Package ‘PASWR’

October 12, 2022

Type Package

Title Probability and Statistics with R

Version 1.3

Date 2022-05-14

Maintainer Alan T. Arnholt <arnholt@appstate.edu>

Description Functions and data sets for the text Probability and Statistics with R.

Depends lattice

Imports MASS, e1071

LazyData TRUE

License GPL-2

RoxygenNote 7.1.2

Encoding UTF-8

NeedsCompilation no

Author Alan T. Arnholt [aut, cre]

Repository CRAN

Date/Publication 2022-05-15 11:50:02 UTC

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Description

Data and functions for the book *Probability and Statistics with R*

Details

Package: PASWR  
Type: Package  
Version: 1.2  
Date: 2016-02-24  
License: GPL (>=2)

Comprehensive and engineering-oriented, *Probability and Statistics with R* provides a thorough treatment of probability and statistics, clear and accessible real-world examples, and fully detailed proofs. The text provides step-by-step explanations for numerous examples in R and S-PLUS for nearly every topic covered, including both traditional and nonparametric techniques. With a wide range of graphs to illustrate complex material as well as a solutions manual, the book also offers an accompanying website that features supporting information, including datasets, functions, and other downloadable material. It is ideal for undergraduate students and for engineers and scientists who must perform statistical analyses.

Author(s)

Alan T. Arnholt  
Maintainer: <arnholtat@appstate.edu>

References


Description

Data regarding aggressive behavior in relation to exposure to violent television programs used in Example 10.5
Apple

Format
A data frame with 16 observations on the following 2 variables:

- violence (an integer vector)
- noviolence (an integer vector)

Details
This is data regarding aggressive behavior in relation to exposure to violent television programs from Gibbons (1997) with the following exposition:

...a group of children are matched as well as possible as regards home environment, genetic factors, intelligence, parental attitudes, and so forth, in an effort to minimize factors other than TV that might influence a tendency for aggressive behavior. In each of the resulting 16 pairs, one child is randomly selected to view the most violent shows on TV, while the other watches cartoons, situation comedies, and the like. The children are then subjected to a series of tests designed to produce an ordinal measure of their aggression factors. (pages 143-144)

Source

References

Examples

```r
with(data = Aggression, 
    wilcox.test(violence, noviolence, paired = TRUE, 
                alternative = "greater"))
```

---

Apple Hardness

Description
An experiment was undertaken where seventeen recently picked (Fresh) apples were randomly selected and measured for hardness. Seventeen apples were also randomly selected from a warehouse (Warehouse) where the apples had been stored for one week. Data are used in Example 8.10.

Format
A data frame with 17 observations on the following 2 variables:

- Fresh (hardness rating measured in kg/meter$^2$)
- Warehouse (hardness rating measured in kg/meter$^2$)
AptSize

Source


Examples

# Figure 8.5
attach(Apple)
par(pty = "s")
Altblue <- "#A9E2FF"
Adkblue <- "#0080FF"
fresh <- qqnorm(Fresh)
old <- qqnorm(Warehouse)
plot(fresh, type = "n", ylab = "Sample Quantiles", xlab = "Theoretical Quantiles")
qqline(Fresh, col = Altblue)
qqline(Warehouse, col = Adkblue)
points(fresh, col = Altblue, pch = 16, cex = 1.2)
points(old, col = Adkblue, pch = 17)
legend(-1.75, 9.45, c("Fresh", "Warehouse"), col = c(Altblue, Adkblue),
text.col = c("black", "black"), pch = c(16, 17), lty = c(1, 1), bg = "gray95", cex = 0.75)
title("Q-Q Normal Plots")
detach(Apple)

# Trellis approach
qqmath(~c(Fresh, Warehouse), type = c("p","r"), pch = c(16, 17),
cex = 1.2, col=c("#A9E2FF", "#0080FF"),
groups=rep(c("Fresh", "Warehouse"), c(length(Fresh), length(Warehouse))),
data = Apple, ylab = "Sample Quantiles", xlab = "Theoretical Quantiles")

AptSize

<table>
<thead>
<tr>
<th>AptSize</th>
<th>Apartment Size</th>
</tr>
</thead>
</table>

Description

Size of apartments in Mendebaldea, Spain and San Jorge, Spain

Format

A data frame with 8 observations on the following 2 variables:

Mendebaldea Mendebaldea apartment size in square meters
SanJorge San Jorge apartment size in square meters

Source

Baberuth

Examples

```r
with(data = AptSize,
    boxplot(Mendebaldea, SanJorge))
```

---

**Baberuth**

**George Herman Ruth**

---

**Description**

Baseball statistics for George Herman Ruth (The Bambino or The Sultan Of Swat)

**Format**

A data frame with 22 observations on the following 14 variables.

- **Year**  year in which the season occurred
- **Team**  team he played for Bos-A, Bos-N, or NY-A
- **G**  games played
- **AB**  at bats
- **R**  runs scored
- **H**  hits
- **X2B**  doubles
- **X3B**  triples
- **HR**  home runs
- **RBI**  runs batted in
- **SB**  stolen bases
- **BB**  base on balls or walks
- **BA**  batting average H/AB
- **SLG**  slugging percentage (total bases/at bats)

**Source**

https://www.baseball-reference.com/about/bat_glossary.shtml

**References**


**Examples**

```r
with(data = Baberuth,
    hist(RBI))
```
Description

Two volunteers each consumed a twelve ounce beer every fifteen minutes for one hour. One hour after the fourth beer was consumed, each volunteer’s blood alcohol was measured with a different breathalyzer from the same company. The numbers recorded in data frame Bac are the sorted blood alcohol content values reported with breathalyzers from company X and company Y. Data are used in Example 9.15.

Format

A data frame with 10 observations on the following 2 variables:

- **X** blood alcohol content measured in g/L
- **Y** blood alcohol content measured in g/L

Source


Examples

```r
with(data = Bac, 
    var.test(X, Y, alternative = "less"))
```

Description

A manufacturer of lithium batteries has two production facilities, A and B. Fifty randomly selected batteries with an advertised life of 180 hours are selected, and tested. The lifetimes are stored in (facilityA). Fifty randomly selected batteries with an advertised life of 200 hours are selected, and tested. The lifetimes are stored in (facilityB).

Format

A data frame with 50 observations on the following 2 variables:

- **facilityA** life time measured in hours
- **facilityB** life time measured in hours
bino.gen

Source

Examples

```r
with(data = Battery,
     qqnorm(facilityA))
with(data = Battery,
     qqline(facilityA))
```

---

### bino.gen

**Simulating Binomial Distribution**

**Description**
Function that generates and displays $m$ repeated samples of $n$ Bernoulli trials with a given probability of success.

**Usage**

```r
bino.gen(samples, n, pi)
```

**Arguments**

- `samples`: number of repeated samples to generate
- `n`: number of Bernoulli trials
- `pi`: probability of success for Bernoulli trial

**Value**

- `simulated.distribution`: Simulated binomial distribution
- `theoretical.distribution`: Theoretical binomial distribution

**Author(s)**

Alan T. Arnholt

**Examples**

```r
bino.gen(1000, 20, 0.75)
```
### Beech Trees

**Description**

Several measurements of 42 beech trees (*Fagus Sylvatica*) taken from a forest in Navarra (Spain).

**Format**

A data frame with 42 observations on the following 4 variables:

- **Dn** diameter of the stem in centimeters
- **H** height of the tree in meters
- **PST** weight of the stem in kilograms
- **PSA** aboveground weight in kilograms

**Source**

*Gobierno de Navarra* and *Gestion Ambiental Viveros y Repoblaciones de Navarra*, 2006. The data were obtained within the European Project FORSEE.

**References**


**Examples**

```
plot(log(PSA) ~ log(Dn), data = biomass)
```

### Body Fat Composition

**Description**

Values from a study reported in the *American Journal of Clinical Nutrition* that investigated a new method for measuring body composition.

**Format**

A data frame with 18 observations on the following 3 variables:

- **age** age in years
- **fat** body fat composition
- **sex** a factor with levels F for female and M for male
Calculus Assessment Scores

Description
Mathematical assessment scores for 36 students enrolled in a biostatistics course according to whether or not the students had successfully completed a calculus course prior to enrolling in the biostatistics course.

Format
A data frame with 18 observations on the following 2 variables:

- **No.Calculus**: assessment score for students with no prior calculus
- **Yes.Calculus**: assessment score for students with prior calculus

Source

Examples
```r
with(data = Calculus,
    z.test(x = Yes.Calculus, y = No.Calculus, sigma.x = 5, sigma.y = 12)$conf)
```
Cars2004EU  


Description

The numbers of cars per 1000 inhabitants (cars), the total number of known mortal accidents (deaths), and the country population/1000 (population) for the 25 member countries of the European Union for the year 2004.

Format

A data frame with 25 observations on the following 4 variables:

- country: a factor with levels Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden, and United Kingdom
- cars: numbers of cars per 1000 inhabitants
- deaths: total number of known mortal accidents
- population: country population/1000

Source


Examples

plot(deaths ~ cars, data = Cars2004EU)

checking.plots  

Checking Plots

Description

Function that creates four graphs that can be used to help assess independence, normality, and constant variance.

Usage

checking.plots(model, n.id = 3, COL = c("#0080FF", "#A9E2FF"))
Arguments

model an aov or lm object
n.id the number of points to identify
COL vector of two colors

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

See Also

twoway.plots, oneway.plots

Examples

mod.aov <- aov(StopDist ~ tire, data = Tire)
checking.plots(mod.aov)
rm(mod.aov)

Chips  Silicon Chips

Description

Two techniques of splitting chips are randomly assigned to 28 sheets so that each technique is applied to 14 sheets. The values recorded in Chips are the number of usable chips from each silicon sheet.

Format

A data frame with 14 observations on the following 2 variables:

**techniqueI** number of usable chips
**techniqueII** number of usable chips

Source

Examples

```r
par(mfrow = c(1, 2))
with(data = Chips, qqnorm(techniqueI))
with(data = Chips, qqline(techniqueI))
with(data = Chips, qqnorm(techniqueII))
with(data = Chips, qqline(techniqueII))
par(mfrow=c(1, 1))
# Trellis Approach
graph1 <- qqmath(~techniqueI, data = Chips, type=c("p", "r"))
graph2 <- qqmath(~techniqueII, data = Chips, type=c("p", "r"))
print(graph1, split=c(1, 1, 2, 1), more = TRUE)
print(graph2, split=c(2, 1, 2, 1), more = FALSE)
rm(graph1, graph2)
```

### Description

CircuitDesigns contains the results from an accelerated life test used to estimate the lifetime of four different circuit designs (lifetimes in thousands of hours).

### Format

A data frame with 26 observations on the following 2 variables:

- **lifetime**: lifetimes in thousands of hours
- **design**: a factor with levels `Design1`, `Design2`, `Design3`, and `Design4`

### Source


### Examples

```r
bwplot(design ~ lifetime, data = CircuitDesigns)
```
Description

This program simulates random samples from which it constructs confidence intervals for either the population mean, the population variance, or the population proportion of successes.

Usage

CIsim(
  samples = 100,
  n = 30,
  parameter = 0.5,
  sigma = 1,
  conf.level = 0.95,
  type = c("Mean", "Var", "Pi")
)

Arguments

- samples: the number of samples desired.
- n: the size of each sample
- parameter: If constructing confidence intervals for the population mean or the population variance, parameter is the population mean (i.e., type is one of either "Mean" or "Var"). If constructing confidence intervals for the population proportion of successes, the value entered for parameter represents the population proportion of successes (\(\pi\)), and as such, must be a number between 0 and 1.
- sigma: is the population standard deviation. sigma is not required if confidence intervals are of type "Pi".
- conf.level: confidence level for the graphed confidence intervals, restricted to lie between zero and one
- type: character string, one of "Mean", "Var", or "Pi", or just the initial letter of each, indicating the type of confidence interval simulation to perform

Details

Default is to construct confidence intervals for the population mean. Simulated confidence intervals for the population variance or population proportion of successes are possible by selecting the appropriate value in the type argument.

Value

Performs specified simulation and draws the resulting confidence intervals on a graphical device.
**Combinations**

**Author(s)**

Alan T. Arnholt <arnholtat@appstate.edu>

**Examples**

```r
CIsim(samples = 100, n = 30, parameter = 100, sigma = 10, conf.level = 0.90)
# Simulates 100 samples of size 30 from a normal distribution with mean 100
# and a standard deviation of 10. From the 100 simulated samples, 90% confidence
# intervals for the Mean are constructed and depicted in the graph.
```

```r
CIsim(100, 30, 100, 10, type = "Var")
# Simulates 100 sample of size 30 from a normal distribution with mean 100
# and a standard deviation of 10. From the 100 simulated samples, 95% confidence
# intervals for the variance are constructed and depicted in the graph.
```

```r
CIsim(100, 50, 0.5, type = "Pi", conf.level = 0.92)
# Simulates 100 samples of size 50 from a binomial distribution where the
# population proportion of successes is 0.5. From the 100 simulated samples,
# 92% confidence intervals for Pi are constructed and depicted in the graph.
```

**Description**

Computes all possible combinations of \( n \) objects taken \( k \) at a time.

**Usage**

```r
Combinations(n, k)
```

**Arguments**

- \( n \)  
  - a number
- \( k \)  
  - a number less than or equal to \( n \)

**Value**

Returns a matrix containing the possible combinations of \( n \) objects taken \( k \) at a time.

**See Also**

`SRS`
Examples

Combinations(5,2)
  # The columns in the matrix list the values of the 10 possible
  # combinations of 5 things taken 2 at a time.

<table>
<thead>
<tr>
<th>CosAma</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Cosmed Versus Amatek</em></td>
</tr>
</tbody>
</table>

Description

The Cosmed is a portable metabolic system. A study at Appalachian State University compared the metabolic values obtained from the Cosmed to those of a reference unit (Amatek) over a range of workloads from easy to maximal to test the validity and reliability of the Cosmed. A small portion of the results for VO2 (ml/kg/min) measurements taken at a 150 watt workload are stored in CosAma.

Format

A data frame with 14 observations on the following 3 variables:

- **subject**  subject number
- **Cosmed**  measured VO2 with Cosmed
- **Amatek**  measured VO2 with Amatek

Source


Examples

bwplot(~(Cosmed - Amatek), data = CosAma)
Depend

Number of Dependent Children for 50 Families

Description

Number of dependent children for 50 families.

Format

A data frame with 50 observations on the following 4 variables.

C1  a numeric vector
number  a numeric vector
Count  a numeric vector
Percent  a numeric vector

Depend

Number of Dependent Children for 50 Families

Description

Number of dependent children for 50 families.

Format

A data frame with 50 observations on the following 4 variables.

C1  a numeric vector
number  a numeric vector
Count  a numeric vector
Percent  a numeric vector

Cows  Butterfat of Cows

Description

Random samples of ten mature (five-year-old and older) and ten two-year-old cows were taken from each of five breeds. The average butterfat percentage of these 100 cows is stored in the variable butterfat with the type of cow stored in the variable breed and the age of the cow stored in the variable age.

Format

A data frame with 100 observations on the following 3 variables:

butterfat  average butterfat percentage
age  a factor with levels 2 years old and Mature
breed  a factor with levels Ayrshire, Canadian, Guernsey, Holstein-Friesian, and Jersey

Source

Canadian record book of purebreed diary cattle.

References


Examples

summary(aov(butterfat ~ breed + age, data = Cows))

Cows  Butterfat of Cows

Depend  Number of Dependent Children for 50 Families
Drosophila

Source


Examples

with(data = Depend, table(C1))

<table>
<thead>
<tr>
<th>Drosophila</th>
<th>Drosophila Melanogaster</th>
</tr>
</thead>
</table>

Description

Drosophila contains per diem fecundity (number of eggs laid per female per day for the first 14 days of life) for 25 females from each of three lines of Drosophila melanogaster. The three lines are Nonselected (control), Resistant, and Susceptible. Data are used in Example 11.5.

Format

A data frame with 75 observations on the following 2 variables:

Fecundity number of eggs laid per female per day for the first 14 days of life

Line a factor with levels Nonselected, Resistant, and Susceptible

Source

The original measurements are from an experiment conducted by R. R. Sokal (Sokal and Rohlf, 1994, p. 237).

References


Examples

summary(aov(Fecundity ~ Line, data = Drosophila))
EDA  

Exploratory Data Analysis

Description

Function that produces a histogram, density plot, boxplot, and Q-Q plot

Usage

EDA(x, trim = 0.05, dec = 3)

Arguments

- **x**: is a numeric vector where NAs and Infs are allowed but will be removed.
- **trim**: is a fraction (between 0 and 0.5, inclusive) of values to be trimmed from each end of the ordered data such that if \( \text{trim} = 0.5 \), the result is the median.
- **dec**: is a number specifying the number of decimals

Details

The function EDA() will not return console window information on data sets containing more than 5000 observations. It will, however, still produce graphical output for data sets containing more than 5000 observations.

Value

Function returns various measures of center and location. The values returned for the quartiles are based on the default \( \text{R} \) definitions for quartiles. For more information on the definition of the quartiles, type \(?\text{quantile}\) and read about the algorithm used by \( \text{type} = 7 \).

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

Examples

EDA(x = rnorm(100))
# Produces four graphs for the 100 randomly
# generated standard normal variates.
Description

Salaries for engineering graduates 10 years after graduation

Format

A data frame with 51 observations on the following 2 variables:

- **salary**: salary 10 years after graduation in thousands of dollars
- **university**: one of three different engineering universities

Source


Examples

```r
boxplot(salary ~ university, data = Engineer, horizontal = TRUE)
# Trellis Approach
bwplot(university ~ salary, data = Engineer)
```

Description

Initial results from a study to determine whether the traditional sitting position or the hamstring stretch position is superior for administering epidural anesthesia to pregnant women in labor as measured by the number of obstructive (needle to bone) contacts (OC)

Format

A data frame with 85 observations on the following 7 variables:

- **Doctor**: a factor with levels Dr. A, Dr. B, Dr. C, and Dr. D
- **kg**: weight in kg of patient
- **cm**: height in cm of patient
- **Ease**: a factor with levels Difficult, Easy, and Impossible indicating the physician’s assessment of how well bone landmarks can be felt in the patient
Treatment a factor with levels Hamstring Stretch and Traditional Sitting

OC number of obstructive contacts

Complications a factor with levels Failure – person got dizzy, Failure – too many OCs, None, Paresthesia, and Wet Tap

Source


Examples

EPIDURAL$Teasy <- factor(EPIDURAL$Ease, levels = c("Easy", "Difficult", "Impossible"))
X <- table(EPIDURAL$Doctor, EPIDURAL$Teasy)
X
par(mfrow = c(2, 2)) # Figure 2.12
barplot(X,
main = "Barplot where Doctor is Stacked \nwithin Levels of Palpitation")
barplot(t(X),
main = "Barplot where Levels of Palpitation \nis Stacked within Doctor")
par(mfrow = c(1, 1))
rm(X)

Traditional Sitting Position Versus Hamstring Stretch Position

Description

Intermediate results from a study to determine whether the traditional sitting position or the hamstring stretch position is superior for administering epidural anesthesia to pregnant women in labor as measured by the number of obstructive (needle to bone) contacts (OC)

Format

A data frame with 342 observations on the following 7 variables:

Doctor a factor with levels Dr. A, Dr. B, Dr. C, and Dr. D
kg weight in kg of patient
cm height in cm of patient
Ease a factor with levels Difficult, Easy, and Impossible indicating the physician’s assessment of how well bone landmarks can be felt in the patient
Treatment  a factor with levels Hamstring Stretch and Traditional Sitting
OC  number of obstructive contacts
Complications  a factor with levels Failure - person got dizzy, Failure - too many OCs, None, Paresthesia, and Wet Tap

Source

Examples

boxplot(OC ~ Treatment, data = EPIDURALf)

<table>
<thead>
<tr>
<th>EURD</th>
<th>European Union Research and Development</th>
</tr>
</thead>
</table>

Description
A random sample of 15 countries’ research and development investments for the years 2002 and 2003 is taken and the results in millions of euros are stored in EURD.

Format
A data frame with 15 observations on the following 3 variables:

Country  a factor with levels Bulgaria, Croatia, Cyprus, Czech Republic, Estonia, France, Hungary, Latvia, Lithuania, Malta, Portugal, Romania, Slovakia, and Slovenia
RD2002  research and development investments in millions of euros for 2002
RD2003  research and development investments in millions of euros for 2003

Source

Examples

qqmath(~(RD2003 - RD2002), data = EURD, type=c("p", "r"))
Description

The carbon retained by leaves measured in kg/ha is recorded for forty-one different plots of mountainous regions of Navarra (Spain), depending on the forest classification: areas with 90% or more beech trees (*Fagus Sylvatica*) are labeled monospecific, while areas with many species of trees are labeled multispecific.

Format

A data frame with 41 observations on the following 3 variables:

- **Plot**  plot number
- **carbon**  carbon retained by leaves measured in kg/ha
- **type**  a factor with levels monospecific and multispecific

Source

*Gobierno de Navarra* and *Gestion Ambiental Viveros y Repoblaciones de Navarra*, 2006. The data were obtained within the European Project FORSEE.

References


Examples

```r
boxplot(carbon ~ type, data=fagus)
```

Description

In a weight loss study on obese cats, overweight cats were randomly assigned to one of three groups and boarded in a kennel. In each of the three groups, the cats’ total caloric intake was strictly controlled (1 cup of generic cat food) and monitored for 10 days. The difference between the groups was that group A was given 1/4 of a cup of cat food every six hours, group B was given 1/3 a cup of cat food every eight hours, and group C was given 1/2 a cup of cat food every twelve hours. The weight of the cats at the beginning and end of the study was recorded and the difference in weights (grams) is stored in the variable *Weight* of the data frame FCD. Data are used in Example 11.4.
**Fertilize**

**Format**

A data frame with 36 observations on the following 2 variables:

- **Weight** difference in weights (grams)
- **Diet** a factor with levels A, B, and C

**Source**


**Examples**

```r
# Figure 11.12
FCD.aov <- aov(Weight ~ Diet, data = FCD)
checking.plots(FCD.aov)
rm(FCD.aov)
```

---

**Fertilize**

**Cross and Auto Fertilization**

**Description**

Plants’ heights in inches obtained from two seeds, one obtained by cross fertilization and the other by auto fertilization, in two opposite but separate locations of a pot are recorded.

**Format**

A data frame with 15 observations on the following 2 variables:

- **cross** height of plant in inches
- **self** height of plant in inches

**Source**

Darwin, C. (1876) *The Effect of Cross and Self-Fertilization in the Vegetable Kingdom*

**References**


**Examples**

```r
with(data = Fertilize,
    t.test(cross, self))
```
**Carrot Shear**

**Description**

Shear measured in kN on frozen carrots from four randomly selected freezers.

**Format**

A data frame with 16 observations on the following 2 variables:

- **shear**: carrot shear measured in kN
- **freezer**: a factor with levels A, B, C, and D

**Source**


**Examples**

```r
summary(aov(shear ~ freezer, data = food))
```

**Pit Stop Times**

**Description**

Pit stop times for two teams at 10 randomly selected Formula 1 races.

**Format**

A data frame with 10 observations on the following 3 variables:

- **Race**: number corresponding to a race site
- **Team1**: pit stop times for team one
- **Team2**: pit stop times for team two

**Source**

Examples

```r
with(data = Formula1,
     boxplot(Team1, Team2))
```

---

**GD**

*Times Until Failure*

---

**Description**

Contains time until failure in hours for a particular electronic component subjected to an accelerated stress test.

**Format**

A data frame with 100 observations on the following variable:

- **attf** times until failure in hours

**Source**


**Examples**

```r
with(data = GD,
     hist(attf, prob = TRUE))
with(data = GD,
     lines(density(attf)))
# Trellis Approach
histogram(~attf, data = GD, type = "density",
          panel = function(x, ...) {
            panel.histogram(x, ...)
            panel.densityplot(x, col = "blue", plot.points = TRUE, lwd = 2)
          })
```
Blood Glucose Levels

Description

Fifteen diabetic patients were randomly selected, and their blood glucose levels were measured in mg/100 ml with two different devices.

Format

A data frame with 15 observations on the following 3 variables:

- **Patient**  patient number
- **Old**  blood glucose level in mg/100 ml using old device
- **New**  blood glucose level in mg/100 ml using new device

Source


Examples

```r
with(data = glucose,
     boxplot(Old, New))
```

GPA and SAT Scores

Description

The admissions committee of a comprehensive state university selected at random the records of 200 second semester freshmen. The results, first semester college GPA and SAT scores, are stored in the data frame Grades. Data are used in Example 12.6.

Format

A data frame with 200 observations on the following 2 variables:

- **sat**  SAT score
- **gpa**  grade point average
### Description

The consumer expenditure survey, created by the U.S. Department of Labor, was administered to 30 households in Watauga County, North Carolina, to see how the cost of living in Watauga county with respect to total dollars spent on groceries compares with other counties. The amount of money each household spent per week on groceries is stored in the variable `groceries`. Data are used in Example 8.3.

### Format

A data frame with 30 observations on the following variable:

- **groceries** total dollars spent on groceries

### Source


### Examples

```r
with(data = Grocery,
    z.test(x = groceries, sigma.x = 30, conf.level = 0.97)$conf)
```
HardWater

Mortality and Water Hardness

Description

Mortality and drinking water hardness for 61 cities in England and Wales.

Format

A data frame with 61 observations on the following 4 variables.

- **location**: a factor with levels North South indicating whether the town is as north as Derby
- **town**: the name of the town
- **mortality**: averaged annual mortality per 100,000 males
- **hardness**: calcium concentration (in parts per million)

Details

These data were collected in an investigation of environmental causes of disease. They show the annual mortality rate per 100,000 for males, averaged over the years 1958-1964, and the calcium concentration (in parts per million) in the drinking water supply for 61 large towns in England and Wales. (The higher the calcium concentration, the harder the water.)

Source


Examples

```r
plot(mortality ~ hardness, data = HardWater)
```

House

House Prices

Description

Random sample of house prices (in thousands of dollars) for three bedroom/two bath houses in Watauga County, NC
HSwrestler

Format

A data frame with 14 observations on the following 2 variables:

- **Neighborhood** a factor with levels Blowing Rock, Cove Creek, Green Valley, Park Valley, Parkway, and Valley Crucis
- **Price** price of house (in thousands of dollars)

Examples

```r
with(data = House,
    t.test(Price))
```

---

<table>
<thead>
<tr>
<th>HSwrestler</th>
<th>High School Wrestlers</th>
</tr>
</thead>
</table>

Description

The body fat of 78 high school wrestlers was measured using three separate techniques, and the results are stored in the data frame HSwrestler. The techniques used were hydrostatic weighing (HWFAT), skin fold measurements (SKFAT), and the Tanita body fat scale (TANFAT). Data are used in Examples 10.11, 12.11, and 12.12.

Format

A data frame with 78 observations on the following 9 variables:

- **AGE** age of wrestler in years
- **HT** height of wrestler in inches
- **WT** weight of wrestler in pounds
- **ABS** abdominal fat
- **TRICEPS** tricep fat
- **SUBSCAP** subscapular fat
- **HWFAT** hydrostatic fat
- **TANFAT** Tanita fat
- **SKFAT** skin fat

Source

Data provided by Dr. Alan Utter, Department of Health Leisure and Exercise Science, Appalachian State University.
References


Examples

```r
FAT <- c(HSwrestler$HWFAT, HSwrestler$TANFAT, HSwrestler$SKFAT)
GROUP <- factor(rep(c("HWFAT", "TANFAT", "SKFAT"), rep(78, 3)))
BLOCK <- factor(rep(1:78, 3))
friedman.test(FAT ~ GROUP | BLOCK)
```

---

**Hubble**

**Hubble Telescope**

Description

The Hubble Space Telescope was put into orbit on April 25, 1990. Unfortunately, on June 25, 1990, a spherical aberration was discovered in Hubble’s primary mirror. To correct this, astronauts had to work in space. To prepare for the mission, two teams of astronauts practiced making repairs under simulated space conditions. Each team of astronauts went through 15 identical scenarios. The times to complete each scenario were recorded in days.

Format

A data frame with 15 observations on the following 2 variables:

- **Team1** days to complete scenario
- **Team2** days to complete scenario

Source


Examples

```r
with(data = Hubble, 
qqnorm(Team1 - Team2))
with(data = Hubble, 
qqline(Team1 - Team2))
# Trellis Approach 
qqmath(~(Team1 - Team2), data = Hubble, type="p", "r")
```
**InsurQuotes**

<table>
<thead>
<tr>
<th>InsurQuotes</th>
<th>Insurance Quotes</th>
</tr>
</thead>
</table>

**Description**

Insurance quotes for two insurers of hazardous waste jobs

**Format**

A data frame with 15 observations on the following 2 variables:

- **companyA** quotes from company A in euros
- **companyB** quotes from company B in euros

**Source**


**Examples**

```r
with(data = InsurQuotes,
     t.test(companyA, companyB))
```

---

**interval.plot**

<table>
<thead>
<tr>
<th>Interval Plot</th>
</tr>
</thead>
</table>

**Description**

Function to graph intervals

**Usage**

```r
interval.plot(ll, ul, parameter = 0)
```

**Arguments**

- **ll**: vector of lower values
- **ul**: vector of upper values
- **parameter**: value of the desired parameter (used when graphing confidence intervals)

**Value**

Draws user-given intervals on a graphical device.
Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

Examples

```r
set.seed(385)
samples <- 100
n <- 625
ll <- numeric(samples)
ul <- numeric(samples)
xbar <- numeric(samples)
for (i in 1:samples){
xbar[i] <- mean(rnorm(n, 80, 25))
ll[i] <- xbar[i] - qnorm(.975)*25/sqrt(n)
ul[i] <- xbar[i] + qnorm(.975)*25/sqrt(n)
}
interval.plot(ll, ul, parameter = 80)
```

---

**janka**  
*Australian Eucalypt Hardwoods*

**Description**

The dataset consists of density and hardness measurements from 36 Australian Eucalypt hardwoods.

**Format**

A data frame with 36 observations on the following 2 variables.

- **Density** a measure of density of the timber
- **Hardness** the Janka hardness of the timber

**Details**

Janka Hardness is an importance rating of Australian hardwood timbers. The test measures the force required to imbed a steel ball into a piece of wood.

**Source**


**Examples**

```r
with(data = janka, plot(Hardness ~ Density, col = "blue"))
```
Kinder

Kindergarten Class

Description
The data frame Kinder contains the height in inches and weight in pounds of 20 children from a kindergarten class. Data are used in Example 12.17.

Format
A data frame with 20 observations on the following 2 variables:

- **ht** height in inches of child
- **wt** weight in pounds of child

Source

Examples

```r
# Figure 12.10
with(data = Kinder,
     plot(wt, ht))
# Trellis Approach
xyplot(ht ~ wt, data = Kinder)
```

ksdist

Simulated Distribution of $D_n$ (Kolmogorov-Smirnov)

Description
Function to visualize the sampling distribution of $D_n$ (the Kolmogorov-Smirnov one sample statistic) and to find simulated critical values.

Usage

```r
ksdist(n = 10, sims = 10000, alpha = 0.05)
```

Arguments

- **n** sample size
- **sims** number of simulations to perform
- **alpha** desired $\alpha$ level
Author(s)

Alan T. Arnholt <arnholt@AppState.edu>

See Also

ksdist

Examples

ksdist(n = 10, sims = 15000, alpha = 0.05)

ksLdist

Simulated Lilliefors’ Test of Normality Values

Description

Function to visualize the sampling distribution of $D_n$ (the Kolmogorov-Smirnov one sample statistic) for simple and composite hypotheses

Usage

ksLdist(n = 10, sims = 10000, alpha = 0.05)

Arguments

n sample size
sims number of simulations to perform
alpha desired $\alpha$ level

Author(s)

Alan T. Arnholt <arnholt@ AppState.edu>

See Also

ksdist

Examples

ksLdist(n = 10, sims = 1500, alpha = 0.05)
**Leddiode**  
*LED Diodes*

**Description**

The diameter in millimeters for a random sample of 15 diodes from each of the two suppliers is stored in the data frame Leddiode.

**Format**

A data frame with 15 observations on the following 2 variables:

- **supplierA**  
diameter in millimeters of diodes from supplier A
- **supplierB**  
diameter in millimeters of diodes from supplier B

**Source**


**Examples**

```r
with(data = Leddiode,  
    boxplot(supplierA, supplierB, col = c("red", "blue")))
```

---

**LostR**  
*Lost Revenue Due to Worker Illness*

**Description**

Data set containing the lost revenue in dollars/day and number of workers absent due to illness for a metallurgic company

**Format**

A data frame with 25 observations on the following 2 variables:

- **NumberSick**  
  number of absent workers due to illness
- **LostRevenue**  
  lost revenue in dollars

**Source**

Examples

```r
xyplot(LostRevenue ~ NumberSick, data = LostR, type=c("p", "r"))
```

---

**MilkCarton**

*Milk Carton Drying Times*

**Description**

A plastics manufacturer makes two sizes of milk containers: half gallon and gallon sizes. The time required for each size to dry is recorded in seconds in the data frame MilkCarton.

**Format**

A data frame with 40 observations on the following 2 variables:

- **Hgallon** drying time in seconds for half gallon containers
- **Wgallon** drying time in seconds for whole gallon containers

**Source**


**Examples**

```r
with(data = MilkCarton,
    boxplot(Hgallon, Wgallon))
```

---

**normarea**

*Normal Area*

**Description**

Function that computes and draws the area between two user specified values in a user specified normal distribution with a given mean and standard deviation.

**Usage**

```r
normarea(lower = -Inf, upper = Inf, m = 0, sig = 1)
```
**Arguments**

- **lower**: the desired lower value
- **upper**: the desired upper value
- **m**: the mean for the population (default is the standard normal with \( m = 0 \))
- **sig**: the standard deviation of the population (default is the standard normal with \( \sigma = 1 \))

**Value**

Draws the specified area in a graphics device

**Author(s)**

Alan T. Arnholt <arnholtat@appstate.edu>

**Examples**

```r
# Finds and graphically illustrates \( P(70 < X < 130) \) given \( X \) is N(100, 15)
normarea(lower = 70, upper = 130, m = 100, sig = 15)
```

---

**nsize**

**Required Sample Size**

**Description**

Function to determine required sample size to be within a given margin of error

**Usage**

```r
nsize(b, sigma = NULL, p = 0.5, conf.level = 0.95, type = c("mu", "pi"))
```

**Arguments**

- **b**: the desired bound
- **sigma**: population standard deviation; not required if using type "pi"
- **p**: estimate for the population proportion of successes; not required if using type "mu"
- **conf.level**: confidence level for the problem, restricted to lie between zero and one
- **type**: character string, one of "mu" or "pi", or just the initial letter of each, indicating the appropriate parameter; default value is "mu"

**Details**

Answer is based on a normal approximation when using type "pi".
Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

Examples

```r
nsizer(b = 0.015, p = 0.5, conf.level = 0.95, type = "pi")
# Returns the required sample size (n) to estimate the population
# proportion of successes with a 0.95 confidence interval
# so that the margin of error is no more than 0.015 when the
# estimate of the population proportion of successes is 0.5.
nsizer(b = 0.02, sigma = 0.1, conf.level = 0.95, type = "mu")
# Returns the required sample size (n) to estimate the population
# mean with a 0.95 confidence interval so that the margin
# of error is no more than 0.02.
```

ntester Normality Tester

Description

Q-Q plots of randomly generated normal data of the same sample size as the tested data are generated and plotted on the perimeter of the graph while a Q-Q plot of the actual data is depicted in the center of the graph.

Usage

```r
ntester(actual.data)
```

Arguments

actual.data is a numeric vector. Missing and infinite values are allowed, but are ignored in the calculation. The length of actual.data must be less than 5000 after dropping nonfinite values.

Details

Q-Q plots of randomly generated normal data of the same size as the tested data are generated and plotted on the perimeter of the graph sheet while a Q-Q plot of the actual data is depicted in the center of the graph. The p-values are calculated based on the Shapiro-Wilk W-statistic. Function will only work on numeric vectors containing less than or equal to 5000 observations. Best used for moderate sized samples (n < 50).

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>
oneway.plots

References


Examples

```r
tester(actual.data = rexp(40, 1))
# Q-Q plot of random exponential data in center plot
# surrounded by 8 Q-Q plots of randomly generated
# standard normal data of size 40.
```

oneway.plots  
*Exploratory Graphs for Single Factor Designs*

Description

Function to create dotplots, boxplots, and design plot (means) for single factor designs

Usage

```r
oneway.plots(Y, fac1, COL = c("#A9E2FF", "#0080FF"))
```

Arguments

- `Y` response variable for a single factor design
- `fac1` predictor variable (factor)
- `COL` a vector with two colors

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

See Also

`twoway.plots`, `checking.plots`

Examples

```r
with(data = Tire, oneway.plots(StopDist, tire))
```
Description

The data frame Phenyl records the level of Q10 at four different times for 46 patients diagnosed with phenylketonuria. The variable Q10.1 contains the level of Q10 measured in micromoles for the 46 patients. Q10.2, Q10.3, and Q10.4 are the values recorded at later times respectively for the 46 patients.

Format

A data frame with 46 observations on the following 4 variables.

- **Q10.1** level of Q10 at time 1 in micromoles
- **Q10.2** level of Q10 at time 2 in micromoles
- **Q10.3** level of Q10 at time 3 in micromoles
- **Q10.4** level of Q10 at time 4 in micromoles

Details

Phenylketonuria (PKU) is a genetic disorder that is characterized by an inability of the body to utilize the essential amino acid, phenylalanine. Research suggests patients with phenylketonuria have deficiencies in coenzyme Q10.

Source


References


Examples

```r
with(data = Phenyl, 
    t.test(Q10.1, conf.level = 0.99))
```
### Phone

**Telephone Call Times**

**Description**

Phone contains times in minutes of long distance telephone calls during a one month period for a small business. Data are used in Example 10.1.

**Format**

A data frame with 23 observations on the following variable:

- **call.time**  time spent on long distance calls in minutes

**Source**


**Examples**

```R
with(data = Phone, 
     SIGN.test(call.time, md = 2.1))
```

### Rat

**Rat Survival Time**

**Description**

The survival time in weeks of 20 male rats exposed to high levels of radiation.

**Format**

A data frame with 20 observations on the following variable:

- **survival.time**  number of weeks survived

**Source**


**References**

Examples

```r
with(data = Rat, 
    EDA(survival.time))
```

---

<table>
<thead>
<tr>
<th>Ratbp</th>
<th>Rat Blood Pressure</th>
</tr>
</thead>
</table>

Description

Twelve rats were chosen, and a drug was administered to six rats, the treatment group, chosen at random. The other six rats, the control group, received a placebo. The drops in blood pressure (mmHg) for the treatment group (with probability distribution F) and the control group (with probability distribution G) are stored in the variables `Treat` and `Cont`, respectively. Data are used in Example 10.18.

Format

A data frame with 6 observations on the following 2 variables:

- **Treat** drops in blood pressure in mmHg for treatment group
- **Cont** drops in blood pressure in mmHg for control group

Source

The data is originally from Ott and Mendenhall (1985, problem 8.17).

References


Examples

```r
with(data = Ratbp, 
    boxplot(Treat, Cont))
```
**Refrigerator**

### Description

Thirty 18 cubic feet refrigerators were randomly selected from a company’s warehouse. The first fifteen had their motors modified while the last fifteen were left intact. The energy consumption (kilowatts) for a 24 hour period for each refrigerator was recorded and stored in the data frame **Refrigerator**. The refrigerators with the design modification are stored in the variable `modelA`, and those without the design modification are stored in the variable `modelB`.

### Format

A data frame with 30 observations on the following 2 variables.

- **modelA** energy consumption in kilowatts for a 24 hour period
- **modelB** energy consumption in kilowatts for a 24 hour period

### Source


### Examples

```r
with(data = Refrigerator, 
    boxplot(modelA, modelB))
```

---

**Roacheggs**

### Description

A laboratory is interested in testing a new child friendly pesticide on *Blatta orientalis* (oriental cockroaches). Scientists apply the new pesticide to 81 randomly selected *Blatta orientalis* oothecae (eggs). The results from the experiment are stored in the data frame **Roacheggs** in the variable `eggs`. A zero in the variable `eggs` indicates that nothing hatched from the egg while a 1 indicates the birth of a cockroach. Data is used in Example 7.16.

### Format

A data frame with 81 observations on the following variable:

- **eggs** numeric vector where a 0 indicates nothing hatched while a 1 indicates the birth of a cockroach.
Source


Examples

```r
p <- seq(0.1, 0.9, 0.001)
negloglike <- function(p){
  -(sum(Roacheggs$eggs)*log(p) + sum(1 - Roacheggs$eggs)*log(1 - p))
}
.nlm(negloglike, 0.2)
rm(negloglike)
```

---

**Salinity**

**Surface Water Salinity**

Description

Surface-water salinity measurements were taken in a bottom-sampling project in Whitewater Bay, Florida. These data are stored in the data frame *Salinity*.

Format

A data frame with 48 observations on the following variable:

- `salinity` surface-water salinity measurements

Source


References


Examples

```r
with(data = Salinity,
     EDA(salinity))
```
Description

To estimate the total surface occupied by fruit trees in 3 small areas (R63, R67, and R68) of Navarra (Spain) in 2001, a sample of 47 square segments has been taken. The experimental units are square segments or quadrats of 4 hectares, obtained by random sampling after overlaying a square grid on the study domain. Data are used in Case Study: Fruit Trees, Chapter 12.

Format

A data frame with 47 observations on the following 17 variables:

- **QUADRAT** number of the sampled segment or quadrat
- **SArea** the small area, a factor with levels R63, R67, and R68
- **WH** area classified as wheat in sampled segment
- **BA** area classified as barley in sampled segment
- **NAR** area classified as non arable in sampled segment
- **COR** area classified as corn in sampled segment
- **SF** area classified as sunflower in sampled segment
- **VI** area classified as vineyard in sampled segment
- **PS** area classified as grass in sampled segment
- **ES** area classified as asparagus in sampled segment
- **AF** area classified as lucerne in sampled segment
- **CO** area classified as rape (*Brassica Napus*) in sampled segment
- **AR** area classified as rice in sampled segment
- **AL** area classified as almonds in sampled segment
- **OL** area classified as olives in sampled segment
- **FR** area classified as fruit trees in sampled segment
- **OBS** the observed area of fruit trees in sampled segment

Source


References

Examples

```r
with(data = satfruit,
pairs(satfruit[, 15:17]))
# Trellis Approach
splom(~data.frame(satfruit[, 15:17]), data = satfruit)
```

---

### SBIQ  
**County IQ**

---

**Description**

A school psychologist administered the Stanford-Binet intelligence quotient (IQ) test in two counties. Forty randomly selected, gifted and talented students were selected from each county. The Stanford-Binet IQ test is said to follow a normal distribution with a mean of 100 and standard deviation of 16.

**Format**

A data frame with 40 observations on the following 2 variables:

- **County1**  IQ scores for county one
- **County2**  IQ scores for county two

**Source**


**Examples**

```r
with(data = SBIQ, qqnorm(County1))  
with(data = SBIQ, qqline(County1))  
# Trellis Approach
qqmath(~County1, data = SBIQ, type=c("p", "r"))
```
Description

Twenty-five patients with schizophrenia were classified as psychotic or nonpsychotic after being treated with an antipsychotic drug. Samples of cerebral fluid were taken from each patient and assayed for dopamine b-hydroxylase (DBH) activity. The dopamine measurements for the two groups are in nmol/(ml)(h)/(mg) of protein.

Format

A data frame with 15 observations on the following 2 variables:

- **nonpsychotic** dopamine activity level for patients classified nonpsychotic
- **psychotic** dopamine activity level for patients classified psychotic

Source


References


Examples

```r
with(data = Schizo, boxplot(nonpsychotic, psychotic, names = c("nonpsychotic", "psychotic"), col = c("green", "red")))
```

---

Score

<table>
<thead>
<tr>
<th>Score</th>
<th>Standardized Test Scores</th>
</tr>
</thead>
</table>

Description

Standardized test scores from a random sample of twenty college freshmen.

Format

A data frame with 20 observations on the following variable:

- **scores** standardized test score
Description
The times recorded are those for 41 successive vehicles travelling northwards along the M1 motorway in England when passing a fixed point near Junction 13 in Bedfordshire on Saturday, March 23, 1985. After subtracting the times, the following 40 interarrival times reported to the nearest second are stored in SDS4 under the variable Times. Data are used in Example 10.17.

Format
A data frame with 40 observations on the following variable:

Times  interarrival times to the nearest second

Source

References

Examples

```r
with(data = SDS4, hist(Times))
```
SIGN.test

Sign Test

Description

This function will test a hypothesis based on the sign test and reports linearly interpolated confidence intervals for one sample problems.

Usage

SIGN.test(
  x,  
  y = NULL,  
  md = 0,  
  alternative = "two.sided",  
  conf.level = 0.95,  
  ...
)

Arguments

x numeric vector; NAs and Inf's are allowed but will be removed.
y optional numeric vector; NAs and Inf's are allowed but will be removed.
md a single number representing the value of the population median specified by the null hypothesis
alternative is a character string, one of "greater", "less", or "two.sided", or the initial letter of each, indicating the specification of the alternative hypothesis. For one-sample tests, alternative refers to the true median of the parent population in relation to the hypothesized value of the median.
conf.level confidence level for the returned confidence interval, restricted to lie between zero and one
...

Details

Computes a “Dependent-samples Sign-Test” if both x and y are provided. If only x is provided, computes the “Sign-Test.”

Value

A list of class htest_S, containing the following components:

statistic the S-statistic (the number of positive differences between the data and the hypothesized median), with names attribute “S”.
p.value the p-value for the test
conf.int is a confidence interval (vector of length 2) for the true median based on linear interpolation. The confidence level is recorded in the attribute conf.level. When the alternative is not "two.sided", the confidence interval will be half-infinite, to reflect the interpretation of a confidence interval as the set of all values k for which one would not reject the null hypothesis that the true mean or difference in means is k. Here infinity will be represented by Inf.

estimate is a vector of length 1, giving the sample median; this estimates the corresponding population parameter. Component estimate has a names attribute describing its elements.

null.value is the value of the median specified by the null hypothesis. This equals the input argument md. Component null.value has a names attribute describing its elements.

alternative records the value of the input argument alternative: "greater", "less", or "two.sided"

data.name a character string (vector of length 1) containing the actual name of the input vector x

Confidence.Intervals a 3 by 3 matrix containing the lower achieved confidence interval, the interpolated confidence interval, and the upper achieved confidence interval

Null Hypothesis

For the one-sample sign-test, the null hypothesis is that the median of the population from which x is drawn is md. For the two-sample dependent case, the null hypothesis is that the median for the differences of the populations from which x and y are drawn is md. The alternative hypothesis indicates the direction of divergence of the population median for x from md (i.e., "greater", "less", "two.sided").

Assumptions

The median test assumes the parent population is continuous.

Note

The reported confidence interval is based on linear interpolation. The lower and upper confidence levels are exact.

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

References

**SimDataST**

**See Also**

`z.test`, `zsum.test`, `tsum.test`

**Examples**

```r
with(data = Phone, SIGN.test(call.time, md = 2.1))
# Computes two-sided sign-test for the null hypothesis
# that the population median is 2.1. The alternative
# hypothesis is that the median is not 2.1. An interpolated
# upper 95% upper bound for the population median will be computed.
```

---

**SimDataST**

*Simulated Data (Predictors)*

**Description**

Simulated data for five variables. Data are used with Example 12.21.

**Format**

A data frame with 200 observations on the following 5 variables:

- **Y1**: a numeric vector
- **Y2**: a numeric vector
- **x1**: a numeric vector
- **x2**: a numeric vector
- **x3**: a numeric vector

**Source**


**Examples**

```r
xyplot(Y1 ~ x1, data = SimDataST, type=c("p", "smooth"))
```
SimDataXT | Simulated Data (Logarithms)

**Description**

Simulated data for four variables. Data are used with Example 12.18.

**Format**

A data frame with 200 observations on the following 4 variables:

- **Y** a numeric vector
- **x1** a numeric vector
- **x2** a numeric vector
- **x3** a numeric vector

**Source**


**Examples**

```r
xyplot(Y ~ x1, data = SimDataXT, type=c("p", "smooth"))
```

---

Soccer | World Cup Soccer

**Description**

Soccer contains how many goals were scored in the regulation 90 minute periods of World Cup soccer matches from 1990 to 2002. Data are used in Example 4.4.

**Format**

A data frame with 575 observations on the following 3 variables:

- **CGT** cumulative goal time in minutes
- **Game** game in which goals were scored
- **Goals** number of goals scored in regulation period
Details

The World Cup is played once every four years. National teams from all over the world compete. In 2002 and in 1998, thirty-six teams were invited; whereas, in 1994 and in 1990, only 24 teams participated. The data frame Soccer contains three columns: CGT, Game, and Goals. All of the information contained in Soccer is indirectly available from the FIFA World Cup website, located at https://www.fifa.com/.

Source


References


Examples

```r
with(data = Soccer,
    table(Goals))
```

---

### SRS

**Simple Random Sample**

**Description**

Computes all possible samples from a given population using simple random sampling

**Usage**

```r
SRS(popvalues, n)
```

**Arguments**

- `popvalues` are values of the population. NAs and Infs are allowed but will be removed from the population.
- `n` the sample size

**Details**

If non-finite values are entered as part of the population, they are removed; and the returned simple random sample computed is based on the remaining finite values.
Value

The function srs() returns a matrix containing the possible simple random samples of size n taken from a population of finite values popvalues.

Author(s)

Alan T. Arnholt <arnholt@apstate.edu>

See Also

combn

Examples

SRS(popvalues = c(5, 8, 3, NA, Inf), n = 2)

Description

In a study conducted at Appalachian State University, students used digital oral thermometers to record their temperatures each day they came to class. A randomly selected day of student temperatures is provided in StatTemps. Information is also provided with regard to subject gender and the hour of the day when the students’ temperatures were measured.

Format

A data frame with 34 observations on the following 3 variables:

- **temperature**  temperature in farenheit
- **gender**  a factor with levels Female and Male
- **class**  a factor with levels 8 a.m. and 9 a.m.

Source


Examples

bwplot(gender ~ temperature, data = StatTemps)
**Stschool**  

**School Satisfaction**

**Description**

A questionnaire is randomly administered to 11 students from State School X and to 15 students from State School Y (the results have been ordered and stored in the data frame Stschool). Data are used in Example 9.11.

**Format**

A data frame with 26 observations on the following 4 variables:

- **X** satisfaction score
- **Y** satisfaction score
- **Satisfaction** combined satisfaction scores
- **School** a factor with levels X and Y

**Source**


**Examples**

```r
with(data = Stschool,
     t.test(X, Y, var.equal = TRUE))
```

---

**Sundig**  

**Workstation Comparison**

**Description**

To compare the speed differences between two different brands of workstations (Sun and Digital), the times each brand took to complete complex simulations was recorded. Five complex simulations were selected, and the five selected simulations were run on both workstations. The resulting times in minutes for the five simulations are stored in data frame Sundig.

**Format**

A data frame with 5 observations on the following 3 variables:

- **SUN** time in seconds for a Sun workstation to complete a simulation
- **DIGITAL** time in seconds for a Digital workstation to complete a simulation
- **d** difference between Sun and Digital

```r
```
Source


Examples

```r
with(data = Sunflower, 
    t.test(SUN, DIGITAL, paired = TRUE)$conf)
```

---

**Sunflower Defoliation**

**Description**

Seventy-two field trials were conducted by applying four defoliation treatments (non defoliated control, 33%, 66%, and 100%) at different growth stages (stage) ranging from pre-flowering (1) to physiological maturity (5) in four different locations of Navarra, Spain: Carcastillo (1), Melida (2), Murillo (3), and Unciti (4). There are two response variables: yield in kg/ha of the sunflower and numseed, the number of seeds per sunflower head. Data are stored in the data frame `sunflower`. Data used in Case Study: Sunflower defoliation from Chapter 11.

**Format**

A data frame with 72 observations on the following 5 variables:

- **location**: a factor with levels A, B, C, and D for locations Carcastillo, Melida, Murillo, and Unciti respectively
- **stage**: a factor with levels stage1, stage2, stage3, stage4, and stage5
- **defoli**: a factor with levels control, treat1, treat2, and treat3
- **yield**: sunflower yield in kg/ha
- **numseed**: number of seeds per sunflower head

**Source**


**References**


**Examples**

```r
summary(aov(yield ~ stage + defoli + stage:defoli, data = sunflower))
```
**SurfaceSpain**

*Surface Area for Spanish Communities*

**Description**

Surface area (km^2) for seventeen autonomous Spanish communities.

**Format**

A data frame with 17 observations on the following 2 variables:

- **community** a factor with levels Andalucia, Aragon, Asturias, Baleares, C.Valenciana, Canarias, Cantabria, Castilla-La Mancha, Castilla-Leon, Cataluna, Extremadura, Galicia, La Rioja, Madrid, Murcia, Navarra, and P.Vasco
- **surface** surface area in km^2

**Source**


**Examples**

```r
with(data = SurfaceSpain,
    barplot(surface, names.arg = community, las = 2))
# Trellis Approach
barchart(community ~ surface, data = SurfaceSpain)
```

---

**Swimtimes**

*Swim Times*

**Description**

Swimmers' improvements in seconds for two diets are stored in the data frame Swimtimes. The values in highfat represent the time improvement in seconds for swimmers on a high fat diet, and the values in lowfat represent the time improvement in seconds for swimmers on a low fat diet. Data are used in Example 10.9.

**Format**

A data frame with 14 observations on the following 2 variables:

- **lowfat** time improvement in seconds
- **highfat** time improvement in seconds
Details

Times for the thirty-two swimmers for the 200 yard individual medley were taken right after the swimmers’ conference meet. The swimmers were randomly assigned to follow one of the diets. The group on diet 1 followed a low fat diet the entire year but lost two swimmers along the way. The group on diet 2 followed the high fat diet the entire year and also lost two swimmers.

Source


Examples

```r
with(data = Swimtimes,
      wilcox.test(highfat, lowfat))
```

<table>
<thead>
<tr>
<th>Tennis</th>
<th>Speed Detector</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

The Yonalasee tennis club has two systems to measure the speed of a tennis ball. The local tennis pro suspects one system (Speed1) consistently records faster speeds. To test her suspicions, she sets up both systems and records the speeds of 12 serves (three serves from each side of the court). The values are stored in the data frame *Tennis* in the variables Speed1 and Speed2. The recorded speeds are in kilometers per hour.

Format

A data frame with 12 observations on the following 2 variables:

- **Speed1** speed in kilometers per hour
- **Speed2** speed in kilometers per hour

Source


Examples

```r
with(data = Tennis,
     boxplot(Speed1, Speed2))
```
TestScores

Statistics Grades

Description
Test grades of 29 students taking a basic statistics course

Format
A data frame with 29 observations on the following variable:

grade  test score

Source

Examples

with(data = TestScores,
     EDA(grade))

Tire

Tire Stopping Distances

Description
The data frame Tire has the stopping distances measured to the nearest foot for a standard sized car to come to a complete stop from a speed of sixty miles per hour. There are six measurements of the stopping distance for four different tread patterns labeled A, B, C, and D. The same driver and car were used for all twenty-four measurements. Data are used in Example 11.1 and 11.2.

Format
A data frame with 24 observations on the following 2 variables:

StopDist  stopping distance measured to the nearest foot
tire  a factor with levels A, B, C, and D

Source
Examples

summary(aov(StopDist ~ tire, data = Tire))

<table>
<thead>
<tr>
<th>TireWear</th>
<th>Tire Wear</th>
</tr>
</thead>
</table>

Description

The data frame TireWear contains measurements for the amount of tread loss after 10,000 miles of driving in thousandths of an inch. Data are used in Example 11.8.

Format

A data frame with 16 observations on the following 3 variables:

- **Wear**: tread loss measured in thousandths of an inch
- **Treat**: a factor with levels A, B, C, and D
- **Block**: a factor with levels Car1, Car2, Car3, and Car4

Source


Examples

```r
par(mfrow = c(1, 2), cex = 0.8)
with(data = TireWear,
    interaction.plot(Treat, Block, Wear, type = "b", legend = FALSE))
with(data = TireWear,
    interaction.plot(Block, Treat, Wear, type = "b", legend = FALSE))
par(mfrow = c(1, 1), cex = 1)
```
Description

The `titanic3` data frame describes the survival status of individual passengers on the Titanic. The `titanic3` data frame does not contain information for the crew, but it does contain actual and estimated ages for almost 80% of the passengers.

Format

A data frame with 1309 observations on the following 14 variables:

- **pclass**: a factor with levels 1st, 2nd, and 3rd
- **survived**: Survival (0 = No; 1 = Yes)
- **name**: Name
- **sex**: a factor with levels female and male
- **age**: age in years
- **sibsp**: Number of Siblings/Spouses Aboard
- **parch**: Number of Parents/Children Aboard
- **ticket**: Ticket Number
- **fare**: Passenger Fare
- **cabin**: Cabin
- **embarked**: a factor with levels Cherbourg, Queenstown, and Southampton
- **boat**: Lifeboat
- **body**: Body IdentificationNumber
- **home.dest**: Home/Destination

Details

Thomas Cason of UVa has greatly updated and improved the `titanic` data frame using the *Encyclopedia Titanica* and created a new dataset called `titanic3`. This dataset reflects the state of data available as of August 2, 1999. Some duplicate passengers have been dropped, many errors have been corrected, many missing ages have been filled in, and new variables have been created.

Source

https://hbiostat.org/data/repo/titanic.html

References

Examples

```r
with(titanic3, 
    table(pclass, sex))
```

<table>
<thead>
<tr>
<th>TOE</th>
<th>Nuclear Energy</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

Nuclear energy (in TOE, tons of oil equivalent) produced in 12 randomly selected European countries during 2003

Format

A data frame with 12 observations on the following variable:

energy  nuclear energy measured in tons of oil equivalent

Source


Examples

```r
with(TOE, 
    plot(density(energy)))
```

<table>
<thead>
<tr>
<th>Top20</th>
<th>Tennis Income</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

Top20 contains data (in millions of dollars) corresponding to the earnings of 15 randomly selected tennis players whose earnings fall somewhere in positions 20 through 100 of ranked earnings.

Format

A data frame with 15 observations on the following variable:

income  yearly income in millions of dollars
tsum.test 65

Source

https://www.atptour.com/

References


Examples

with(data = Top20,
     EDA(income))

---

### tsum.test

**Summarized t-test**

#### Description

Performs a one-sample, two-sample, or a Welch modified two-sample t-test based on user supplied summary information. Output is identical to that produced with `t.test`.

#### Usage

```r
 tsum.test(
   mean.x, 
   s.x = NULL, 
   n.x = NULL, 
   mean.y = NULL, 
   s.y = NULL, 
   n.y = NULL, 
   alternative = c("two.sided", "less", "greater"), 
   mu = 0, 
   var.equal = FALSE, 
   conf.level = 0.95, 
   ... 
)
```

#### Arguments

- **mean.x**: a single number representing the sample mean of `x`
- **s.x**: a single number representing the sample standard deviation of `x`
- **n.x**: a single number representing the sample size of `x`
- **mean.y**: a single number representing the sample mean of `y`
- **s.y**: a single number representing the sample standard deviation of `y`
n.y               a single number representing the sample size of y
alternative       is a character string, one of "greater", "less", or "two.sided", or just
                  the initial letter of each, indicating the specification of the alternative hypothesis.
                  For one-sample tests, alternative refers to the true mean of the parent population in relation to the hypothesis value mu. For the standard two-sample tests, alternative refers to the difference between the true population mean for x and that for y, in relation to mu. For the one-sample and paired t-tests, alternative refers to the true mean of the parent population in relation to the hypothesized value mu. For the standard and Welch modified two-sample t-tests, alternative refers to the difference between the true population mean for x and that for y, in relation to mu. For the one-sample t-tests, alternative refers to the true mean of the parent population in relation to the hypothesized value mu.
mu                is a single number representing the value of the mean or difference in means specified by the null hypothesis.
var.equal         logical flag: if TRUE, the variances of the parent populations of x and y are assumed equal. Argument var.equal should be supplied only for the two-sample tests.
conf.level        is the confidence level for the returned confidence interval; it must lie between zero and one.
...               Other arguments passed onto tsum.test()

Details
If y is NULL, a one-sample t-test is carried out with x. If y is not NULL, either a standard or Welch modified two-sample t-test is performed, depending on whether var.equal is TRUE or FALSE.

Value
A list of class htest, containing the following components:

statistic        the t-statistic, with names attribute "t"
parameters       is the degrees of freedom of the t-distribution associated with statistic. Component parameters has names attribute "df".
p.value          the p-value for the test
conf.int         is a confidence interval (vector of length 2) for the true mean or difference in means. The confidence level is recorded in the attribute conf.level. When alternative is not "two.sided", the confidence interval will be half-infinite, to reflect the interpretation of a confidence interval as the set of all values k for which one would not reject the null hypothesis that the true mean or difference in means is k. Here infinity will be represented by Inf.
estimate        is a vector of length 1 or 2, giving the sample mean(s) or mean of differences; these estimate the corresponding population parameters. Component estimate has a names attribute describing its elements.
null.value is the value of the mean or difference in means specified by the null hypothesis. This equals the input argument \( \mu \). Component null.value has a names attribute describing its elements.

alternative records the value of the input argument alternative: "greater", "less" or "two.sided".

data.name is a character string (vector of length 1) containing the names x and y for the two summarized samples.

**Null Hypothesis**

For the one-sample t-test, the null hypothesis is that the mean of the population from which \( x \) is drawn is \( \mu \). For the standard and Welch modified two-sample t-tests, the null hypothesis is that the population mean for \( x \) less that for \( y \) is \( \mu \).

The alternative hypothesis in each case indicates the direction of divergence of the population mean for \( x \) (or difference of means for \( x \) and \( y \)) from \( \mu \) (i.e., "greater", "less", or "two.sided").

**Test Assumptions**

The assumption of equal population variances is central to the standard two-sample t-test. This test can be misleading when population variances are not equal, as the null distribution of the test statistic is no longer a t-distribution. If the assumption of equal variances is doubtful with respect to a particular dataset, the Welch modification of the t-test should be used.

The t-test and the associated confidence interval are quite robust with respect to level toward heavy-tailed non-Gaussian distributions (e.g., data with outliers). However, the t-test is non-robust with respect to power, and the confidence interval is non-robust with respect to average length, toward these same types of distributions.

**Confidence Intervals**

For each of the above tests, an expression for the related confidence interval (returned component conf.int) can be obtained in the usual way by inverting the expression for the test statistic. Note that, as explained under the description of conf.int, the confidence interval will be half-infinite when alternative is not "two.sided"; infinity will be represented by Inf.

**Author(s)**

Alan T. Arnholt <arnholtat@appstate.edu>

**References**

twoway.plots

Exploratory Graphs for Two Factor Designs

description
Function creates side-by-side boxplots for each factor, a design plot (means), and an interaction plot.

Usage

twoway.plots(Y, fac1, fac2, COL = c("#A9E2FF", "#0080FF"))

Arguments

Y    response variable
fac1  factor one
fac2  factor two
COL   a vector with two colors

Author(s)
Alan T. Arnholt <arnholtat@appstate.edu>

See Also

oneway.plots, checking.plots

Examples

with(data = TireWear, twoway.plots(Wear, Treat, Block))
URLaddress

<table>
<thead>
<tr>
<th>URLaddress</th>
<th>Megabytes Downloaded</th>
</tr>
</thead>
</table>

Description

The manager of a URL commercial address is interested in predicting the number of megabytes downloaded, \( \text{megasd} \), by clients according to the number minutes they are connected, \( \text{mconnected} \). The manager randomly selects (megabyte, minute) pairs, and records the data. The pairs (\( \text{megasd} \), \( \text{mconnected} \)) are stored in the data frame \( \text{URLaddress} \).

Format

A data frame with 30 observations on the following 2 variables:

- \( \text{megasd} \) megabytes downloaded
- \( \text{mconnected} \) number of minutes connected

Source


Examples

```r
xyplot(mconnected ~ megasd, data = URLaddress, type=c("p", "r"))
```

vit2005

| Apartments in Vitoria |

Description

Descriptive information and the appraised total price (in Euros) for apartments in Vitoria, Spain.

Format

A data frame with 218 observations on the following 16 variables:

- \( \text{row.labels} \) the number of the observation
- \( \text{totalprice} \) the market total price (in Euros) of the apartment including garage(s) and storage room(s)
- \( \text{area} \) the total living area of the apartment in square meters
**category**  a factor indicating the condition of the apartment with levels 2A, 2B, 3A, 3B, 4A, 4B, and 5A. The factors are ordered so that 2A is the best and 5A is the worst.

**age**  age of the apartment

**floor**  floor on which the apartment is located

**rooms**  total number of rooms including bedrooms, dining room, and kitchen

**out**  a factor indicating the percent of the apartment exposed to the elements. The levels E100, E75, E50, and E25, correspond to complete exposure, 75% exposure, 50% exposure, and 25% exposure respectively.

**conservation**  is an ordered factor indicating the state of conservation of the apartment. The levels 1A, 2A, 2B, and 3A are ordered from best to worst conservation.

**toilets**  the number of bathrooms

**garage**  the number of garages

**elevator**  indicates the absence (0) or presence (1) of elevators.

**streetcategory**  an ordered factor from best to worst indicating the category of the street with levels S2, S3, S4, and S5

**heating**  a factor indicating the type of heating with levels 1A, 3A, 3B, and 4A which correspond to: no heating, low-standard private heating, high-standard private heating, and central heating respectively.

**tras**  the number of storage rooms outside of the apartment

**Source**


**Examples**

```r
modTotal <- lm(totalprice ~ area + as.factor(elevator) + area:as.factor(elevator), data = vit2005)
modSimpl <- lm(totalprice ~ area, data = vit2005)
anova(modSimpl,modTotal)
rm(modSimpl, modTotal)
```

**Wait**  **Waiting Time**

**Description**

A statistician records how long he must wait for his bus each morning. Data are used in Example 10.4.
**Washer**

**Format**

A data frame with 15 observations on the following variable:

- **wt** waiting time in minutes

**Source**


**Examples**

```r
with(data = Wait, 
    wilcox.test(wt, mu = 6, alternative = "less"))
```

---

**Washer Diameter**

**Description**

Diameter of washers.

**Format**

A data frame with 20 observations on the following variable:

- **diameters** diameter of washer in cm

**Source**


**Examples**

```r
with(data = Washer, 
    EDA(diameters))
```
Water  

* Sodium Content of Water *

Description

An independent agency measures the sodium content in 20 samples from source X and in 10 samples from source Y and stores them in data frame `Water`. Data are used in Example 9.12.

Format

A data frame with 30 observations on the following 4 variables:

- **X**  sodium content measured in mg/L
- **Y**  sodium content measured in mg/L
- **Sodium** combined sodium content measured in mg/L
- **Source** a factor with levels X and Y

Source


Examples

```
with(data = Water,
     t.test(X, Y, alternative = "less"))
```

WCST  

* Wisconsin Card Sorting Test *

Description

The following data are the test scores from a group of 50 patients from the *Virgen del Camino* Hospital (Pamplona, Spain) on the Wisconsin Card Sorting Test.

Format

A data frame with 50 observations on the following variable:

- **score**  score on the Wisconsin Card Sorting Test
Details

The “Wisconsin Card Sorting Test” is widely used by psychiatrists, neurologists, and neuropsychologists with patients who have a brain injury, neurodegenerative disease, or a mental illness such as schizophrenia. Patients with any sort of frontal lobe lesion generally do poorly on the test.

Source


Examples

densityplot(~score, data = WCST, ref = TRUE)

WeightGain

Weight Gain in Rats

Description

The data come from an experiment to study the gain in weight of rats fed on four different diets, distinguished by amount of protein (low and high) and by source of protein (beef and cereal).

Format

A data frame with 40 observations on the following 4 variables.

ProteinSource a factor with levels Beef Cereal
ProteinAmount a factor with levels High Low
weightgain weight gain in grams

Details

The design of the experiment is a completely randomized with ten rats on each of the four treatments.

Source


Examples

aov(weightgain ~ ProteinSource*ProteinAmount, data = WeightGain)
Description

Seventeen Spanish communities and their corresponding surface area (in hectares) dedicated to growing wheat.

Format

A data frame with 17 observations on the following 3 variables:

- community: a factor with levels Andalucia, Aragon, Asturias, Baleares, C.Valenciana, Canarias, Cantabria, Castilla-La Mancha, Castilla-Leon, Cataluna, Extremadura, Galicia, La Rioja, Madrid, Murcia, Navarra, and P. Vasco
- hectares: surface area measured in hectares
- acres: surface area measured in acres

Source


Examples

```r
with(data = WheatSpain,
    boxplot(hectares))
```

Description

USA’s 2004 harvested wheat surface by state

Format

A data frame with 30 observations on the following 2 variables.

- STATES: a factor with levels AR, CA, CO, DE, GA, ID, IL, IN, KS, KY, MD, MI, MO, MS, MT, NC, NE, NY, OH, OK, OR, Other, PA, SC, SD, TN, TX, VA, WA, and WI
- ACRES: wheat surface area measured in 1000s of acres
WilcoxE.test

Source


Examples

with(data = wheatUSA2004, hist(ACRES))

WilcoxE.test

Wilcoxon Exact Test

Description

Performs exact one sample and two sample Wilcoxon tests on vectors of data.

Usage

wilcoxE.test(
  x,
  y = NULL,
  mu = 0,
  paired = FALSE,
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95
)

Arguments

x is a numeric vector of data values. Non-finite (i.e. infinite or missing) values will be omitted.

y an optional numeric vector of data values

mu a number specifying an optional parameter used to form the null hypothesis

paired a logical indicating whether you want a paired test

alternative a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "less", or "greater". You can specify just the initial letter.

conf.level confidence level of the interval
Details

If only x is given, or if both x and y are given and paired = TRUE, a Wilcoxon signed rank test of
the null hypothesis that the distribution of x (in the one sample case) or of x - y (in the paired two
sample case) is symmetric about \( \mu \) is performed.

Otherwise, if both x and y are given and paired = FALSE, a Wilcoxon rank sum test is done. In
this case, the null hypothesis is that the distribution of x and y differ by a location shift \( \mu \), and the
alternative is that they differ by some other location shift (and the one-sided alternative "greater"
is that x is shifted to the right of y).

Value

A list of class htest, containing the following components:

- statistic: the value of the test statistic with a name describing it
- p.value: the p-value for the test
- null.value: the location parameter \( \mu \)
- alternative: a character string describing the alternative hypothesis
- method: the type of test applied
- data.name: a character string giving the names of the data
- conf.int: a confidence interval for the location parameter
- estimate: an estimate of the location parameter

Note

The function is rather primitive and should only be used for problems with fewer than 19 observa-
tions as the memory requirements are rather large.

Author(s)

Alan T. Arnholt <arnholtat@appstate.edu>

References

  Wiley & Sons.

See Also

wilcox.test
Examples

```r
# Wilcoxon Signed Rank Test
PH <- c(7.2, 7.3, 7.3, 7.4)
wilcoxE.test(PH, mu = 7.25, alternative = "greater")
# Wilcoxon Signed Rank Test (Dependent Samples)
with(data = Aggression,
wilcoxE.test(violence, noviolence, paired = TRUE, alternative = "greater"))
# Wilcoxon Rank Sum Test
x <- c(7.2, 7.2, 7.3, 7.3)
y <- c(7.3, 7.3, 7.4, 7.4)
wilcoxE.test(x, y)
rm(PH, x, y)
```

### Wool

<table>
<thead>
<tr>
<th>Wool Production</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
</tbody>
</table>

### Description

Random sample of wool production in kilograms on 5 different days at two different locations

### Format

A data frame with 15 observations on the following 2 variables:

- **textileA**  wool production in thousands of kilograms
- **textileB**  wool production in thousands of kilograms

### Source


### Examples

```r
with(data = Wool,
t.test(textileA, textileB))
```
Description

This function is based on the standard normal distribution and creates confidence intervals and tests hypotheses for both one and two sample problems.

Usage

```r
z.test(
  x,
  sigma.x = NULL,
  y = NULL,
  sigma.y = NULL,
  sigma.d = NULL,
  alternative = c("two.sided", "less", "greater"),
  mu = 0,
  paired = FALSE,
  conf.level = 0.95,
  ...
)
```

Arguments

- `x` a (non-empty) numeric vector of data values
- `sigma.x` a single number representing the population standard deviation for `x`
- `y` an optional (non-empty) numeric vector of data values
- `sigma.y` a single number representing the population standard deviation for `y`
- `sigma.d` a single number representing the population standard deviation for the paired differences
- `alternative` character string, one of "greater", "less", or "two.sided", or the initial letter of each, indicating the specification of the alternative hypothesis. For one-sample tests, alternative refers to the true mean of the parent population in relation to the hypothesized value `mu`. For the standard two-sample tests, alternative refers to the difference between the true population mean for `x` and that for `y`, in relation to `mu`.
- `mu` a single number representing the value of the mean or difference in means specified by the null hypothesis
- `paired` a logical indicating whether you want a paired z-test
- `conf.level` confidence level for the returned confidence interval, restricted to lie between zero and one
- `...` Other arguments passed onto `z.test()`
Details

If \( y \) is NULL, a one-sample z-test is carried out with \( x \) provided \( \sigma_x \) is not NULL. If \( y \) is not NULL, a standard two-sample z-test is performed provided both \( \sigma_x \) and \( \sigma_y \) are finite. If \( \text{paired} = \text{TRUE} \), a paired z-test where the differences are defined as \( x - y \) is performed when the user enters a finite value for \( \sigma_d \) (the population standard deviation for the differences).

Value

A list of class \texttt{htest}, containing the following components:

- \texttt{statistic} the z-statistic, with names attribute \texttt{z}
- \texttt{p.value} the p-value for the test
- \texttt{conf.int} is a confidence interval (vector of length 2) for the true mean or difference in means. The confidence level is recorded in the attribute \texttt{conf.level}. When alternative is not "two.sided," the confidence interval will be half-infinite, to reflect the interpretation of a confidence interval as the set of all values \( k \) for which one would not reject the null hypothesis that the true mean or difference in means is \( k \). Here, infinity will be represented by \texttt{Inf}.
- \texttt{estimate} vector of length 1 or 2, giving the sample mean(s) or mean of differences; these estimate the corresponding population parameters. Component \texttt{estimate} has a names attribute describing its elements.
- \texttt{null.value} the value of the mean or difference of means specified by the null hypothesis. This equals the input argument \texttt{mu}. Component \texttt{null.value} has a names attribute describing its elements.
- \texttt{alternative} records the value of the input argument \texttt{alternative}: "greater", "less", or "two.sided".
- \texttt{data.name} a character string (vector of length 1) containing the actual names of the input vectors \( x \) and \( y \)

Null Hypothesis

For the one-sample z-test, the null hypothesis is that the mean of the population from which \( x \) is drawn is \( \mu \). For the standard two-sample z-test, the null hypothesis is that the population mean for \( x \) less that for \( y \) is \( \mu \). For the paired z-test, the null hypothesis is that the mean difference between \( x \) and \( y \) is \( \mu \).

The alternative hypothesis in each case indicates the direction of divergence of the population mean for \( x \) (or difference of means for \( x \) and \( y \)) from \( \mu \) (i.e., "greater", "less", or "two.sided").

Test Assumptions

The assumption of normality for the underlying distribution or a sufficiently large sample size is required along with the population standard deviation to use Z procedures.
Confidence Intervals

For each of the above tests, an expression for the related confidence interval (returned component conf.int) can be obtained in the usual way by inverting the expression for the test statistic. Note that, as explained under the description of conf.int, the confidence interval will be half-infinite when alternative is not "two.sided"; infinity will be represented by Inf.

Author(s)

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References


See Also

zsum.test, tsum.test

Examples

```r
with(data = Grocery, z.test(x = groceries, sigma.x = 30, conf.level = 0.97)$conf)
# Example 8.3 from PASWR.
x <- rnorm(12)
z.test(x, sigma.x = 1)
# Two-sided one-sample z-test where the assumed value for
# sigma.x is one. The null hypothesis is that the population
# mean for 'x' is zero. The alternative hypothesis states
# that it is either greater or less than zero. A confidence
# interval for the population mean will be computed.
x <- c(7.8, 6.6, 6.5, 7.4, 7.3, 7., 6.4, 7.1, 6.7, 7.6, 6.8)
y <- c(4.5, 5.4, 6.1, 6.1, 5.4, 5., 4.1, 5.5)
z.test(x, sigma.x=0.5, y, sigma.y=0.5, mu=2)
# Two-sided standard two-sample z-test where both sigma.x
# and sigma.y are both assumed to equal 0.5. The null hypothesis
# is that the population mean for 'x' less that for 'y' is 2.
# The alternative hypothesis is that this difference is not 2.
# A confidence interval for the true difference will be computed.
z.test(x, sigma.x = 0.5, y, sigma.y = 0.5, conf.level = 0.90)
# Two-sided standard two-sample z-test where both sigma.x and
# sigma.y are both assumed to equal 0.5. The null hypothesis
# is that the population mean for 'x' less that for 'y' is zero.
# The alternative hypothesis is that this difference is not
# zero. A 90% confidence interval for the true difference will
# be computed.
```
zsum.test

\[ r(x, y) \]

---

**zsum.test**  
*Summarized z-test*

**Description**

This function is based on the standard normal distribution and creates confidence intervals and tests hypotheses for both one and two sample problems based on summarized information the user passes to the function. Output is identical to that produced with `z.test`.

**Usage**

```r
zsum.test(
  mean.x,
  sigma.x = NULL,
  n.x = NULL,
  mean.y = NULL,
  sigma.y = NULL,
  n.y = NULL,
  alternative = c("two.sided", "less", "greater"),
  mu = 0,
  conf.level = 0.95,
  ...
)
```

**Arguments**

- `mean.x`: a single number representing the sample mean of `x`
- `sigma.x`: a single number representing the population standard deviation for `x`
- `n.x`: a single number representing the sample size for `y`
- `mean.y`: a single number representing the sample mean of `y`
- `sigma.y`: a single number representing the population standard deviation for `y`
- `n.y`: a single number representing the sample size for `y`
- `alternative`: is a character string, one of "greater", "less", or "two.sided", or the initial letter of each, indicating the specification of the alternative hypothesis. For one-sample tests, `alternative` refers to the true mean of the parent population in relation to the hypothesized value `mu`. For the standard two-sample tests, `alternative` refers to the difference between the true population mean for `x` and that for `y`, in relation to `mu`.
- `mu`: a single number representing the value of the mean or difference in means specified by the null hypothesis
- `conf.level`: confidence level for the returned confidence interval, restricted to lie between zero and one
- `...`: Other arguments passed onto `z.test()`
Details

If y is NULL, a one-sample z-test is carried out with x provided sigma.x is finite. If y is not NULL, a standard two-sample z-test is performed provided both sigma.x and sigma.y are finite.

Value

A list of class htest, containing the following components:

- statistic: the z-statistic, with names attribute z
- p.value: the p-value for the test
- conf.int: is a confidence interval (vector of length 2) for the true mean or difference in means. The confidence level is recorded in the attribute conf.level. When alternative is not "two.sided," the confidence interval will be half-infinite, to reflect the interpretation of a confidence interval as the set of all values k for which one would not reject the null hypothesis that the true mean or difference in means is k. Here, infinity will be represented by Inf.
- estimate: vector of length 1 or 2, giving the sample mean(s) or mean of differences; these estimate the corresponding population parameters. Component estimate has a names attribute describing its elements.
- null.value: the value of the mean or difference in means specified by the null hypothesis. This equals the input argument mu. Component null.value has a names attribute describing its elements.
- alternative: records the value of the input argument alternative: "greater", "less", or "two.sided".
- data.name: a character string (vector of length 1) containing the names x and y for the two summarized samples.

Null Hypothesis

For the one-sample z-test, the null hypothesis is that the mean of the population from which x is drawn is mu. For the standard two-sample z-test, the null hypothesis is that the population mean for x less that for y is mu.

The alternative hypothesis in each case indicates the direction of divergence of the population mean for x (or difference of means for x and y) from mu (i.e., "greater", "less", or "two.sided").

Test Assumptions

The assumption of normality for the underlying distribution or a sufficiently large sample size is required along with the population standard deviation to use Z procedures.

Confidence Intervals

For each of the above tests, an expression for the related confidence interval (returned component conf.int) can be obtained in the usual way by inverting the expression for the test statistic. Note that, as explained under the description of conf.int, the confidence interval will be half-infinite when alternative is not "two.sided"; infinity will be represented by Inf.
Author(s)

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References


See Also

z.test, tsum.test

Examples

zsum.test(mean.x = 56/30, sigma.x = 2, n.x = 30, alternative="greater", mu = 1.8)
# Example 9.7 part a. from PASWR.
x <- rnorm(12)
zsum.test(mean(x), sigma.x = 1, n.x = 12)
# Two-sided one-sample z-test where the assumed value for
# sigma.x is one. The null hypothesis is that the population
# mean for 'x' is zero. The alternative hypothesis states
# that it is either greater or less than zero. A confidence
# interval for the population mean will be computed.
# Note: returns same answer as:
# z.test(x, sigma.x = 1)

x <- c(7.8, 6.6, 6.5, 7.4, 7.3, 7.0, 6.4, 7.1, 6.7, 7.6, 6.8)
y <- c(4.5, 5.4, 6.1, 6.1, 5.4, 5.0, 4.1, 5.5)
zsum.test(mean(x), sigma.x = 0.5, n.x = 11, mean(y), sigma.y = 0.5, n.y = 8, mu = 2)
# Two-sided standard two-sample z-test where both sigma.x
# and sigma.y are both assumed to equal 0.5. The null hypothesis
# is that the population mean for 'x' less that for 'y' is 2.
# The alternative hypothesis is that this difference is not 2.
# A confidence interval for the true difference will be computed.
# Note: returns same answer as:
# z.test(x, sigma.x = 0.5, y, sigma.y = 0.5)

x <- c(7.8, 6.6, 6.5, 7.4, 7.3, 7.0, 6.4, 7.1, 6.7, 7.6, 6.8)
y <- c(4.5, 5.4, 6.1, 6.1, 5.4, 5.0, 4.1, 5.5)
zsum.test(mean(x), sigma.x = 0.5, n.x = 11, mean(y), sigma.y = 0.5, n.y = 8, conf.level=0.90)
# Two-sided standard two-sample z-test where both sigma.x and
# sigma.y are both assumed to equal 0.5. The null hypothesis
# is that the population mean for 'x' less that for 'y' is zero.
# The alternative hypothesis is that this difference is not
# zero. A 90% confidence interval for the true difference will
# be computed. Note: returns same answer as:
z.test(x, sigma.x=0.5, y, sigma.y=0.5, conf.level=0.90)
rm(x, y)
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