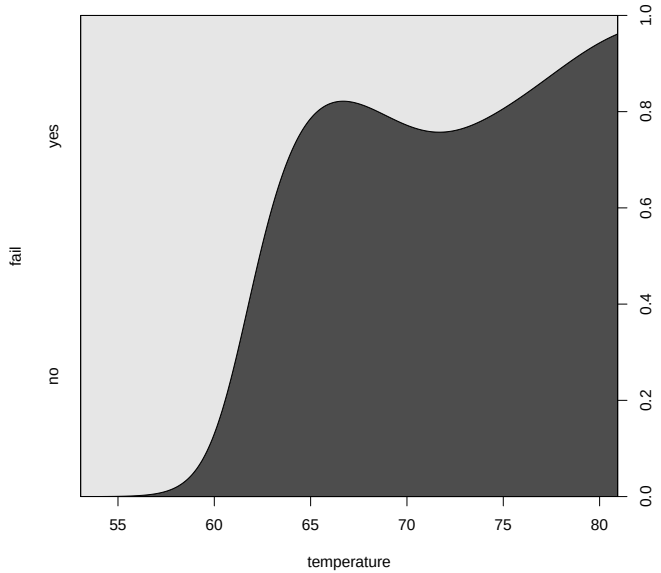
pie

```
library(plotrix)
pie3D(c(10,10,10,20,30,20), labels=c("Nature","Science","Ce
Cancer","Other"),col=2:7)
```



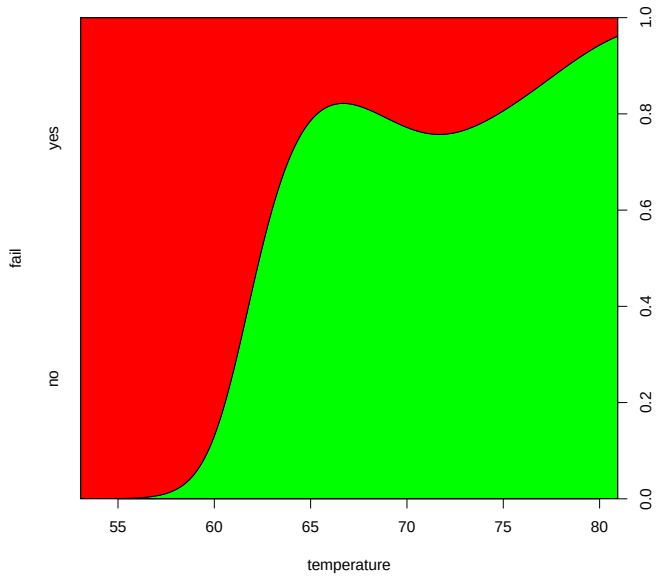
cdplot

```
cdplot(temperature, fail)
```



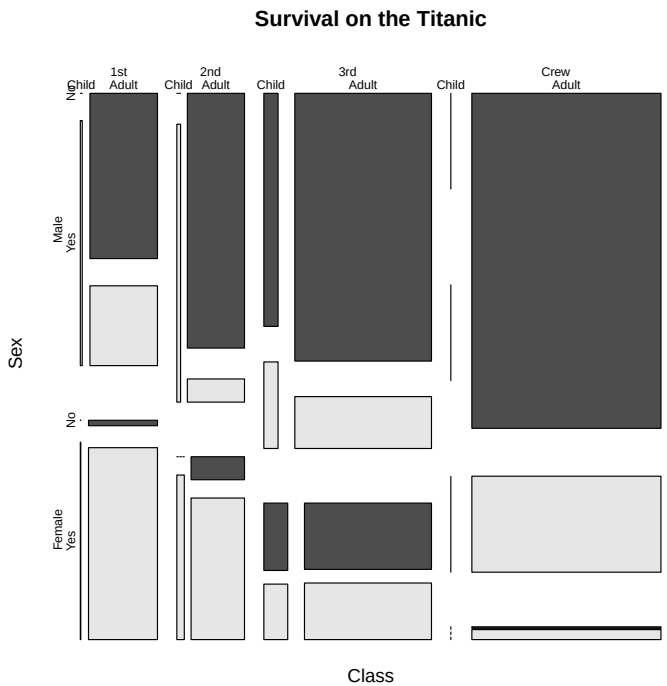
cdplot

```
cdplot(temperature, fail, col=c("green", "red"))
```



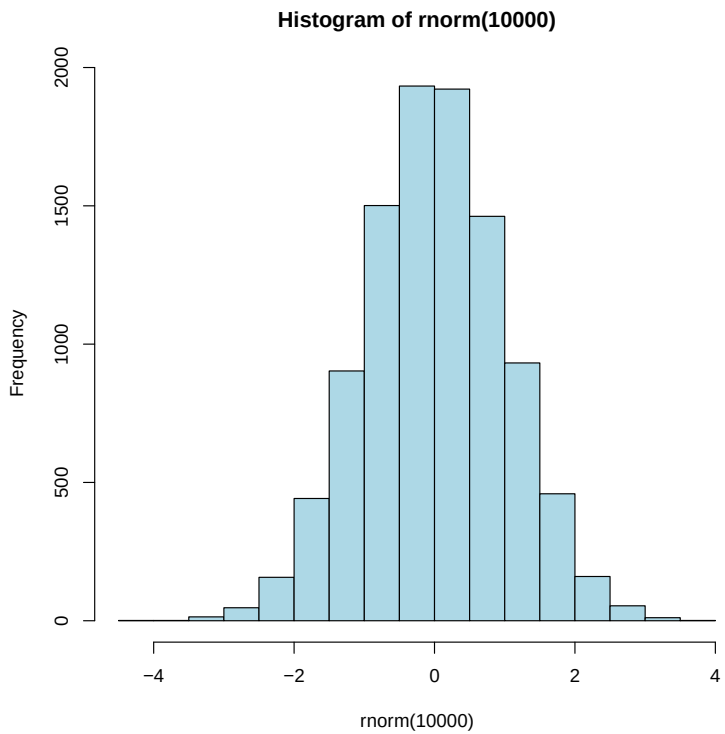
mosaicplot

```
require(stats)
mosaicplot(Titanic, main = "Survival on the Titanic",
color = TRUE)
```



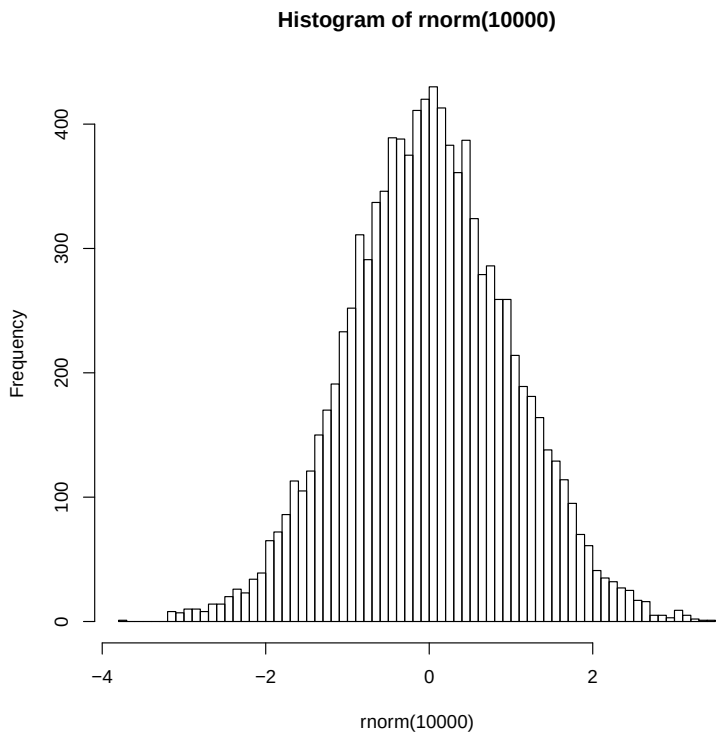
hist

```
hist(rnorm(10000), col="lightblue")
```



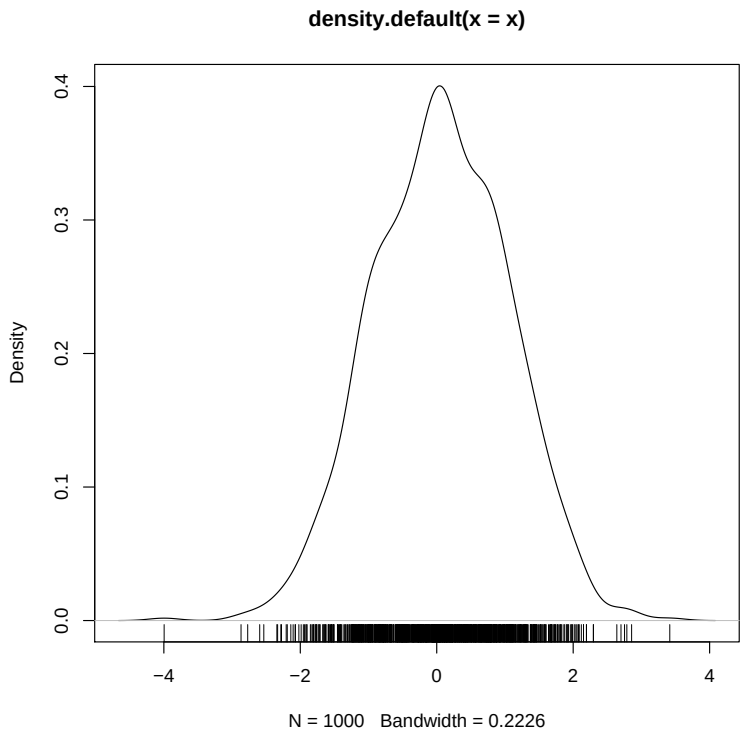
hist

```
hist(rnorm(10000), breaks=100)
```



density + rug

```
x = rnorm(1000)
plot(density(x))
rug(x)
```



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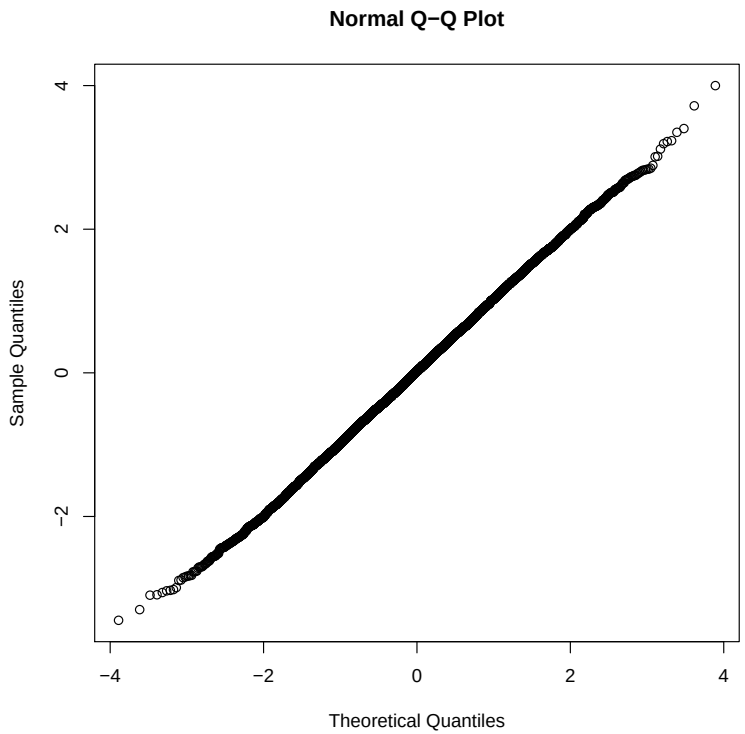
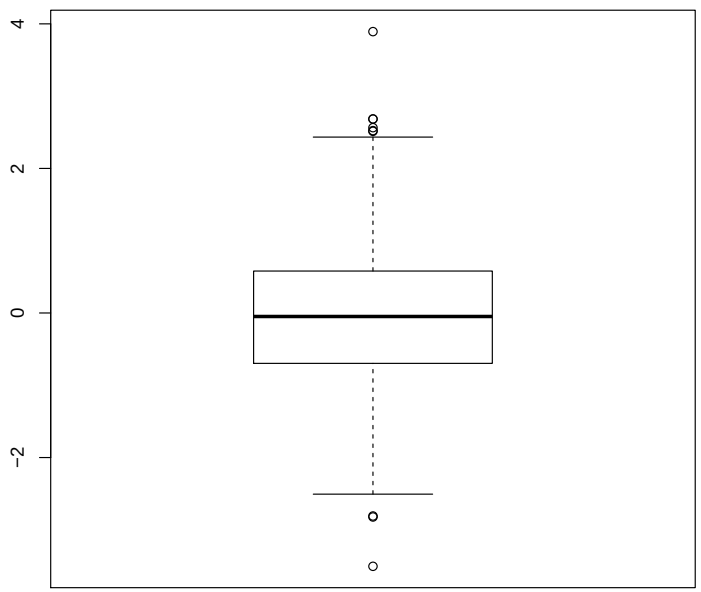
Q-Q plot

```
qqnorm(rnorm(10000))
```



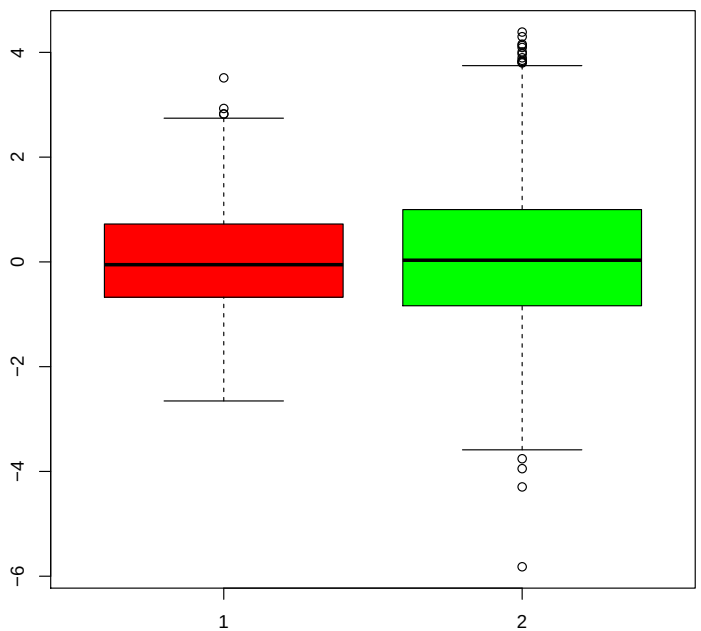
boxplot

```
boxplot(rnorm(1000))
```



boxplot

```
boxplot(cbind(rnorm(1000),rnorm(1000)+rnorm(1000)), col=c("
```



Next

1 Object-Oriented Programming

2 Data Visualization

3 R Package
- R Package Development
- devtools

4 Bioconductor

5 Reproducible Research in R

R Package

- Hadley: In R, the fundamental unit of shareable code is the package.
- Hilary Parker: Seriously, it doesn’ t have to be about sharing your code (although that is an added benefit!). It is about saving yourself time.

References

- Writing R Extensions:
  http://cran.r-project.org/manuals.html
- R Packages from Hadley:
  http://r-pkgs.had.co.nz/
- Writing an R package from scratch:
  http://hilaryparker.com/2014/04/29/writing-an-r-package-from-scratch/
- 开发R程序包之忍者篇:
  http://cos.name/2011/05/write-r-packages-like-a-ninja/

R Package from Scratch

see cgr directory

Why devtools?

- This book espouses my philosophy of package development:
- anything that can be automated, should be automated.
- Do as little as possible by hand.
- Do as much as possible with functions.

Next

1 Object-Oriented Programming

2 Data Visualization

3 R Package

4 Bioconductor
- Overview
- ggbio

5 Reproducible Research in R

Overview

Bioconductor

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, 934 software packages, and an active user community.

Goals

- To provide widespread access to a broad range of powerful statistical and graphical methods for the analysis of genomic data.
- To facilitate the inclusion of biological metadata in the analysis of genomic data, e.g. literature data from PubMed, annotation data from Entrez genes.
- To provide a common software platform that enables the rapid development and deployment of extensible, scalable, and interoperable software.
- To further scientific understanding by producing high-quality documentation and reproducible research.
- To train researchers on computational and statistical methods for the analysis of genomic data.

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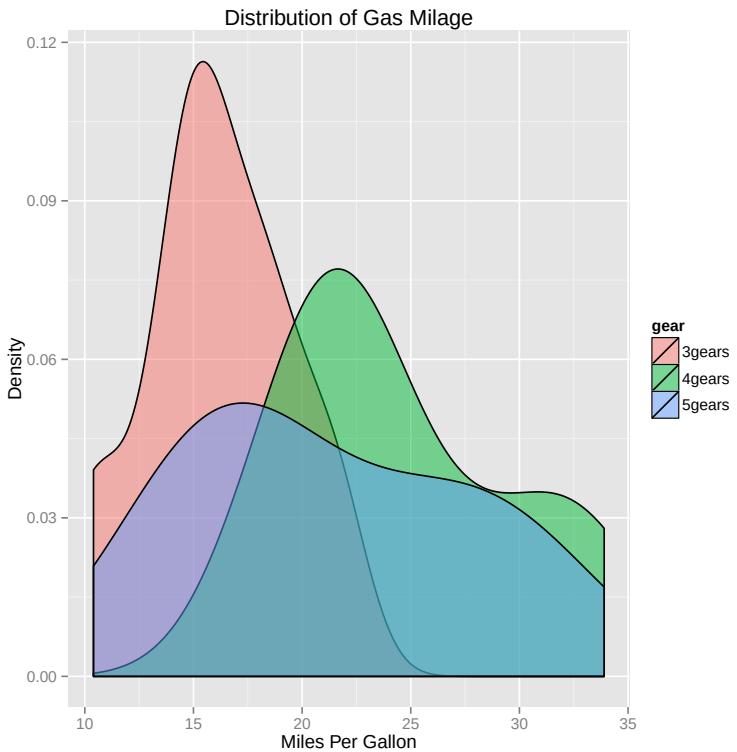
see GNBF5010-2013/4. Biological Data Analysis and Visualization in R/slides.pdf

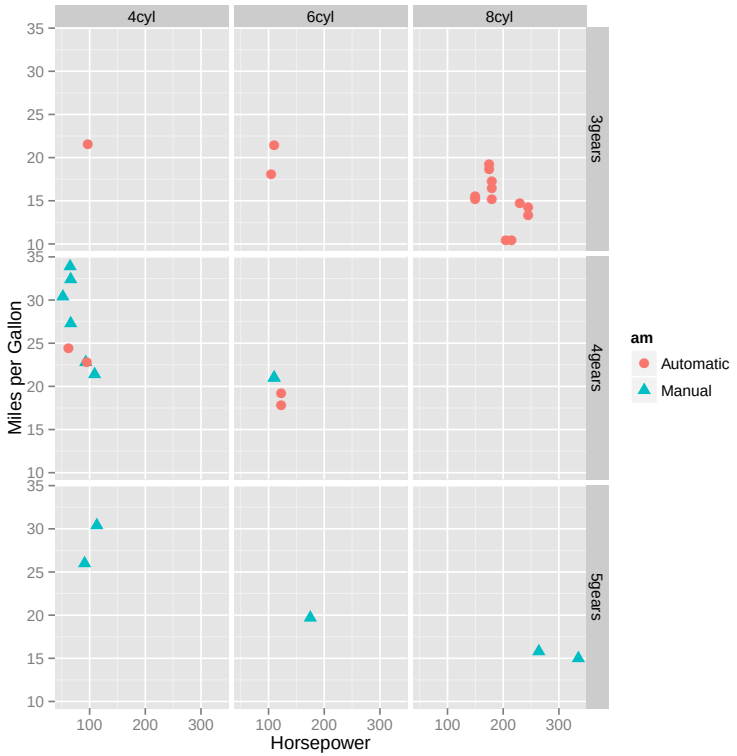
ggplot2

```
qplot(mpg, data=mtcars, geom="density", fill=gear, alpha=I(.
5), main="Distribution of Gas Milage", xlab="Miles Per
Gallon", ylab="Density")
```



ggplot2

```
qplot(hp, mpg, data=mtcars, shape=am, color=am, facets=gear ~
size=I(3), xlab="Horsepower", ylab="Miles per Gallon")
```



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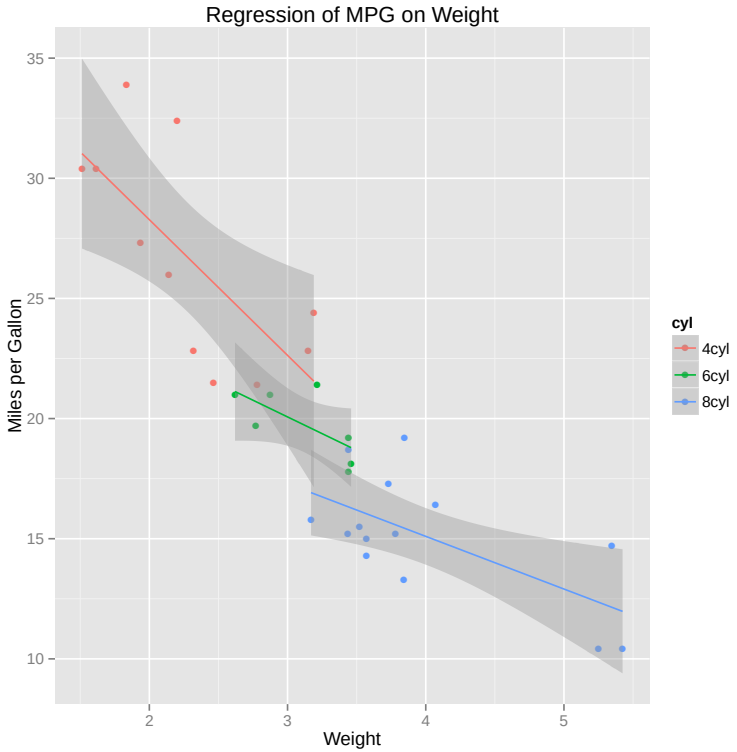
ggplot2

```
qplot(wt, mpg, data=mtcars, geom=c("point", "smooth"),
method="lm", formula=y x, color=cyl, main="Regression
of MPG on Weight", xlab="Weight", ylab="Miles per Gallon")
```



ggplot2

```
qplot(gear, mpg, data=mtcars, geom=c("boxplot", "jitter"),
fill=gear, main="Mileage by Gear Number", xlab="", ylab="Mile
per Gallon")
```

ggbio

- ggplot2 + bioconductor = ggbio
- Website: http://www.tengfei.name/ggbio/
- Author: Tengfei Yin at Seven Bridges Genomics

ggbio Examples

```
source("http://bioconductor.org/biocLite.R")
biocLite("ggbio")
library(ggbio)
example(autoplot)
```

Next

1 Object-Oriented Programming

2 Data Visualization

3 R Package

4 Bioconductor

5 Reproducible Research in R
- knitr
- Interactive Report and Shiny

Overview

- Official website: http://yihui.name/knitr/
- Reference: Dynamic Documents with R and knitr
- Author: Yihui Xie

Examples

- the slides of the R lectures are generated by knitr
  - Knitr
  - XeLaTeX
- see knitr directory for the Knitr example in Markdown

Interactive Report

- Google Analytics
- 百度统计 from Baidu.com
- 数据魔方 from Taobao.com

Shiny Overview

- A web application framework for R
- Turn your analyses into interactive web applications
- No HTML, CSS, or JavaScript knowledge required
- http://shiny.rstudio.com/

Example

see shinyApp directory