Package ‘ILS’

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Description It performs interlaboratory studies (ILS) to detect those laboratories that provide non-consistent results when comparing to others. It permits to work simultaneously with various testing materials, from standard univariate, and functional data analysis (FDA) perspectives. The univariate approach based on ASTM E691-08 consist of estimating the Mandel’s h and k statistics to identify those laboratories that provide more significant different results, testing also the presence of outliers by Cochran and Grubbs tests, Analysis of variance (ANOVA) techniques are provided (F and Tuckey tests) to test differences in means corresponding to different laboratories per each material. Taking into account the functional nature of data retrieved in analytical chemistry, applied physics and engineering (spectra, thermograms, etc.). ILS package provides a FDA approach for finding the Mandel’s k and h statistics distribution by smoothing bootstrap resampling.
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<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>boot.sim.set</td>
<td>2</td>
</tr>
<tr>
<td>cox.trend</td>
<td>3</td>
</tr>
<tr>
<td>DSC</td>
<td>4</td>
</tr>
<tr>
<td>func.ils.formula</td>
<td>5</td>
</tr>
<tr>
<td>Glucose</td>
<td>5</td>
</tr>
<tr>
<td>grubbs.test</td>
<td>6</td>
</tr>
<tr>
<td>h.qcs</td>
<td>7</td>
</tr>
<tr>
<td>IDT</td>
<td>9</td>
</tr>
<tr>
<td>ILS</td>
<td>10</td>
</tr>
<tr>
<td>ils.fqdata</td>
<td>10</td>
</tr>
<tr>
<td>ils.fqcs</td>
<td>11</td>
</tr>
<tr>
<td>k.qcs</td>
<td>12</td>
</tr>
<tr>
<td>lab.aov</td>
<td>14</td>
</tr>
<tr>
<td>lab.qcdata</td>
<td>15</td>
</tr>
<tr>
<td>lab.qcs</td>
<td>16</td>
</tr>
<tr>
<td>mandel.fqcs</td>
<td>17</td>
</tr>
<tr>
<td>outliers.ils</td>
<td>19</td>
</tr>
<tr>
<td>plot.ils.fqdata</td>
<td>19</td>
</tr>
<tr>
<td>plot.ils.fqcs</td>
<td>21</td>
</tr>
<tr>
<td>plot.lab.qcdata</td>
<td>22</td>
</tr>
<tr>
<td>plot.lab.qcs</td>
<td>22</td>
</tr>
<tr>
<td>plot.mandel.fqcs</td>
<td>23</td>
</tr>
<tr>
<td>TG</td>
<td>24</td>
</tr>
</tbody>
</table>

Index 26

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>boot.sim.set</td>
<td>2</td>
</tr>
<tr>
<td>Bootstrap samples of a functional statistic</td>
<td></td>
</tr>
</tbody>
</table>

Description

data.bootstrap provides bootstrap samples for functional data.

Usage

boot.sim.set(x, smo = 0.05)

Arguments

x An object of class fdata.
smo The smoothing parameter for the bootstrap samples.
cochran.test

Function to compute the Cochran test statistic

Description

Function to estimate the Cochran test statistic.

Usage

cochran.test(x, ...)

## Default S3 method:
cochran.test(
x,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL,
  alpha = 0.05,
  ...
)

## S3 method for class 'lab.qcdata'
cochran.test(x, alpha = 0.05, ...)

Arguments

x An object of class `lab.qcdata` (Univariate Quality Control Data).
...
Other arguments passed to or from methods.
var.index A scalar with the column number corresponding to the observed variable (the critical to quality variable). Alternatively can be a string with the name of the quality variable.
replicate.index A scalar with the column number corresponding to the index each replicate.
material.index A scalar corresponding to the replicated number.
laboratory.index A scalar that defines the index number of each laboratory.
data.name A string specifying the name of the variable which appears on the plots. If name is not provided, it is taken from the object given as data.
alpha The significance level (0.05 by default)
References


Examples

```r
library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
cochran.test(Glucose.qcdata)
```

---

DSC  
**Differential Scanning Calorimetry curves**

Description

90 samples of calcium oxalate were analyzed by differential scanning calorimetry technique (DSC), obtaining 90 DSC curves showing from an SDT device the difference of heat between a sample and an oxalate reference value depending on the temperature that the samples are heated at a constant temperature rate. The data set consists of 15 TG curves of 1000 observations from each of the 6 laboratories. Laboratory 2 to Laboratory 4 uses the same simultaneous SDT analyzer in similar conditions, Laboratory 6 uses a simultaneous SDT analyzer with an old calibration, and Laboratory 7 uses a simultaneous SDT analyzer with a calibration (2 degrees Celsius displaced from the zinc melting point).

Format

5 x 1000 x 6 dimension array, where each matrix consists of the 15 DSC curves obtained by testing 15 different oxalate samples, and evaluated at 1000 different temperature values. These 15 curves were obtained for each of the 6 laboratories that performed the experiments.

Xi  Differential Scanning Calorimetry curves.

References

func.ils.formula

Examples

```r
library(ILS)
data(DSC)
summary(DSC)
```

---

**func.ils.formula**

*Descriptive measures for functional data.*

---

**Description**

Central and dispersion measures for functional data.

**Usage**

```r
func.ils.formula(formula, data = NULL, drop = FALSE, func = func.mean)
```

**Arguments**

- `formula` A formula, such as `y ~ group`, where `y` is a `fdata` object to be split into groups according to the grouping variable group (usually a factor).
- `data` List that containing the variables in the formula. The item called "df" is a data frame with the grouping variable. The item called "y" is a `fdata` object.
- `drop` Logical indicating if levels that do not occur should be dropped (if `f` is a factor or a list).
- `func` Measures for functional data.

---

**Glucose**

*Glucose in Serum*

**Description**

Dataset corresponding to serum glucose (measurements of glucose concentration in blood used to control diabetes) testing. Eight laboratories conducted tests to five different blood samples tagged with different references, ranging them from low sugar content to very high. Three replicates were obtained for each sample. It is retrieved from ASTM E 691 standard.

**Format**

A data frame with 120 observations composed of the following 4 variables:

- **Glucose** Glucose content in Serum.
- **Replicate** Number of glucose measurement corresponding to each material.
- **Material** Level of glucose, ranging from low content of sugar to very high level of glucose in blood.
- **Laboratory** Laboratories conducted tests.
References


Examples

library(ILS)
data(Glucose)
summary(Glucose)
attach(Glucose)
str(Glucose)
table(Replicate,Material,Laboratory)
table(Laboratory,Material)
st <- with(Glucose, tapply(Glucose, list(Material,Laboratory), mean))
st

grubbs.test

Function to compute the Grubbs test statistic

Description

Function to estimate the Grubbs test statistic.

Usage

grubbs.test(x, ...)

## Default S3 method:
grubbs.test(x,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL,
  alpha = 0.05,
  ...
)

## S3 method for class 'lab.qcdata'
grubbs.test(x, alpha = 0.05, ...)

Arguments

x    An object of class `lab.qcdata` (Univariate Quality Control Data).
...
var.index A scalar with the column number corresponding to the observed variable (the critical to quality variable). Alternatively can be a string with the name of the quality variable.
replicate.index A scalar with the column number corresponding to the index each replicate.
material.index A scalar corresponding to the replicated number.
laboratory.index A scalar that defines the index number of each laboratory.
data.name A string specifying the name of the variable which appears on the plots. If name is not provided, it is taken from the object given as data.
alpha The significance level (0.05 for default)

References


Examples

```r
library(ILS)
data(Glucose)
Glucose.qcdata<- lab.qcdata(Glucose)
str(Glucose.qcdata)
grubbs.test(Glucose.qcdata)
```

---

**h.qcs**

*Function to estimate the univariate Mandel’s h statistic*

**Description**

This function is used to compute the Mandel’s h statistic.
Usage

h.qcs(x, ...)

## Default S3 method:

h.qcs(
  x,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL,
  alpha = 0.05,
  ...
)

## S3 method for class 'lab.qcdata'

h.qcs(x, alpha = 0.05, ...)

Arguments

x

An object of class lab.qcdata (Univariate Quality Control Data).

...  Other arguments passed to or from methods.

var.index

A scalar with the column number corresponding to the observed variable (the
critical to quality variable). Alternatively can be a string with the name of the
quality variable.

replicate.index

A scalar with the column number corresponding to the index each replicate.

material.index  A scalar corresponding to the replicated number.

laboratory.index

A scalar that defines the index number of each laboratory.

data.name

A string specifying the name of the variable which appears on the plots. If name
is not provided, it is taken from the object given as data.

alpha

The significance level (0.05 by default)

References

Wilrich Peter-T. (2013), Critical values of Mandel’s h and k, the Grubbs and the Cochran test

ASTM E 691 (1999), Standard practice for conducting an interlaboratory study to determine the
precision of a test method. American Society for Testing and Materials. West Conshohocken, PA,
USA.

Examples

library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
h<- h.qcs(Glucose.qcdata, alpha = 0.005)
summary(h)
plot(h)

---

**IDT**

Dataset composed of the initial decomposition temperature (IDT) of different samples of Calcium Oxalate, obtained by 7 different laboratories

**Description**

Initial decomposition temperature (IDT) is a parameter defined by temperature at which a material loss 5% of its weight when it is heated using a constant rate. One hundred and five calcium oxalate samples were tested by thermogravimetric analysis (TG), obtaining 105 TG curves from which the IDT is extracted. Summarizing, IDT dataset is composed of the IDT values of calcium oxalate obtained by 7 different laboratories that analyze 15 oxalate samples each one.: Laboratory 1 uses a simultaneous thermal analyzer (STA) with an old calibration program, Laboratory 2 to Laboratory 4 use a SDT simultaneous analyzer, Laboratory 6 utilizes a SDT simultaneous analyzer with an old calibration, and Laboratory 7 uses a SDT simultaneous analyzer with a biased calibration (2 degrees Celsius shifted from the zinc melting point).

**Format**

Dataframe of dimension 105 x 44. The first column corresponds to IDT variable, the second (Sample) is the replicate number, the third is the tested material (Material), and fourth is the laboratory.

- **IDT** Initial decomposition temperature.
- **Sample** The replicate number.
- **Run** Tested material.
- **Laboratory** Laboratories conducted tests.

**References**


**Examples**

```r
library(ILS)
data(IDT)
summary(IDT)
attach(IDT)
str(IDT)
table(Sample,Run,Laboratory)
table(Laboratory,Run)
st <- with(IDT, tapply(IDT, list(Run,Laboratory), mean))
```
ILS  
*Interlaboratory Study*

**Description**

Interlaboratory Study

**Details**

It performs interlaboratory studies (ILS) to detect those laboratories that provide non-consistent results when comparing to others. It permits to work simultaneously with various testing materials, from standard univariate, and functional data analysis (FDA) perspectives. The univariate approach based on ASTM E691-08 consist of estimating the Mandel’s h and k statistics to identify those laboratories that provide more significant different results, testing also the presence of outliers by Cochran and Grubbs tests. Analysis of variance (ANOVA) techniques are provided (F and Tuckey tests) to test differences in the testing variable means corresponding to test differences in means corresponding to differente laboratories per each material. Taking into account the functional nature of data retrieved in analytical chemistry, applied physics and engineering (spectra, thermograms, etc.). ILS package provides a FDA approach for functional Mandel’s k and h statistics by smoothing bootstrap resampling of distribution.

**ils.fqcd**  
*Functional Quality Control Data*

**Description**

It Creates an object of class `ils.fqcd` to perform statistical quality control. This object is used to plot functional data.

**Usage**

```r
ils.fqcd(  
x,  
p = NULL,  
index.laboratory = NULL,  
argvals = NULL,  
rangeval = NULL,  
names = NULL
)
```
**ils.fqcs**

**Arguments**

- `x` A \((n \times m)\) matrix or data-frame. The \(m\) is the number of points observed in each curve, and \(n\) is the number of curves for each laboratory.
- `p` The number of laboratories.
- `index.laboratory` The laboratory index. The index laboratory length should be equal a `p`.
- `argvals` Argvals, by default: `1:m`.
- `rangeval` The range of discretization points, by default: `range(argvals)`.
- `names` Optional. A list with tree components: main an overall title, xlab title for x axis and ylab title for y axis.

**References**


**Examples**

```r
library(ILS)
data(TG)
delta <- seq(from = 40 ,to = 850 ,length.out = 1000 )
fqcdata <- ils.fqcdata(TG, p = 7, argvals = delta)
xlab <- "Temperature (C)"
ylab <- "Mass (%)"
main <- "TG curves obtained from calcium oxalate"
plot(x = fqcdata, main = main, xlab=xlab, ylab=ylab,col = 1:7,legend = TRUE)
```

---

**ils.fqcs**

It develops an object of class 'ils.fqcs'

**Description**

Create an object of class 'ils.fqcs' to perform statistical quality control. This function is used to compute requested FDA.

**Usage**

```r
ils.fqcs(x, ...)
```

## Default S3 method:
`ils.fqcs(x, argvals = NULL, rangeval = NULL, ...)`

## S3 method for class 'ils.fqcdata'
ils.fqcs(x, ...)

## S3 method for class 'ils.fqcs'
print(x, ...)

## S3 method for class 'ils.fqcs'
summary(object, ...)

**Arguments**

- **x**
  - An object of class `ils.fqcs` for which a print is desired.
- **...**
  - Other arguments passed to or from methods.
- **argvals**
  - Argvals, by default: 1:m.
- **rangeval**
  - The range of discretization points, by default: range(argvals).
- **object**
  - An object of class `ils.fqcs` for which a summary is desired.

**References**


**Examples**

```r
library(ILS)
data(TG)
delta <- seq(from = 40 ,to = 850 ,length.out = 1000 )
fqcdata <- ils.fqcdata(TG, p = 7, argvals = delta)
xlab <- "Temperature/ C"
ylab <- "Mass/ %"
fqcstat <- ils.fqcs(fqcdata)
plot(fqcstat, xlab = xlab, ylab = ylab,legend = TRUE)
```

---

**k.qcs**  
*Function to calculate the Mandel’s k statistic*

**Description**

This function is used to compute the statistic $k$ of Mandel.
k.qcs

Usage

k.qcs(x, ...)

## Default S3 method:
k.qcs(
  x,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL,
  alpha = 0.05,
  ...
)

## S3 method for class 'lab.qcdata'
k.qcs(x, alpha = 0.05, ...)

Arguments

x An object of class lab.qcdata (Univariate Quality Control Data).

... Other arguments passed to or from methods.

var.index A scalar with the column number corresponding to the observed variable (the critical to quality variable). Alternatively can be a string with the name of the quality variable.

replicate.index A scalar with the column number corresponding to the index each replicate.

material.index A scalar corresponding to the replicated number.

laboratory.index A scalar that defines the index number of each laboratory.

data.name A string specifying the name of the variable which appears on the plots. If name is not provided, it is taken from the object given as data.

alpha The significance level (0.05 by default)

References


Examples

library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
k<- k.qcs(Glucose.qcdata, alpha = 0.005)
summary(k)
plot(k)

lab.aov

Function to compute the AOV

Description

Function to compute the analysis of variance of ILS data, taking into account the laboratories and material factors.

Usage

lab.aov(x, ...)

## Default S3 method:
lab.aov(
  x,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL,
  level = 0.95,
  plot = FALSE,
  pages = 0,
  ...
)

## S3 method for class 'lab.qcdata'
lab.aov(x, level = 0.95, plot = FALSE, pages = 0, ...)

Arguments

x An object of class lab.qcdata (Univariate Quality Control Data).

... Other arguments passed to or from methods.

var.index A scalar with the column number corresponding to the observed variable (the critical to quality variable). Alternatively can be a string with the name of the quality variable.

replicate.index A scalar with the column number corresponding to the index each replicate.

material.index A scalar corresponding to the replicated number.

laboratory.index A scalar that defines the index number of each laboratory.
lab.qcdata

Description

It creates a 'lab.qcdata' class object to perform the interlaboratory study. This object is used to plot ILS data and more.

Usage

lab.qcdata(
  data,
  var.index = 1,
  replicate.index = 2,
  material.index = 3,
  laboratory.index = 4,
  data.name = NULL
)

References


Examples

## Not run:
library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
lab.aov(Glucose.qcdata,level = 0.95, plot = TRUE, pages = 1)

## End(Not run)
Arguments

data A matrix or data-frame that contains the data, replicate index, type of material, and the laboratory.

var.index A scalar with the column number corresponding to the observed variable (the critical to quality variable). Alternatively can be a string with the name of the quality variable.

replicate.index A scalar with the column number corresponding to the index each replicate.

material.index A scalar corresponding to the replicated number.

laboratory.index A scalar that defines the index number of each laboratory.

data.name A string specifying the name of the variable which appears on the plots. If name is not provided, it is taken from the object given as data.

Examples

library(ILLS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
summary(Glucose.qcdata)

lab.qcs Create an object of class 'lab.qcs' to perform statistical quality control. This function is used to compute statistics required for plotting Statistics

Description

It develops an object of lab.qcs-codelinkclass to perform statistical quality control. This function is used to compute the requested statistics to be summarized and plotted.

Usage

lab.qcs(x, ...)

## S3 method for class 'lab.qcs'
print(x, ...)

## S3 method for class 'lab.qcs'
summary(object, ...)

Arguments

x An object of class lab.qcs for which a print is desired.

... Other arguments passed to or from methods.

object An object of class lab.qcs for which a summary is desired.
Examples

```r
library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
Glucose.qcs <- lab.qcs(Glucose.qcdata)
str(Glucose.qcs)
summary(Glucose.qcs)
```

`mandel.fqcs`  
This function is used to compute the FDA Mandel's h and k statistic

Description

It develops an object of 'mandel.fqcs' class to perform statistical quality control analysis. This function is used to compute the functional approach of Mandel's h and k statistic. It is specifically designed to deal with experimental data results defined by curves such as thermograms and spectra.

Usage

```r
mandel.fqcs(x, ...)
```

## Default S3 method:

```r
mandel.fqcs(
  x,
  p = NULL,
  index.laboratory = NULL,
  argvals = NULL,
  rangeval = NULL,
  names = NULL,
  ...
)
```

## S3 method for class 'ils.fqcdata'

```r
mandel.fqcs(
  x,
  fdep = depth.mode,
  outlier = TRUE,
  trim = 0.01,
  alpha = 0.01,
  nb = 200,
  smo = 0.05,
  ...
)
```
Arguments

- **x**: A \((n \times m)\) matrix or data-frame. The \(m\) is the number of points observed in each curve, and \(n\) is the number of curves for each laboratory.
- **...**: Other arguments passed to or from other methods.
- **p**: The number of laboratories.
- **index.laboratory**: The laboratory index. The index laboratory length should be equal a \(p\).
- **argvals**: Argvals, by default: 1:m.
- **rangeval**: The range of discretization points, by default: range(argvals).
- **names**: Optional. A list with tree components: main an overall title, xlab title for x axis and ylab title for y axis.
- **fdep**: Type of depth measure, by default depth.mode.
- **outlier**: = TRUE
- **trim**: The alpha of the trimming.
- **alpha**: Significance level, by default 1%.
- **nb**: The number of bootstrap samples.
- **smo**: The smoothing parameter for the bootstrap samples.

References


Examples

```r
## Not run:
library(ILS)
data(TG)
delta <- seq(from = 40 , to = 850 , length.out = 1000 )
fqcd <- ils.fqcd(TG, p = 7, argvals = delta)
mandel.tg <- mandel.fqcs(fqcd.tg, nb = 200)
plot(mandel.tg,legend = F,col=c(rep(3,5),1,1))
## End(Not run)
```
outliers.ils  

Detecting outliers for functional dataset

Description

Procedure for detecting functional outliers.

Usage

outliers.ils(x, fdep = depth.FM, trim = 0.01)

Arguments

x An object of class fdata.
fdep Type of depth measure, by default depth.mode.
trim The percentage of the trimming, by default is 1%.

plot.ils.fqcdata  

Plotting method for 'ils.fqcdata' objects

Description

Generic function to plot objects of 'ils.fqcdata' class

Usage

## S3 method for class 'ils.fqcdata'
plot(
x,
  type = "l",
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  ylim = NULL,
  x.co = NULL,
  y.co = NULL,
  legend = TRUE,
  col = NULL,
  ...
)
Arguments

x
An object class of ils.fqcdata (Functional Quality Control Data)

type
1-character string giving the type of plot desired. The following values are possible for fdata class object: "l" for lines (by default), "p" for points, , "o" for overplotted points and lines, "b", "c" for (empty if "c") points joined by lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines. The following values are possible for fdata2d class object: "image.contour" (by default) to display three-dimensional data and add the contour lines, "image" to display three-dimensional data, "contour" to display a contour plot, "persp" to display a perspective plots of a surface over the x-y plane and "filled.contour" to display a contour plot with the areas between the contours filled in solid color.

main
Main title for the plot.

xlab
Title for the x axis.

ylab
Title for the y axis.

ylim
The y limits of the plot.

x.co
It specifies the x co-ordinates to be used to place a legend.

y.co
It specifies the y co-ordinates to be used to place a legend.

legend
Logical argument. Default is TRUE then The legend default is used.

col
Color specifications

... Other arguments passed to matplot function (for fdata class).

References


Examples

## Not run:
library(ILS)
data(TG)
delta <- seq(from = 40 ,to = 850 ,length.out = 1000 )
fqcdata <- ils.fqcdata(TG, p = 7, argvals = delta)
windows()
xlab <- "Temperature (C)"
ylab <- "Mass (%)"
main <- "TG curves obtained from calcium oxalate"
plot(x = fqcdata, main = main, xlab=xlab, ylab=ylab,legend = TRUE)
## End(Not run)
plot.ils.fqcs

Plotting method for 'ils.fqcs' objects

Description
Generic function to plot objects of 'ils.fqcs' class. Results of functional ILS studies are graphically shown.

Usage
## S3 method for class 'ils.fqcs'
plot(x, type = "l", xlab = NULL, ylab = NULL, legend = TRUE, col = NULL, ...)

Arguments
x An object of class ils.fqcs (Functional Quality Control Statistics).
type 1-character string giving the type of plot desired. The following values are possible for fdata class object: "l" for lines (by default), "p" for points, "o" for overplotted points and lines, "b", "c" for (empty if "c") points joined by lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines. The following values are possible for fdata2d class object: "image.contour" (by default) to display three-dimensional data and add the contour lines, "image" to display three-dimensional data, "contour" to display a contour plot, "persp" to display a perspective plots of a surface over the x-y plane and "filled.contour" to display a contour plot with the areas between the contours filled in solid color.
xlab Title for the x axis.
ylab Title for the y axis.
legend Logical argument. Default is TRUE then The legend default is used.
col Color specifications.
... Other arguments to be passed to or from methods.

References

Examples
library(ILS)
data(TG)
delta <- seq(from = 40 ,to = 850 ,length.out = 1000 )
plot.lab.qcs

plot.lab.qcdata

Plot method for 'lab.qcdata' objects

Description

Generic function for plotting objects of 'lab.qcdata' class. Results of univariate ILS studies are graphically shown.

Usage

## S3 method for class 'lab.qcdata'
plot(x, xlab = NULL, ylab = NULL, col = "blue", ...)

Arguments

x An object of class lab.qcdata (Univariate Quality Control Data).
xlab Title for the x axis.
ylab Title for the y axis.
col Color of type material, when there only one.
... Other arguments to be passed to or from methods.

Examples

library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
str(Glucose.qcdata)
plot(Glucose.qcdata)

plot.lab.qcs

Plot method for 'lab.qcs' objects

Description

Generic function for plotting objects of 'lab.qcs' class. Results of univariate ILS studies are graphically shown.
Usage

## S3 method for class 'lab.qcs'
plot(x, title = NULL, xlab = NULL, ylab = NULL, col = NULL, ylim = NULL, ...)

Arguments

x An object of class lab.qcs (Univariate Quality Control Statistics).
title Main title for the plot.
xlab Title for the x axis.
ylab Title for the y axis.
col Color specifications.
ylim A Numeric vectors of length 2 (coordinates ranges).
... Other arguments to be passed to or from methods.

Examples

library(ILS)
data(Glucose)
Glucose.qcdata <- lab.qcdata(Glucose)
Glucose.qcs <- lab.qcs(Glucose.qcdata)
plot(Glucose.qcs)

Description

Generic function to plot objects of 'mandel.fqcs' class. Results of functional ILS studies are graphically shown.

Usage

## S3 method for class 'mandel.fqcs'
plot(  
  x,  
  xlab = NULL,  
  ylab = NULL,  
  x.co = NULL,  
  y.co = NULL,  
  legend = TRUE,  
  col = NULL,  
  ...  
)

plot.mandel.fqcs Plotting method for 'mandel.fqcs' objects
Arguments

- **x**: An object of class `mandel.fqcs`.
- **xlab**: Title for the x axis.
- **ylab**: Title for the y axis.
- **x.co**: It specifies the x co-ordinates to be used to place a legend.
- **y.co**: It specifies the y co-ordinates to be used to place a legend.
- **legend**: Logical argument. Default is `TRUE` then the legend default is used.
- **col**: Color specifications.
- **...**: Other arguments to be passed to or from methods.

References


Examples

```r
## Not run:
library(ILS)
data(TG)
delta <- seq(from = 40 , to = 850 , length.out = 1000 )
fqcdas <- ils fqcdas(TG , p = 7 , argvals = delta)
mandel.tg <- mandel.fqcs(fqcdas , nb = 200)
plot(mandel.tg , legend = F , col = c(rep(3 , 5) , 1 , 1))
## End(Not run)
```

# $H(t)$ and $K(t)$

TG  

**Thermogravimetry curves**

Description

One hundred and five Calcium oxalate samples were tested by thermogravimetric (TG) analysis, obtaining 105 TG curves that shows the mass loss of oxalate depending on time when samples are heated at a constant temperature rate. Dataset is composed by fifteen TG curves of 1000 observations each of overall 7 different laboratories. Laboratory 1 uses a simultaneous thermal analyzer (STA) with an old calibration program, Laboratory 2 to Laboratory 4 use a SDT simultaneous analyzer, Laboratory 6 utilizes a SDT simultaneous analyzer with an old calibration, and Laboratory 7 uses a SDT simultaneous analyzer with a biased calibration (2 degrees Celsius shifted from the zinc melting point).
Format

A 15 x 1000 x 7 dimension array, where each matrix consists of the 15 TG curves obtained testing 15 different oxalate samples, and evaluated in 1000 different values of temperature. These 15 curves were obtained for each of the overall 7 laboratories that have performed the experiments.

Vi Thermogravimetric.

References


Examples

```r
library(ILS)
data(TG)
summary(TG)
```
Index

* datasets
  Glucose, 5
boot.sim.set, 2
cochran.test, 3
DSC, 4
func.ils.formula, 5
Glucose, 5
grubbs.test, 6
h.qcs, 7
IDT, 9
ILS, 10
ils.fqcdta, 10
ils.fqcs, 11
k.qcs, 12
lab.aov, 14
lab.qcdata, 15
lab.qcs, 16
mandel.fqcs, 17
outliers.ils, 19
plot.ils.fqcdta, 19
plot.ils.fqcs, 21
plot.lab.qcdata, 22
plot.lab.qcs, 22
plot.mandel.fqcs, 23
print.ils.fqcs(ils.fqcs), 11
print.lab.qcs(lab.qcs), 16
summary.ils.fqcs(ils.fqcs), 11
summary.lab.qcs(lab.qcs), 16
TG, 24