Package ‘ellipse’

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  ellipse-package .................................................. 2
  ellipse .......................................................... 3
  ellipse.arima0 .................................................. 4
  ellipse(glm) .................................................... 5
  ellipse.lm ........................................................ 6
  ellipse.nls ....................................................... 7
  ellipse.profile .................................................. 8
Functions for drawing ellipses and ellipse-like confidence regions

Description

This package contains various routines for drawing ellipses and ellipse-like confidence regions, implementing the plots described in Murdoch and Chow (1996).

There are also routines implementing the profile plots described in Bates and Watts (1988).

Details

There are three groups of routines in the ellipse package. The first consists of those involved with `plotcorr`, which implements the plots described in Murdoch and Chow (1996). These display correlations using ellipses, whose shape is that of the contours of a bivariate normal distribution with matching correlation.

The second group implements a version of the profile plots described in Bates and Watts (1988); see `ellipse.profile` and `pairs.profile`.

The last group provide the basis for the others, drawing ellipses based on various S objects, including scalar correlations, covariance matrices `arima`, `lm`, and `nls` fits: see `ellipse`.

Author(s)

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References


ellipse

Make an ellipse

Description

A generic function returning an ellipse or other outline of a confidence region for two parameters.

Usage

ellipse(x, ...)
## Default S3 method:
ellipse(x, scale = c(1, 1), centre = c(0, 0), level = 0.95,
t = sqrt(qchisq(level, 2)), which = c(1, 2), npoints = 100, center = centre,
...)

Arguments

x
An object. In the default method the parameter x should be a correlation between -1 and 1 or a square positive definite matrix at least 2x2 in size. It will be treated as the correlation or covariance of a multivariate normal distribution.

... Descendant methods may require additional parameters.

scale
If x is a correlation matrix, then the standard deviations of each parameter can be given in the scale parameter. This defaults to c(1, 1), so no rescaling will be done.

centre
The centre of the ellipse will be at this position.

level
The confidence level of a pairwise confidence region. The default is 0.95, for a 95% region. This is used to control the size of the ellipse being plotted. A vector of levels may be used.

t
The size of the ellipse may also be controlled by specifying the value of a t-statistic on its boundary. This defaults to the appropriate value for the confidence region.

which
This parameter selects which pair of variables from the matrix will be plotted. The default is the first 2.

npoints
The number of points used in the ellipse. Default is 100.

center An alternative to centre to accommodate US spelling.

Details

The default method uses the \((\cos(\theta + d/2), \cos(\theta - d/2))\) parametrization of an ellipse, where \(\cos(d)\) is the correlation of the parameters.

Value

An npoints x 2 matrix is returned with columns named according to the row names of the matrix x (default 'x' and 'y'), suitable for plotting.
References

See Also
ellipse.lm, ellipse.nls, ellipse.profile, ellipse.profile.nls, ellipse.arima0, plotcorr

Examples
# Plot an ellipse corresponding to a 95% probability region for a
# bivariate normal distribution with mean 0, unit variances and
# correlation 0.8.
plot(ellipse(0.8), type = 'l')

ellipse.arima0

Outline an approximate pairwise confidence region

Description
This function produces the ellipsoidal outline of an approximate pairwise confidence region for an ARIMA model fit.

Usage
## S3 method for class 'arima0'
ellipse(x, which = c(1, 2), level = 0.95, t = sqrt(qchisq(level, 2)), ...)

Arguments

x The first argument should be an arima0 object, usually resulting from a call to arima0().

which Which selects the pair of parameters to be plotted. The default is the first two.

level The confidence level of the region. Default 95%.

t The t statistic on the boundary of the ellipse.

... Other ellipse.default parameters may also be used.

Details
The summary function is used to obtain the approximate covariance matrix of the fitted parameters.

Value
A matrix with columns x and y to outline the confidence region.
**ellipse.glm**

See Also

`ellipse`

Examples

```r
data(USAccDeaths)
fit <- arima0(USAccDeaths, order = c(0, 1, 1), seasonal = list(order = c(0, 1, 1)))
# Plot the approximate 95% confidence region for the first two parameters
# of the model
plot(ellipse(fit), type = 'l')
points(fit$coef[1], fit$coef[2])
```

**Description**

This function produces the ellipsoidal outline of an approximate pairwise confidence region for a generalized linear model fit.

**Usage**

```r
## S3 method for class 'glm'
ellipse(x, which = c(1, 2), level = 0.95, t, npoints = 100,
dispersion, ...)
```

**Arguments**

- `x`  
  The first argument should be a `glm` object, usually resulting from a call to `glm()`.

- `which`  
  Which selects the pair of parameters to be plotted. The default is the first two.

- `level`  
  The confidence level of the region. Default 95%.

- `t`  
  The t statistic on the boundary of the ellipse. For Binomial or Poisson families, \( \sqrt{\text{qchisq}(\text{level}, 2)} \) is used; for other distributions, \( \sqrt{2 \times \text{qf}(\text{level}, 2, \text{df})} \) where \( \text{df} \) is the residual degrees of freedom.

- `npoints`  
  How many points to return in the ellipse.

- `dispersion`  
  The value of dispersion to use. If specified, it is treated as fixed, and the chi-square limits for \( t \) are used. If missing, it is taken from `summary(x)`.

- `...`  
  Other `ellipse.default` parameters may also be used.

**Details**

The summary function is used to obtain the approximate covariance matrix of the fitted parameters, the dispersion estimate, and the degrees of freedom.

**Value**

A matrix with columns named according to which to outline the confidence region.
**See Also**

`ellipse.default`

**Examples**

```r
## Dobson (1990) Page 93: Randomized Controlled Trial:

counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
glm.D93 <- glm(counts ~ outcome + treatment, family=poisson())

# Plot an approximate 95 % confidence region for the two Outcome parameters

plot(ellipse(glm.D93, which = c(2,3)), type = 'l')
points(glm.D93$coefficients[2], glm.D93$coefficients[3])
```

---

**Description**

This function produces the ellipsoidal outline of a pairwise confidence region for a linear model fit.

**Usage**

```r
## S3 method for class 'lm'
ellipse(x, which = c(1, 2), level = 0.95, t = sqrt(2 * qf(level, 2, x$df.residual)), ...)
```

**Arguments**

- `x` The first argument should be an `lm` object, usually resulting from a call to `lm()`.
- `which` Which selects the pair of parameters to be plotted. The default is the first two.
- `level` The confidence level of the region. Default 95%.
- `t` The t statistic on the boundary of the ellipse.
- `...` Other `ellipse.default` parameters may also be used.

**Details**

The summary function is used to obtain the covariance matrix of the fitted parameters.

**Value**

A matrix with columns `x` and `y` to outline the confidence region.
ellipse.nls

See Also

ellipse.default

Examples

# Plot the estimate and joint 90% confidence region for the displacement and cylinder
# count linear coefficients in the mtcars dataset
data(mtcars)
fit <- lm(mpg ~ disp + cyl , mtcars)
plot(ellipse(fit, which = c('disp', 'cyl'), level = 0.90), type = 'l')
points(fit$coefficients['disp'], fit$coefficients['cyl'])

---

ellipse.nls  Outline an approximate pairwise confidence region

Description

This function produces the ellipsoidal outline of an approximate pairwise confidence region for a
nonlinear model fit.

Usage

## S3 method for class 'nls'
ellipse(x, which = c(1, 2), level = 0.95,
    t = sqrt(2 * qf(level, 2, s$df[2])), ...)  

Arguments

x  The first argument should be an nls object, usually resulting from a call to nls().
which  Which selects the pair of parameters to be plotted. The default is the first two.
level  The confidence level of the region. Default 95%.
t  The t statistic on the boundary of the ellipse.
...  Other ellipse.default parameters may also be used.

Details

The summary function is used to obtain the approximate covariance matrix of the fitted parameters.

Value

A matrix with columns x and y to outline the confidence region.

See Also

ellipse.default, ellipse.profile
Examples

# Plot an approximate 95% confidence region for the weight and displacement
# parameters in the Michaelis Menten model
data(Puromycin)
fit <- nls(rate ~ Vm*conc/(K + conc), data = Puromycin, subset = state=="treated",
          start = list(K = 0.05, Vm = 200))
plot(ellipse(fit,which=c("Vm","K")), type = 'l')
params <- fit$m$s$getPars()
points(params[['Vm']],params[['K']])

Description

This routine approximates a contour of a function based on the profile of that function.

Usage

## S3 method for class 'profile'
elipse(x, which = c(1, 2), level = 0.95, t = sqrt(qchisq(level, 2)),
      npoints = 100, ...)

Arguments

x An object of class profile, e.g. from profile.glm in the MASS package.
which Which pair of parameters to use.
level The ellipse.profile function defaults assume that the profiled function is -2 times
       the log likelihood of a regular model. With this assumption the level
       argument specifies the confidence level for an asymptotic confidence region.
t The square root of the value to be contoured.
npoints How many points to use in the ellipse.
... Extra arguments are not used.

Details

This function uses the 4 point approximation to the contour as described in Appendix 6 of Bates
and Watts (1988). It produces the exact contour for quadratic surfaces, and good approximations
for mild deviations from quadratic. If the surface is multimodal, the algorithm is likely to produce
nonsense.

Value

An npoints x 2 matrix with columns having the chosen parameter names, which approximates a
contour of the function that was profiled.


References


See Also

profile, ellipse.nls

Examples

# Plot an approximate 95% confidence region for the Puromycin parameters Vm and K, and overlay the ellipsoidal region

data(Puromycin)
Purboth <- nls(formula = rate ~ ((Vm + delV * (state == "treated")) * conc)/(K + conc), data = Puromycin, start = list(Vm = 160, delV = 40, K = 0.05))
Pur.prof <- profile(Purboth)
plot(ellipse(Pur.prof, which = c("Vm", "K")), type = "l")
lines(ellipse(Purboth, which = c("Vm", "K")), lty = 2)
params <- Purboth$m$getPars()
points(params["Vm"],params["K"])

Description

This routine approximates a pairwise confidence region for a glm model.

Usage

## S3 method for class 'profile.glm'
ellipse(x, which = c(1, 2), level = 0.95, t, npoints = 100, dispersion, ...)

Arguments

x
Which
level
t
npoints

An object of class profile.glm.
Which pair of parameters to use.
The level argument specifies the confidence level for an asymptotic confidence region.
The square root of the value to be contoured. By default, this is qchisq(level, 2) for models with fixed dispersion (i.e. binomial and Poisson), and 2 * qf(level, 2, df) for other models, where df is the residual degrees of freedom.
How many points to use in the ellipse.
dispersion: If specified, fixed dispersion is assumed, otherwise the dispersion is taken from the model.
...
Extra parameters which are not used (for compatibility with the generic).

Details

This function uses the 4 point approximation to the contour as described in Appendix 6 of Bates and Watts (1988). It produces the exact contour for quadratic surfaces, and good approximations for mild deviations from quadratic. If the surface is multimodal, the algorithm is likely to produce nonsense.

Value

An npoints x 2 matrix with columns having the chosen parameter names, which approximates a contour of the function that was profiled.

References


See Also

profile, glm, ellipse.glm

Examples

```
## MASS has a pairs.profile function that conflicts with ours, so
## do a little trickery here
noMASS <- is.na(match('package:MASS', search()))
if (noMASS) require(MASS)

## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
glm.D93 <- glm(counts ~ outcome + treatment, family=poisson())

## Plot an approximate 95% confidence region for the two outcome variables
prof.D93 <- profile(glm.D93)
plot(ellipse(prof.D93, which = 2:3), type = 'l')
lines(ellipse(glm.D93, which = 2:3, lty = 2)
params <- glm.D93$coefficients
points(params[2],params[3])

## Clean up our trickery
if (noMASS) detach('package:MASS')
```
**ellipse.profile.nls**  
*Pairwise profile sketch*

### Description

This routine approximates a pairwise confidence region for a nonlinear regression model.

### Usage

```r
# S3 method for class 'profile.nls'
ellipse(x, which = c(1, 2), level = 0.95,
       t = sqrt(2 * qf(level, 2, attr(x, "summary")$df[2])),
       npoints = 100, ...)
```

### Arguments

- `x` An object of class `profile.nls`.
- `which` Which pair of parameters to use.
- `level` The `level` argument specifies the confidence level for an asymptotic confidence region.
- `t` The square root of the value to be contoured.
- `npoints` How many points to use in the ellipse.
- `...` Extra parameters which are not used (for compatibility with the generic).

### Details

This function uses the 4 point approximation to the contour as described in Appendix 6 of Bates and Watts (1988). It produces the exact contour for quadratic surfaces, and good approximations for mild deviations from quadratic. If the surface is multimodal, the algorithm is likely to produce nonsense.

### Value

An `npoints x 2` matrix with columns having the chosen parameter names, which approximates a contour of the function that was profiled.

### References


### See Also

`profile.ellipse.nls`
Examples

```r
# Plot an approximate 95% confidence region for the Puromycin # parameters Vm and K, and overlay the ellipsoidal region
data(Puromycin)
Purboth <- nls(formula = rate ~ ((Vm + delV * (state == "treated")) * conc)/(K + conc), data = Puromycin, start = list(Vm = 160, delV = 40, K = 0.05))
Pur.prof <- profile(Purboth)
plot(ellipse(Pur.prof, which = c("Vm", "K")), type = "l")
lines(ellipse(Purboth, which = c("Vm", "K")), lty = 2)
params <- Purboth$m$getPars()
points(params["Vm"],params["K"])
```

Description

A matrix of scatterplots is produced.

Usage

```r
pairs(x, ...)
## Default S3 method:
pairs(x, ...)
## S3 method for class "formula"
pairs(formula, data = NULL, ..., subset, na.action = stats::na."
```

Arguments

- `x` An object containing the data to plot.
- `formula, data, subset, na.action` See `pairs`.
- `...` Other arguments to pass to the methods.

Details

The `ellipse` package defines a `pairs.profile` method for profile objects. Unfortunately, so does the `MASS` package. The `ellipse::pairs` generic is supplied to allow users to choose to use the version in this package. See the `pairs.profile` help page for more details.

Value

Typically no useful value is produced; this generic function is called for the side effect of producing the display.
pairs.profile

See Also

pairs.profile for the method from this package.

Examples

example(pairs, "graphics")

Description

This function produces pairwise plots of profile traces, profile sketches, and ellipse approximations
to confidence intervals.

Usage

## S3 method for class 'profile'
pairs(x, labels = c(names(x), "Profile tau"), panel = lines, invert = TRUE,
     plot.tau = TRUE, plot.trace = TRUE, plot.sketch = TRUE,
     plot.ellipse = FALSE, level = 0.95, ...)

Arguments

x An object of class profile, generally the result of the profile() function.
labels The labels to use for each variable. These default to the variable names.
panel The function to use to draw the sketch in each panel.
invert Whether to swap the axes so things look better.
plot.tau Whether to do the profile tau (profile t) plots.
plot.trace Whether to do the profile trace plots.
plot.sketch Whether to do the profile sketch plots.
plot.ellipse Whether to do the ellipse approximations.
level The nominal confidence level for the profile sketches and ellipses.
... Other plotting parameters.

Details

This function implements the plots used in Bates and Watts (1988) for nonlinear regression diagnostics.

Unfortunately, the MASS package also defines a pairs.profile method. The ellipse::pairs generic is supplied to allow users to choose to use the version in this package.

If x is a profile object, then ellipse::pairs(x) is guaranteed to call the method from this package.
If you’d rather use the MASS method, then two steps are needed: you need to be sure that MASS
is loaded, then call \texttt{graphics::pairs(x)}. (If \texttt{MASS} is not loaded, you’ll get the default method from the \texttt{graphics} package, which will trigger an error since it doesn’t know about profile objects.)

If both \texttt{ellipse} and \texttt{MASS} are loaded, then \texttt{pairs(x)} is slightly ambiguous: the method that is called depends on the ordering of \texttt{ellipse} and \texttt{graphics} (not \texttt{MASS}!) in the search list. In almost all cases \texttt{ellipse} will precede \texttt{graphics}, so the \texttt{ellipse} method will usually be the default.

If \( x \) is any object other than a profile object, \texttt{ellipse::pairs(x)} will pass the call on to \texttt{graphics::pairs(x)}, and the standard method will be called.

\section*{Side Effects}

Produces a plot on the current device for each pair of variables in the profile object.

\section*{References}


\section*{See Also}

\texttt{profile}, \texttt{ellipse.profile}, \texttt{ellipse.nls}

\section*{Examples}

\begin{verbatim}
# Plot everything for the Puromycin data
data(Puromycin)
Purboth <- nls(formula = rate ~ ((Vm + delV * (state == "treated") * conc)/(K + conc), data = Puromycin,
    start = list(Vm = 160, delV = 40, K = 0.05))
Pur.prof <- profile(Purboth)
ellipse::pairs(Pur.prof, plot.ellipse = TRUE)

# Show the corresponding plot from MASS:
if (requireNamespace("MASS"))
  graphics::pairs(Pur.prof)
\end{verbatim}

\section*{Description}

This function plots a correlation matrix using ellipse-shaped glyphs for each entry. The ellipse represents a level curve of the density of a bivariate normal with the matching correlation.
plotcorr

Usage

plotcorr(corr, outline = TRUE, col = 'grey', numbers = FALSE,
         type = c("full","lower","upper"),
         diag = (type == "full"), bty = "n", axes = FALSE,
         xlab = "", ylab = "", asp = 1,
         cex.lab = par("cex.lab"), cex = 0.75*par("cex"),
         mar = 0.1 + c(2,2,4,2), ...)

Arguments

corr A matrix containing entries between -1 and 1 to be plotted as correlations.
outline Whether the ellipses should be outlined in the default colour.
col Which colour(s) to use to fill the ellipses.
numbers Whether to plot numerical correlations in place of ellipses. If numbers is TRUE,
then the correlations will be rounded to a single decimal place and placed on the
plot.
type Character. Plot "full" matrix or just "upper" or "lower" triangular part of it.
diag Logical. Plot diagonal elements or not.
bty, axes, xlab, ylab, asp, mar, cex.lab, ...
         Graphical parameters which will be passed to plot when plotting.
cex Graphical parameter which will be passed to text when plotting.

Details

The ellipses being plotted will be tangent to a unit character square, with the shape chosen to match
the required correlation. If numbers = FALSE, the col vector will be recycled to colour each of the
ellipses; if TRUE, it will be ignored.

Author(s)

Duncan Murdoch; Gregor Gorjanc suggested the type and diag options.

References

Murdoch, D.J. and Chow, E.D. (1996). A graphical display of large correlation matrices. The

See Also

ellipse

Examples

save.par <- par(ask = interactive())

# Plot the correlation matrix for the mtcars data full model fit
data(mtcars)
fit <- lm(mpg ~ ., mtcars)
plotcorr(summary(fit, correlation = TRUE)$correlation)

# Plot a second figure with numbers in place of the ellipses
plotcorr(summary(fit, correlation = TRUE)$correlation, numbers = TRUE)

# Colour the ellipses to emphasize the differences. The color range is based on RColorBrewer's Reds and Blues (suggested by Gregor Gorjanc)

corr.mtcars <- cor(mtcars)
ord <- order(corr.mtcars[1,])
xc <- corr.mtcars[ord, ord]
colors <- c("#A50F15", "#DE2D26", "#FB6A4A", "#FCAE91", "#FEE5D9", "white", "#EFF3FF", "#BDD7E7", "#6BAED6", "#3182BD", "#08519C")
plotcorr(xc, col=colors[5*xc + 6])

plotcorr(xc, col=colors[5*xc + 6], type = "upper")
plotcorr(xc, col=colors[5*xc + 6], type = "lower", diag = TRUE)
par(save.par)
Index

* dplot
  ellipse, 3
  ellipse-package, 2
  ellipse.arima0, 4
  ellipse.glm, 5
  ellipse.lm, 6
  ellipse.nls, 7
  ellipse.profile, 8
  ellipse.profile.glm, 9
  ellipse.profile.nls, 11
  pairs.profile, 13
* hplot
  plotcorr, 14
* models
  ellipse.profile, 8
  ellipse.profile.glm, 9
  ellipse.profile.nls, 11
* nonlinear
  ellipse.nls, 7
  pairs.profile, 13
* package
  ellipse-package, 2
* regression
  ellipse.glm, 5
  ellipse.lm, 6
  pairs.profile, 13
* ts
  ellipse.arima0, 4

arima, 2

ellipse, 2, 3, 5, 15
ellipse-package, 2
ellipse.arima0, 4, 4
ellipse.default, 6, 7
ellipse.glm, 5, 10
ellipse.lm, 4, 6
ellipse.nls, 4, 7, 9, 11, 14
ellipse.profile, 2, 4, 7, 8, 14
ellipse.profile.glm, 9

glm, 10
lm, 2
nls, 2
pairs, 12, 12, 13
pairs.profile, 2, 12, 13, 13
plot, 15
plotcorr, 2, 4, 14
profile, 8–11, 14
profile.glm, 8, 9
profile.nls, 11
text, 15