Table of Useful R commands

Command	Purpose
help()	Obtain documentation for a given R command
example()	View some examples on the use of a command
c(), scan()	Enter data manually to a vector in R
seq()	Make arithmetic progression vector
rep()	Make vector of repeated values
data()	Load (often into a data.frame) built-in dataset
View()	View dataset in a spreadsheet-type format
str()	Display internal structure of an R object
read.csv(), read.table()	Load into a data.frame an existing data file
library(), require()	Make available an R add-on package
dim()	See dimensions (# of rows/cols) of data.frame
length()	Give length of a vector
ls()	Lists memory contents
rm()	Removes an item from memory
names()	Lists names of variables in a data.frame
hist()	Command for producing a histogram
histogram()	Lattice command for producing a histogram
stem()	Make a stem plot
table()	List all values of a variable with frequencies
xtabs()	Cross-tabulation tables using formulas
mosaicplot()	Make a mosaic plot
cut()	Groups values of a variable into larger bins
mean(), median()	Identify "center" of distribution
by()	apply function to a column split by factors
summary()	Display 5-number summary and mean
var(), sd()	Find variance, sd of values in vector
sum()	Add up all values in a vector
quantile()	Find the position of a quantile in a dataset
barplot()	Produces a bar graph
barchart()	Lattice command for producing bar graphs
boxplot()	Produces a boxplot
bwplot()	Lattice command for producing boxplots

Command	Purpose
plot()	Produces a scatterplot
xyplot()	Lattice command for producing a scatterplot
lm()	Determine the least-squares regression line
anova()	Analysis of variance (can use on results of lm())
predict()	Obtain predicted values from linear model
nls()	estimate parameters of a nonlinear model
residuals()	gives (observed - predicted) for a model fit to data
sample()	take a sample from a vector of data
replicate()	repeat some process a set number of times
cumsum()	produce running total of values for input vector
ecdf()	builds empirical cumulative distribution function
dbinom(), etc.	tools for binomial distributions
dpois(), etc.	tools for Poisson distributions
pnorm(), etc.	tools for normal distributions
qt(), etc.	tools for student t distributions
pchisq(), etc.	tools for chi-square distributions
binom.test()	hypothesis test and confidence interval for 1 proportion
prop.test()	inference for 1 proportion using normal approx.
chisq.test()	carries out a chi-square test
fisher.test()	Fisher test for contingency table
t.test()	student t test for inference on population mean
qqnorm(), qqline()	tools for checking normality
addmargins()	adds marginal sums to an existing table
prop.table()	compute proportions from a contingency table
par()	query and edit graphical settings
power.t.test()	power calculations for 1- and 2-sample t
anova()	compute analysis of variance table for fitted model

Examples of usage

help()

```
help(mean)
```

example()

```
require(lattice)
example(histogram)
```

c(), rep() seq()

```
> x = c(8, 6, 7, 5, 3, 0, 9)
> x

[1] 8 6 7 5 3 0 9

> names = c("Owen", "Luke", "Anakin", "Leia", "Jacen", "Jaina")
> names

[1] "Owen"   "Luke"   "Anakin" "Leia"   "Jacen"  "Jaina"

> heartDeck = c(rep(1, 13), rep(0, 39))
> heartDeck

 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[49] 0 0 0 0

> y = seq(7, 41, 1.5)
> y

 [1]  7.0  8.5 10.0 11.5 13.0 14.5 16.0 17.5 19.0 20.5 22.0 23.5 25.0 26.5 28.0 29.5 31.0 32.5 34.0
[20] 35.5 37.0 38.5 40.0
```

data(), dim(), names(), View(), str()

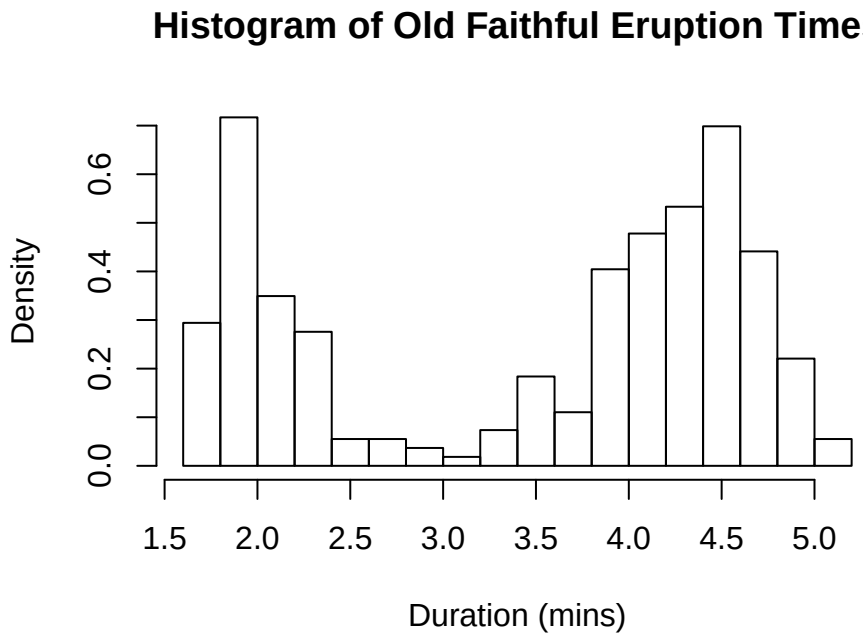
```
> data(iris)
> names(iris)

[1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"

> dim(iris)

[1] 150   5

> str(iris)

'data.frame':        150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

> View(iris)
```

`ls()`, `rm()`

```
> data(iris)
> data(faithful)
> data(Puromycin)
> data(LakeHuron)
> ls()
[1] "faithful"  "heartDeck" "iris"      "LakeHuron" "names"     "Puromycin" "x"         "y"
> newVector = 1:12
> ls()
[1] "faithful"  "heartDeck" "iris"      "LakeHuron" "names"     "newVector" "Puromycin" "x"
[9] "y"
> rm(faithful)
> ls()
[1] "heartDeck" "iris"      "LakeHuron" "names"     "newVector" "Puromycin" "x"         "y"
```

`hist()`

```
data(faithful)
hist(faithful$eruptions)
hist(faithful$eruptions, n=15)
hist(faithful$eruptions, breaks=seq(1.5,5.25,.25), col="red")
hist(faithful$eruptions, freq=F, n=15, main="Histogram of Old Faithful Eruption Times", xlab="Duration (mins)")
```



library(), require()

```
> library(abd)
> require(lattice)
```

histogram()

```
require(lattice)
data(iris)
histogram(iris$Sepal.Length, breaks=seq(4,8,.25))
histogram(~ Sepal.Length, data=iris, main="Iris Sepals", xlab="Length")
histogram(~ Sepal.Length | Species, data=iris, col="red")
histogram(~ Sepal.Length | Species, data=iris, n=15, layout=c(1,3))
```

read.csv()

```
> As.in.H2O = read.csv("http://www.calvin.edu/~scofield/data/comma/arsenicInWater.csv")
```

read.table()

```
> senate = read.table("http://www.calvin.edu/~scofield/data/tab/rc/senate99.dat", sep="\t", header=T)
```

mean(), median(), summary(), var(), sd(), quantile(),

```
> counties=read.csv("http://www.calvin.edu/~stob/data/counties.csv")
> names(counties)
[1] "County"         "State"          "Population"     "HousingUnits"   "TotalArea"
[6] "WaterArea"      "LandArea"       "DensityPop"     "DensityHousing"
> x = counties$LandArea
> mean(x, na.rm = T)
[1] 1126.214
> median(x, na.rm = T)
[1] 616.48
> summary(x)
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
     1.99    431.70    616.50   1126.00    923.20 145900.00
> sd(x, na.rm = T)
[1] 3622.453
> var(x, na.rm = T)
[1] 13122165
> quantile(x, probs=seq(0, 1, .2), na.rm=T)
       0%       20%       40%       60%       80%      100%
     1.99    403.29    554.36    717.94   1043.82 145899.69
```

`sum()`

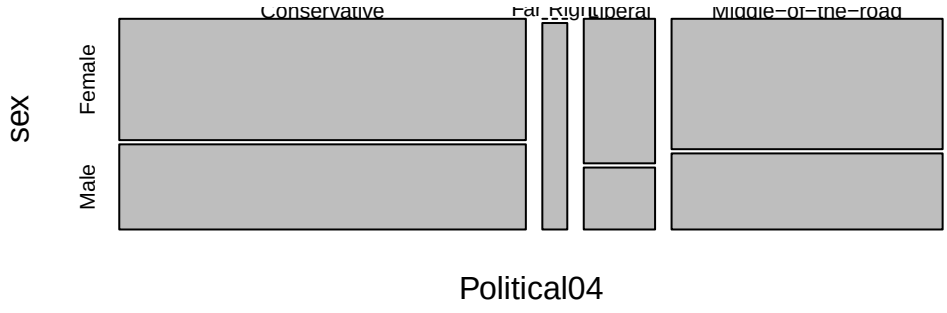
```
> firstTwentyIntegers = 1:20
> sum(firstTwentyIntegers)

[1] 210

> die = 1:6
> manyRolls = sample(die, 100, replace=T)
> sixFreq = sum(manyRolls == 6)
> sixFreq / 100

[1] 0.14
```

`stem()`

```
> monarchs = read.csv("http://www.calvin.edu/~scofield/data/comma/monarchReigns.csv")
> stem(monarchs$years)

  The decimal point is 1 digit(s) to the right of the |

  0 | 0123566799
  1 | 0023333579
  2 | 012224455
  3 | 355589
  4 | 4
  5 | 069
  6 | 3
```

`table()`, `table()`, `mosaicplot()`, `cut()`

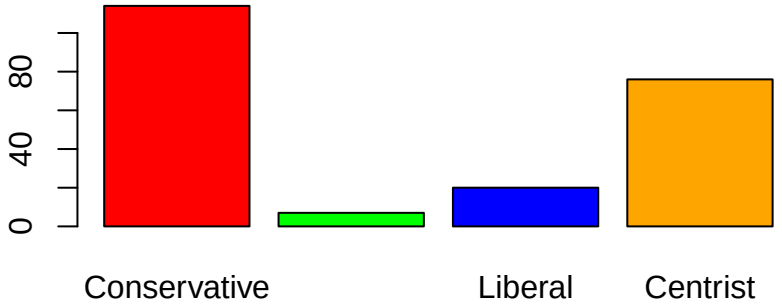
```
> pol = read.csv("http://www.calvin.edu/~stob/data/csbv.csv")
> table(pol$sex)

Female   Male
   133     88

> table(pol$sex, pol$Political04)

        Conservative Far Right Liberal Middle-of-the-road
  Female           67         0      14                48
  Male             47         7       6                28

> xtabs(~sex, data=pol)

sex
Female   Male
   133     88

> xtabs(~Political04 + Political07, data=pol)

                  Political07
Political04          Conservative Far Left Far Right Liberal Middle-of-the-road
  Conservative                 58        0         2      13                39
  Far Right                     4        0         3       0                 0
  Liberal                       0        1         1      14                 4
  Middle-of-the-road           20        0         0      22                32

> mosaicplot(~Political04 + sex, data=pol)
```



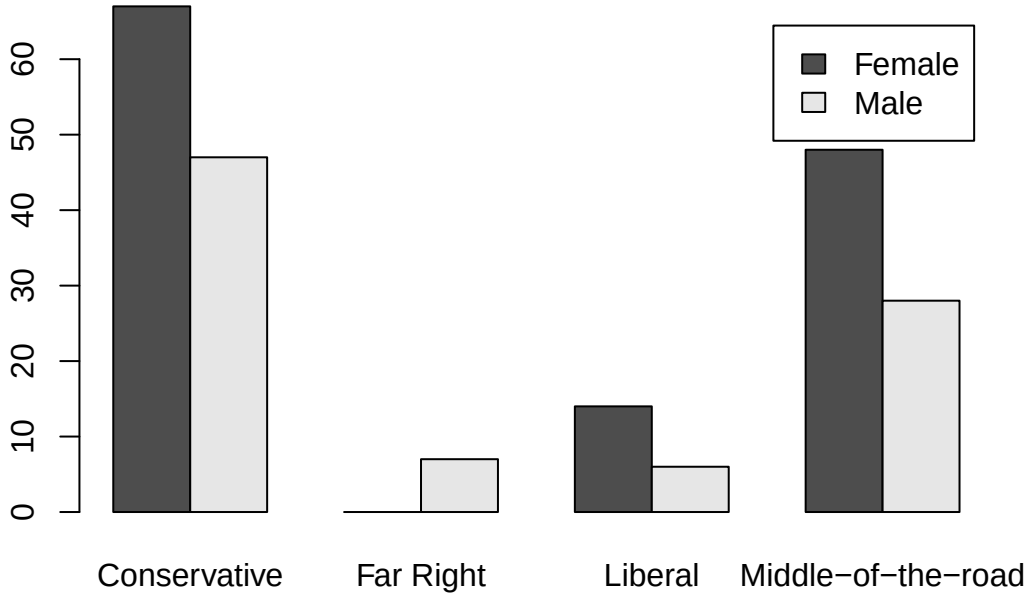

```
> monarchs = read.csv("http://www.calvin.edu/~scofield/data/comma/monarchReigns.csv")
> table(monarchs$years)

 0  1  2  3  5  6  7  9 10 12 13 15 17 19 20 21 22 24 25 33 35 38 39 44 50 56 59 63
 1  1  1  1  1  2  1  2  2  1  4  1  1  1  1  1  3  2  2  1  3  1  1  1  1  1  1  1

> xtabs(~years, data=monarchs)

years
 0  1  2  3  5  6  7  9 10 12 13 15 17 19 20 21 22 24 25 33 35 38 39 44 50 56 59 63
 1  1  1  1  1  2  1  2  2  1  4  1  1  1  1  1  3  2  2  1  3  1  1  1  1  1  1  1

> cut(monarchs$years, breaks=seq(0,65,5))

 [1] (20,25] (10,15] (30,35] (15,20] (30,35] (5,10]  (15,20] (55,60] (30,35] (15,20] (45,50] (20,25]
[13] (10,15] (5,10]  (35,40] (20,25] <NA>    (0,5]   (20,25] (35,40] (5,10]  (0,5]   (40,45] (20,25]
[25] (20,25] (20,25] (0,5]   (10,15] (5,10]  (10,15] (10,15] (30,35] (55,60] (5,10]  (5,10]  (60,65]
[37] (5,10]  (20,25] (0,5]   (10,15]
13 Levels: (0,5] (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] ... (60,65]

> table(cut(monarchs$years, breaks=seq(0,65,5)))

  (0,5]  (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] (50,55] (55,60]
      4       7       6       3       8       0       4       2       1       1       0       2
(60,65]
      1

> fiveYrLevels = cut(monarchs$years, breaks=seq(0,65,5))
> xtabs(~fiveYrLevels)

fiveYrLevels
  (0,5]  (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] (50,55] (55,60]
      4       7       6       3       8       0       4       2       1       1       0       2
(60,65]
      1
```

`barplot()`

```
pol = read.csv("http://www.calvin.edu/~stob/data/csbv.csv")
barplot(table(pol$Political04), main="Political Leanings, Calvin Freshman 2004")
barplot(table(pol$Political04), horiz=T)
barplot(table(pol$Political04),col=c("red","green","blue","orange"))
barplot(table(pol$Political04),col=c("red","green","blue","orange"),
        names=c("Conservative","Far Right","Liberal","Centrist"))
```

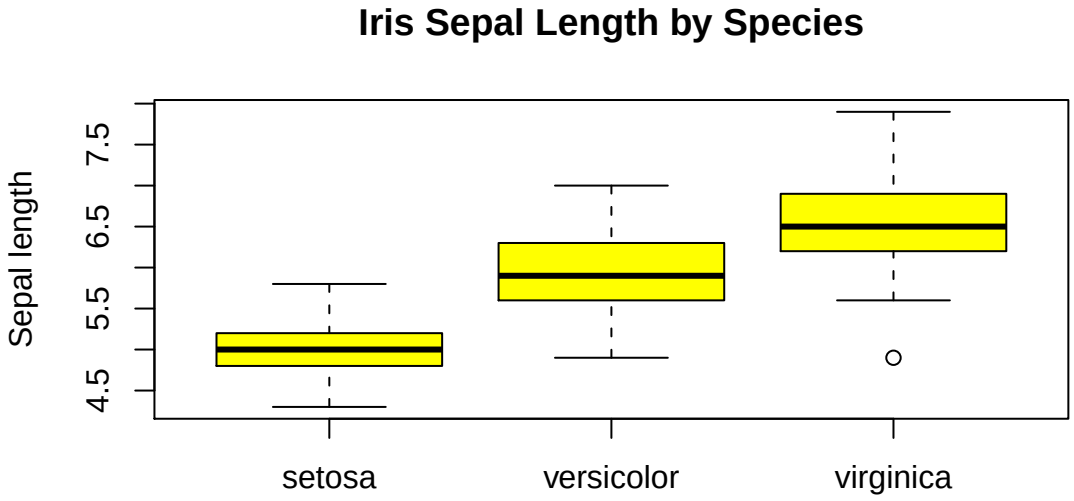



```
barplot(xtabs(~sex + Political04, data=pol), legend=c("Female","Male"), beside=T)
```



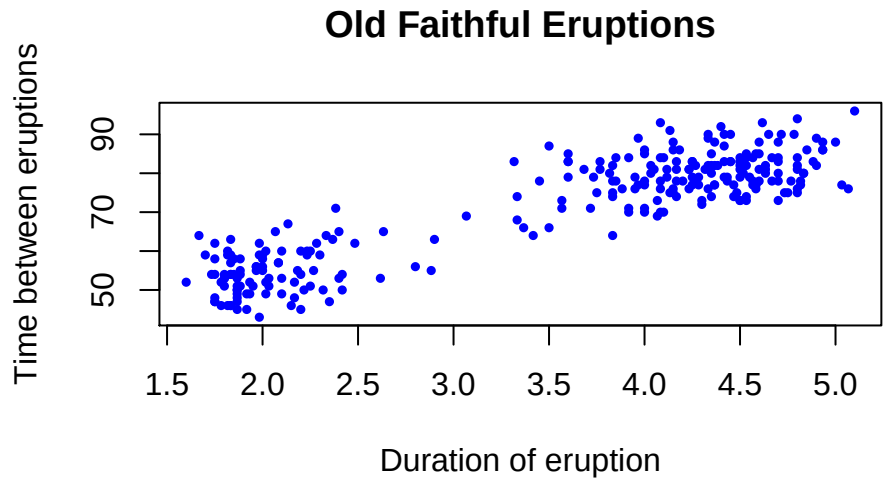
`boxplot()`

```
data(iris)
boxplot(iris$Sepal.Length)
boxplot(iris$Sepal.Length, col="yellow")
boxplot(Sepal.Length ~ Species, data=iris)
boxplot(Sepal.Length ~ Species, data=iris, col="yellow", ylab="Sepal length",main="Iris Sepal Length by Species")
```



`plot()`

```
data(faithful)
plot(waiting~eruptions,data=faithful)
plot(waiting~eruptions,data=faithful,cex=.5)
plot(waiting~eruptions,data=faithful,pch=6)
plot(waiting~eruptions,data=faithful,pch=19)
plot(waiting~eruptions,data=faithful,cex=.5,pch=19,col="blue")
plot(waiting~eruptions, data=faithful, cex=.5, pch=19, col="blue", main="Old Faithful Eruptions",
     ylab="Wait time between eruptions", xlab="Duration of eruption")
```

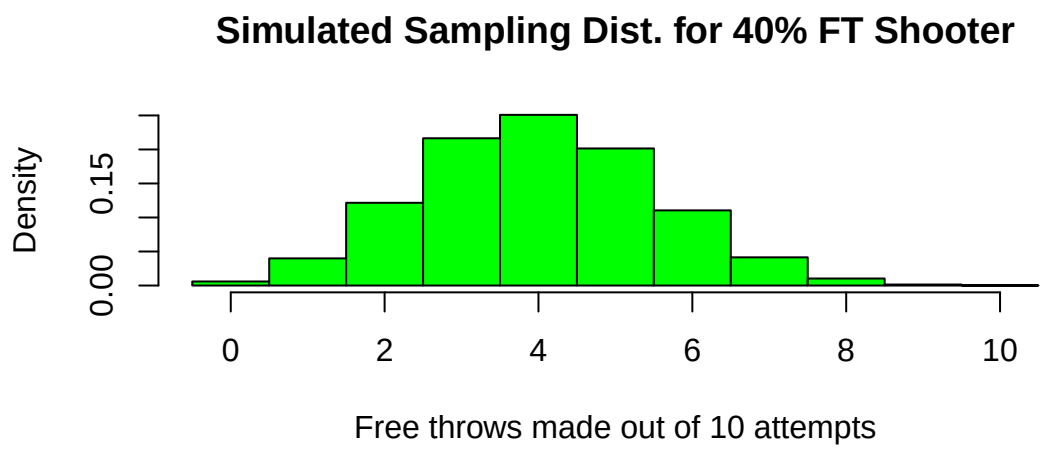


`sample()`

```
> sample(c("Heads","Tails"), size=1)
[1] "Heads"
> sample(c("Heads","Tails"), size=10, replace=T)
 [1] "Heads" "Heads" "Heads" "Tails" "Tails" "Tails" "Tails" "Tails" "Tails" "Heads"
> sample(c(0, 1), 10, replace=T)
 [1] 1 0 0 1 1 0 0 1 0 0
> sum(sample(1:6, 2, replace=T))
[1] 10
> sample(c(0, 1), prob=c(.25,.75), size=10, replace=T)
 [1] 1 1 1 0 1 1 1 1 1 1
> sample(c(rep(1,13),rep(0,39)), size=5, replace=F)
[1] 0 0 0 0 0
```

`replicate()`

```
> sample(c("Heads","Tails"), 2, replace=T)
[1] "Tails" "Heads"
> replicate(5, sample(c("Heads","Tails"), 2, replace=T))
     [,1]    [,2]    [,3]    [,4]    [,5]
[1,] "Heads" "Tails" "Heads" "Tails" "Heads"
[2,] "Heads" "Tails" "Heads" "Heads" "Heads"
> ftCount = replicate(100000, sum(sample(c(0, 1), 10, rep=T, prob=c(.6, .4))))
> hist(ftCount, freq=F, breaks=-0.5:10.5, xlab="Free throws made out of 10 attempts",
+      main="Simulated Sampling Dist. for 40% FT Shooter", col="green")
```



`dbinom()`, `pbinom()`, `qbinom()`, `rbinom()`, `binom.test()`, `prop.test()`

```
> dbinom(0, 5, .5)      # probability of 0 heads in 5 flips

[1] 0.03125

> dbinom(0:5, 5, .5)    # full probability dist. for 5 flips

[1] 0.03125 0.15625 0.31250 0.31250 0.15625 0.03125

> sum(dbinom(0:2, 5, .5))    # probability of 2 or fewer heads in 5 flips

[1] 0.5

> pbinom(2, 5, .5)    # same as last line

[1] 0.5

> flip5 = replicate(10000, sum(sample(c("H","T"), 5, rep=T)=="H"))
> table(flip5) / 10000   # distribution (simulated) of count of heads in 5 flips

flip5
     0      1      2      3      4      5
0.0310 0.1545 0.3117 0.3166 0.1566 0.0296

> table(rbinom(10000, 5, .5)) / 10000    # shorter version of previous 2 lines

     0      1      2      3      4      5
0.0304 0.1587 0.3087 0.3075 0.1634 0.0313

> qbinom(seq(0,1,.2), 50, .2)    # approx. 0/.2/.4/.6/.8/1-quantiles in Binom(50,.2) distribution

[1]  0  8  9 11 12 50

> binom.test(29, 200, .21)    # inference on sample with 29 successes in 200 trials

        Exact binomial test

data:  29 and 200
number of successes = 29, number of trials = 200, p-value = 0.02374
alternative hypothesis: true probability of success is not equal to 0.21
95 percent confidence interval:
 0.09930862 0.20156150
sample estimates:
probability of success
                 0.145

> prop.test(29, 200, .21)    # inference on same sample, using normal approx. to binomial

        1-sample proportions test with continuity correction

data:  29 out of 200, null probability 0.21
X-squared = 4.7092, df = 1, p-value = 0.03
alternative hypothesis: true p is not equal to 0.21
95 percent confidence interval:
 0.1007793 0.2032735
sample estimates:
    p
0.145
```

pchisq(), qchisq(), chisq.test()

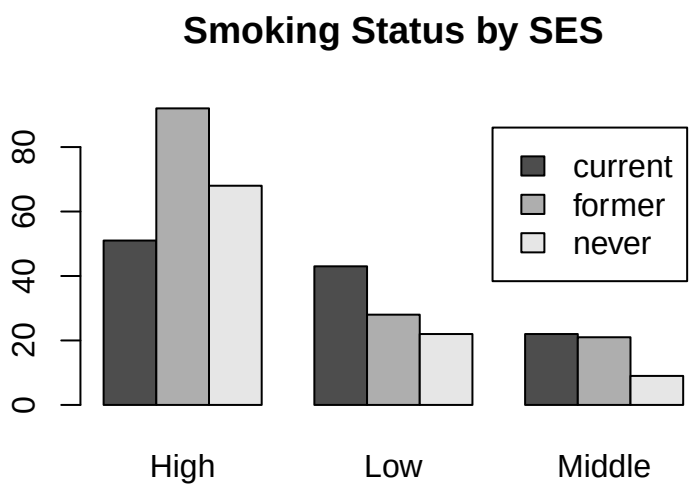
```
> 1 - pchisq(3.1309, 5)   # gives P-value associated with X-squared stat 3.1309 when df=5

[1] 0.679813

> pchisq(3.1309, df=5, lower.tail=F)   # same as above

[1] 0.679813

> qchisq(c(.001,.005,.01,.025,.05,.95,.975,.99,.995,.999), 2)  # gives critical values like Table A

 [1]  0.002001001  0.010025084  0.020100672  0.050635616  0.102586589  5.991464547  7.377758908
 [8]  9.210340372 10.596634733 13.815510558

> qchisq(c(.999,.995,.99,.975,.95,.05,.025,.01,.005,.001), 2, lower.tail=F)  # same as above

 [1]  0.002001001  0.010025084  0.020100672  0.050635616  0.102586589  5.991464547  7.377758908
 [8]  9.210340372 10.596634733 13.815510558

> observedCounts = c(35, 27, 33, 40, 47, 51)
> claimedProbabilities = c(.13, .13, .14, .16, .24, .20)
> chisq.test(observedCounts, p=claimedProbabilities)   # goodness-of-fit test, assumes df = n-1

        Chi-squared test for given probabilities

data:  observedCounts
X-squared = 3.1309, df = 5, p-value = 0.6798
```

addmargins()

```
> blood = read.csv("http://www.calvin.edu/~scofield/data/comma/blood.csv")
> t = table(blood$Rh, blood$type)
> addmargins(t)        # to add both row/column totals

       A  AB   B   O Sum
  Neg  6   1   2   7  16
  Pos 34   3   9  38  84
  Sum 40   4  11  45 100

> addmargins(t, 1)     # to add only column totals

      A AB  B  O
  Neg  6  1  2  7
  Pos 34  3  9 38
  Sum 40  4 11 45

> addmargins(t, 2)     # to add only row totals

      A AB  B  O Sum
  Neg  6  1  2  7  16
  Pos 34  3  9 38  84
```

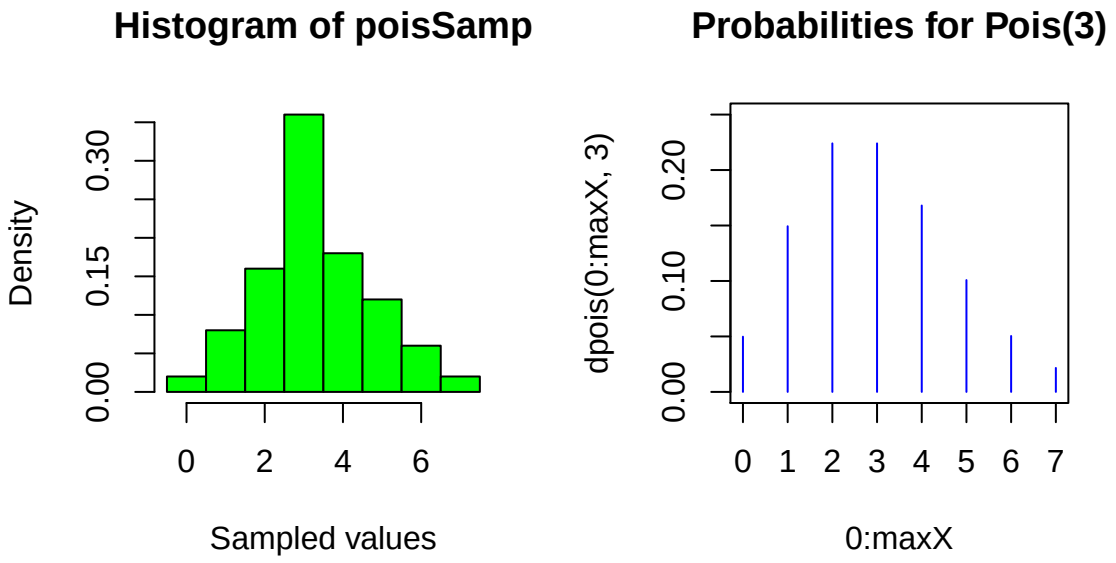
`prop.table()`

```
> smoke = matrix(c(51,43,22,92,28,21,68,22,9),ncol=3,byrow=TRUE)
> colnames(smoke) = c("High","Low","Middle")
> rownames(smoke) = c("current","former","never")
> smoke = as.table(smoke)
> smoke

        High Low Middle
current   51  43     22
former    92  28     21
never     68  22      9

> summary(smoke)

Number of cases in table: 356
Number of factors: 2
Test for independence of all factors:
        Chisq = 18.51, df = 4, p-value = 0.0009808

> prop.table(smoke)

              High        Low     Middle
current 0.14325843 0.12078652 0.06179775
former  0.25842697 0.07865169 0.05898876
never   0.19101124 0.06179775 0.02528090

> prop.table(smoke, 1)

             High       Low    Middle
current 0.4396552 0.3706897 0.1896552
former  0.6524823 0.1985816 0.1489362
never   0.6868687 0.2222222 0.0909091

> barplot(smoke,legend=T,beside=T,main='Smoking Status by SES')
```



`par()`

```
> par(mfrow = c(1,2))      # set figure so next two plots appear side-by-side
> poisSamp = rpois(50, 3)    # Draw sample of size 50 from Pois(3)
> maxX = max(poisSamp)     # will help in setting horizontal plotting region
> hist(poisSamp, freq=F, breaks=-.5:(maxX+.5), col="green", xlab="Sampled values")
> plot(0:maxX, dpois(0:maxX, 3), type="h", ylim=c(0,.25), col="blue", main="Probabilities for Pois(3)")
```



`fisher.test()`

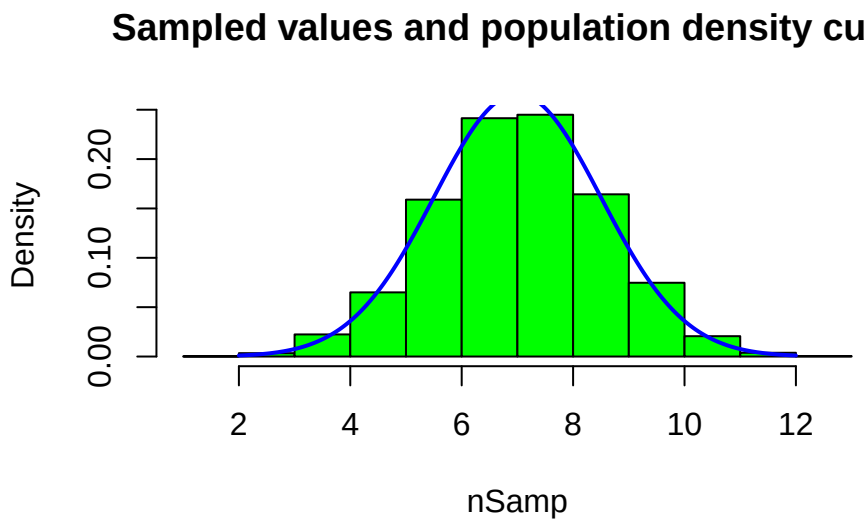
```
> blood = read.csv("http://www.calvin.edu/~scofield/data/comma/blood.csv")
> tblood = xtabs(~Rh + type, data=blood)
> tblood      # contingency table for blood type and Rh factor

     type
Rh     A AB  B  O
  Neg  6  1  2  7
  Pos 34  3  9 38

> chisq.test(tblood)

        Pearson's Chi-squared test

data:  tblood
X-squared = 0.3164, df = 3, p-value = 0.957

> fisher.test(tblood)

        Fisher's Exact Test for Count Data

data:  tblood
p-value = 0.8702
alternative hypothesis: two.sided
```

`dpois()`, `ppois()`

```
> dpois(2:7, 4.2)   # probabilities of 2, 3, 4, 5, 6 or 7 successes in Pois(4.211)
[1] 0.13226099 0.18516538 0.19442365 0.16331587 0.11432111 0.06859266
> ppois(1, 4.2)   # probability of 1 or fewer successes in Pois(4.2); same as sum(dpois(0:1, 4.2))
[1] 0.077977
> 1 - ppois(7, 4.2)   # probability of 8 or more successes in Pois(4.2)
[1] 0.06394334
```

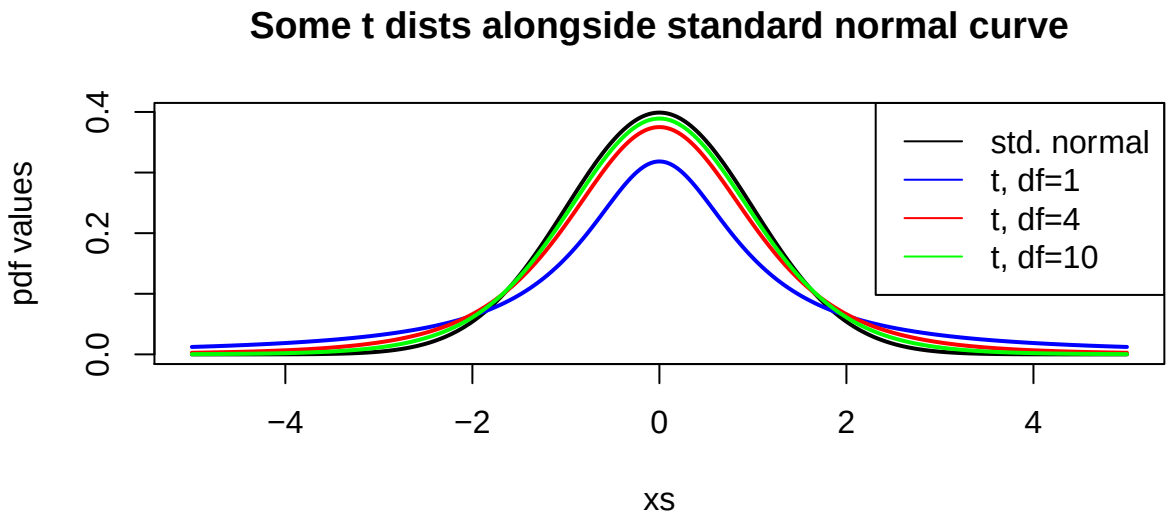
`pnorm()` `qnorm()`, `rnorm()`, `dnorm()`

```
> pnorm(17, 19, 3)     # gives Prob[X < 17], when X ~ Norm(19, 3)
[1] 0.2524925
> qnorm(c(.95, .975, .995))       # obtain z* critical values for 90, 95, 99% CIs
[1] 1.644854 1.959964 2.575829
> nSamp = rnorm(10000, 7, 1.5)    # draw random sample from Norm(7, 1.5)
> hist(nSamp, freq=F, col="green", main="Sampled values and population density curve")
> xs = seq(2, 12, .05)
> lines(xs, dnorm(xs, 7, 1.5), lwd=2, col="blue")
```



qt(), pt(), rt(), dt()

```
> qt(c(.95, .975, .995), df=9)    # critical values for 90, 95, 99% CIs for means

[1] 1.833113 2.262157 3.249836

> pt(-2.1, 11)     # gives Prob[T < -2.1] when df = 11

[1] 0.02980016

> tSamp = rt(50, 11)     # takes random sample of size 50 from t-dist with 11 dfs
> # code for comparing several t distributions to standard normal distribution
> xs = seq(-5,5,.01)
> plot(xs, dnorm(xs), type="l", lwd=2, col="black", ylab="pdf values",
+      main="Some t dists alongside standard normal curve")
> lines(xs, dt(xs, 1), lwd=2, col="blue")
> lines(xs, dt(xs, 4), lwd=2, col="red")
> lines(xs, dt(xs, 10), lwd=2, col="green")
> legend("topright",col=c("black","blue","red","green"),
+        legend=c("std. normal","t, df=1","t, df=4","t, df=10"), lty=1)
```



by()

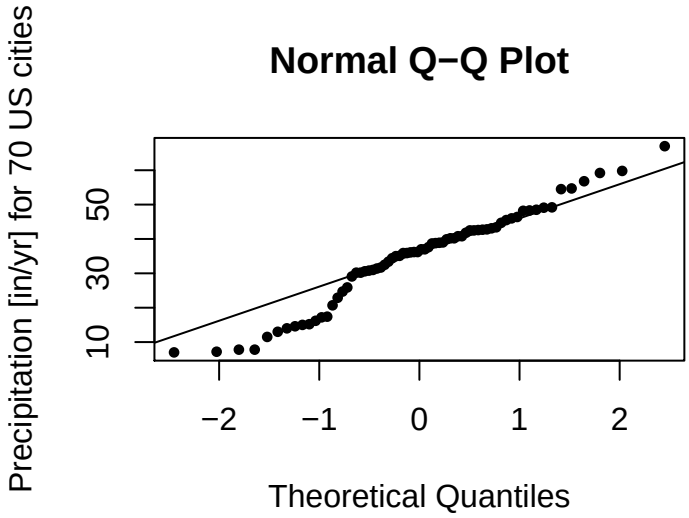
```
> data(warpbreaks)
> by(warpbreaks$breaks, warpbreaks$tension, mean)

warpbreaks$tension: L
[1] 36.38889
------------------------------------------------------------------------
warpbreaks$tension: M
[1] 26.38889
------------------------------------------------------------------------
warpbreaks$tension: H
[1] 21.66667
```

`t.test()`

```
> data(sleep)
> t.test(extra ~ group, data=sleep)     # 2-sample t with group id column

        Welch Two Sample t-test

data:  extra by group
t = -1.8608, df = 17.776, p-value = 0.0794
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -3.3654832  0.2054832
sample estimates:
mean in group 1 mean in group 2
           0.75            2.33

> sleepGrp1 = sleep$extra[sleep$group==1]
> sleepGrp2 = sleep$extra[sleep$group==2]
> t.test(sleepGrp1, sleepGrp2, conf.level=.99)       # 2-sample t, data in separate vectors

        Welch Two Sample t-test

data:  sleepGrp1 and sleepGrp2
t = -1.8608, df = 17.776, p-value = 0.0794
alternative hypothesis: true difference in means is not equal to 0
99 percent confidence interval:
 -4.027633  0.867633
sample estimates:
mean of x mean of y
     0.75      2.33
```

`qqnorm()`, `qqline()`

```
> qqnorm(precip, ylab = "Precipitation [in/yr] for 70 US cities", pch=19, cex=.6)
> qqline(precip)    # Is this line helpful?  Is it the one you would eyeball?
```



power.t.test()

```
> power.t.test(n=20, delta=.1, sd=.4, sig.level=.05)   # tells how much power at these settings

     Two-sample t test power calculation

              n = 20
          delta = 0.1
             sd = 0.4
      sig.level = 0.05
          power = 0.1171781
    alternative = two.sided

 NOTE: n is number in *each* group

> power.t.test(delta=.1, sd=.4, sig.level=.05, power=.8)   # tells sample size needed for desired power

     Two-sample t test power calculation

              n = 252.1281
          delta = 0.1
             sd = 0.4
      sig.level = 0.05
          power = 0.8
    alternative = two.sided

 NOTE: n is number in *each* group
```

anova()

```
require(lattice)
require(abd)
data(JetLagKnees)
xyplot(shift ~ treatment, JetLagKnees, type=c('p','a'), col="navy", pch=19, cex=.5)
anova( lm( shift ~ treatment, JetLagKnees ) )

Analysis of Variance Table

Response: shift
          Df Sum Sq Mean Sq F value   Pr(>F)
treatment  2 7.2245  3.6122  7.2894 0.004472 **
Residuals 19 9.4153  0.4955
---
Signif. codes:  0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1
```