

Table of Useful R commands

Command	Purpose	Command	Purpose
<code>help()</code>	Obtain documentation for a given R command	<code>plot()</code>	Produces a scatterplot
<code>example()</code>	View some examples on the use of a command	<code>xyplot()</code>	Lattice command for producing a scatterplot
<code>c()</code> , <code>scan()</code>	Enter data manually to a vector in R	<code>lm()</code>	Determine the least-squares regression line
<code>seq()</code>	Make arithmetic progression vector	<code>anova()</code>	Analysis of variance (can use on results of <code>lm()</code>)
<code>rep()</code>	Make vector of repeated values	<code>predict()</code>	Obtain predicted values from linear model
<code>data()</code>	Load (often into a <code>data.frame</code>) built-in dataset	<code>nls()</code>	estimate parameters of a nonlinear model
<code>View()</code>	View dataset in a spreadsheet-type format	<code>residuals()</code>	gives (observed - predicted) for a model fit to data
<code>str()</code>	Display internal structure of an R object	<code>sample()</code>	take a sample from a vector of data
<code>read.csv()</code> , <code>read.table()</code>	Load into a <code>data.frame</code> an existing data file	<code>replicate()</code>	repeat some process a set number of times
<code>library()</code> , <code>require()</code>	Make available an R add-on package	<code>cumsum()</code>	produce running total of values for input vector
<code>dim()</code>	See dimensions (# of rows/cols) of <code>data.frame</code>	<code>ecdf()</code>	builds empirical cumulative distribution function
<code>length()</code>	Give length of a vector	<code>dbinom()</code> , etc.	tools for binomial distributions
<code>ls()</code>	Lists memory contents	<code>dpois()</code> , etc.	tools for Poisson distributions
<code>rm()</code>	Removes an item from memory	<code>pnorm()</code> , etc.	tools for normal distributions
<code>names()</code>	Lists names of variables in a <code>data.frame</code>	<code>qt()</code> , etc.	tools for student <i>t</i> distributions
<code>hist()</code>	Command for producing a histogram	<code>pchisq()</code> , etc.	tools for chi-square distributions
<code>histogram()</code>	Lattice command for producing a histogram	<code>binom.test()</code>	hypothesis test and confidence interval for 1 proportion
<code>stem()</code>	Make a stem plot	<code>prop.test()</code>	inference for 1 proportion using normal approx.
<code>table()</code>	List all values of a variable with frequencies	<code>chisq.test()</code>	carries out a chi-square test
<code>xtabs()</code>	Cross-tabulation tables using formulas	<code>fisher.test()</code>	Fisher test for contingency table
<code>mosaicplot()</code>	Make a mosaic plot	<code>t.test()</code>	student <i>t</i> test for inference on population mean
<code>cut()</code>	Groups values of a variable into larger bins	<code>qqnorm()</code> , <code>qqline()</code>	tools for checking normality
<code>mean()</code> , <code>median()</code>	Identify “center” of distribution	<code>addmargins()</code>	adds marginal sums to an existing table
<code>by()</code>	apply function to a column split by factors	<code>prop.table()</code>	compute proportions from a contingency table
<code>summary()</code>	Display 5-number summary and mean	<code>par()</code>	query and edit graphical settings
<code>var()</code> , <code>sd()</code>	Find variance, sd of values in vector	<code>power.t.test()</code>	power calculations for 1- and 2-sample <i>t</i>
<code>sum()</code>	Add up all values in a vector	<code>anova()</code>	compute analysis of variance table for fitted model
<code>quantile()</code>	Find the position of a quantile in a dataset		
<code>barplot()</code>	Produces a bar graph		
<code>barchart()</code>	Lattice command for producing bar graphs		
<code>boxplot()</code>	Produces a boxplot		
<code>bwplot()</code>	Lattice command for producing boxplots		

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 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()

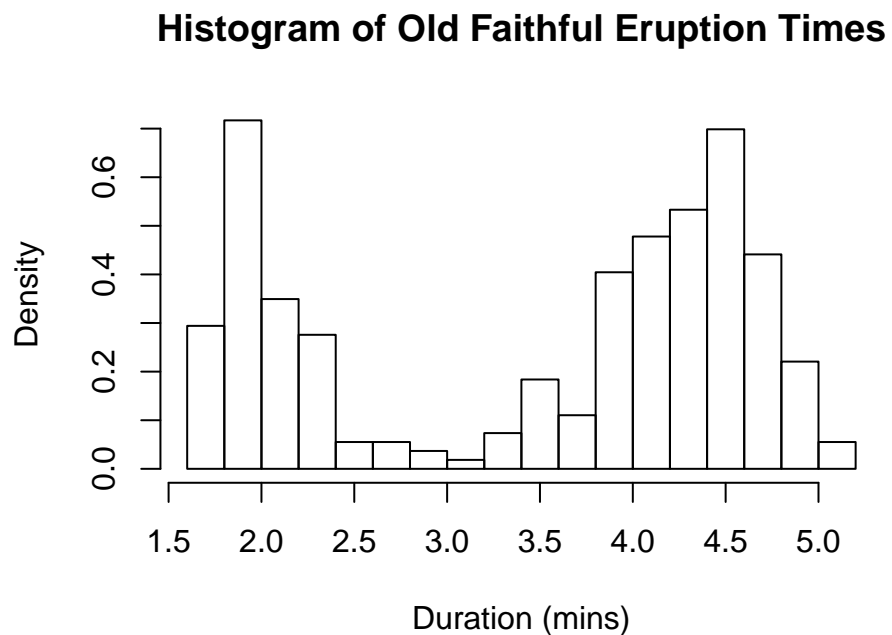
[1] "faithful" "heartDeck" "iris"      "LakeHuron" "names"     "newVector" "Puromycin" "x"
[9] "y"

> 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

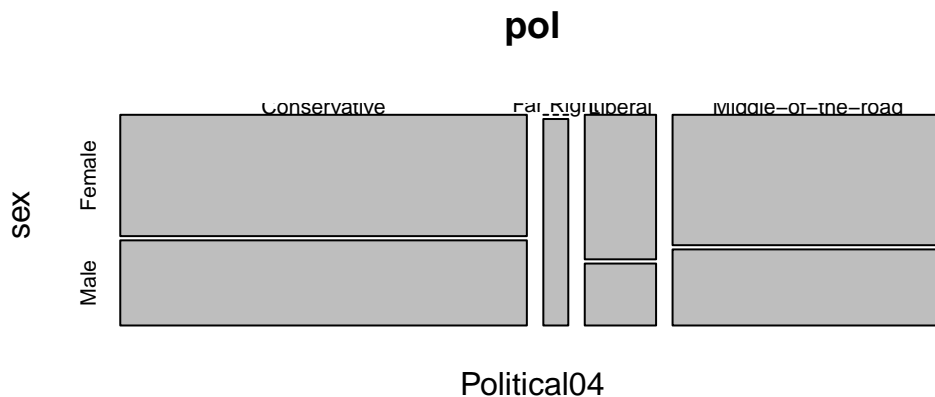
> xtabs(~sex, data=pol)

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)))

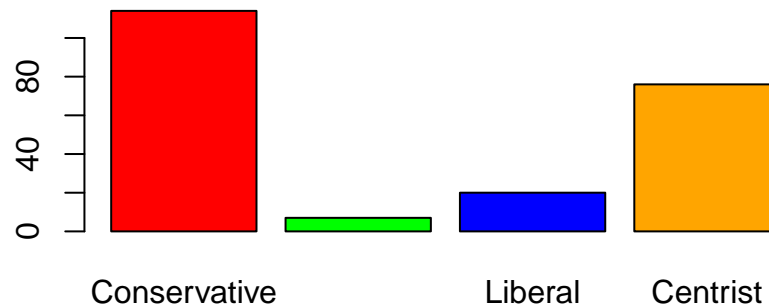
 (0,5] (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] (50,55] (55,60]
      4      7      6      3      8      0      4      2      1      1      0      2
(60,65]
      1

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

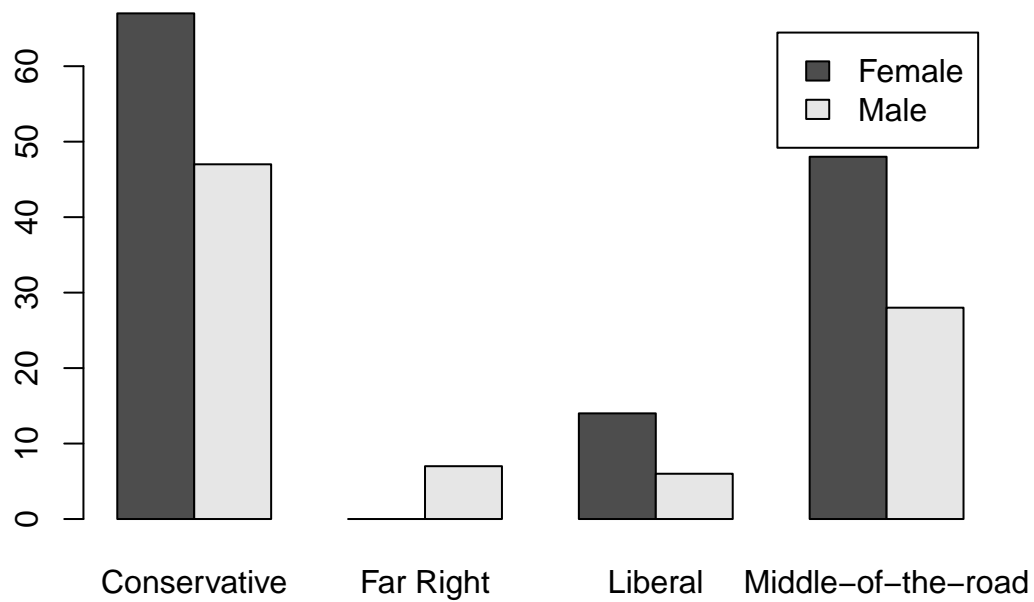
fiveYrLevels
 (0,5] (5,10] (10,15] (15,20] (20,25] (25,30] (30,35] (35,40] (40,45] (45,50] (50,55] (55,60]
      4      7      6      3      8      0      4      2      1      1      0      2
(60,65]
      1
```

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"))
```



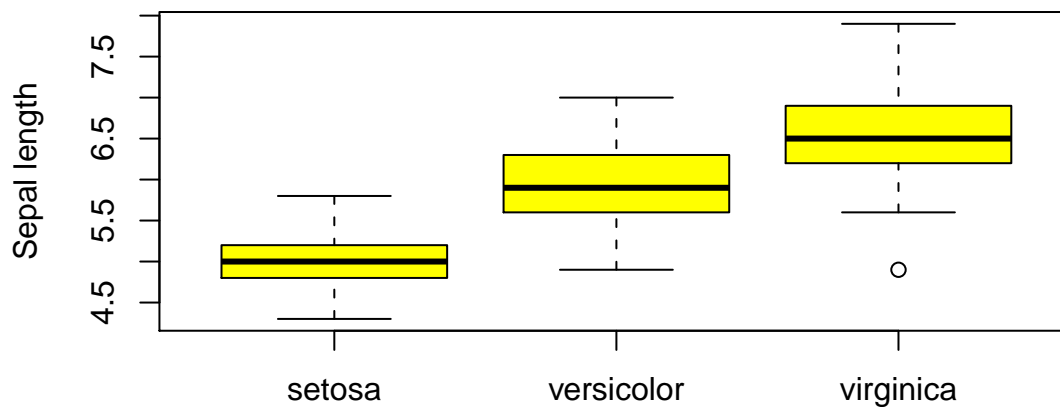
```
barplot(xtabs(~sex + Political04, data=pol), legend=c("Female", "Male"), beside=T)
```



```
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")
```

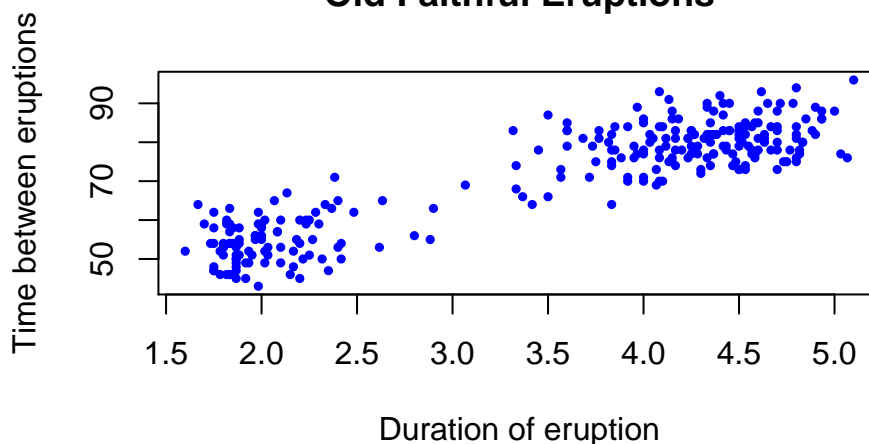
Iris Sepal Length by Species



```
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")
```

Old Faithful Eruptions

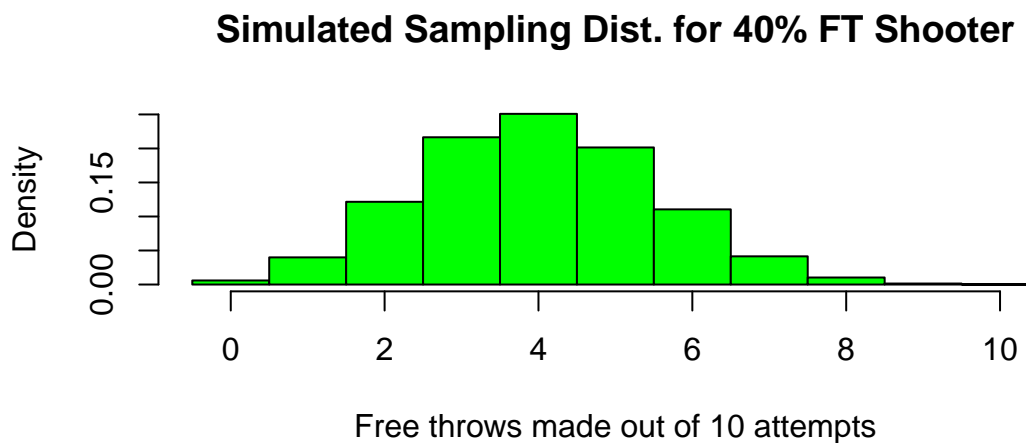


sample()

```
> 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

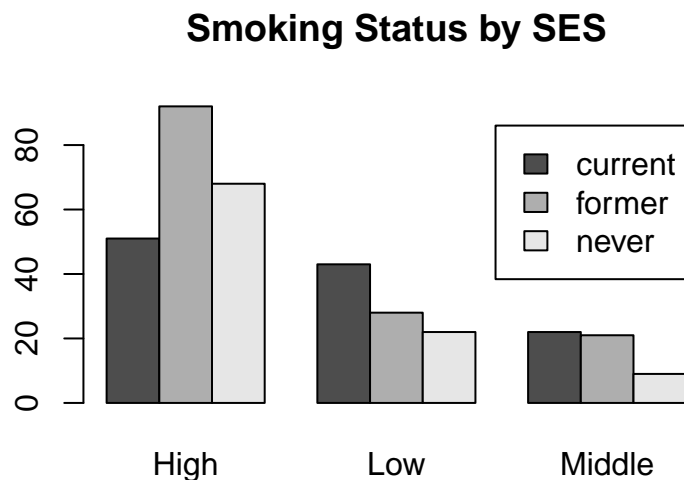
> prop.table(smoke)

      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

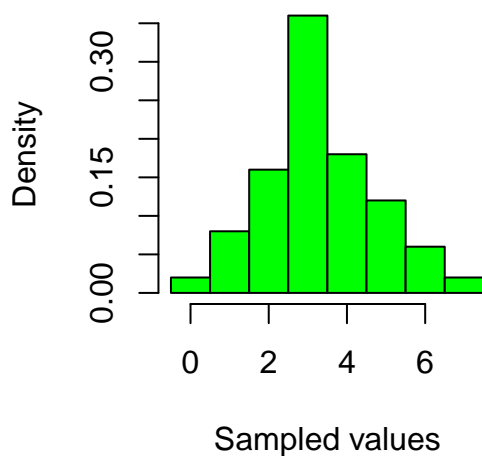
> barplot(smoke,legend=T,beside=T,main='Smoking Status by SES')
```



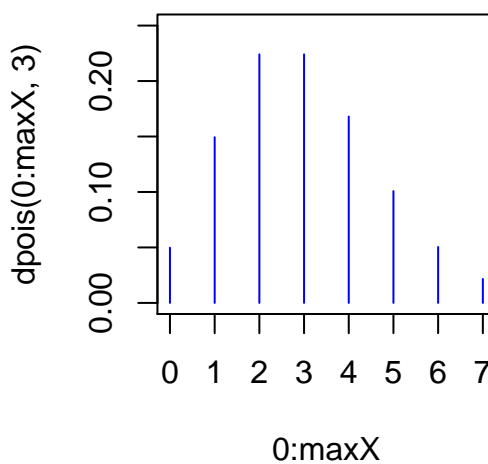
par()

```
> 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)")
```

Histogram of poisSamp



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
```

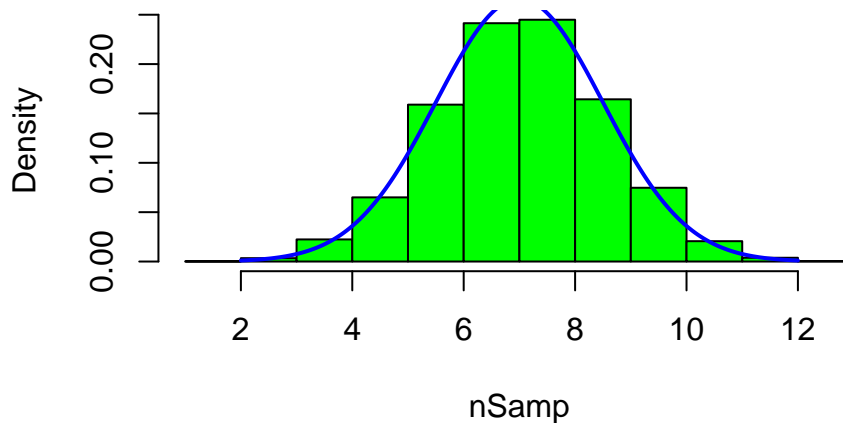
pnorm(), qnorm(), rnorm(), dnorm()

```
> 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")
```

Sampled values and population density curve



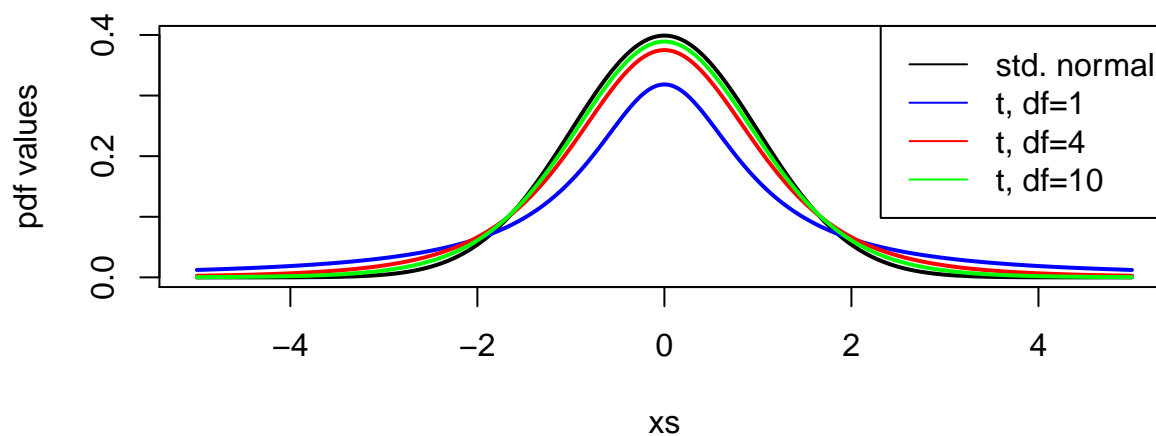
qt(), pt(), rt(), dt()

```
> 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)
```

Some t dists alongside standard normal curve



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

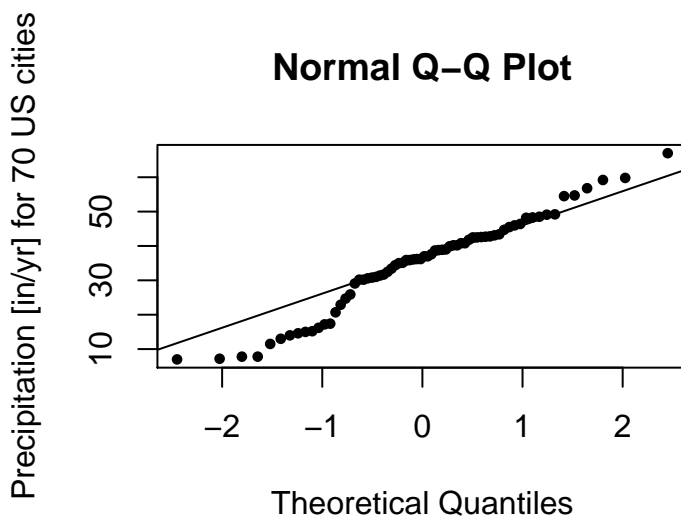
> sleepGrp1 = sleep$extra[sleep$group==1]
> sleepGrp2 = sleep$extra[sleep$group==2]
> t.test(sleepGrp1, sleepGrp2, conf.level=.99)    # 2-sample t, data in separate vectors

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
```

