Basic statistics

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Contents

In this course we'll review R functions for generating basic descriptive and inferential statistics.

1 Descriptive statistics

1.1 Methodology

Arithmetic mean of a single sample

The mean is the sum of the numbers $\sum y$ divided by the number of numbers $n = \sum 1$ (summing over the number of numbers in the vector called y).

```
arithmetic.mean <- function(x) sum(x)/length(x)
x<-c(1:100)
arithmetic.mean(x)

## [1] 50.5

mean(x)

## [1] 50.5

salary=c(2000,2100,2200,2300,2350,2450,2500,2700,2900,2850,3500,3800,2600,
         3000,3300,3200,4000,3100,4200)
mean(salary)

## [1] 2897.368

mean(salary,trim=0.2)

## [1] 2826.923

mean(salary,trim=0.5)

## [1] 2850
```

Median of a single sample

The median (or 50th percentile) is the middle value of the sorted values of a vector of numbers.

```
sort(x)[ceiling(length(x)/2)]

## [1] 50
```

There is slight hitch here, of course, because if the vector contains an even number of numbers, then there is no middle value. The logic here is that we need to work out the arithmetic average of the two values of y on either side of the middle. The question now arises as to how we know, in general, whether the vector y contains an odd or an even number of numbers, so that we can decide which of the two methods to use.

```
med <- function(x) {
odd.even <- length(x)%%2
if (odd.even == 0) (sort(x)[length(x)/2]+sort(x)[1+ length(x)/2])/2
else
```

```
sort(x)[ceiling(length(x)/2)]
}
med(x)

## [1] 50.5

median(x)

## [1] 50.5
```

You could write the same function in a single (long) line by using ifelse instead of if.

```
med <- function(x) ifelse(length(x)%%2==1, sort(x)[ceiling(length(x)/2)],
       (sort(x)[length(x)/2]+sort(x)[1+ length(x)/2])/2 )
salary=c(2000,2100,2200,2300,2350,2450,2500,2700,2900,2850,3500,3800,2600,
         3000,3300,3200,4000,3100,4200)
mean(salary)

## [1] 2897.368

med(salary)

## [1] 2850

salary=c(2000,2100,2200,2300,2350,2450,2500,2700,2900,2850,3500,3800,2600,
         3000,3300,3200,4000,3100,15000)
mean(salary)

## [1] 3465.789

med(salary)

## [1] 2850
```

Geometric mean

For processes that change multiplicatively rather than additively, neither the arithmetic mean nor the median is an ideal measure of central tendency. Under these conditions, the appropriate measure is the geometric mean.

$$\hat{y} = \sqrt[n]{\prod y}$$

Harmonic mean

Consider the following problem. An elephant has a territory which is a square of side 2 km. Each morning, the elephant walks the boundary of this territory. He begins the day at a sedate pace, walking the first side of the territory at a speed of 1 km/hr. On the second side, he has sped up to 2 km/hr. By the third side he has accelerated to an impressive 4 km/hr, but this so wears him out, that he has to return on the final side at a sluggish 1 km/hr. So what is his average speed over the ground? You might say he travelled at 1, 2, 4 and 1 km/hr so the average speed is $(1 + 2 + 4 + 1)/4 = 8/4 = 2$ km/hr. But that is wrong. Can you see how to work out the right answer? Recall that velocity is defined as distance travelled divided by time taken. The distance travelled is easy: it is just $4 \times 2 = 8$ km. The time taken is a bit harder. The first edge was 2 km long, and travelling at 1 km/hr this

must have taken 2 hr. The second edge was 2 km long, and travelling at 2 km/hr this must have taken 1 hr. The third edge was 2 km long and travelling at 4 km/hr this must have taken 0.5 hr. The final edge was 2 km long and travelling at 1 km/hr this must have taken 2 hr. So the total time taken was $2 + 1 + 0.5 + 2 = 5.5$ hr. So the average speed is not 2 km/hr but $8/5.5 = 1.4545$ km/hr.

$$\tilde{y} = \frac{1}{(\sum(1/y))/n}$$

```
harmonic <- function (x) 1/mean(1/x)
harmonic(c(1,2,4,1))

## [1] 1.454545
```

Variance

A measure of variability is perhaps the most important quantity in statistical analysis. The greater the variability in the data, the greater will be our uncertainty in the values of parameters estimated from the data, and the less will be our ability to distinguish between competing hypotheses about the data.

The variance of a sample is measured as a function of 'the sum of the squares of the difference between the data and the arithmetic mean'. This important quantity is called the 'sum of squares':

$$SS = \sum(y - \bar{y})^2$$

To complete our calculation of the variance we need the degrees of freedom (d.f.). This important concept in statistics is defined as follows:

$$d.f. = n - k$$

which is the sample size, n, minus the number of parameters, k, estimated from the data. For the variance, we have estimated one parameter from the data, $\bar{}$y, and so there are $n - 1$ degrees of freedom. In a linear regression, we estimate two parameters from the data, the slope and the intercept, and so there are $n - 2$ degrees of freedom in a regression analysis.

We always calculate variance as

$$\text{variance} = \frac{\text{sum of squares}}{\text{degrees of freedom}}$$

```
y <- c(13,7,5,12,9,15,6,11,9,7,12)
variance <- function(x) sum((x - mean(x))^2)/(length(x)-1)
variance(y)

## [1] 10.25455

var(y)

## [1] 10.25455
```

Exercise

Write a funtion to calculate mean, variance, standard deviation, median, variable coefficient, skewness and kurtosis of data.

Variance ratio test

How do we know if two variances are significantly different from one another? Write a funtion to calculate statistic of Variance ratio test.

1.2 Basic method

First, we'll look at measures of central tendency, variability, and distribution shape for continuous variables. For illustrative purposes, we'll use several of the variables from the Motor Trend Car Road Tests (mtcars) dataset you first saw in chapter 1. Our focus will be on miles per gallon (mpg), horsepower (hp), and weight (wt). install.packages("pastecs"), install.packages("Hmisc")

```
vars <- c("mpg", "hp", "wt")
head(mtcars[vars])
```

```
##                    mpg  hp    wt
## Mazda RX4         21.0 110 2.620
## Mazda RX4 Wag     21.0 110 2.875
## Datsun 710        22.8  93 2.320
## Hornet 4 Drive    21.4 110 3.215
## Hornet Sportabout 18.7 175 3.440
## Valiant           18.1 105 3.460
```

```
summary(mtcars[vars])
```

```
##       mpg              hp              wt
##  Min.   :10.40   Min.   : 52.0   Min.   :1.513
##  1st Qu.:15.43   1st Qu.: 96.5   1st Qu.:2.581
##  Median :19.20   Median :123.0   Median :3.325
##  Mean   :20.09   Mean   :146.7   Mean   :3.217
##  3rd Qu.:22.80   3rd Qu.:180.0   3rd Qu.:3.610
##  Max.   :33.90   Max.   :335.0   Max.   :5.424
```

```
library(Hmisc)
describe(mtcars[vars])
```

```
## mtcars[vars]
##
##  3  Variables      32  Observations
## ---------------------------------------------------------------------------
## mpg
##       n missing  unique    Info    Mean     .05     .10     .25     .50
##      32       0      25       1   20.09   12.00   14.34   15.43   19.20
##     .75     .90     .95
##   22.80   30.09   31.30
##
## lowest : 10.4 13.3 14.3 14.7 15.0, highest: 26.0 27.3 30.4 32.4 33.9
## ---------------------------------------------------------------------------
## hp
##       n missing  unique    Info    Mean     .05     .10     .25     .50
##      32       0      22       1   146.7   63.65   66.00   96.50  123.00
##     .75     .90     .95
##  180.00  243.50  253.55
```

```
##
## lowest :  52  62  65  66  91, highest: 215 230 245 264 335
## ---------------------------------------------------------------------------
## wt
##       n missing  unique    Info    Mean     .05     .10     .25     .50
##      32       0      29       1   3.217   1.736   1.956   2.581   3.325
##     .75     .90     .95
##   3.610   4.048   5.293
##
## lowest : 1.513 1.615 1.835 1.935 2.140
## highest: 3.845 4.070 5.250 5.345 5.424
## ---------------------------------------------------------------------------
```

```
library(pastecs)
stat.desc(mtcars[vars])
```

```
##                      mpg           hp          wt
## nbr.val       32.0000000   32.0000000  32.0000000
## nbr.null       0.0000000    0.0000000   0.0000000
## nbr.na         0.0000000    0.0000000   0.0000000
## min           10.4000000   52.0000000   1.5130000
## max           33.9000000  335.0000000   5.4240000
## range         23.5000000  283.0000000   3.9110000
## sum          642.9000000 4694.0000000 102.9520000
## median        19.2000000  123.0000000   3.3250000
## mean          20.0906250  146.6875000   3.2172500
## SE.mean        1.0654240   12.1203173   0.1729685
## CI.mean.0.95   2.1729465   24.7195501   0.3527715
## var           36.3241028 4700.8669355   0.9573790
## std.dev        6.0269481   68.5628685   0.9784574
## coef.var       0.2999881    0.4674077   0.3041285
```

1.3 Descriptive statistics by group

When comparing groups of individuals or observations, the focus is usually on the descriptive statistics of each group, rather than the total sample.

```
aggregate(mtcars[vars], by = list(am = mtcars$am), mean)
```

```
##   am      mpg       hp       wt
## 1  0 17.14737 160.2632 3.768895
## 2  1 24.39231 126.8462 2.411000
```

```
aggregate(mtcars[vars], by = list(am = mtcars$am), sd)
```

```
##   am      mpg       hp        wt
## 1  0 3.833966 53.90820 0.7774001
## 2  1 6.166504 84.06232 0.6169816
```

Unfortunately, aggregate() only allows you to use single value functions such as mean, standard deviation, and the like in each call. It won't return several statistics at once. install.packages("psych")

```
library(psych)
describeBy(mtcars[vars], mtcars$am)

## group: 0
##     vars  n   mean    sd median trimmed   mad   min    max  range  skew
## mpg    1 19  17.15  3.83  17.30   17.12  3.11 10.40  24.40  14.00  0.01
## hp     2 19 160.26 53.91 175.00  161.06 77.10 62.00 245.00 183.00 -0.01
## wt     3 19   3.77  0.78   3.52    3.75  0.45  2.46   5.42   2.96  0.98
##     kurtosis    se
## mpg    -0.80  0.88
## hp     -1.21 12.37
## wt      0.14  0.18
## ------------------------------------------------------------
## group: 1
##     vars  n   mean    sd median trimmed   mad   min    max  range skew
## mpg    1 13  24.39  6.17  22.80   24.38  6.67 15.00  33.90  18.90 0.05
## hp     2 13 126.85 84.06 109.00  114.73 63.75 52.00 335.00 283.00 1.36
## wt     3 13   2.41  0.62   2.32    2.39  0.68  1.51   3.57   2.06 0.21
##     kurtosis    se
## mpg    -1.46  1.71
## hp      0.56 23.31
## wt     -1.17  0.17
```

1.4 An advanced example

The describe.by() function doesn't allow you to specify an arbitrary function, so you can use the following command.

```
mystats <- function(x, na.omit = FALSE) {
if (na.omit)  x <- x[!is.na(x)]
m <- mean(x)
n <- length(x)
s <- sd(x)
skew <- sum((x - m)^3/s^3)/n
kurt <- sum((x - m)^4/s^4)/n - 3
return(c(n = n, mean = m, stdev = s, skew = skew, kurtosis = kurt))
}
library(reshape)
dfm <- melt(mtcars, measure.vars = c("mpg", "hp", "wt"), id.vars = c("am", "cyl"))
cast(dfm, am + cyl + variable ~ ., mystats)

##    am cyl variable  n       mean      stdev          skew   kurtosis
## 1   0   4      mpg  3  22.900000  1.4525839  6.851657e-02 -2.3333333
## 2   0   4       hp  3  84.666667 19.6553640 -3.804217e-01 -2.3333333
## 3   0   4       wt  3   2.935000  0.4075230 -3.807326e-01 -2.3333333
## 4   0   6      mpg  4  19.125000  1.6317169  4.817573e-01 -1.9076891
## 5   0   6       hp  4 115.250000  9.1787799 -9.395461e-02 -2.3303515
## 6   0   6       wt  4   3.388750  0.1162164 -7.349455e-01 -1.6967507
## 7   0   8      mpg 12  15.050000  2.7743959 -2.843325e-01 -0.9635443
## 8   0   8       hp 12 194.166667 33.3598379  2.785849e-01 -1.4385375
## 9   0   8       wt 12   4.104083  0.7683069  8.542070e-01 -1.1433587
```

```
## 10  1   4      mpg  8  28.075000  4.4838599 -2.078592e-01 -1.6584985
## 11  1   4       hp  8  81.875000 22.6554156  1.373411e-01 -1.8105587
## 12  1   4       wt  8   2.042250  0.4093485  3.488929e-01 -1.1451272
## 13  1   6      mpg  3  20.566667  0.7505553 -3.849002e-01 -2.3333333
## 14  1   6       hp  3 131.666667 37.5277675  3.849002e-01 -2.3333333
## 15  1   6       wt  3   2.755000  0.1281601 -1.154378e-01 -2.3333333
## 16  1   8      mpg  2  15.400000  0.5656854  0.000000e+00 -2.7500000
## 17  1   8       hp  2 299.500000 50.2045815  0.000000e+00 -2.7500000
## 18  1   8       wt  2   3.370000  0.2828427 -1.137979e-15 -2.7500000
```

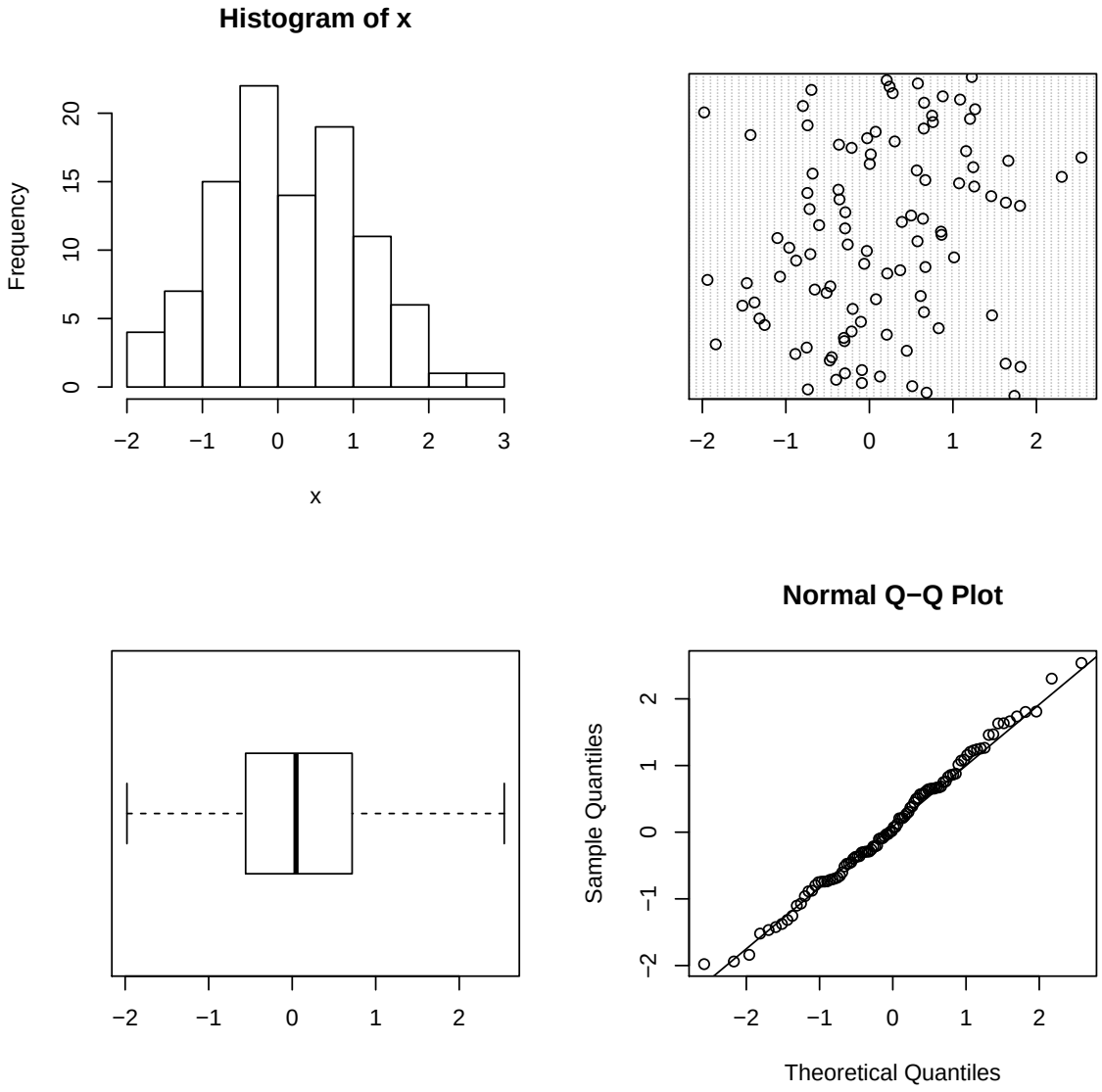
or install.packages("doBy")

```
#summaryBy(formula, data=dataframe, FUN=function)
library(doBy)
summaryBy(mpg+hp+wt~am, data=mtcars, FUN=mystats)

##   am mpg.n mpg.mean mpg.stdev   mpg.skew mpg.kurtosis hp.n  hp.mean
## 1  0    19 17.14737  3.833966 0.01395038   -0.8031783   19 160.2632
## 2  1    13 24.39231  6.166504 0.05256118   -1.4553520   13 126.8462
##   hp.stdev     hp.skew hp.kurtosis wt.n  wt.mean  wt.stdev   wt.skew
## 1 53.90820 -0.01422519  -1.2096973   19 3.768895 0.7774001 0.9759294
## 2 84.06232  1.35988586   0.5634635   13 2.411000 0.6169816 0.2103128
##   wt.kurtosis
## 1   0.1415676
## 2  -1.1737358
```

1.5 Describe the data using a Graph

```
COM <- function (x)   {
    par(mfrow=c(2,2))              # Combine four graph
    hist(x)                        # histogram
    dotchart(x)                    # dotchart
    boxplot(x,horizontal=T)        # boxplot
    qqnorm(x);qqline(x)            # normal
    par(mfrow=c(1,1))              # reset the enviroment
  }
x <- rnorm(100)
COM(x)
```



2 Frequency tables

One way tables

You can generate simple frequency counts using the table() function.

```
library("vcd")

## Loading required package:  grid

mytable <- with(Arthritis, table(Improved))
mytable

## Improved
```

```
##   None   Some Marked
##     42     14     28

prop.table(mytable)

## Improved
##      None      Some    Marked
## 0.5000000 0.1666667 0.3333333

prop.table(mytable)*100

## Improved
##     None     Some   Marked
## 50.00000 16.66667 33.33333
```

Two way tables

For two-way tables, the format for the table() function is mytable <- table(A, B), where A is the row variable, and B is the column variable.

```
mytable <- with(Arthritis, table(Treatment,Improved))
mytable

##           Improved
## Treatment None Some Marked
##   Placebo   29    7      7
##   Treated   13    7     21

mytable <- xtabs(~ Treatment+Improved, data=Arthritis)
mytable

##           Improved
## Treatment None Some Marked
##   Placebo   29    7      7
##   Treated   13    7     21

DF <- as.data.frame(UCBAdmissions)
head(DF)

##      Admit Gender Dept Freq
## 1 Admitted   Male    A  512
## 2 Rejected   Male    A  313
## 3 Admitted Female    A   89
## 4 Rejected Female    A   19
## 5 Admitted   Male    B  353
## 6 Rejected   Male    B  207

xtabs(Freq ~ Gender + Admit, DF)

##         Admit
## Gender   Admitted Rejected
##   Male       1198     1493
##   Female      557     1278
```

You can generate marginal frequencies using the addmargins() functions.

```
addmargins(mytable)
```

```
##           Improved
## Treatment None Some Marked Sum
##   Placebo   29    7      7  43
##   Treated   13    7     21  41
##   Sum       42   14     28  84
```

```
addmargins(prop.table(mytable))
```

```
##           Improved
## Treatment       None       Some     Marked        Sum
##   Placebo 0.34523810 0.08333333 0.08333333 0.51190476
##   Treated 0.15476190 0.08333333 0.25000000 0.48809524
##   Sum     0.50000000 0.16666667 0.33333333 1.00000000
```

NOTE: The table() function ignores missing values (NAs) by default. To include NA as a valid category in the frequency counts, include the table option useNA="ifany".

3 Correlations

Correlation coefficients are used to describe relationships among quantitative variables. The sign ± indicates the direction of the relationship (positive or inverse) and the magnitude indicates the strength of the relationship (ranging from 0 for no relationship to 1 for a perfectly predictable relationship).

R can produce a variety of correlation coefficients, including Pearson, Spearman, Kendall, partial, polychoric, and polyserial. The cor() function produces all three correlation coefficients, whereas the cov() function provides covariances.

```
#cor(x, use= , method= )
cor(1:10, 2:11)
```

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

```
states<- state.x77[,1:5]
cov(states)
```

```
##               Population      Income   Illiteracy     Life Exp      Murder
## Population 19931683.7588 571229.7796  292.8679592 -407.8424612 5663.523714
## Income       571229.7796 377573.3061 -163.7020408  280.6631837 -521.894286
## Illiteracy      292.8680   -163.7020    0.3715306   -0.4815122    1.581776
## Life Exp       -407.8425    280.6632   -0.4815122    1.8020204   -3.869480
## Murder         5663.5237   -521.8943    1.5817755   -3.8694804   13.627465
```

```
cor(states)
```

```
##             Population     Income Illiteracy    Life Exp     Murder
## Population  1.00000000  0.2082276  0.1076224 -0.06805195  0.3436428
## Income      0.20822756  1.0000000 -0.4370752  0.34025534 -0.2300776
## Illiteracy  0.10762237 -0.4370752  1.0000000 -0.58847793  0.7029752
## Life Exp   -0.06805195  0.3402553 -0.5884779  1.00000000 -0.7808458
## Murder      0.34364275 -0.2300776  0.7029752 -0.78084575  1.0000000
```

```
cor(states, method="spearman")

##            Population     Income Illiteracy   Life Exp     Murder
## Population  1.0000000  0.1246098  0.3130496 -0.1040171  0.3457401
## Income      0.1246098  1.0000000 -0.3145948  0.3241050 -0.2174623
## Illiteracy  0.3130496 -0.3145948  1.0000000 -0.5553735  0.6723592
## Life Exp   -0.1040171  0.3241050 -0.5553735  1.0000000 -0.7802406
## Murder      0.3457401 -0.2174623  0.6723592 -0.7802406  1.0000000
```

The default options are use="everything" and method="pearson". Notice that you get square matrices by default (all variables crossed with all other variables). You can also produce nonsquare matrices.

```
x <- states[,c("Population", "Income", "Illiteracy")]
y <- states[,c("Life Exp", "Murder")]
cor(x,y)

##               Life Exp     Murder
## Population -0.06805195  0.3436428
## Income      0.34025534 -0.2300776
## Illiteracy -0.58847793  0.7029752
```

Testing correlations for significance

The corr.test() function provided in the psych package allows you to testing correlations for significance. install.packages("psych")

```
library(psych)
corr.test(states, use="complete")

## Call:corr.test(x = states, use = "complete")
## Correlation matrix
##            Population Income Illiteracy Life Exp Murder
## Population       1.00   0.21       0.11    -0.07   0.34
## Income           0.21   1.00      -0.44     0.34  -0.23
## Illiteracy       0.11  -0.44       1.00    -0.59   0.70
## Life Exp        -0.07   0.34      -0.59     1.00  -0.78
## Murder           0.34  -0.23       0.70    -0.78   1.00
## Sample Size
## [1] 50
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##            Population Income Illiteracy Life Exp Murder
## Population       0.00   0.44       0.91     0.91   0.09
## Income           0.15   0.00       0.01     0.09   0.43
## Illiteracy       0.46   0.00       0.00     0.00   0.00
## Life Exp         0.64   0.02       0.00     0.00   0.00
## Murder           0.01   0.11       0.00     0.00   0.00
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

The use= options can be "pairwise" or "complete" (for pairwise or listwise deletion of missing values, respectively). The method= option is "pearson" (the default), "spearman", or "kendall".

Partial correlations

A partial correlation is a correlation between two quantitative variables, controlling for one or more other quantitative variables. You can use the pcor() function in the ggm package to provide partial correlation coefficients. install.packages("ggm")

```
#pcor(u, S)
library(ggm)

## Loading required package:  igraph
## Warning:  package 'igraph' was built under R version 3.2.4
##
## Attaching package:  'igraph'
## The following objects are masked from 'package:stats':
##
##    decompose, spectrum
## The following object is masked from 'package:base':
##
##    union
##
## Attaching package:  'ggm'
## The following object is masked from 'package:igraph':
##
##    pa
## The following object is masked from 'package:Hmisc':
##
##    rcorr

pcor(c(1,5,2,3,4), cov(states))

## [1] 0.4476116
```

where u is a vector of numbers, with the first two numbers the indices of the variables to be correlated, and the remaining numbers the indices of the conditioning variables (that is, the variables being partialed out). S is the covariance matrix among the variables.

Another example

install.packages("MSG")

```
library("MSG")
par(mfrow = c(1, 2), pch = 20, ann = FALSE, mar = c(2, 2, 0.5, 0.2))
plot(BinormCircle, col = rgb(1, 0, 0))
plot(BinormCircle, col = rgb(1, 0, 0, alpha = 0.01))
attach(BinormCircle)
cor(V1,V2)
detach(BinormCircle)
```

4 Probability functions

Random Sampling

The sample function draws randomly from a specified set of (scalar) objects allowing you to sample from arbitrary distributions.

```
set.seed(1)
sample(1:10, 4)

## [1] 3 4 5 7

sample(1:10, 4)

## [1] 3 9 8 5

sample(letters, 5)

## [1] "q" "b" "e" "x" "p"

sample(1:10) ## permutation

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

sample(1:10)

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

sample(1:10, replace = TRUE) ## Sample w/replacement

##  [1] 2 9 7 8 2 8 5 9 7 8
```

In R, probability functions take the form [dpqr]distribution_abbreviation(). where the first letter refers to the aspect of the distribution returned:

d = density

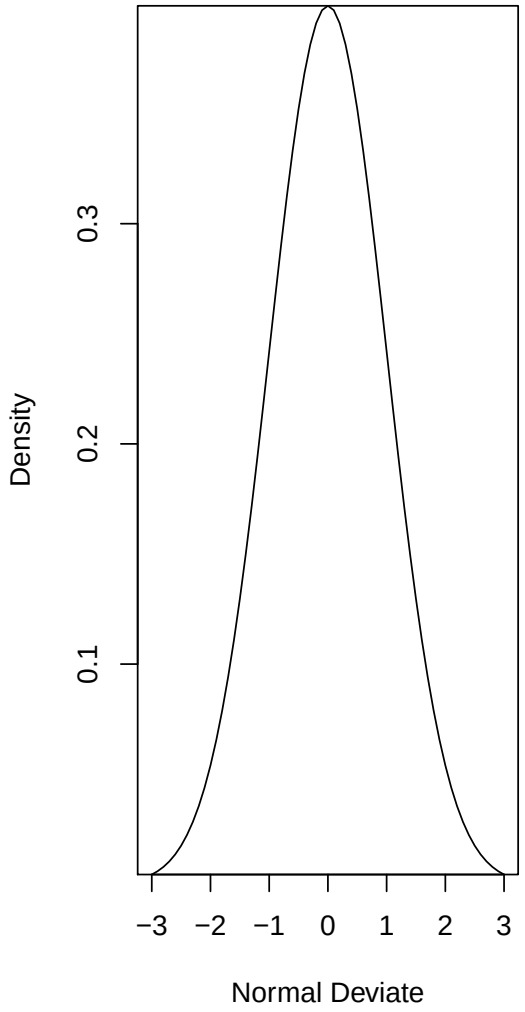
p = distribution function

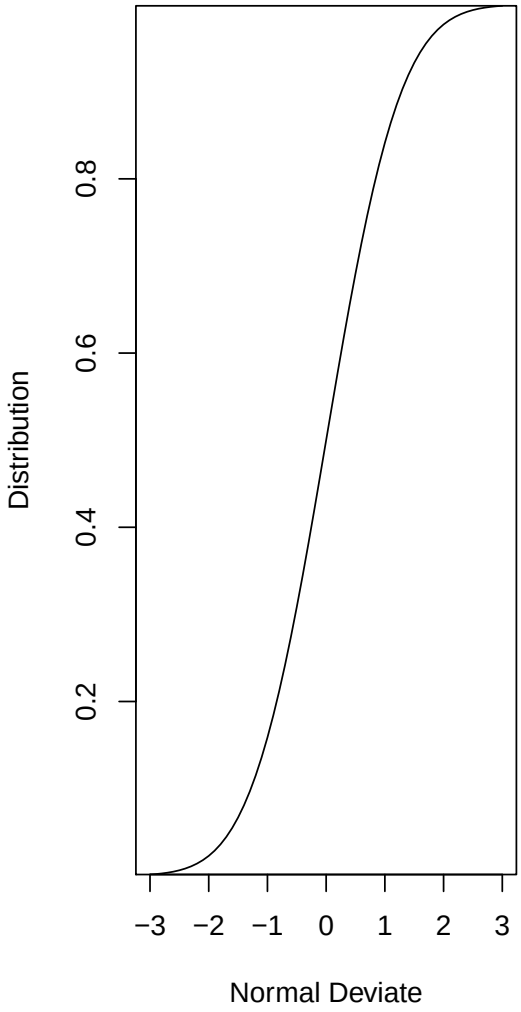
q = quantile function

r = random generation (random deviates)

To see how these work, let's look at functions related to the normal distribution. If you don't specify a mean and a standard deviation, the standard normal distribution is assumed (mean=0, sd=1).

```
par(mfrow=c(1,2))
x <- pretty(c(-3,3), 60)
y <- dnorm(x)
z <- pnorm(x)
plot(x, y, type = "l", xlab = "Normal Deviate", ylab = "Density", yaxs = "i" )
plot(x, z, type = "l", xlab = "Normal Deviate", ylab = "Distribution", yaxs = "i" )
```





What is the area under the standard normal curve to the left of z=1.96?

```
pnorm(1.96)
```

```
## [1] 0.9750021
```

What is the value of the 90th percentile of a normal distribution with a mean of 500 and a standard deviation of 100?

```
qnorm(.95)
```

```
## [1] 1.644854
```

```
qnorm(.9, mean=500, sd=100)
```

```
## [1] 628.1552
```

Generate 50 random normal deviates with a mean of 50 and a standard deviation of 10.

```
rnorm(50, mean=50, sd=10)

##  [1] 51.33336 58.04190 49.42893 55.03608 60.85769 43.09046 37.15401
##  [8] 50.46726 47.64293 44.57112 45.66690 43.50528 57.26751 61.51912
## [15] 59.92160 45.70487 62.38304 47.20654 67.57903 55.60746 45.47216
## [22] 41.67957 38.33429 39.34409 34.36218 61.56537 58.32047 47.72671
## [29] 52.66137 46.23297 74.41365 42.04661 49.45123 52.50141 56.18243
## [36] 48.27376 27.76100 37.36386 53.58729 49.88955 40.59351 48.84175
## [43] 41.85031 52.42263 35.74902 53.65941 52.48413 50.65288 50.19156
## [50] 52.57338
```

Setting the seed for random number generation

Each time you generate pseudo-random deviates, a different seed, and therefore different results, are produced. To make your results reproducible, you can specify the seed explicitly, using the set.seed() function . An example is given in the next listing. Here, the runif() function is used to generate pseudo-random numbers from a uniform distribution on the interval 0 to 1.

```
runif(5)

## [1] 0.2581659 0.7293096 0.4525708 0.1751268 0.7466983

runif(5)

## [1] 0.1049876 0.8645449 0.6146450 0.5571595 0.3287773

set.seed(1234)
runif(5)

## [1] 0.1137034 0.6222994 0.6092747 0.6233794 0.8609154

set.seed(1234)
runif(5)

## [1] 0.1137034 0.6222994 0.6092747 0.6233794 0.8609154
```

Generating multivariate normal data

```
library(MASS)
options(digits=3)
set.seed(1234)
mean <- c(230.7, 146.7, 3.6)
sigma <- matrix( c(15360.8, 6721.2, -47.1, 6721.2, 4700.9, -16.5,
         -47.1,  -16.5,   0.3), nrow=3, ncol=3)
mydata <- mvrnorm(500, mean, sigma)
mydata <- as.data.frame(mydata)
names(mydata) <- c("y", "x1", "x2")
dim(mydata)
```

```
## [1] 500   3
```

```
head(mydata, n=10)
```

```
##        y    x1   x2
## 1   98.8  41.3 3.43
## 2  244.5 205.2 3.80
## 3  375.7 186.7 2.51
## 4  -59.2  11.2 4.71
## 5  313.0 111.0 3.45
## 6  288.8 185.1 2.72
## 7  134.8 165.0 4.39
## 8  171.7  97.4 3.64
## 9  167.2 101.0 3.50
## 10 121.1  94.5 4.10
```

Generating Poisson data

```
rpois(10, 1)
```

```
##  [1] 3 0 0 0 0 0 0 2 1 2
```

```
rpois(10, 2)
```

```
##  [1] 1 4 3 1 0 1 1 4 1 1
```

```
rpois(10, 20)
```

```
##  [1] 18 17 27 19 11 33 24 25 11 11
```

```
ppois(2, 2) ## Cumulative distribution Pr(x <= 2)
```

```
## [1] 0.677
```

```
ppois(4, 2) ## Pr(x <= 4)
```

```
## [1] 0.947
```

```
ppois(6, 2) ## Pr(x <= 6)
```

```
## [1] 0.995
```

Generating Random Numbers From a Linear Model

Suppose we want to simulate from the following linear model

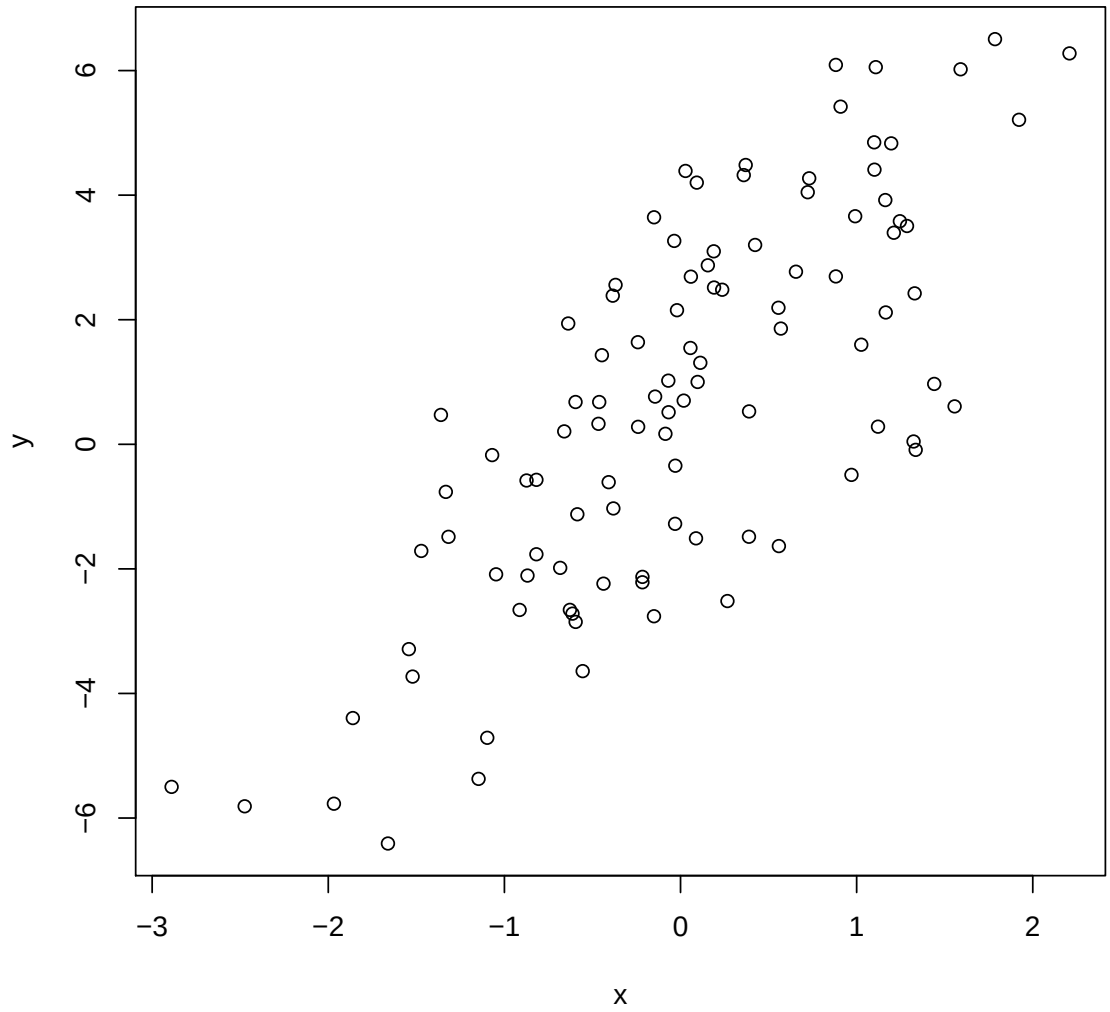
$$y = \beta_0 + \beta_1 x + \varepsilon$$

where $\varepsilon \sim N(0, 2^2)$. Assume $x \sim N(0, 1^2)$, $\beta_0 = 0.5$, and $\beta_1 = 2$.

```r
set.seed(20)
x <- rnorm(100)
e <- rnorm(100, 0, 2)
y <- 0.5 + 2 * x + e
summary(y)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   -6.41   -1.54    0.68    0.69    2.93    6.51

plot(x, y)
```

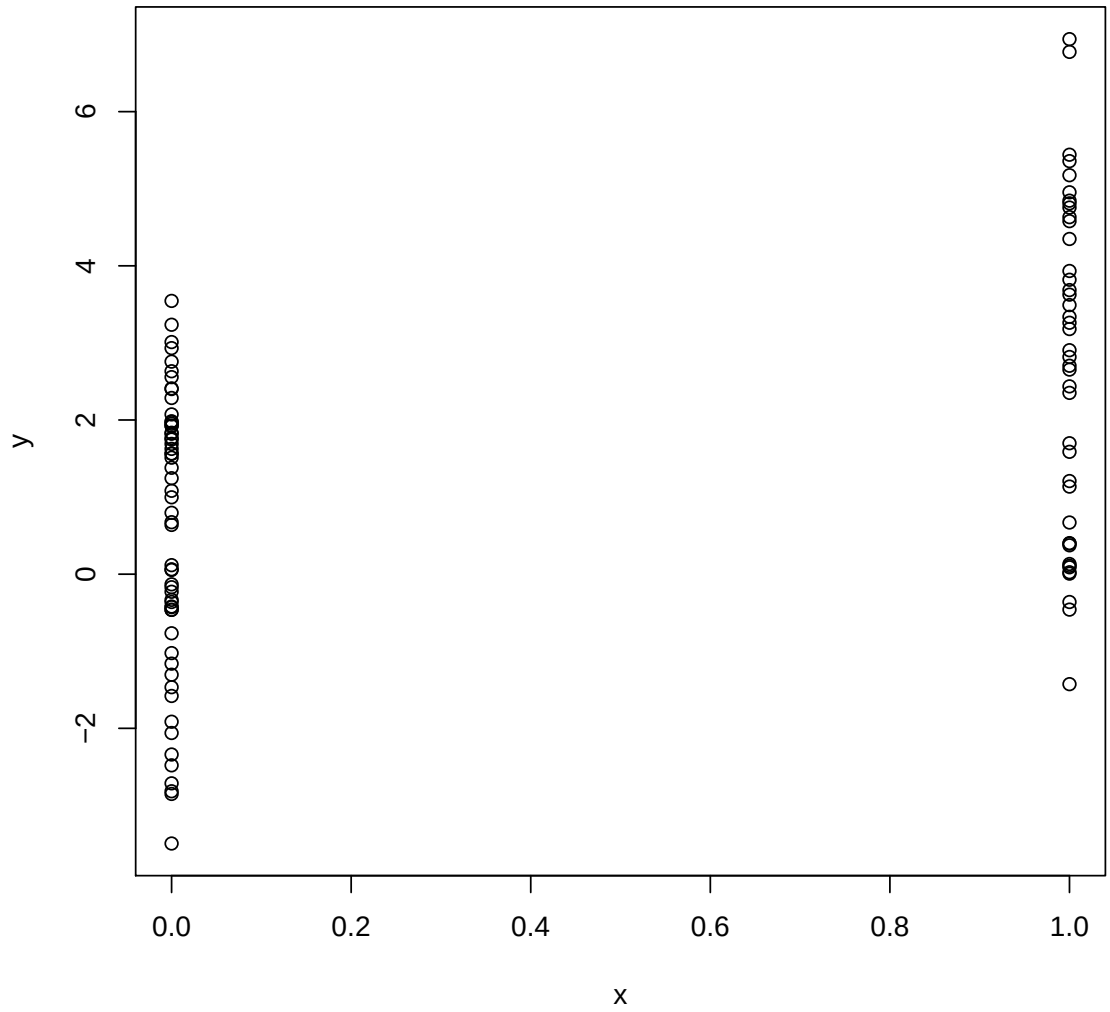


What if x is binary?

```r
set.seed(10)
x <- rbinom(100, 1, 0.5)
e <- rnorm(100, 0, 2)
y <- 0.5 + 2 * x + e
summary(y)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   -3.49   -0.14    1.58    1.43    2.84    6.94

plot(x, y)
```



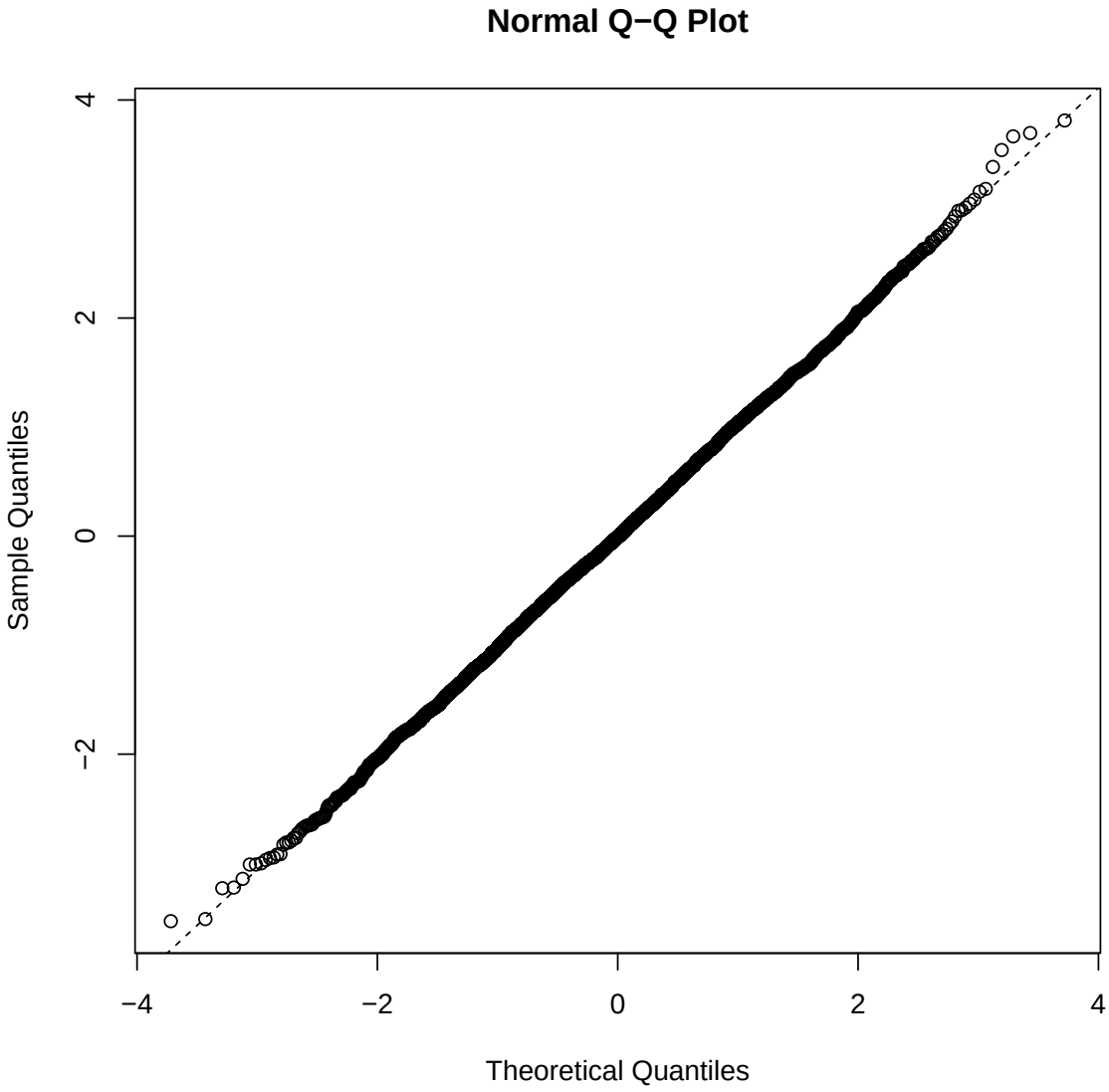
Testing normality

The simplest test of normality (and in many ways the best) is the 'quantile–quantile plot'. This plots the ranked samples from our distribution against a similar number of ranked quantiles taken from a normal distribution. If our sample is normally distributed then the line will be straight. Departures from normality show up as various sorts of non-linearity (e.g. S-shapes or banana shapes). The functions you need are qqnorm and qqline (quantile–quantile plot against a normal distribution)

```
y <- rnorm(5000)
shapiro.test(y)

##
##  Shapiro-Wilk normality test
##
## data:  y
## W = 1, p-value = 0.8

qqnorm(y)
qqline(y,lty=2)
```



5 Simulation

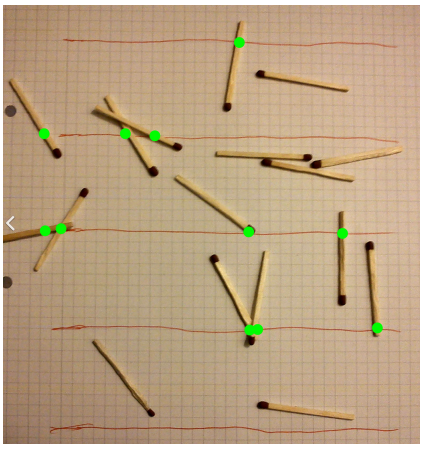
5.1 Buffon's needle problem

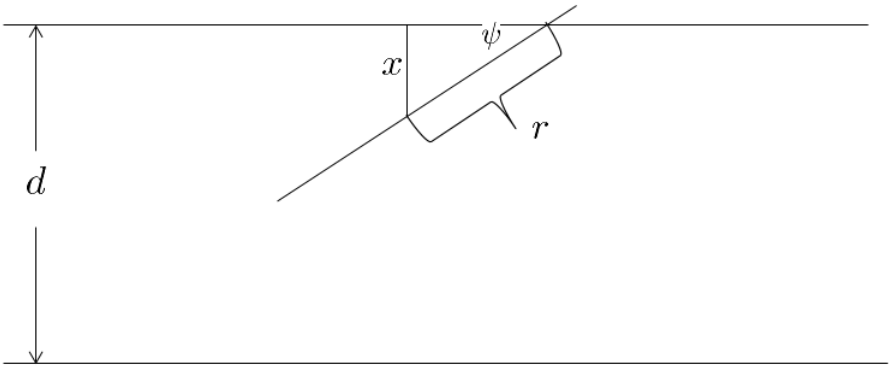
In mathematics, Buffon's needle problem is a question first posed in the 18th century by Georges-Louis Leclerc, Comte de Buffon:

Suppose we have a floor made of parallel strips of wood, each the same width, and we drop a needle onto the floor. What is the probability that the needle will lie across a line between two strips?

Buffon's needle was the earliest problem in geometric probability to be solved; it can be solved using integral geometry. The solution, in the case where the needle length is not greater than the width of the strips, can be used to design a Monte Carlo method for approximating the number π, although that was not the original motivation for de Buffon's question.

With the position random variables defined in this way, we clearly have $0 \leq x \leq d/2$ and $0 \leq \psi \leq \pi$.





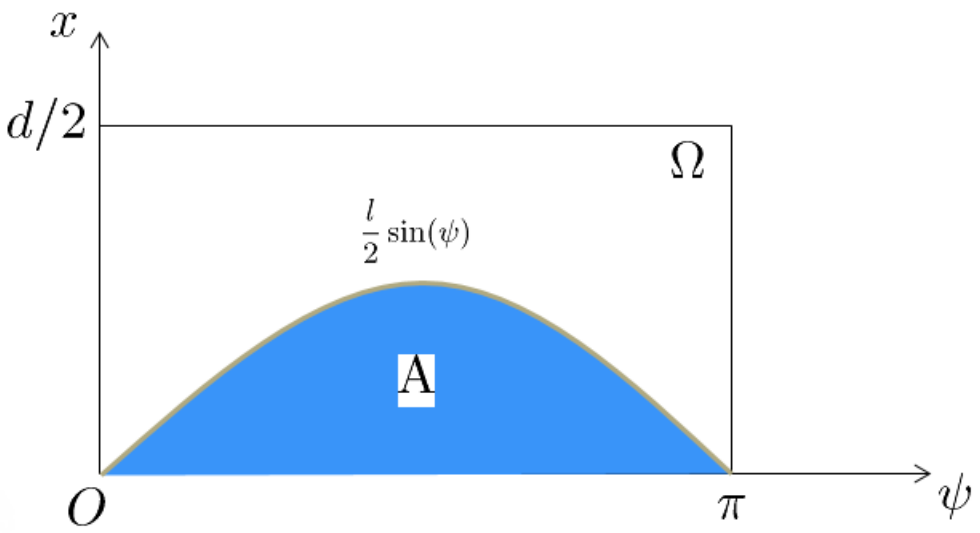
The needle hitting a line, which means

$$x \leq \frac{l}{2}\sin(\psi)$$

Working in the joint sample space. We are asked for the probability that the needle intersects one of the parallel lines. To answer this question, all we need do is identify the set of points in the joint sample space.

$$P(A) = \frac{S_A}{S_\Omega} = \frac{\int_0^\pi \frac{l}{2}\sin\psi d\psi}{\frac{d}{2}\pi} = \frac{2l}{d\pi}$$

$$\pi = \frac{2lN}{dn}$$




```
install.packages(animation)
buffon.needle(namx=500, interval=0)
```

```
buffon<-function(n, l=0.8, a=1){
   k<-0
   theta<-runif(n,0, pi); x<-runif(n,0, a/2)
    for (i in 1:n){
    if (x[i]<= l/2*sin(theta[i]))
      k<-k+1
  }
   2*l*n/(k*a)
}
buffon(10000)

## [1] 3.11
```

Exercise

Let X_n and Y_n be iid random variables each having a uniform distribution with joint probability density function are

$$f(x,y) = \begin{cases} 1, & 0 < x < 1, 0 < y < 1 \\ 0, & \text{others} \end{cases}$$

then $P(X^2 + Y^2 \leq 1) = \pi/4$, calculate π.

```
MC1 <- function(n){
   k <- 0; x <- runif(n); y <- runif(n)
   for (i in 1:n){
      if (x[i]^2+y[i]^2 < 1)
         k <- k+1
```

```
   }
   4*k/n
}
MC1(10000)

## [1] 3.14
```

5.2 Central limit theorem

Let $X_1, X_2, \ldots X_n$ denote the observations of a random sample from a distribution that has mean μ and positive variance σ^2. Then the random variable

$$Y_n = \frac{\sum_{i=1}^{n} X_i - n\mu}{\sqrt{n}\sigma} = \frac{\sqrt{n}(\bar{X}_n - \mu)}{\sigma}$$

converges in distribution to a random variable which has a normal distribution with mean zero and variance 1.

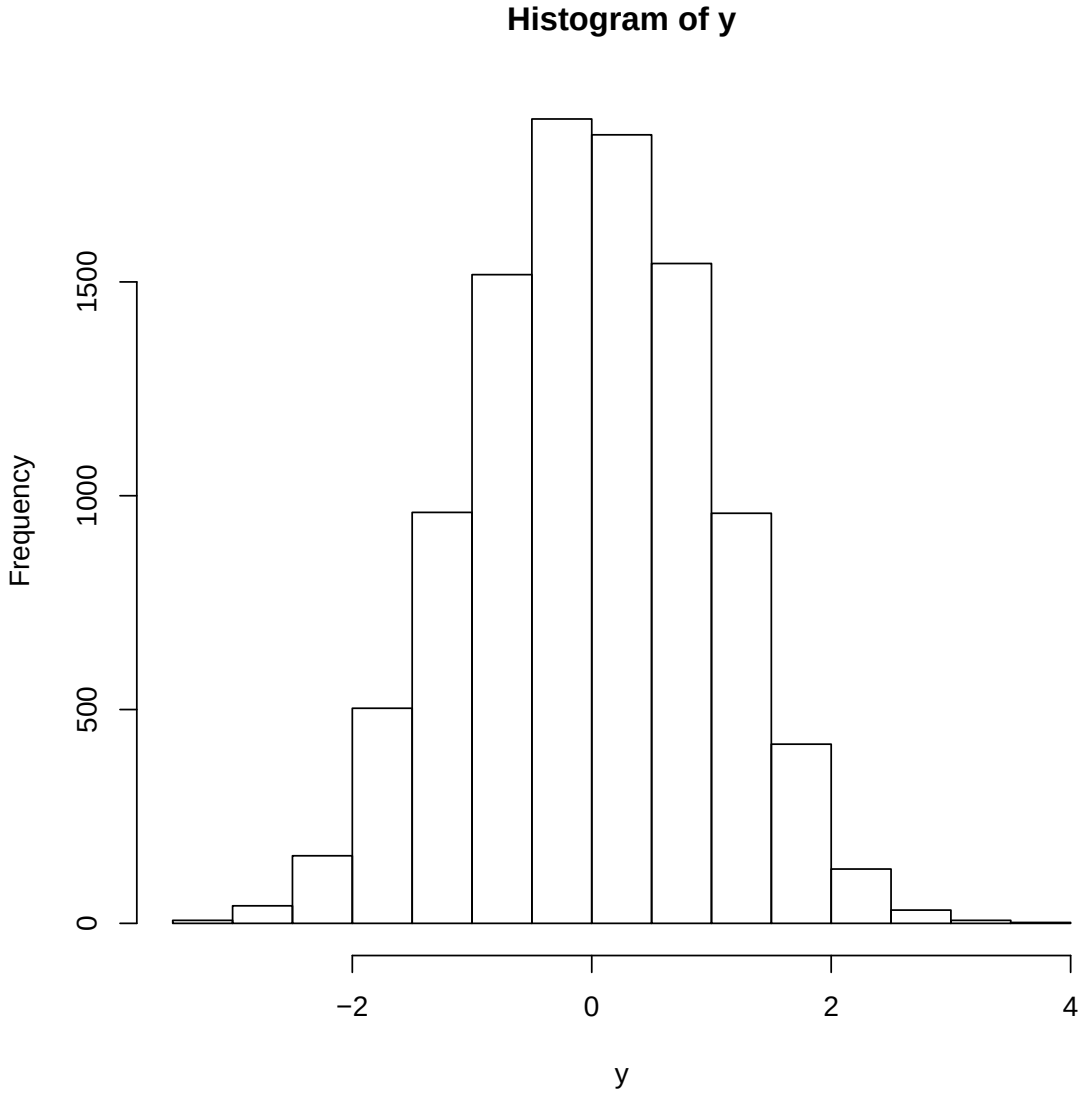
```
f=function(n) rchisq(n,5)
clt.ani(FUN = f)
```

5.3 Create random variables

The following step can create random variables obeying normal distribution

1. Suppose X be a iid random variable and sample from a uniform distribution. Creating $x_1, x_2, \ldots x_{12}$.
2. Calculating $y = x_1 + x_2 + \cdots + x_{12} - 6$. According to Central limit theorem, y is a random variable sample from a normal distribution with parameter $N(0, 1)$.
3. Calculating $z = \mu + \sigma y$. z is a normal distribution from $N(\mu, \sigma^2)$.
4. Repeat (1)-(4) k times.

```
MCN <- function(k){
        y <- numeric()
        for (i in 1:k){
                x <- runif(n=12,min=0,max=1)
                y[i]<-sum(x)-6
        }
        hist(y)
}
MCN(10000)
```



5.4 Monte Carlo Experiments

Since the least-squares estimators under the assumptions of CLRM have certain desirable statistical features summarized in the BLUE property. In this section, we prove this property more formally. But in practice how does one know that the BLUE property holds? For example, how does one find out if the OLS estimators are unbiased? The answer is provided by the so-called Monte Carlo experiments, which are essentially computer simulation, or sampling, experiments.

Consider the following model:

$$Y_i = \beta_i + \beta_2 X_i + u_i \tag{1}$$

A Monte Carlo experiment proceeds as follows:

1. Suppose the true values of the parameters are as follows: $\beta_1 = 20$ and $\beta_2 = 0.6$.

2. You choose the sample size, say $n = 25$.

3. You fix the values of X for each observation. In all you will have 25 X values.

4. Suppose you go to a random number table, choose 25 values, and call them u_i (these days most statistical packages have built-in random number generators).

5. Since you know β_1, β_2, X_i, and u_i, using (1) you obtain 25 Y_i values.

6. Now using the 25 Y_i values thus generated, you regress these on the 25 X values chosen in step 3, obtaining $\hat{\beta}_1$ and $\hat{\beta}_2$, the least-squares estimators.

7. Suppose you repeat this experiment 99 times, each time using the same β_1, β_2, and X values. Of course, the u_i values will vary from experiment to experiment. Therefore, in all you have 100 experiments, thus generating 100 values each of β_1 and β_2. (In practice, many such experiments are conducted, sometimes 1000 to 2000.)

8. You take the averages of these 100 estimates and call them $\bar{\hat{\beta}}_1$ and $\bar{\hat{\beta}}_2$.

9. If these average values are about the same as the true values of β_1 and β_2 assumed in step 1, this Monte Carlo experiment "establishes" that the least-squares estimators are indeed unbiased. Recall that under CLRM $E(\hat{\beta}_1) = \beta_1$ and $E(\hat{\beta}_2) = \beta_2$.

These steps characterize the general nature of the Monte Carlo experiments. Such experiments are often used to study the statistical properties of various methods of estimating population parameters. They are particularly useful to study the behavior of estimators in small, or finite, samples.

```
###MCMC
beta0=1:1000
beta1=1:1000
b1=20;b2=0.6;n=25
x=10:34

for(i in 1:1000){
u=rnorm(25)
y=b1+b2*x+u
lm.m=lm(y~x)
beta0[i]=as.numeric(coef(lm.m)[1])
beta1[i]=as.numeric(coef(lm.m)[2])
}
#beta0
#beta1
mean(beta0)

## [1] 20

mean(beta1)

## [1] 0.6
```

Monte Carlo integration

Calculate

$$\theta = \int_0^1 e^{-x} dx$$

```
m <- 10000
#1
k<-0
for (i in 1:m){
        x<-runif(1)
        y<-runif(1)
        ifelse(y<=exp(-x),k<-k+1,k<-k)
}
J<-k/m;J

## [1] 0.631

#2
x <- runif(m)
theta.hat <- mean(exp(-x))
print(theta.hat)

## [1] 0.634

#TURE
print(1 - exp(-1))

## [1] 0.632
```

If we need to calculate $\int_a^b g(x)dx$, and $a < b$, then

$$y = (x - a)/(b - a)$$

and

$$\int_a^b g(x)dx = \int_0^1 g(y(b-a)+a)(b-a)dy$$

Further, if $c \leq g(x) \leq d$,

$$f(y) = \frac{1}{d-c}[g(a + (b-a)y) - c]$$

The above Equation is $0 \leq f(y) \leq 1$. Finally,

$$\int_a^b g(x)dx = S_0 \int_0^1 f(y)dy + c(b-a)$$

where $S_0 = (b-a)(d-c)$.

Exercise

Calculate

$$\int_0^1 e^{-x^2/2}/\sqrt{2\pi}dx$$

```r
#1
m<-10000;k<-0
for (i in 1:m){
        x<-runif(1)
        y<-runif(1)
        ifelse(y<=exp(((-x^2)/2))/sqrt(2*pi),k<-k+1,k<-k)
}
J<-k/m;J

## [1] 0.343

#2
x <- runif(m)
theta.hat <- mean(exp(((-x^2)/2))/sqrt(2*pi))
print(theta.hat)

## [1] 0.341

#TURE
#0.341344
```

5.5 Bootstrap

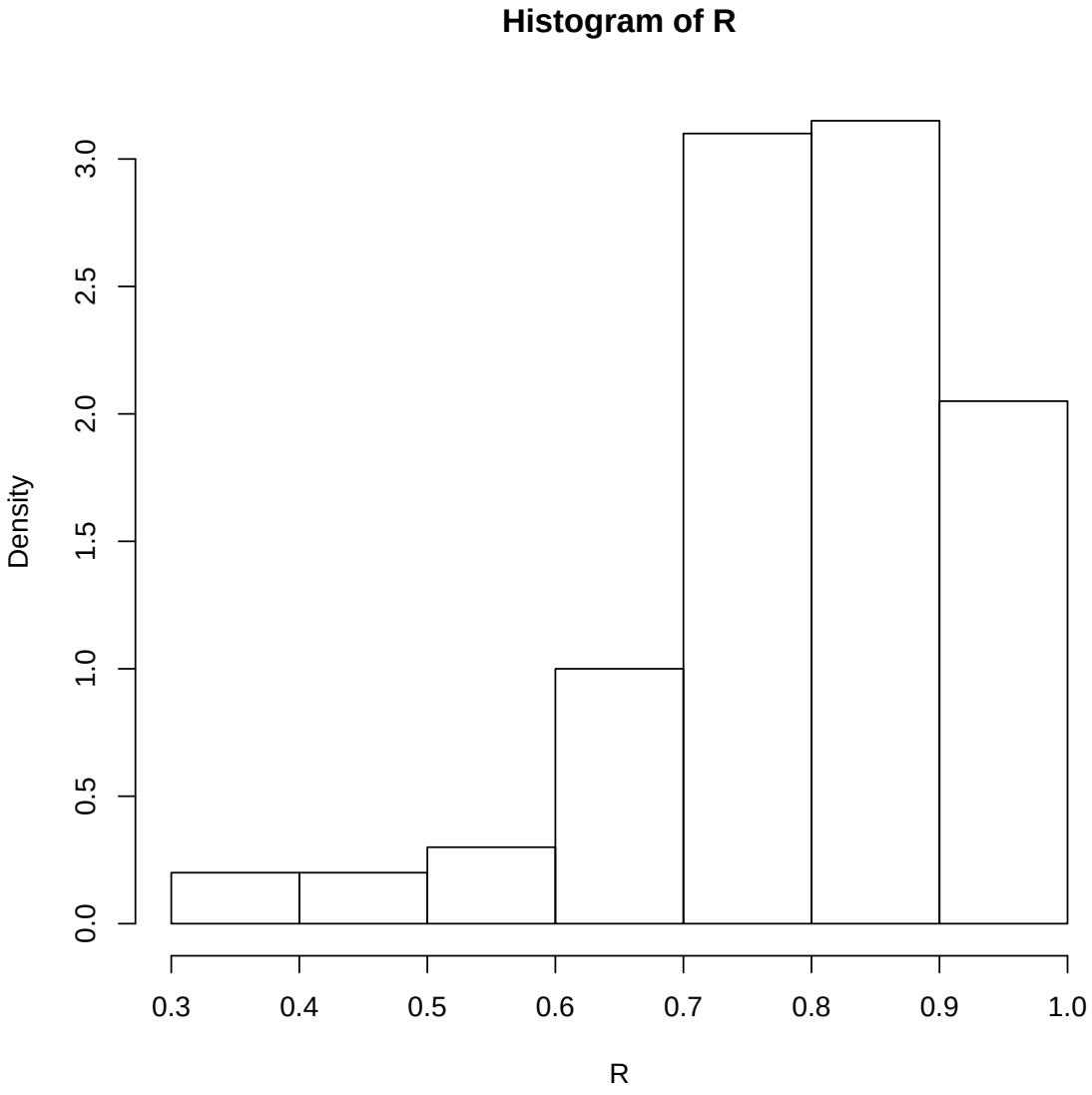
```r
library(bootstrap) #for the law data
head(law)

##   LSAT GPA
## 1  576 339
## 2  635 330
## 3  558 281
## 4  578 303
## 5  666 344
## 6  580 307

print(cor(law$LSAT, law$GPA))

## [1] 0.776

#set up the bootstrap
B <- 200 #number of replicates
n <- nrow(law) #sample size
R <- numeric(B) #storage for replicates
#bootstrap estimate of standard error of R
for (b in 1:B) {
        #randomly select the indices
        i <- sample(1:n, size = n, replace = TRUE)
        LSAT <- law$LSAT[i] #i is a vector of indices
        GPA <- law$GPA[i]
        R[b] <- cor(LSAT, GPA)
}
#output
hist(R, prob = TRUE)
```


Histogram of R
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
R

```
mean(R)
```

```
## [1] 0.794
```