

# Package ‘pistar’

September 27, 2013

**Type** Package

**Title** Rudas, Clogg and Lindsay Mixture Index of Fit

**Version** 0.5.1

**Date** 2013-09-27

**Author** Juraj Medzihorsky <juraj.medzihorsky@gmail.com>

**Maintainer** Juraj Medzihorsky <juraj.medzihorsky@gmail.com>

**Depends** methods

**Description** Functions for estimating the Rudas, Clogg and Lindsay mixture index of fit.

**License** GPL (>= 2)

## R topics documented:

pistar-package . . . . .	2
Fienberg1980a . . . . .	2
freq.table . . . . .	3
pearson2pistar . . . . .	4
piplot.ct . . . . .	5
PiplotCT-class . . . . .	7
pistar . . . . .	7
Pistar-class . . . . .	8
pistar.2by2 . . . . .	9
pistar.bvn . . . . .	10
pistar.ct . . . . .	11
pistar.ll . . . . .	14
pistar.mvn . . . . .	16
pistar.uv . . . . .	18
Pistar2by2-class . . . . .	21
PistarBVN-class . . . . .	21
PistarCT-class . . . . .	22
PistarCUV-class . . . . .	23
PistarDUV-class . . . . .	24
PistarLL-class . . . . .	25
PistarMVN-class . . . . .	25
PistarRCL-class . . . . .	26

PistarUV-class . . . . . 27

pool.jack . . . . . 28

rcl.em . . . . . 29

rcl.s . . . . . 30

summary.Pistar . . . . . 31

SummaryPistar-class . . . . . 32

**Index** 34

---

pistar-package	<i>Rudas, Clogg, and Lindsay Mixture Index of Fit</i>
----------------	---

---

**Description**

Functions for the Rudas, Clogg and Lindsay  $\pi^*$  mixture index of fit.

**Details**

Package: pistar  
Type: Package  
Version: 0.5.1  
Date: 2013-09-27  
License: GPL ( $\geq 2$ )

Functions for the Rudas, Clogg and Lindsay  $\pi^*$  mixture index of fit.

**Note**

The author would like to thank Tamas Rudas for invaluable advice in the development of this package.  
Work on the package was supported in part by Central European University grant BPF/5182/20123/R.

**Author(s)**

Juraj Medzihorsky <juraj.medzihorsky@gmail.com>

---

Fienberg1980a	<i>Citation Practices in Two Operations Research Journals</i>
---------------	---

---

**Description**

Citation practices in two operations reserch journals from Fienberg (1980a) analyzed by Rudas (2002) using the mixture index of fit.  
Reprinted by permission of The Applied Probability Trust. First published in Fienberg, S. E. (1980a) Using loglinear models to analyze cross-classified categorical data, *The Mathematical Scientist*, 5, 13-30. Copyright (c) Applied Probability Trust 1980.

**Usage**

```
data(Fienberg1980a)
```

**Format**

A 2-dimensional 2-by-4 array cross-tabulating observations of 336 papers in two operations research journals, *Management Science* (MS) and *Operations Research* (OR), from their 1969 and 1970 issues. Each papers is classified into one of four categories based on whether it refers to other papers from these two journals.

The variables and their levels are as follows:

No	Name	Levels
1	citing	MS, OR
2	cited	none, MS, OR, both

**Source**

Fienberg, S. E. (1980a) Using loglinear models to analyze cross-classified categorical data, *The Mathematical Scientist*, 5, 13-30.

**References**

Fienberg, S. E. (1980a) Using loglinear models to analyze cross-classified categorical data, *The Mathematical Scientist*, 5, 13-30.

Rudas, T. (2002) 'A Latent Class Approach to Measuring the Fit of a Statistical Model' in Hage-naars, J. A. and McCutcheon, A. L. (eds.) *Applied Latent Class Analysis*. Cambridge University Press. 345-365.

**Examples**

```
data(Fienberg1980a)
Fienberg1980a
```

---

freq.table

*Frequency Table of Integers in a Vector*


---

**Description**

freq.table is used to obtain a frequency table of values from a numeric vector. Unlike table it includes the frequency of each integer value on the interval from the smallest to the largest observed value, and thus can contain also zeros.

**Usage**

```
freq.table(x)
```

**Arguments**

x                      a numeric vector.

**Details**

`freq.table` first coerces the input vector into type integer and then creates a table of frequencies of all integers on the closed interval from the smallest to the largest inputted integer.

**Value**

A named vector of frequencies.

**Author(s)**

Juraj Medzihorsky

**See Also**

[table](#)

**Examples**

```
set.seed(1989)
y <- c(rpois(1e1, 3), rpois(1e1, 1e1))
freq.table(y)
# compare with table()
table(y)
```

---

pearson2pistar

*Pearson to  $\pi^*$  Conversion*

---

**Description**

`pearson2pistar` is used to convert Pearson product-moment correlation coefficient into the  $\pi^*$  mixture index of fit using the relationship between them described by Rudas, Clogg, and Lindsay (1994).

**Usage**

```
pearson2pistar(coeff)
```

**Arguments**

`coeff` value of Pearson product-moment correlation coefficient to be converted.

**Details**

The relationship between  $\pi^*$  and Pearson  $\rho$  is:

$$\pi^* = 1 - \sqrt{\frac{1 - |\rho|}{1 + |\rho|}}$$

**Value**

Value of  $\pi^*$  corresponding to the supplied value of Pearson product-moment correlation coefficient.

**Author(s)**

Juraj Medzihorsky

**References**

Rudas, T., Clogg, C. C., Lindsay, B. G. (1994) A New Index of Fit Based on Mixture Methods for the Analysis of Contingency Tables. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 56, No. 4, 623-639.

**See Also**[corpistar.bvn](#)**Examples**

```
pearson2pistar(0.5)

curve(pearson2pistar, from=-1,
      xlab=expression(rho),
      ylab=expression(pi^symbol('*')))
```

piplot.ct

*Pre-analysis Plot for [pistar.ct](#)***Description**

piplot.ct is used to inform the choice of the interval on which to look for  $\pi^*$  with [pistar.ct](#). It plots log-likelihood ratio statistic values of a two-point mixture of a user-supplied model and an unrestricted component fit to a contingency table on a specified number of equally-spaced points on a supplied interval.

**Usage**

```
piplot.ct(fn, data, ..., from = .Machine$double.neg.eps^0.25,
          to = 1 - .Machine$double.neg.eps^0.25, n = 10, draw = TRUE,
          color = "black", zero_line = TRUE, add = FALSE, values = FALSE)
```

**Arguments**

fn	a user-supplied function that inputs a contingency table of observed values and outputs a contingency table of predicted values. The function must output a named list with the contingency table of predicted values named 'fit'.
data	a contingency table.
...	further arguments passed to the user-supplied function.
from	numeric: lower bound of the interval of out-of-model proportions to be explored.
to	numeric: upper bound of the interval of out-of-model proportions to be explored.
n	numeric: number of equally-spaced points from the interval of out-of-model proportions to be explored.
draw	logical: draw a plot or lines?

color	color of the line.
zero_line	logical: plot a horizontal line at 0?
add	logical: add the line to a plot?
values	logical: return a dataframe with explored out-of-model proportions and their corresponding log-likelihood ratio statistics?

## Details

Developed from John M. Grego's `clr.plot`

## Value

A plot. If `values = TRUE` returns also an object of class 'PiplotCT' with the following slots:

pi	numeric vector of explored out-of-model proportions
lr	numeric vector of corresponding log-likelihood ratio statistics
lr_plus_eps	lr plus the value of eps

## Author(s)

Juraj Medzihorsky, developed from John M. Grego's `clr.plot`

## References

Grego, J.M. `clr.plot` function available at <http://www.stat.sc.edu/~grego/courses/stat770/CLR.txt>

## See Also

[pistar.ct rcl.em](#)

## Examples

```
data(Fienberg1980a)

mf <- function(data) loglin(data, list(1, 2), fit=TRUE, print=FALSE)

a <- piplot.ct(fn=mf, data=Fienberg1980a, values=TRUE)

a

plot(a, color='red')
```

---

PiplotCT-class	Class "PiplotCT"
----------------	------------------

---

### Objects from the Class

Objects can be created by calls of the form `new("PiplotCT", ...)`.

### Slots

```
call: Object of class "language" ~~
pi: Object of class "numeric" ~~
lr: Object of class "numeric" ~~
lr_plus_eps: Object of class "numeric" ~~
```

### Methods

```
plot signature(x = "PiplotCT"): ...
print signature(x = "PiplotCT"): ...
show signature(object = "PiplotCT"): ...
```

### Examples

```
showClass("PiplotCT")
```

---

pistar	<i>The Mixture Index of Fit</i>
--------	---------------------------------

---

### Description

`pistar` is a wrapper function for all functions estimating the Rudas-Clogg-Lindsay  $\pi^*$  mixture index of fit from package **pistar**.

### Usage

```
pistar(proc, ...)
```

### Arguments

proc	"uv" for <code>pistar.uv</code> "ct" for <code>pistar.ct</code> "ll" for <code>pistar.ll</code> "2by2" for <code>pistar.2by2</code> "mvn" for <code>pistar.mvn</code> "bvn" for <code>pistar.bvn</code>
...	arguments passed to the function.

**Value**

An object of class "Pistar".

**Author(s)**

Juraj Medzihorsky

**Examples**

```
# create data in a 2-by-2 table
H <- matrix(rpois(4, 20), ncol=2)

# find pi* for independence (i.e. odds ratio of 1)
h <- pistar(proc='2by2', data=H, alpha=1, jack=FALSE)

h
```

---

Pistar-class	<i>Class "Pistar"</i>
--------------	-----------------------

---

**Objects from the Class**

Objects can be created by calls of the form `new("Pistar", ...)`.

**Slots**

```
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

**Methods**

```
print signature(x = "Pistar"): ...
show signature(object = "Pistar"): ...
summary signature(object = "Pistar"): ...
```

**Examples**

```
showClass("Pistar")
```



pistar.2by2

*The Mixture Index of Fit for Odds Ratios in 2-by-2 Tables***Description**

pistar.2by2 is used to estimate  $\pi^*$  for a given cross-product ratio (i.e. odds ratio) in a 2-by-2 table using the method devised by Clogg, Rudas, and Xi (1995).

**Usage**

```
pistar.2by2(data, alpha = 1, jack = FALSE, verbose = TRUE)
```

**Arguments**

data	a 2-by-2 contingency table.
alpha	numeric: cross-product ratio
jack	logical: perform jackknife?
verbose	logical: print during estimation?

**Value**

Object of class "Pistar", "PistarCT", and "Pistar2by2" with the following slots:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit. <b>est</b> for the supplied data and odds ratio. <b>jack</b> vector of values from jackknife.
pred	a list of predicted values with three items: <b>model</b> the model component multiplied by $(1 - \pi^*)$ <b>unres</b> the unrestricted component multiplied by $\pi^*$ <b>combi</b> the two-point mixture, i.e. $(1 - \pi^*)M + \pi^*U$
data	the supplied data.
param	a list of with a single item <b>est</b> numeric: the supplied value of cross-product ratio.

**References**

Clogg, C. C., Rudas, T., & Xi, L. (1995). A new index of structure for the analysis of models for mobility tables and other cross-classifications. *Sociological Methodology*, 197-222.

Rudas, T., Zwick, R., (1997) Estimating the Importance of Differential Item Functioning. *Journal of Educational and Behavioral Statistics*, Vol. 22, No. 1 (Spring, 1997), pp. 31-45

**Examples**

```
H <- matrix((1:4)*1e1, byrow=TRUE, ncol=2)

h <- pistar.2by2(H, alpha=1, jack=TRUE)

h

str(h)

plot(h)

summary(h)
```

pistar.bvn

*The Mixture Index of Fit for Bivariate Normal Independence***Description**

pistar.bvn is used to estimate the  $\pi^*$  mixture index of fit for independence in a bivariate normal distribution using the relationship between  $\pi^*$  and Pearson correlation coefficient.

**Usage**

```
pistar.bvn(x, y, conf = 0.95, na.action, alt = "two.sided", verbose = TRUE)
```

**Arguments**

x	a numeric vector containing the first variable.
y	a numeric vector containing the second variable.
conf	confidence level.
na.action	passed to cor.test.
alt	alternative hypothesis, determines the shape of the confidence interval; passed to cor.test.
verbose	logical: print during estimation?

**Value**

Object of class "Pistar", and "PistarBVN" with the following slots:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit: <b>est</b> for the supplied data. <b>jack</b> vector of values from jackknife.
pred	not yet implemented.
data	a data.frame with the supplied data.
param	not yet implemented.
interval	confidence interval for $\pi^*$ .
conf	confidence level.
alt	the supplied alternative hypothesis.

**Author(s)**

Juraj Medzihorsky

**References**

Rudas, T., Clogg, C. C., Lindsay, B. G. (1994) A New Index of Fit Based on Mixture Methods for the Analysis of Contingency Tables. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 56, No. 4, 623-639.

**See Also**

[cor.test](#) [pearson2pistar](#)

**Examples**

```
# simulate data
set.seed(1989)
n <- 1e2
a <- rnorm(n)
b <- rnorm(n)

# find pi*
o <- pistar.bvn(x=a, y=b)

o
```

---

pistar.ct

---

*The Mixture Index of Fit for a Contingency Table*


---

**Description**

pistar.ct is used to find the value of the  $\pi^*$  for any user-supplied model fit to a contingency table. The only requirements are (1) that the model inputs only a contingency table with non-negative continuous cell values, and (2) outputs a named list in which the predicted values are a contingency table named "fit". Optionally parameter estimates of interest can be outputted as a vector named "param" in the output list.

$\pi^*$  for the model of interest is estimated using the algorithm of Rudas, Clogg, and Lindsay (1994). Standard errors for  $\pi^*$  and any other parameter estimates of interest can be obtained by jackknife as proposed by Dayton (2003).

**Usage**

```
pistar.ct(data, fn, from = .Machine$double.neg.eps^0.25,
           to = 1 - .Machine$double.neg.eps^0.25, jack = FALSE,
           method = "uniroot", u_iter = 1e3, zeta = 1,
           lr_eps = .Machine$double.neg.eps^0.25,
           max_dif = .Machine$double.neg.eps^0.5, chi_stat = 0, verbose = TRUE)
```

## Arguments

data	a contingency table.
fn	a user supplied function that estimates the model of interests. Must input only the observed values as a contingency table containing non-negative continuous cell values. Must output the predicted values as a contingency table as item named "fit" in a named list. Optionally can output parameter estimates of interest as a vector named "param" in the output named list.
from	numeric: lower bound of the interval of out-of-model proportions to be explored.
to	numeric: upper bound of the interval of out-of-model proportions to be explored.
jack	logical: perform jackknife?
method	character: method with to look for $\pi^*$ . "uniroot" uses uniroot, can be expected to be faster "split" uses a simple binary search from rcl.s.
u_iter	maximum number of iterations for method uniroot if method "uniroot".
zeta	weighing constant; default is 1. The EM algorithm might crash due to very low cell values and in such case increasing the zeta might help.
lr_eps	penalty for finding $\pi^*$ , the largest small positive number that can be still considered practically indistinguishable from 0.
max_dif	largest acceptable difference, passed to rcl.em and rcl.s.
chi_stat	$\chi^2$ statistic penalty; default 0. Supply a different e.g. if you want to find the lower endpoint of a one-sided confidence interval for $\pi^*$ .
verbose	logical: print during estimation?

## Details

The EM algorithm implemented here was proposed by Rudas, Clogg and Lindsay (1994). The jackknife procedure was proposed by Dayton (2003). The function is developed from J.M.Grego's `clr` and `clr.root` functions.

## Value

Object of class "Pistar", "PistarCT", and "PistarRCL" with the following slots:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit. <b>est</b> for the supplied data. <b>jack</b> vector of values from jackknife.
pred	a list of predicted values with three items: <b>model</b> the model component multiplied by $(1 - \pi^*)$ <b>unres</b> the unrestricted component multiplied by $\pi^*$ <b>combi</b> the two-point mixture, i.e. $(1 - \pi^*)M + \pi^*U$
data	an array with the supplied data.
param	a list of requested estimates of the parameters of interest of the model fit to an <b>unscaled</b> model density, i.e. to $M$ and <b>not</b> $(1 - \pi)M$ . <b>est</b> the estimated values. <b>jack</b> from each jackknife replication.
llrs	a list of values of log-likelihood ratio statistics

**est** for the supplied data.  
**jack** vector of values from each jackknife.  
 iter a list of the numbers of iterations of either uniroot or rcl.s  
**est** for the supplied data.  
**jack** from each jackknife replication.

### Author(s)

Juraj Medzihorsky

Developed from J.M.Grego's c1r and c1r.root functions.

### References

Dayton, C. M. (2003) Applications and computational strategies for the two-point mixture index of fit. *British Journal of Mathematical & Statistical Psychology*, 56, 1-13.

Grego, J. M. c1r and c1r.root functions available at <http://www.stat.sc.edu/~grego/courses/stat770/CLR.txt>

Rudas, T., Clogg, C. C., Lindsay, B. G. (1994) A New Index of Fit Based on Mixture Methods for the Analysis of Contingency Tables. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 56, No. 4, 623-639.

Rudas, T. (2002) 'A Latent Class Approach to Measuring the Fit of a Statistical Model' in Hage-naars, J. A. and McCutcheon, A. L. (eds.) *Applied Latent Class Analysis*. Cambridge University Press. 345-365.

### See Also

[piplot.ct](#) [rcl.em](#) [rcl.s](#)

### Examples

```
# load data
data(Fienberg1980a)

# define a function: log-linear model of independence in a
# 2-way table
mf <- function(x){
  loglin(table=x, margin=list(1,2), fit=TRUE, print=FALSE)
}

# find pi*
p <- pistar(proc='ct', data=Fienberg1980a, fn=mf, jack=FALSE)

p

summary(p)

plot(p)
```

---

pistar.ll

---

*The Mixture Index of Fit for Log-linear Models*


---

## Description

pistar.ll is used to find the value of the  $\pi^*$  index of fit for any log-linear model estimated with loglin;  $\pi^*$  is estimated using the algorithm of Rudas, Clogg, and Lindsay (1994). Standard errors for  $\pi^*$  and any other estimates of parameters of interest can be obtained by jackknife as proposed by Dayton (2003).

## Usage

```
pistar.ll(data, margin = list(1, 2), start = rep(1, length(data)), eps = 0.1,
          iter = 1e3, param = TRUE, print = FALSE,
          from = .Machine$double.neg.eps^0.25,
          to = 1 - .Machine$double.neg.eps^0.25, jack = FALSE,
          lr_eps = .Machine$double.neg.eps^0.25,
          max_dif = .Machine$double.neg.eps^0.5, chi_stat = 0, u_iter = 1e3,
          tol = .Machine$double.eps^0.25, verbose = TRUE)
```

## Arguments

data	a contingency table.
margin	passed to loglin.
start	start argument of loglin.
eps	eps argument of loglin.
iter	maximum number of iterations for loglin.
param	logical: return parameter estimates?
print	logical: should loglin print during fitting?
from	numeric: lower bound of the interval of out-of-model proportions to be explored.
to	numeric: upper bound of the interval of out-of-model proportions to be explored.
jack	logical: perform jackknife?
lr_eps	penalty for finding $\pi^*$ , the largest small positive number that can be still considered practically indistinguishable from 0.
max_dif	largest acceptable difference, passed to rcl.em.
chi_stat	$\chi^2$ statistic penalty; default 0. Supply a different e.g. if you want to find the lower endpoint of a one-sided confidence interval for $\pi^*$ .
u_iter	maximum number of iterations for method uniroot.
tol	tolerance passed to loglin.
verbose	logical: print during estimation?

## Details

This is a version of the algorithm implemented in pistar.ct for log-linear models that is speed-optimized.

**Value**

Object of class "Pistar", "PistarCT", "PistarRCL", and "PistarLL" with the following slots:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit. <b>est</b> for the supplied data. <b>jack</b> vector of values from jackknife.
pred	a list of predicted values with three items: <b>model</b> the model component multiplied by $(1 - \pi^*)$ <b>unres</b> the unrestricted component multiplied by $\pi^*$ <b>combi</b> the two-point mixture, i.e. $(1 - \pi^*)M + \pi^*U$
data	the supplied data.
param	a list of requested estimates of the parameters of interest of the model fit to an <b>unscaled</b> model density, i.e. to $M$ and <b>not</b> $(1 - \pi)M$ . <b>est</b> the estimated values. <b>jack</b> from each jackknife replication.
llrs	a list of values of log-likelihood ratio statistics <b>est</b> for the supplied data. <b>jack</b> vector of values from each jackknife.
iter	a list of the numbers of iterations of either <code>uniroot</code> or <code>rcl.s</code> <b>est</b> for the supplied data. <b>jack</b> from each jackknife replication.

**Author(s)**

Juraj Medzihorsky

Developed from J.M.Grego's `clr` and `clr.root` functions.

**References**

Dayton, C. M. (2003) Applications and computational strategies for the two-point mixture index of fit. *British Journal of Mathematical & Statistical Psychology*, 56, 1-13.

Grego, J. M. `clr` and `clr.root` functions available at <http://www.stat.sc.edu/~grego/courses/stat770/CLR.txt>

Rudas, T., Clogg, C. C., Lindsay, B. G. (1994) A New Index of Fit Based on Mixture Methods for the Analysis of Contingency Tables. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 56, No. 4, 623-639.

Rudas, T. (2002) 'A Latent Class Approach to Measuring the Fit of a Statistical Model' in Hage-naars, J. A. and McCutcheon, A. L. (eds.) *Applied Latent Class Analysis*. Cambridge University Press. 345-365.

**See Also**

[pistar.ct loglin](#)

## Examples

```
data(HairEyeColor)

# check if the data is an "array"
is(HairEyeColor, "array")

# it is not, so it first needs to be converted:
HEC <- array(HairEyeColor,
  dim=dim(HairEyeColor),
  dimnames=dimnames(HairEyeColor))

# find  $\pi^*$  for independence in a 3-way table
p <- pistar(proc='ll', data=HEC, margin=list(1, 2, 3), jack=FALSE)

p

summary(p)

# plot does not work for n-way tables if n > 2
# plot(p)

# create data
H <- matrix((1:4)*1e1, byrow=TRUE, ncol=2)

# find  $\pi^*$  and model parameter estimates and perform jackknife
h <- pistar(proc='ll', data=H, margin=list(1, 2), param=TRUE, jack=TRUE)

h

summary(h)
```

---

pistar.mvn

---

*The Mixture Index of Fit for Multivariate Normal Independence*


---

## Description

pistar.mvn is used to estimate the value of the  $\pi^*$  mixture index of fit for independence in multivariate normal distribution using the procedure of Knott (2005). Standard errors can be obtained using jackknife as proposed by Dayton (2003).

## Usage

```
pistar.mvn(data, cor_matrix = FALSE, max_dif = .Machine$double.neg.eps^0.5,
  jack = FALSE, seed = 1989, lag = c(5, 10), verbose = TRUE)
```

## Arguments

data	a matrix, or a correlation matrix.
cor_matrix	logical: is the supplied data a correlation matrix? If TRUE jackknife cannot be performed.



max_dif	numeric: maximal acceptable difference between selected iterations for the convergence diagnostic. See 'Details'.
jack	logical: perform jackknife?
seed	seed for random number generation.
lag	parameters of the convergence diagnostic, see 'Details'.
verbose	logical: print during estimation?

### Details

The function was developed from code published by Knott (2005).

A simple convergence diagnostic was added to Knott's (2005) procedure. The absolute values of the differences between the value of  $\pi^*$  at the current iteration and between lag iterations and stops the iterations as successful if all the differences are smaller than the constant supplied as max\_dif argument. To check if the algorithm has converged to a global or a local minimum check test in the output and restart the procedure with a different seed if needed (see Knott 2005 for more details).

### Value

Object of class "Pistar", and "PistarMVN" with the following components:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit: <b>est</b> for the supplied data. <b>jack</b> vector of values from jackknife.
pred	not yet implemented.
data	the supplied data.
param	not yet implemented.
trace	a list of traces from the iterations: <b>est</b> vector from estimation with supplied data. <b>jack</b> list of traces from jackknife.
iter	a list of numbers of the iterations: <b>est</b> from estimation with supplied data. <b>jack</b> a list of traces from jackknife.
test	a test statistic to evaluate if the procedure has converged to a local or global optimum. See Knott (2005) for more details. <b>est</b> Vector from estimation with supplied data. <b>jack</b> List of vectors from jackknife.

### Author(s)

Juraj Medzihorsky

Developed from code published by Knott (2005).

### References

- Dayton, C. M. (2003) Applications and computational strategies for the two-point mixture index of fit. *British Journal of Mathematical & Statistical Psychology*, 56, 1-13.
- Knott, M. (2005) A measure of independence for a multivariate normal distribution and some connections with factor analysis, *Journal of Multivariate Analysis*, 96, 374-383.

## Examples

```
# simulate data
set.seed(1989)
n <- 1e2
A <- cbind(rnorm(n), rnorm(n))

# find pi*
a <- pistar(proc='mvn', data=A, jack=FALSE)

a

summary(a)

plot(a)
```

---

pistar.uv

---

*The Mixture Index of Fit for Univariate Distributions*


---

## Description

pistar.uv is used to estimate the  $\pi^*$  index of fit for any user-supplied univariate distribution. The user must supply a probability mass or density function that inputs the data as the first argument and the parameters as the next arguments. See ‘Details’ for the estimation procedures. Standard errors available via jackknife as suggested by Dayton (2003).

## Usage

```
pistar.uv(data, dfn, n_par = NULL, inits = NULL, discrete = FALSE,
          freq = FALSE, lower = NULL, upper = NULL, jack = FALSE,
          method = "Nelder-Mead", control = list(maxit = 2000),
          verbose = TRUE, npk = 1e3, eps = .Machine$double.neg.eps^0.5)
```

## Arguments

data	a vector or a frequency table.
dfn	function: probability mass or density function that inputs the data as the first argument and the parameters as the arguments that immediately follow it.
n_par	numeric: number of parameters. Either n_par or inits must be supplied. If only n_par is supplied initial values are generated internally and might not always be suitable.
inits	a vector or list of initial values of parameters supplied to optim. If named the parameter names are preserved in the output.
discrete	logical: is the distribution discrete?
freq	logical: is the supplied data a frequency table? Relevant only if discrete is TRUE.
lower	numeric: a vector of lower bounds for parameters.
upper	numeric: a vector of upper bounds for parameters.
jack	logical: perform jackknife?

method	method argument for <code>optim</code> . Default "Brent" for mono-parameter functions and "Nelder-Mead" for multi-parameter functions. See <code>optim</code> for details on methods.
control	list supplied to <code>optim</code> , see <code>optim</code> .
verbose	logical: print during estimation?
npk	an integer indicating the number of points for density; used if <code>discrete = FALSE</code> .
eps	numeric: the smallest number practically indistinguishable from 0. Used only if <code>discrete = TRUE</code> .

## Details

The general procedure for discrete and continuous distributions is the same: a general purpose optimization method is used to find such values of the parameters of the supplied distribution that minimize the following quantity: 1 minus the inverse of the ratio of the model and the observed density at the point of their supports where this ratio is highest. This quantity is  $\pi^*$ .

The procedure for discrete distributions differs from the one for the continuous distributions in the method used to obtain the observed density. In the discrete case the observed frequencies are used for the observed density. In the continuous case a kernel density is estimated using density with gaussian kernel.

## Value

Object of class "Pistar", and "PistarUV" and depending on the `discrete` argument of the function either "PistarDUV" or "PistarCUV" with the following slots:

call	the matched call.
pistar	a list of estimated values of the mixture index of fit. <b>est</b> for the supplied data. <b>jack</b> vector of values from jackknife.
pred	if <code>discrete = TRUE</code> a list of predicted values with three items: <b>model</b> the model component multiplied by $(1 - \pi^*)$ <b>unres</b> the unrestricted component multiplied by $\pi^*$ <b>combi</b> the two-point mixture, i.e. $(1 - \pi^*)M + \pi^*U$ if <code>discrete = FALSE</code> the list also contains three components with the same names, but they contain the values of the scaled densities at npk (i.e. by default 1e3) points.
data	the supplied data.
param	a list of parameter estimates of interest: <b>est</b> the estimated values. <b>jack</b> from each jackknife replication.
meth	method of <code>optim</code> used.
conv	a list of integer codes from <code>optim</code> that indicate convergence of the optimization algorithm. Any value that is not 0 suggests problems. See <code>optim</code> for details. <b>est</b> from estimation with the supplied data. <b>jack</b> from jackknife replications.
mess	a list of messages passed from <code>optim</code> . See <code>optim</code> for details. <b>est</b> From the main estimation. <b>jack</b> From jackknife replications.

**Note**

The application of the mixture index of fit for discrete distributions was proposed by Dayton (2003).

**Author(s)**

Juraj Medzihorsky

**References**

Dayton, C. M. (2003) Applications and computational strategies for the two-point mixture index of fit. *British Journal of Mathematical & Statistical Psychology*, 56, 1-13.

**See Also**

[optim density freq.table](#)

**Examples**

```
# (1) discrete
# simulate data
set.seed(1989)
e <- c(rpois(1e3, 2), rpois(2e2, 5))

# make a frequency table
te <- freq.table(e)

# define a function for a slice from Poisson
md <- function(x, l, lo=0, up=5){
  z <- dpois(x, l)
  z[x<lo] <- 0
  z[x>up] <- 0
  z <- z/sum(z)
  return(z)
}

# find pi*
pe <- pistar(proc='uv', data=te, dfn=md, n_par=1,
  discrete=TRUE, freq=TRUE, jack=FALSE)

pe

summary(pe)

plot(pe)

# (2) continuous
# simulate data
set.seed(1989)
y <- c(rnorm(1e2, 0, 2), runif(2e1, -1, 1))

# find pi* and parameters for normal dist.
py <- pistar(proc='uv', data=y, dfn=dnorm, n_par=2, discrete=FALSE,
  jack=FALSE)

py
```

```
summary(py)
```

```
plot(py)
```

---

Pistar2by2-class	Class "Pistar2by2"
------------------	--------------------

---

### Objects from the Class

Objects can be created by calls of the form `new("Pistar2by2", ...)`.

### Slots

```
data: Object of class "array" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "**PistarCT**", directly. Class "**Pistar**", by class "PistarCT", distance 2.

### Methods

No methods defined with class "Pistar2by2" in the signature.

### Examples

```
showClass("Pistar2by2")
```

---

PistarBVN-class	Class "PistarBVN"
-----------------	-------------------

---

### Objects from the Class

Objects can be created by calls of the form `new("PistarBVN", ...)`.

### Slots

```
data: Object of class "data.frame" ~~
interval: Object of class "numeric" ~~
conf: Object of class "numeric" ~~
alt: Object of class "character" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

**Extends**

Class "[Pistar](#)", directly.

**Methods**

**plot** signature(x = "PistarBVN"): ...

**Examples**

```
showClass("PistarBVN")
```

---

PistarCT-class	<i>Class "PistarCT"</i>
----------------	-------------------------

---

**Usage**

```
## S4 method for signature 'PistarCT'
plot(x, y, ...)
```

**Arguments**

x	object of class PistarCT
y	ignored
...	optional

**Objects from the Class**

Objects can be created by calls of the form `new("PistarCT", ...)` or `PistarCT(...)`.

**Slots**

```
data: Object of class "array" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

**Extends**

Class "[Pistar](#)", directly.

**Methods**

**plot** signature(x = "PistarCT"): ...

**Author(s)**

Juraj Medzihorsky

**Examples**

```
showClass("PistarCT")
```

---

PistarCUV-class	Class "PistarCUV"
-----------------	-------------------

---

### Usage

```
## S4 method for signature 'PistarCUV'
plot(x, model_col = 'blue', unres_col = 'grey', combi_col = 'black', lty = 1, lwd = 1,
     pos = 'topright', bty = 'n', ... )
```

### Arguments

x	object of class "PistarCUV".
model_col	color for the model component.
unres_col	color for the unrestricted component.
combi_col	color for the predicted values from the two-point mixture.
lty	line type.
lwd	line width.
pos	position of the legend, see legend.
bty	box type of the legend, see legend.
...	optional arguments passed further to plot.

### Objects from the Class

Objects can be created by calls of the form `new("PistarCUV", ...)` or `PistarCUV(...)`.

### Slots

```
data: Object of class "numeric" ~~
meth: Object of class "character" ~~
conv: Object of class "list" ~~
mess: Object of class "list" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "[PistarUV](#)", directly. Class "[Pistar](#)", by class "PistarUV", distance 2.

### Methods

```
plot signature(x = "PistarCUV"): ...
```

### Examples

```
showClass("PistarCUV")
```

---

PistarDUV-class	<i>Class "PistarDUV"</i>
-----------------	--------------------------

---

### Usage

```
## S4 method for signature 'PistarDUV'
plot(x, model_col = 'blue', unres_col = 'grey', combi_col = 'black', pos = 'topright', bty = 'n')
```

### Arguments

x	object of class "PistarDUV".
model_col	color for the model component.
unres_col	color for the unrestricted component.
combi_col	color for the predicted values from the two-point mixture.
pos	position of the legend, see legend.
bty	box type of the legend, see legend.
...	optional arguments passed further to plot.

### Objects from the Class

Objects can be created by calls of the form `new("PistarDUV", ...)` or `PistarDUV(...)`.

### Slots

```
data: Object of class "table" ~~
meth: Object of class "character" ~~
conv: Object of class "list" ~~
mess: Object of class "list" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "[PistarUV](#)", directly. Class "[Pistar](#)", by class "PistarUV", distance 2.

### Methods

```
plot signature(x = "PistarDUV"): ...
```

### Examples

```
showClass("PistarDUV")
```



---

PistarLL-class	Class "PistarLL"
----------------	------------------

---

### Objects from the Class

Objects can be created by calls of the form `new("PistarLL", ...)`.

### Slots

```
llrs: Object of class "list" ~~
iter: Object of class "list" ~~
data: Object of class "array" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "[PistarRCL](#)", directly. Class "[PistarCT](#)", by class "PistarRCL", distance 2. Class "[Pistar](#)", by class "PistarRCL", distance 3.

### Methods

No methods defined with class "PistarLL" in the signature.

### Examples

```
showClass("PistarLL")
```

---

PistarMVN-class	Class "PistarMVN"
-----------------	-------------------

---

### Usage

```
## S4 method for signature 'PistarMVN'
plot(x, lty = 1, lwd = 1, col = 'black', ... )
```

### Arguments

<code>x</code>	object of class "PistarMVN".
<code>lty</code>	line type.
<code>lwd</code>	line width.
<code>col</code>	color of the line.
<code>...</code>	optional arguments passed further.

### Objects from the Class

Objects can be created by calls of the form `new("PistarMVN", ...)` or `PistarMVN()`.

### Slots

```
data: Object of class "data.frame" ~~
trace: Object of class "list" ~~
iter: Object of class "list" ~~
test: Object of class "list" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "[Pistar](#)", directly.

### Methods

**plot** signature(x = "PistarMVN"): ...

### Examples

```
showClass("PistarMVN")
```

---

PistarRCL-class	<i>Class "PistarRCL"</i>
-----------------	--------------------------

---

### Objects from the Class

Objects can be created by calls of the form `new("PistarRCL", ...)`.

### Slots

```
llrs: Object of class "list" ~~
iter: Object of class "list" ~~
data: Object of class "array" ~~
call: Object of class "language" ~~
pistar: Object of class "list" ~~
pred: Object of class "list" ~~
param: Object of class "list" ~~
```

### Extends

Class "[PistarCT](#)", directly. Class "[Pistar](#)", by class "PistarCT", distance 2.

**Methods**

No methods defined with class "PistarRCL" in the signature.

**Examples**

```
showClass("PistarRCL")
```

---

PistarUV-class	Class "PistarUV"
----------------	------------------

---

**Objects from the Class**

Objects can be created by calls of the form `new("PistarUV", ...)`.

**Slots**

meth: Object of class "character" ~~

conv: Object of class "list" ~~

mess: Object of class "list" ~~

call: Object of class "language" ~~

pistar: Object of class "list" ~~

pred: Object of class "list" ~~

param: Object of class "list" ~~

**Extends**

Class "[Pistar](#)", directly.

**Methods**

No methods defined with class "PistarUV" in the signature.

**Examples**

```
showClass("PistarUV")
```

pool.jack

*Jackknife Standard Errors and Confidence Intervals***Description**

pool.jack is used to obtain standard errors and confidence intervals from the output of jackknife procedures.

**Usage**

```
pool.jack(data, ct = TRUE, estimate, jack_est, side = NULL, conf = 0.95,
          lower = -Inf, upper = Inf, bias = FALSE)
```

**Arguments**

data	the data.
ct	logical: is the data a contingency table?
estimate	the value of the estimate.
jack_est	the vector of estimates from jackknife replications.
side	NULL for a two-sided c.i., "lower" or "upper" for a one-sided interval. "auto" selects "lower" if the estimate is larger than 0 and "upper" if it is smaller than 0.
conf	confidence level expressed as a number between 0 and 1. e.g. for a 95% confidence interval supply 0.95
lower	lowest possible value for one-sided c.i.
upper	largest possible value for one-sided c.i.
bias	logical: apply bias correction? Bias correction currently not implemented.

**Value**

A named list with the following components:

se	standard error.
low	lower endpoint of c.i.
upp	upper endpoint of c.i.
conf	confidence level of the c.i.
side	"lower" and "upper" for one-sided c.i., "both" for a two-sided c.i.
bias	implementation of bias correction not finished.

**Author(s)**

Juraj Medzihorsky

**References**

Efron, Bradley, and Robert Tibshirani. (1993). An introduction to the bootstrap. Vol. 57. CRC press.

rcl.em

*Rudas-Clogg-Lindsay EM Algorithm***Description**

rcl.em is used to fit a two-point mixture composed of a user-supplied model of interest and an unrestricted distribution fit to a contingency table with supplied mixing proportions using the Rudas-Clogg-Lindsay (1994) EM algorithm.

**Usage**

```
rcl.em(pi_out, FNEM, data, max_dif = .Machine$double.neg.eps^0.5,
      zeta = 1, lr_only = TRUE, chi_stat = 0,
      lr_eps = .Machine$double.neg.eps^0.25)
```

**Arguments**

pi_out	out-of-model proportion, i.e. the mixing weight of the unrestricted component
FNEM	user-supplied function that estimates the model of interests. Must input only the observed values as a contingency table. Must output the predicted values as a contingency table as item named "fit" in a named list. Optionally can output parameter estimates of interest as a vector named "param" in the outputted named list.
data	a contingency table.
max_dif	largest acceptable difference, i.e. the largest number practically indistinguishable from 0.
zeta	weighing constant; default is 1. The EM algorithm might crash due to very low cell values; in such case increasing the zeta might help.
lr_only	logical: return only the value of the log-likelihood ratio statistic?
chi_stat	$\chi^2$ statistic penalty; default 0. Supply a different value e.g. if you want to find the lower endpoint of a one-sided confidence interval for $\pi^*$ .
lr_eps	penalty for finding $\pi^*$ , the largest small positive number that can be still considered practically indistinguishable from 0.

**Value**

A named list with the following components: (if lr\_only is TRUE then the list contains only the "lr" component)

pi_out	the out-of-model proportion, i.e. the mixing weight of the unrestricted component
param	a vector of the estimated parameter values fit to an <b>unscaled</b> model density, i.e. to $M$ and <b>not</b> $(1 - \pi)M$ .
lr	general contingency table log-likelihood ratio statistic for the two-point mixture.
model	scaled density of predicted values following the model of interest, i.e. $(1 - \pi)M$ .
unrestricted	Scaled density of predicted values following unrestricted component, i.e. $\pi U$
predicted	values predicted by the two-point mixture, i.e. $(1 - \pi)M + \pi U$ .

**Author(s)**

Juraj Medzihorsky

Developed from J.M.Grego's functions, see 'References'

**References**

Rudas, T., Clogg, C. C., Lindsay, B. G. (1994) A New Index of Fit Based on Mixture Methods for the Analysis of Contingency Tables. *Journal of the Royal Statistical Society. Series B (Methodological)*, Vol. 56, No. 4, 623-639.

Grego, J. M. `clr` and `clr.root` functions available at <http://www.stat.sc.edu/~grego/courses/stat770/CLR.txt>

**See Also**

[pistar.ct](#)

---

rcl.s

*Simple Line-Splitting Function*

---

**Description**

'rcl.s' is used to find the input values under which a user-supplied function outputs a specified value by searching on a user-specified interval

**Usage**

```
rcl.s(FNS, ..., y_goal = .Machine$double.neg.eps^0.5,
      x_lo = .Machine$double.neg.eps^0.25,
      x_up = 1 - .Machine$double.neg.eps^0.25,
      s_tol = .Machine$double.neg.eps^0.5,
      s_mit = 1e2, trace_plot = FALSE)
```

**Arguments**

FNS	user-supplied function. Must input only a single number and output only a single number.
...	arguments passed to the user-supplied function.
y_goal	the goal output value.
x_lo	the lower endpoint of the interval for the input value.
x_up	the upper endpoint of the interval for the input value.
s_tol	tolerance value for convergence diagnostic. If the absolute value of the difference between the output value at the current iteration and the goal output value is less than this tolerance value the algorithm terminates successfully.
s_mit	maximum number of iterations.
trace_plot	logical: return also a traceplot?

**Value**

A dataframe with the following columns:

pi	input values.
lr	output values.

If trace\_plot = TRUE also a plot.

**Author(s)**

Juraj Medzihorsky

---

summary.Pistar	<i>Summarizing "Pistar" Objects</i>
----------------	-------------------------------------

---

**Description**

summary method for class "Pistar"

**Usage**

```
## S4 method for signature 'Pistar'
summary(object, conf = 0.95, pi_side = NULL, par_side = NULL,
        lower = NULL, upper = NULL, bias = FALSE, ...)

## S4 method for signature 'SummaryPistar'
print(x, digits = 2, ...)
```

**Arguments**

object	an object of class "pistar"
x	an object of class "summary.pistar"
digits	integer indicating the number of decimal places to print
conf	Confidence level expressed as a number between 0 and 1. e.g. for a 95% confidence interval supply 0.95
pi_side	Sidedness of c.i. for $\pi^*$ . NULL for a two-sided c.i., "lower" or "upper" for a one-sided interval. "auto" selects "lower" if the estimate is larger than 0 and "upper" if it is smaller than 0.
par_side	Sidedness of c.i. for reported estimates of parameters other than $\pi^*$ . NULL for a two-sided c.i., "lower" or "upper" for a one-sided interval. "auto" selects "lower" if the estimate is larger than 0 and "upper" if it is smaller than 0.
lower	lowest possible value for one-sided c.i.
upper	largest possible value for one-sided c.i.
bias	logical: Apply bias correction? Bias correction currently not implemented.
...	arguments to be passed to methods; not used

**Value**

Object of class "SummaryPistar", a list with the following slots

oldcall	the matched call inherited from the input object of class "Pistar"
pred	inherited from the input object of class "Pistar"
est	A data.frame with the parameter estimates, optionally also with standard errors, lower and upper endpoints of c.i., sidedness of the c.i., and bias (the last is not currently fully implemented)

**Author(s)**

Juraj Medzihorsky

**Examples**

```
# create data:
H <- matrix((1:4)*1e1, byrow=TRUE, ncol=2)

# pi* for independence in a 2-by-2 table
h <- pistar(proc='2by2', data=H, alpha=1, jack=TRUE)

# print 'pistar' object
h

# summarize 'pistar' object
s <- summary(h)

# print 'summary.pistar' object
s

# print the 'summary.pistar' object to 4 decimal places
print(s, digits=4)

# compare the structure of the objects
str(h)
str(s)
```

---

SummaryPistar-class	Class "SummaryPistar"
---------------------	-----------------------

---

**Objects from the Class**

Objects can be created by calls of the form `new("SummaryPistar", ...)` or `SummaryPistar`.

**Slots**

oldcall: Object of class "language" ~~  
 pred: Object of class "list" ~~  
 est: Object of class "data.frame" ~~



### **Methods**

```
print signature(x = "SummaryPistar"): ...  
show signature(object = "SummaryPistar"): ...
```

### **Examples**

```
showClass("SummaryPistar")
```

# Index

- \*Topic **LCA**
  - pistar.ct, 11
- \*Topic **classes**
  - PiplotCT-class, 7
  - Pistar-class, 8
  - Pistar2by2-class, 21
  - PistarBVN-class, 21
  - PistarCT-class, 22
  - PistarCUV-class, 23
  - PistarDUV-class, 24
  - PistarLL-class, 25
  - PistarMVN-class, 25
  - PistarRCL-class, 26
  - PistarUV-class, 27
  - SummaryPistar-class, 32
- \*Topic **correlation**
  - pearson2pistar, 4
- \*Topic **datasets**
  - Fienberg1980a, 2
- \*Topic **frequency**
  - freq.table, 3
- \*Topic **index of fit**
  - pistar, 7
- \*Topic **jackknife**
  - pool.jack, 28
- \*Topic **latent class analysis**
  - pistar.ct, 11
- \*Topic **line-splitting**
  - rcl.s, 30
- \*Topic **loglin**
  - pistar.ll, 14
- \*Topic **mixture**
  - pistar.ct, 11
  - pistar.ll, 14
  - rcl.em, 29
- \*Topic **multivariate normal**
  - pistar.mvn, 16
- \*Topic **package**
  - pistar-package, 2
- \*Topic **pearson**
  - pearson2pistar, 4
- \*Topic **pistar**
  - pearson2pistar, 4
  - piplot.ct, 5
  - pistar, 7
  - pistar-package, 2
  - pistar.2by2, 9
  - pistar.bvn, 10
  - pistar.ct, 11
  - pistar.ll, 14
  - pistar.mvn, 16
  - pistar.uv, 18
  - summary.Pistar, 31
- \*Topic **table**
  - freq.table, 3
- \*Topic **univariate**
  - pistar.uv, 18
- cor, 5
- cor.test, 11
- density, 20
- Fienberg1980a, 2
- freq.table, 3, 20
- loglin, 15
- optim, 20
- pearson2pistar, 4, 11
- piplot.ct, 5, 13
- PiplotCT (PiplotCT-class), 7
- PiplotCT-class, 7
- Pistar, 21–27
- Pistar (Pistar-class), 8
- pistar, 7
- Pistar-class, 8
- pistar-package, 2
- pistar.2by2, 7, 9
- pistar.bvn, 5, 7, 10
- pistar.ct, 5–7, 11, 15, 30
- pistar.ll, 7, 14
- pistar.mvn, 7, 16
- pistar.uv, 7, 18
- Pistar2by2 (Pistar2by2-class), 21
- Pistar2by2-class, 21
- PistarBVN (PistarBVN-class), 21

PistarBVN-class, [21](#)  
 PistarCT, [21](#), [25](#), [26](#)  
 PistarCT (PistarCT-class), [22](#)  
 PistarCT-class, [22](#)  
 PistarCUV (PistarCUV-class), [23](#)  
 PistarCUV-class, [23](#)  
 PistarDUV (PistarDUV-class), [24](#)  
 PistarDUV-class, [24](#)  
 PistarLL (PistarLL-class), [25](#)  
 PistarLL-class, [25](#)  
 PistarMVN (PistarMVN-class), [25](#)  
 PistarMVN-class, [25](#)  
 PistarRCL, [25](#)  
 PistarRCL (PistarRCL-class), [26](#)  
 PistarRCL-class, [26](#)  
 PistarUV, [23](#), [24](#)  
 PistarUV (PistarUV-class), [27](#)  
 PistarUV-class, [27](#)  
 plot, PiplotCT-method (PiplotCT-class), [7](#)  
 plot, PistarCT-method (PistarCT-class),  
     [22](#)  
 plot, PistarCUV-method  
     (PistarCUV-class), [23](#)  
 plot, PistarDUV-method  
     (PistarDUV-class), [24](#)  
 plot, PistarMVN-method  
     (PistarMVN-class), [25](#)  
 pool.jack, [28](#)  
 print, PiplotCT-method (PiplotCT-class),  
     [7](#)  
 print, Pistar-method (Pistar-class), [8](#)  
 print, SummaryPistar-method  
     (summary.Pistar), [31](#)  
  
 rcl.em, [6](#), [13](#), [29](#)  
 rcl.s, [13](#), [30](#)  
  
 show, PiplotCT-method (PiplotCT-class), [7](#)  
 show, Pistar-method (Pistar-class), [8](#)  
 show, SummaryPistar-method  
     (SummaryPistar-class), [32](#)  
 summary, Pistar-method (summary.Pistar),  
     [31](#)  
 summary.Pistar, [31](#)  
 SummaryPistar (SummaryPistar-class), [32](#)  
 SummaryPistar-class, [32](#)  
  
 table, [4](#)