Package ‘dafs’

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**abaz.df**

**DNA from drinking containers**

**Description**

The amount of DNA left on different types of drinking containers.

**Usage**

```r
data(abaz.df)
```

**Format**

A data frame with 21 columns.

- **[.1]** person
  - factor
  - A label (A..F) for the 6 experimental subjects
- **[.2]** sample
  - factor
  - A treatment factor indicating the different beverage/container combinations
- **[.3]** ab.sample
  - factor
  - An abbreviated treatment label
- **[.4]** time
  - factor
  - time when DNA concentration was measured. Levels: 24hrs, 48hrs
- **[.5]** amylase
  - numeric
  - the relative amount of alpha-amylase activity
- **[.6]** quant
  - numeric
- **[.7]** amp.volume
  - numeric
- **[.8]** dna.conc
  - numeric
- **[.9]** gel.profile
  - factor
- **[.10]** failed.profile
  - factor
  - the failure or success of obtaining a usable DNA profile
- **[.11:21]** d3..fga
  - numeric
  - Total peak heights at each locus

**Author(s)**

Abaz et al.

**References**


**abduct.age.df**

**Victim abduct and the age data**

**Description**

This data was studied to investigate whether there was a relationship between whether the victim had been abducted and the age of the victims in certain crimes. The age of the victims had been classified as 0-10 and 11+.
Usage

data(abduct.age.df)

References


anneal.df

Annealing float glass

Description

Rushton was interested in the effect of annealing on the refractive index of glass. It is well known that annealing float glass changes the refractive index (RI). The change in RI - called delta-RI - can tell a forensic scientist something about the glass that they are examining.

In this data set, 3 replicate measurements were made from 150 squares of glass from a single pane. Each fragment was measured pre and post annealing.

Usage

data(anneal.df)

Format

A data frame with 900 observations on 3 variables.

[,1] ri numeric The fragment’s refractive index
[,2] temp numeric The fragment’s match temperature - this will be almost perfectly correlated with ri
[,3] anneal factor either pre or post for pre or post annealing

Author(s)

K.P. Rushton

References

bennett.df

Description
This data is known as the Anscombe quartet. Each of sets has two variables, x and y. In each data set, x and y have the same mean (9 and 7.5), the same standard deviation (3.32 and 2.03) and the same correlation (0.82).

Usage
data(anscombe.df)

References

bennett.df

Bennett data

Description
This data has 10 rows and 49 columns corresponding 10 refractive index (RI) measurements from 49 different locations in a windowpane.

Usage
data(bennett.df)

References

bottle.df

Bottle data

Description
This data contains the elemental concentration of five different elements (Manganese, Barium, Strontium, Zirconium, and Titanium) in samples of glass taken from six different Heineken beer bottles at four different locations (Base, Body, Shoulder, and Neck). Five repeat measurements are made on each sample at each location.

Usage
data(bottle.df)

References
**Description**

This data has 10 refractive index (RI) measurement from recovered glass fragments and ..... 

**Usage**

```r
data(casework.df)
```

**Author(s)**

James Curran

---

**cck196.df**  
*CCK-196G/A data*

**Description**

This data has genotype of Cholecystokinin (CCK) gene promoter regions of -196G/A from selected suicide victims (S) and from control subjects (C).

**Usage**

```r
data(cck196.df)
```

**References**


---

**cck45.df**  
*CCK-45C/T data*

**Description**

This data has genotype of Cholecystokinin (CCK) gene promoter regions of -45C/T from selected suicide victims (S) and from control subjects (C).

**Usage**

```r
data(cck45.df)
```

**References**

Description

This data has number of misleading signatures in comparisons of 16 genuine signatures and 64 simulated signatures from 15 document examiners.

Usage

data(docexam.df)

References


Description

This data measured deoxypyridinoline (DPD) to estimate human age. DPD is a nonreducible collagen crosslink that can be measured in human dentin samples extracted from permanent individual molars. Measurements were made in dentin samples from 22 patients with ages ranging from 15 to 73.

Usage

data(dpd.df)

References

Textile fibres in human hair data

Description

This data comes from a population study of textile fibres in human hair in Cambridgeshire, UK, 2002. It was carried out using 26 volunteers, and 12149 fibres were recovered from a variety of hair lengths using low adhesive tape and classified according to colour, generic type and fibre length. This data has percentage distribution of fibres in head hair according to colour.

Usage

data(fiber.color.df)

References


fitPvalue

Return the P-value from an F-test for a linear model

Description

This functions the P-value from the (null) hypothesis that all of the linear predictors are zero or not-significant.

Usage

fitPvalue(fit)

Arguments

fit a lm object.

Details

summary returns an invisible vector called fstatistic that contains the F-statistic and the degrees of freedom used to test the hypothesis that all of the linear predictors are zero or not-significant. This function takes those values and returns the appropriate upper tail probability from the F-distribution.

Value

A P-value
formatScientificTeX

Author(s)
James Curran

See Also
summary.lm

Examples

```r
x = runif(100, 1, 10)
y = 2 + 3*x + rnorm(100)
fit = lm(y~x)
fitPvalue(fit)
```

formatScientificTeX

Format a number in scientific notation into LaTeX.

**Description**

Format a number in standard scientific format XXX.XXEXXX into a string that can be typeset by LaTeX.

**Usage**

```r
formatScientificTeX(x, width, digits)
```

**Arguments**

- **x**
  The number to be formatted. This number does not need to be in scientific format.
- **width**
  width and digits are interpreted in the same way that they are for the C function sprintf. The number will be formatted so that it takes x times 10 to the power of y, where x is formatted so that the number has width characters in total (including a decimal point) and digits decimal places.
- **digits**
  See width.

**Details**

If x = 300.123, width = 4 and digits = 1, then this function will return "3.0\times 10^2"

**Value**

A string that will format in a LaTeX inline math environment.

**Author(s)**
James Curran
See Also

sprintf

Examples

fmtST(300.123, 1, 4)

---

gc.df  FBI-Gc data

Description

This data has the human group-specific component (Gc) genotypes of African Americans, Caucasians, and South Western Hispanics. The Gc locus has alleles A, B, and C and hence, the possible genotype are AA, AB, AC, BB, BC, and CC.

Usage

data(gc.df)

References

FBI reference database

---

ghb.df  Gamma-hydroxybutyric acid data

Description

This data comes from a gamma-hydroxybutyric acid (GHB) experiment, which has three groups of individuals: (1) volunteers with no alcoholic history, (2) alcoholics who were waiting to start a GHB treatment program but had not yet received the drug, (3) alcoholics currently being treated with GHB, and measured the endogenous GHB concentration (ug/mL) in each.

Usage

data(ghb.df)

References

**gustafson.df**  

**Teeth data**

**Description**  
This data is collected from 41 teeth, which were scored on a number of variables.

**Usage**  
data(gustafson.df)

**References**  

**halfnorm**  

**Produce a half normal plot**

**Description**  
Produce a half normal plot for a fitted `lm` or `glm` object. This function should work for any class that implements `residuals`.

**Usage**  
halfnorm(fit)

**Arguments**  
fit A `lm` or `glm` object.

**Details**  
The absolute value of the residuals are plotted against the positive quantiles of the normal distribution. The largest 5 percent of the empirical quantiles are labelled to help identify potential outliers.

**Value**  
No values are returned.

**Note**  
The labelling of the largest 5 percent is utterly arbitrary.

**Author(s)**  
J.M. Curran
intPlot  

Modified Interactions Plot for Two-way Analysis of Variance

Description

This is a modified version of the function interactionPlots from the s20x library which produces greyscale plots.

Displays data with intervals for each combination of the two factors and shows the mean differences between levels of the first factor for each level of the second factor. Note that there should be more than one observation for each combination of factors.

Usage

intPlot(y, ...)
  ## Default S3 method:
  intPlot(y,
         fac1 = NULL,
         fac2 = NULL,
         xlab = NULL,
         xlab2 = NULL,
         ylab = NULL,
         data.order = TRUE,
         exlim = 0.1,
         jitter = 0.02,
         conf.level = 0.95,
         interval.type = "tukey",
         pooled = TRUE,
         tick.length = 0.1,
         interval.distance = 0.2,
         col.width = 2/3,
         xlab.distance = 0.1,
         xlen = 1.5,
         ylen = 1,
         ...
  )

## S3 method for class 'formula'
intPlot(y,
        data,
        xlab = NULL,
        xlab2 = NULL,
        ylab = NULL,
        data.order = TRUE,
        exlim=0.1,
        jitter=0.02,
        conf.level=0.95,
        interval.type = "tukey",
        pooled = TRUE,
tick.length = 0.1,
interval.distance = 0.2,
col.width = 2/3,
xlab.distance = 0.1,
xlen=1.5,
ylen = 1,
...)

Arguments

y

either a formula of the form: y~fac1+fac2 where y is the response and fac1 and fac2 are the two explanatory variables used as factors, or a single response vector.

fac1

if 'y' is a vector, then fac1 contains the levels of factor 1 which correspond to the y value.

fac2

if 'y' is a vector, then fac1 contains the levels of factor 2 which correspond to the y value.

data

an optional data frame containing the variables in the model.

xlab

an optional label for the x-axis. If not specified the name of fac1 will be used.

xlab2

an optional label for the lines. If not specified the name of fac2 will be used.

ylab

An optional label for the y-axis. If not specified the name of y will be used.

data.order

if TRUE the levels of fac1 and fac2 will be set to unique(fac1) and unique(fac2) respectively.

exlim

provide extra limits.

jitter

the amount of horizontal jitter to show in the plot. The actual jitter is determined as the function is called, and will likely be different each time the function is used.

conf.level

confidence level of the intervals.

interval.type

four options for intervals appearing on plot: "tukey", "hsd", "lsd" or "ci".

pooled

two options: pooled or unpooled standard deviation used for plotted intervals.

tick.length

size of tick, in inches.

interval.distance

distance, as a fraction of the column width, between the points and interval. This is in addition to the extra space allocated for the jitter.

col.width

width of a factor ‘column’, as a fraction of the space between the centres of two columns.

xlab.distance

distance of x-axis labels from bottom of plot, as a fraction of the overall height of the plot.

xlen, ylen

xxx

...

optional arguments.

Examples

library(s20x)
data(mtcars)
intPlot(wt~vs+gear, mtcars)
Description

This data comes from a pilot experiment, which fired a sequence of 10 shots through a set of six paper targets that were equally spaced from 3 ft to 18 ft and recorded the size of the pellet pattern at 18 ft. They then repeated the experiment with five of the targets removed and a single target at 18 ft. The third variable indicate with and without intermediate targets.

Usage

data(jauhari1.df)

References


Description

This data comes from a pilot experiment by Jauhari et al. They fired a sequence of 10 shots through a set of six paper targets that were equally spaced from 3 ft to 18 ft and recorded the size of the pellet pattern at 18 ft.

Usage

data(jauhari2.df)

References

In this data set are the results of 93 human cadaver crash tests. The tests were used in the development of thoracic injury risk functions with consideration of age and restraint condition. The data can be used with logistic regression models by recoding the variable fracture into <6 and >=6, or with a Poisson/quasi-Poisson/negative binomial GLM.

Usage

data(kent.df)

Value

A data frame with ... variables

Author(s)

Kent. R, and Petrie, J.

References


Examples

data(kent.df)

# recode the response fracture to minor injury (<6 rib fractures) and severe injury (>=6 rib fractures)
#kent.df = within(kent.df, {
  # injury = factor(ifelse(fractures<6,'minor','severe'),
  # levels = c('severe','minor'))
#
# fit a binomial GLM
# kent.fit = glm(injury~cmax*
kerckring.df  Kerckring data

Description
This data was analyzed the process of Kerckring on the occipital bone of numbers black and white perinates. The process of Kerckring is a projection of bone occasionally observed emerging from the inferior margin of the supraoccipital portion of the occipital squamous at the midline. Its status was regarded as either absent or present.

Usage
data(kerckring.df)

References

---

last  Return the last element of a vector.

Description
Return the last element of a vector

Usage
last(x)

Arguments

    x            a vector

Author(s)
James Curran

Examples

    x = 1:10
    last(x)
liver.df

Liver data

Description

The data record information on the presence or absence of extramedullary haematopoiesis (EMH) symptoms in 51 liver of sudden infant death (SIDS) and 102 non-SIDS cases.

Usage

data(liver.df)

References


morphine.df

Morphine concentration in heart and peripheral blood samples

Description

Data was compiled from 126 morphine-involved cases investigated by the Office of the Chief Medical Examiner, State of Maryland, USA. An investigation was conducted into whether comparison of morphine concentrations from a central and peripheral site could be used to determine whether a morphine death was acute or delayed. Fifty cases were identified as 'acute' because the urine free morphine concentration by radioimmunoassay (RIA) was less than 25 ng/mL; 76 cases were classified as 'random' because they had a urine morphine concentration greater than 25 ng/mL by RIA. The average heart blood to peripheral blood morphine concentration ratio in the acute deaths was 1.40. The average heart blood to peripheral blood morphine concentration ratio in the random deaths was 1.18. Because there was considerable overlap between the two groups of data, the authors conclude that it was not possible to predict 'acute' opiate intoxication deaths versus 'delayed' deaths when the only information available is heart and peripheral blood free morphine concentrations.

Usage

data(morphine.df)

Author(s)

Levine et al.
References


nasal.spline.df  Nasal spine data

Description

This data was analyzed the projection of the anterior nasal spine on the maxillae of numbers black and white perinates. The anterior nasal spine was assessed by its forward projection away from the frontal plane of the anterior maxillary surface. This was best assessed from the lateral and/or superior perspective. Projection was described as slight, moderate or pronounced.

Usage

data(nasal.spline.df)

References


newton.df  Glass strata data

Description

This data has refractive index (RI) measurements for 30 fragments on each of the five strata - float surface (FS), near float surface (NFS), bulk (B), near anti-float (NAFS), and anti-float (AFS).

Usage

data(newton.df)

References

nzglass.df

New Zealand glass RI data

Description
This data has refractive index (RI) measurements made on glass fragments recovered in New Zealand case work.

Usage
data(nzglass.df)

Author(s)
John Buckleton, Sally Coulson, Tony Gummer, Angus Newton, Gerhard Wevers, Kevan Walsh (and ESR)

pairsDAFS

Modified Pairwise Scatter Plots with Histograms and Correlations

Description
This is a modified version of the pairs20x function from the s20x library which produces greyscale plots.
Plots pairwise scatter plots with histograms and correlations for the data frame.

Usage
pairsDAFS(x, ...)

Arguments
x a data frame.
... optional arguments which are passed to the generic pairs function.

Value
Returns the plots.

Examples
```r
# peruvian indians
library(s20x)
data(peru.df)
pairsDAFS(peru.df)
```
**palatal.df**  
*Palatal arch shape data*

**Description**

This data was analyzed the shape of the palatal arch on the maxillae of numbers black and white perinates. Palatal arch shape was determined by the curve formed by the inner alveolar margin. In order to determine shape, the separate maxillary halves were joined together at the midline. If the inner alveolar margins were observed to converge gradually along a continuous arc towards the midline, the palate was considered parabolic. On the other hand, if the inner alveolar margins were parallel to each other without converging until anterior of the premolars, the palate was considered hyperbolic. If the palate fell somewhere in between, it was considered intermediate.

**Usage**

```r
data(palatal.df)
```

**References**


---

**plotBoth**  
*Produce postscript and pdf images simultaneously*

**Description**

Produce simulataneous postscript and pdf images using a user defined plot function.

**Usage**

```r
plotBoth(plotfn, filename, control = plotBoth.control(), ...)
```

**Arguments**

- `plotfn`  
  A function containing the plotting commands

- `filename`  
  The name of the output file - .eps and .pdf will be appended to the postscript and pdf images respectively

- `control`  
  The results of plotBoth.control controls font embedding and plotting.

- `...`  
  Any additional arguments that need to be fed to plotfn

**Author(s)**

J.M. Curran
plotBoth.control

See Also

plotBoth.control

Examples

## Not run: plotBoth(function()
  plot(rnorm(100),rnorm(100)), 'test')
## End(Not run)

plotBoth.control  Control over plotBoth function

Description

Gives user control over font embedding and plot generation.

Usage

plotBoth.control(genPlots = .genPlots, embedF = .embedF, embedFoptions = .embedFoptions)

Arguments

genPlots    TRUE or FALSE depending on whether plotBoth should produce a plot
embedF     TRUE or FALSE depending on whether font embedding is desired
embedFoptions  A string containing all the font embedding options to be sent to Ghostscript

Value

A list containing the values of the variables genPlots, embedF, and embedFoptions

Author(s)

J Curran
plotRegDiagPlots  
Plot some standard regression diagnostic plots

Description

Produces 3 plots in a 2 x 2 array. The plots are a plot of residuals versus predicted values (pred-res plot), a histogram of the residuals with a normal distribution superimposed, and a normal QQ-plot of the residuals.

Usage

plotRegDiagPlots(fit)

Arguments

fit  
A lm object

Author(s)

J Curran

See Also

plot.lm

Examples

x = runif(100)
y = 3*x+2+dnorm(100)
fit = lm(y~x)
plotRegDiagPlots(fit)

printANODEVTable  
Print an analysis of deviance (ANODEV) table for a GLM

Description

Formats the column headings an table for a GLM using the input of xtable.

Usage

printANODEVTable(xtbl,  
sanitize.text.function = function(x){x},
test = NULL, ...)

printANOVATable

Arguments

  xtbl  The output of xtable applied to the summary output of a normal GLM.
  sanitize.text.function
    Don't change this
  test  "Chisq" or "F" depending on the desired test
  ...  Extra arguments to be fed to print.xtable

Value

  A LaTeX formatted ANODEV table

Author(s)

  J Curran

See Also

  print.xtable

Description

  Formats the column headings an ANOVA table for a normal GLM using the input of xtable.

Usage

  printANOVATable(xtbl, sanitize.text.function = function(x){x}, ...)

Arguments

  xtbl  The output of xtable applied to the summary output of a normal GLM.
  sanitize.text.function
    Don't change this
  ...  Extra arguments to be fed to print.xtable

Value

  A LaTeX formatted ANOVA table

Author(s)

  J Curran

See Also

  print.xtable
printCI

Produce a formatted confidence interval

Description
Takes a vector of length two and prints out a confidence interval in a user specified format.

Usage
printCI(x, fmt)

Arguments
x A vector of length two containing the lower and upper bounds of a confidence interval
fmt A format string to be used by sprintf. Note that this format string is repeated twice in the code for each bound of the confidence interval.

Value
A string containing the formatted CI

Author(s)
James Curran

See Also
sprintf

Examples
n = 100
x = rnorm(n)
mx = mean(x)
se = sd(x)/sqrt(n)
clip = mx + qnorm(c(0.025,0.975))*se
printCI(ci, '%5.2f')
printRegTable

*Print a regression table*

**Description**

Formats the column headings a regression table using the input of `xtable`.

**Usage**

```r
printRegTable(xtbl, sanitize.text.function = function(x){x},
               test = 't', ...)
```

**Arguments**

- `xtbl` - The output of `xtable` applied to the `summary` output of a normal GLM.
- `sanitize.text.function` - Don’t change this
- `test` - “t” or “z” depending on the desired test
- `...` - Extra arguments to be fed to `print.xtable`

**Value**

A LaTeX formatted regression table

**Author(s)**

J Curran

**See Also**

`print.xtable`

---

**pvalue**

*Formats an P-value figure for LaTeX*

**Description**

Produces a math-mode formatted string for a P-value.

**Usage**

```r
pvalue(p, fmt = "$P = %.4f")
```
### Arguments

- **p**  
  The P-value

- **fmt**  
  A formatting string for LaTeX

### Value

A string that will be correctly formatted by LaTeX

### Author(s)

J Curran

### See Also

Sweave

### Examples

```r
p = 0.04
pvalue(p)
```

---

### Description

This data is combined from two calibration experiments which are conducted by Dr. Grzegorz Zadora and Bennett. The factor owner has two levels, RB for Rachel Bennett, and GZ for Grzegorz Zadora. The calibration of the instrument was established using standard glasses (Locke Scientific) set B1-B12 (RI=1.52912-1.520226).

### Usage

```r
data(ri.calibration.df)
```

### References

ri.calibration2.df

GRIM2 calibration data

Description
This data comes from a 2nd generation Glass Refractive Index Measurer (GRIM2) calibration experiment. The calibration of the instrument was established using standard glasses (Locke Scientific) set B1-B12 (RI=1.52912-1.520226). Each of the twelve reference sample glasses B1-B12 was measured five times.

Usage
data(ri.calibration2.df)

References
Dr. Grzegorz Zadora from the Institute for Forensic Research in Krakow, Poland.

Rsq

Formats an R-squared figure for LaTeX

Description
Produces a math-mode formatted string for R-squared.

Usage
Rsq(R, fmt = "$R^2 = %6.4f\$", adj = FALSE)

Arguments

R
The R-squared value

fmt
A formatting string for LaTeX

adj
If TRUE appends 'adjusted ' to the format string

Value
A string that will be correctly formatted by LaTeX

Author(s)
J Curran

See Also
Sweave
Salting out effects in forensic blood alcohol determination

Description

Blood alcohol measurements determined by headspace gas chromatography have been challenged on the grounds that the presence of the preservative sodium fluoride in blood samples artificially increases headspace alcohol concentrations due to a salting out effect. Blood samples containing varying amounts of ethanol and sodium fluoride (NaF) were tested using semi-automated headspace gas chromatography with n-propyl alcohol as the internal standard to assess the validity of this challenge. Miller et al found, in fact, that under these test conditions the measured alcohol levels are systematically depressed as the amount of sodium fluoride in the blood sample increases.

Blood was drawn from each of six subjects near the time of estimated peak blood alcohol concentration. Each subject had three blood samples taken to which 0, 5, and 10mg/mL of NaF were added. The blood alcohol concentration for each tube was determined twice for each tube.

Usage

data(salting1.df)

Format

A data frame containing four variables

| [1] | subject | numeric factor | subject identifier 1-6 |
| [2] | tube    | numeric factor | tube 1,2,3 for each subject |
| [3] | rep     | numeric factor | levels 1,2 indicating replicate measurement |
| [4] | NaF     | numeric factor | the level of sodium fluoride added in mg/mL |
| [5] | conc    | numeric       | alcohol concentration in g/100mL |

Details

Note that the blocking and treatment factors in this data frame are numeric. Therefore, to use them as such will require the use of factor or ordered.

Author(s)

B. A. Miller et al.
References


Description

Blood alcohol measurements determined by headspace gas chromatography have been challenged on the grounds that the presence of the preservative sodium fluoride in blood samples artificially increases headspace alcohol concentrations due to a salting out effect. Blood samples containing varying amounts of ethanol and sodium fluoride (NaF) were tested using semi-automated headspace gas chromatography with n-propyl alcohol as the internal standard to assess the validity of this challenge. Miller et al found, in fact, that under these test conditions the measured alcohol levels are systematically depressed as the amount of sodium fluoride in the blood sample increases.

Blood was drawn from each of four subjects at two time points, first near the time of estimated peak blood alcohol concentration and then approximately 1.5 hours later. Samples were initially analyzed with NaF at manufacturer’s levels (ca. 10 mg/mL).

Usage

data(salting2.df)

Format

A data frame containing four variables

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>[,1]</td>
<td>subject</td>
<td>numeric factor</td>
<td>subject identifier 1-4</td>
</tr>
<tr>
<td>[,2]</td>
<td>time</td>
<td>numeric factor</td>
<td>time sample taken 0 or 1.5h</td>
</tr>
<tr>
<td>[,3]</td>
<td>NaF</td>
<td>numeric factor</td>
<td>the level of sodium fluoride added in mg/mL</td>
</tr>
<tr>
<td>[,4]</td>
<td>EtOH</td>
<td>numeric</td>
<td>alcohol concentration in g/100mL</td>
</tr>
</tbody>
</table>

Details

Note that the blocking and treatment factors in this data frame are numeric. Therefore, to use them as such will require the use of factor or ordered.

Author(s)

B. A. Miller et al.
References


sex.age.df Victims data

Description

This data is collected gender and age of victims in certain crimes. The age of the victims had been classified as 0-10 and 11+.

Usage
data(sex.age.df)

References


shadeDens Add a shaded region to a pdf plot

Description

Useful for shading regions of interest (critical regions perhaps) on a theoretical pdf to illustrate concepts such as P-values.

Usage
shadeDens(x0, x1, dens, col = "lightgrey", n.points = 200, lty = 1,...)

Arguments

x0 A starting x-value for the region to be shaded
x1 An ending x-value for the region to be shaded
dens A function that calculates the pdf
col A color for the shaded region
n.points The number of points to calculate the pdf at over the interval [x0,x1]
lty Line type
... Additional arguments to be fed to dens such as degrees of freedom, mean or standard deviation
Details

Adds a filled polygon to an existing pdf plot.

Author(s)

J Curran

Examples

```r
x = seq(-4.5, 4.5, by = 0.01)
plot(x, dnorm(x), type = 'l')
x0 = qnorm(0.975)
x1 = 4.5
shadeDens(x0, x1, dnorm)
```

Description

In order to test the validity of range-of-fire estimates obtained by the application of regression analysis to shotgun pellet patterns, a blind study was conducted in which questioned pellet patterns were fired at randomly selected ranges between 3.0 and 15.2 m (10 and 50 ft) with two different 12-gauge shotguns, each firing a different type of buckshot cartridge. Test firings at known ranges were also conducted with the same weapons and ammunition.

Usage

```r
data(shotgun.df)
```

Format

A data frame with 3 variables:

1. range numeric the range in feet of the firing
2. sqrt.area numeric the square root of the area of the smallest rectangle that would enclose the pellet pattern
3. model factor the model of shotgun used in the experiment

Author(s)

J.M. Curran

References

**squamous.df**  
*Occipital squamous bone data*

**Description**

This data has been recorded the shape of the occipital squamous bone as narrow, equal, or greater for different races.

**Usage**

```r
data(squamous.df)
```

**References**


**StangleBook**  
*Stangle a set of files*

**Description**

Stangle more than one file at once. This is a helper function to Stangle all the chapters in Data Analysis for Forensic Scientists (DAFS) at once. I have put it into the library for completeness and in the hope that someone else might find it useful.

**Usage**

```r
StangleBook(idx = 0:6,  
  fileList = paste(paste("Chapter", idx, "/", sep = ""),  
                  paste("ch", idx, ".rnw", sep = ""),  
                  sep = ")
```

**Arguments**

- **idx**
  
  There seven chapters in Data Analysis for Forensic Scientists. Corresponding to each chapter is a folder named ChapterI where I is a number from 0 to 6, and an Sweave file named chI.rnw. This parameter lets the user select which subset of files need to be run through Stangle

- **fileList**
  
  This parameter may be altered to suit the structure of your book. By default it is set to create a list of files that have the same name and directory structure as DAFS. The function iterates over a set of file names specified by this parameter.
SweaveBook

Value
No values are returned

Author(s)
James Curran

See Also
Stangle

SweaveBook
Sweave a set of files

Description
Sweave more than one file at once. This is a helper function to Sweave all the chapters in Data Analysis for Forensic Scientists (DAFS) at once. I have put it into the library for completeness and in the hope that someone else might find it useful.

Usage
```
SweaveBook(idx = 0:6, 
    fileList = paste(paste("Chapter", idx, "/", sep = ""), 
        paste("ch", idx, ".rnw", sep = ""), 
        sep = ""))
```

Arguments
idx
There seven chapters in Data Analysis for Forensic Scientists. Corresponding to each chapter is a folder named ChapterI where I is a number from 0 to 6, and an Sweave file named chI.rnw. This parameter lets the user select which subset of files need to be run through Sweave

fileList
This parameter may be altered to suit the structure of your book. By default it is set to create a list of files that have the same name and directory structure as DAFS. The function iterates over a set of file names specified by this parameter.

Value
No values are returned

Author(s)
James Curran

See Also
Sweave
tryptase.df  Tryptase data

Description
This data has tryptase concentrations, which was measured in blood from the femoral vein in 60 deaths: 39 control cases who died rapidly (within minutes) from natural causes (sudden cardiac death and acute aortic dissection), 16 with death caused by prolonged asphyxia (traumatic compression of the chest and suffocation due to body position or smothering), and five anaphylactic deaths. In 44 of these cases, tryptase was measured in both heart (Tryp.cor) and femoral blood (Tryp.fem).

Usage
data(tryptase.df)

References

velocity.df  Calibration data

Description
This data is about calibration between gun powder loading and speed.

Usage
data(velocity.df)

References
Vitreous Humour Carbohydrate Deficient Transferrin

Description

This data has the carbohydrate-deficient transferrin concentration in vitreous humour (VH-CDT) in 21 alcoholics and 7 non-alcoholics.

Usage

data(vhcdt.df)

Format

The data consist of a data frame with 28 observations on 7 variables.

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>age integer age in years</td>
</tr>
<tr>
<td>[2]</td>
<td>alc factor levels (Y, N)</td>
</tr>
<tr>
<td>[3]</td>
<td>vhcdt1 double vitreous humour carbohydrate deficient transferrin concentration (micrograms per liter)</td>
</tr>
<tr>
<td>[4]</td>
<td>vhcdt2 double vitreous humour carbohydrate deficient transferrin concentration (micrograms per liter)</td>
</tr>
<tr>
<td>[5]</td>
<td>vhtf double vitreous humour transferrin (micrograms per liter)</td>
</tr>
<tr>
<td>[6]</td>
<td>td integer time interval to autopsy since found dead</td>
</tr>
<tr>
<td>[7]</td>
<td>td integer time interval to autopsy since found alive</td>
</tr>
</tbody>
</table>

vhcdt1 had a detection limit of 5 micrograms per liter. Observations below this level were coded as 2.5. Similarly in the second assay a detection limit of 2.5 micrograms per liter was used. Observations below this threshold were coded as 1.125.

Author(s)

Berkowicz, A. et al.

References

Description

This data comes from a glass fragments experiment, count the number of glass fragments on the ground that were recovered after a window pane was shot with a handgun. The projectile velocity was controlled by altering the amount of gunpowder added to each bullet. The hardness (as measured on the Rockwell scale of hardness) of each projectile was altered by changing the amount of antimony (Sb) added to the projectile lead during casting. The profile of the projectile was changed by using a round-nose (RN) or wad-cutter (WC) mold. A full factorial design was used to allocate combinations of the factors (velocity, hardness, and profile) to the experimental units (shots). There were four velocity levels, three hardness levels, and two profile levels.

Usage

data(wong.df)

References

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