Package ‘genridge’

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Type Package

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Description The genridge package introduces generalizations of the standard univariate ridge trace plot used in ridge regression and related methods. These graphical methods show both bias (actually, shrinkage) and precision, by plotting the covariance ellipsoids of the estimated coefficients, rather than just the estimates themselves. 2D and 3D plotting methods are provided, both in the space of the predictor variables and in the transformed space of the PCA/SVD of the predictors.

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https://friendly.github.io/genridge/

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`genridge-package` *Generalized ridge trace plots for ridge regression*

Description

The genridge package introduces generalizations of the standard univariate ridge trace plot used in ridge regression and related methods (Friendly, 2012). These graphical methods show both bias (actually, shrinkage) and precision, by plotting the covariance ellipsoids of the estimated coefficients, rather than just the estimates themselves. 2D and 3D plotting methods are provided, both in the space of the predictor variables and in the transformed space of the PCA/SVD of the predictors.

Details

This package provides computational support for the graphical methods described in Friendly (2013). Ridge regression models may be fit using the function `ridge`, which incorporates features of `lm.ridge`. In particular, the shrinkage factors in ridge regression may be specified either in terms of the constant added to the diagonal of $X^T X$ matrix (`lambda`), or the equivalent number of degrees of freedom.

More importantly, the `ridge` function also calculates and returns the associated covariance matrices of each of the ridge estimates, allowing precision to be studied and displayed graphically.

This provides the support for the main plotting functions in the package:

`plot.ridge`: Bivariate ridge trace plots

`pairs.ridge`: All pairwise bivariate ridge trace plots plot3d.ridge: 3D ridge trace plots

traceplot: Traditional univariate ridge trace plots

In addition, the function pca.ridge transforms the coefficients and covariance matrices of a ridge object from predictor space to the equivalent, but more interesting space of the PCA of $X^T X$ or the SVD of **X**. The main plotting functions also work for these objects, of class c("ridge", "pcaridge").

Finally, the functions precision and vif.ridge provide other useful measures and plots.

Author(s)

Michael Friendly

Maintainer: Michael Friendly <friendly@yorku.ca>

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

Arthur E. Hoerl and Robert W. Kennard (1970). Ridge Regression: Biased Estimation for Nonorthogonal Problems, *Technometrics*, 12(1), pp. 55-67.

Arthur E. Hoerl and Robert W. Kennard (1970). Ridge Regression: Applications to Nonorthogonal Problems *Technometrics*, 12(1), pp. 69-82.

See Also

lm.ridge

Examples

```
# see examples for ridge, etc.
```

Acetylene *Acetylene Data*

Description

The data consist of measures of yield of a chemical manufacturing process for acetylene in relation to numeric parameters.

Format

A data frame with 16 observations on the following 4 variables.

yield conversion percentage yield of acetylene

temp reactor temperature (celsius)

ratio H2 to N-heptone ratio

time contact time (sec)

Details

Marquardt and Snee (1975) used these data to illustrate ridge regression in a model containing quadratic and interaction terms, particularly the need to center and standardize variables appearing in high-order terms.

Typical models for these data include the interaction of `temp:ratio`, and a squared term in `temp`

Source

SAS documentation example for `PROC REG`, *Ridge Regression for Acetylene Data*.

References

Marquardt, D.W., and Snee, R.D. (1975), "Ridge Regression in Practice," *The American Statistician*, **29**, 3-20.

Marquardt, D.W. (1980), "A Critique of Some Ridge Regression Methods: Comment," *Journal of the American Statistical Association*, Vol. 75, No. 369 (Mar., 1980), pp. 87-91

Examples

```
data(Acetylene)

# naive model, not using centering
amod0 <- lm(yield ~ temp + ratio + time + I(time^2) + temp:time, data=Acetylene)

y <- Acetylene[,"yield"]
X0 <- model.matrix(amod0)[,-1]

lambda <- c(0, 0.0005, 0.001, 0.002, 0.005, 0.01)
aridge0 <- ridge(y, X0, lambda=lambda)

traceplot(aridge0)
traceplot(aridge0, X="df")
pairs(aridge0, radius=0.2)
```

`biplot.pcaridge` *Biplot of Ridge Regression Trace Plot in SVD Space*

Description

`biplot.pcaridge` supplements the standard display of the covariance ellipsoids for a ridge regression problem in PCA/SVD space with labeled arrows showing the contributions of the original variables to the dimensions plotted.

Usage

```
## S3 method for class 'pcaridge'
biplot(
  x,
  variables = (p - 1):p,
  labels = NULL,
  asp = 1,
  origin,
  scale,
  var.lab = rownames(V),
  var.lwd = 1,
  var.col = "black",
  var.cex = 1,
  xlab,
  ylab,
  prefix = "Dim ",
  suffix = TRUE,
  ...
)
```

Arguments

`x`	A `pcaridge` object computed by `pca.ridge` or a `ridge` object.
`variables`	The dimensions or variables to be shown in the the plot. By default, the *last* two dimensions, corresponding to the smallest singular values, are plotted for `class("pcaridge")` objects or the *first* two variables for `class("ridge")` objects.
`labels`	A vector of character strings or expressions used as labels for the ellipses. Use `labels=NULL` to suppress these.
`asp`	Aspect ratio for the plot. The default value, `asp=1` helps ensure that lengths and angles are preserved in these plots. Use `asp=NA` to override this.
`origin`	The origin for the variable vectors in this plot, a vector of length 2. If not specified, the function calculates an origin to make the variable vectors approximately centered in the plot window.
`scale`	The scale factor for variable vectors in this plot. If not specified, the function calculates a scale factor to make the variable vectors approximately fill the plot window.
`var.lab`	Labels for variable vectors. The default is the names of the predictor variables.
`var.lwd, var.col, var.cex`	Line width, color and character size used to draw and label the arrows representing the variables in this plot.
`xlab, ylab`	Labels for the plot dimensions. If not specified, `prefix` and `suffix` are used to construct informative dimension labels.
`prefix`	Prefix for labels of the plot dimensions.
`suffix`	Suffix for labels of the plot dimensions. If `suffix=TRUE` the percent of variance accounted for by each dimension is added to the axis label.

... Other arguments, passed to plot.pcaridge

Details

The biplot view showing the dimensions corresponding to the two *smallest* singular values is particularly useful for understanding how the predictors contribute to shrinkage in ridge regression.

This is only a biplot in the loose sense that results are shown in two spaces simultaneously – the transformed PCA/SVD space of the original predictors, and vectors representing the predictors projected into this space.

biplot.ridge is a similar extension of plot.ridge, adding vectors showing the relation of the PCA/SVD dimensions to the plotted variables.

class("ridge") objects use the transpose of the right singular vectors, t(x$svd.V) for the dimension weights plotted as vectors.

Value

None

Author(s)

Michael Friendly, with contributions by Uwe Ligges

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://datavis.ca/papers/genridge-jcgs.pdf

See Also

plot.ridge, pca.ridge

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

plridge <- pca(lridge)

plot(plridge, radius=0.5)

# same, with variable vectors
biplot(plridge, radius=0.5)
# add some other options
biplot(plridge, radius=0.5, var.col="brown", var.lwd=2, var.cex=1.2, prefix="Dimension ")

# biplots for ridge objects, showing PCA vectors
```

```
plot(lridge, radius=0.5)
biplot(lridge, radius=0.5)
biplot(lridge, radius=0.5, asp=NA)
```

---

contourf *Enhanced Contour Plots*

Description

This is an enhancement to contour, written as a wrapper for that function. It creates a contour plot, or adds contour lines to an existing plot, allowing the contours to be filled and returning the list of contour lines.

Usage

```
contourf(
  x = seq(0, 1, length.out = nrow(z)),
  y = seq(0, 1, length.out = ncol(z)),
  z,
  nlevels = 10,
  levels = pretty(zlim, nlevels),
  zlim = range(z, finite = TRUE),
  col = par("fg"),
  color.palette = colorRampPalette(c("white", col)),
  fill.col = color.palette(nlevels + 1),
  fill.alpha = 0.5,
  add = FALSE,
  ...
)
```

Arguments

x, y	locations of grid lines at which the values in z are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If x is a list, its components x$x and x$y are used for x and y, respectively. If the list has component x$z this is used for z.
z	a matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.
nlevels	number of contour levels desired **iff** levels is not supplied
levels	numeric vector of levels at which to draw contour lines
zlim	z-limits for the plot. x-limits and y-limits can be passed through ...
col	color for the lines drawn
color.palette	a color palette function to be used to assign fill colors in the plot

`fill.col` a call to the `color.palette` function or an an explicit set of colors to be used in the plot. Use `fill.col=NULL` to suppress the filled polygons. a vector of fill colors corresponding to levels. By default, a set of possibly transparent colors is calculated ranging from white to `col`, using transparency given by `fill.alpha`

`fill.alpha` transparency value for `fill.col`, either a hex character string, or a numeric value between 0 and 1. Use `fill.alpha=NA` to suppress transparency.

`add` logical. If `TRUE`, add to a current plot.

`...` additional arguments passed to `contour`, including all arguments of `contour.default` not mentioned above, as well as additional graphical parameters passed by `contour.default` to more basic functions.

Value

Returns invisibly the list of contours lines, with components `levels`, `x`, `y`. See `contourLines`.

Author(s)

Michael Friendly

See Also

`contour`, `contourLines`

`contourplot` from package lattice.

Examples

```
x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
contourf(x,y,volcano, col="blue")
contourf(x,y,volcano, col="blue", nlevels=6)

# return value, unfilled, other graphic parameters
res <- contourf(x,y,volcano, col="blue", fill.col=NULL, lwd=2)
# levels used in the plot
sapply(res, function(x) x[[1]])
```

Detroit *Detroit Homicide Data for 1961-1973*

Description

The data set `Detroit` was used extensively in the book by Miller (2002) on subset regression. The data are unusual in that a subset of three predictors can be found which gives a very much better fit to the data than the subsets found from the Efroymson stepwise algorithm, or from forward selection or backward elimination. They are also unusual in that, as time series data, the assumption of independence is patently violated, and the data suffer from problems of high collinearity.

As well, ridge regression reveals somewhat paradoxical paths of shrinkage in univariate ridge trace plots, that are more comprehensible in multivariate views.

Format

A data frame with 13 observations on the following 14 variables.

`Police` Full-time police per 100,000 population

`Unemp` Percent unemployed in the population

`MfgWrk` Number of manufacturing workers in thousands

`GunLic` Number of handgun licences per 100,000 population

`GunReg` Number of handgun registrations per 100,000 population

`HClear` Percent of homicides cleared by arrests

`WhMale` Number of white males in the population

`NmfgWrk` Number of non-manufacturing workers in thousands

`GovWrk` Number of government workers in thousands

`HrEarn` Average hourly earnings

`WkEarn` Average weekly earnings

`Accident` Death rate in accidents per 100,000 population

`Assaults` Number of assaults per 100,000 population

`Homicide` Number of homicides per 100,000 of population

Details

The data were originally collected and discussed by Fisher (1976) but the complete dataset first appeared in Gunst and Mason (1980, Appendix A). Miller (2002) discusses this dataset throughout his book, but doesn't state clearly which variables he used as predictors and which is the dependent variable. (`Homicide` was the dependent variable, and the predictors were `Police` ... `WkEarn`.) The data were obtained from StatLib.

A similar version of this data set, with different variable names appears in the `bestglm` package.

Source

https://lib.stat.cmu.edu/datasets/detroit

References

Fisher, J.C. (1976). Homicide in Detroit: The Role of Firearms. *Criminology*, **14**, 387–400.

Gunst, R.F. and Mason, R.L. (1980). *Regression analysis and its application: A data-oriented approach*. Marcel Dekker.

Miller, A. J. (2002). *Subset Selection in Regression*. 2nd Ed. Chapman & Hall/CRC. Boca Raton.

Examples

```
data(Detroit)

# Work with a subset of predictors, from Miller (2002, Table 3.14),
# the "best" 6 variable model
#    Variables: Police, Unemp, GunLic, HClear, WhMale, WkEarn
# Scale these for comparison with other methods

Det <- as.data.frame(scale(Detroit[,c(1,2,4,6,7,11)]))
Det <- cbind(Det, Homicide=Detroit[,"Homicide"])

# use the formula interface; specify ridge constants in terms
# of equivalent degrees of freedom
dridge <- ridge(Homicide ~ ., data=Det, df=seq(6,4,-.5))

# univariate trace plots are seemingly paradoxical in that
# some coefficients "shrink" *away* from 0
traceplot(dridge, X="df")
vif(dridge)
pairs(dridge, radius=0.5)


plot3d(dridge, radius=0.5, labels=dridge$df)

# transform to PCA/SVD space
dpridge <- pca(dridge)

# not so paradoxical in PCA space
traceplot(dpridge, X="df")
biplot(dpridge, radius=0.5, labels=dpridge$df)

# show PCA vectors in variable space
biplot(dridge, radius=0.5, labels=dridge$df)
```

---

diab *Diabetes Progression*

Description

These data consist of observations on 442 patients, with the response of interest being a quantitative measure of disease progression one year after baseline.

There are ten baseline variables: age, sex, body-mass index (`bmi`), average blood pressure (`map`) and six blood serum measurements.

Usage

```
data("diab")
```

Format

A data frame with 442 observations on the following 11 variables.

`prog` disease progression, a numeric vector

`age` age, a numeric vector

`sex` integer, a numeric vector

`bmi` body mass index, a numeric vector

`map` mean arterial blood pressure, a numeric vector

`tc` blood serum TC, a numeric vector

`ldl` blood serum low-density lipoprotein ("bad cholersterol"), a numeric vector

`hdl` blood serum high-density lipoprotein ("good cholersterol"), a numeric vector

`tch` blood serum TCH, a numeric vector

`ltg` blood serum lamotrigine, a numeric vector

`glu` blood serum glucose, a numeric vector

Details

Efron & Hastie describe their analysis using the centered predictor variables standardized to unit L2 norm. `ridge` does not (yet) provide this scaling.

Source

The dataset was taken from the web site for Efron & Hastie (2021), *Computer Age Statistical Inference*, `https://hastie.su.domains/CASI_files/DATA/diabetes.csv`.

References

Efron, B., Hastie, T., Johnstone, I., & Tibshirani, R. (2004). Least Angle Regression. *The Annals of Statistics*, **32**(2), 407-499. doi:10.1214/009053604000000067

Efron, B., & Hastie, T. (2021). *Computer Age Statistical Inference, Student Edition: Algorithms, Evidence, and Data Science*, Cambridge University Press. doi:10.1017/9781108914062

Examples

```
data(diab)
## maybe str(diab) ; plot(diab) ...
```

`Manpower` *Hospital manpower data*

Description

The hospital manpower data, taken from Myers (1990), table 3.8, are a well-known example of highly collinear data to which ridge regression and various shrinkage and selection methods are often applied.

The data consist of measures taken at 17 U.S. Naval Hospitals and the goal is to predict the required monthly man hours for staffing purposes.

Format

A data frame with 17 observations on the following 6 variables.

`Hours` monthly man hours (response variable)

`Load` average daily patient load

`Xray` monthly X-ray exposures

`BedDays` monthly occupied bed days

`AreaPop` eligible population in the area in thousands

`Stay` average length of patient's stay in days

Details

Myers (1990) indicates his source was "Procedures and Analysis for Staffing Standards Development: Data/Regression Analysis Handbook", Navy Manpower and Material Analysis Center, San Diego, 1979.

Source

Raymond H. Myers (1990). *Classical and Modern Regression with Applications*, 2nd ed., PWS-Kent, pp. 130-133.

References

Donald R. Jensen and Donald E. Ramirez (2012). Variations on Ridge Traces in Regression, *Communications in Statistics - Simulation and Computation*, 41 (2), 265-278.

See Also

`manpower` for the same data, and other analyses

Examples

```
data(Manpower)
mmod <- lm(Hours ~ ., data=Manpower)
vif(mmod)
# ridge regression models, specified in terms of equivalent df
mridge <- ridge(Hours ~ ., data=Manpower, df=seq(5, 3.75, -.25))
vif(mridge)

# univariate ridge trace plots
traceplot(mridge)
traceplot(mridge, X="df")

# bivariate ridge trace plots
plot(mridge, radius=0.25, labels=mridge$df)
pairs(mridge, radius=0.25)


# 3D views
# ellipsoids for Load, Xray & BedDays are nearly 2D
plot3d(mridge, radius=0.2, labels=mridge$df)
# variables in model selected by AIC & BIC
plot3d(mridge, variables=c(2,3,5), radius=0.2, labels=mridge$df)

# plots in PCA/SVD space
mpridge <- pca(mridge)
traceplot(mpridge, X="df")
biplot(mpridge, radius=0.25)
```

---

pairs.ridge *Scatterplot Matrix of Bivariate Ridge Trace Plots*

Description

Displays all possible pairs of bivariate ridge trace plots for a given set of predictors.

Usage

```
## S3 method for class 'ridge'
pairs(
  x,
  variables,
  radius = 1,
  lwd = 1,
  lty = 1,
  col = c("black", "red", "darkgreen", "blue", "darkcyan", "magenta", "brown",
    "darkgray"),
```

```
    center.pch = 16,
    center.cex = 1.25,
    digits = getOption("digits") - 3,
    diag.cex = 2,
    diag.panel = panel.label,
    fill = FALSE,
    fill.alpha = 0.3,
    ...
)
```

Arguments

x	A ridge object, as fit by ridge
variables	Predictors in the model to be displayed in the plot: an integer or character vector, giving the indices or names of the variables.
radius	Radius of the ellipse-generating circle for the covariance ellipsoids.
lwd, lty	Line width and line type for the covariance ellipsoids. Recycled as necessary.
col	A numeric or character vector giving the colors used to plot the covariance ellipsoids. Recycled as necessary.
center.pch	Plotting character used to show the bivariate ridge estimates. Recycled as necessary.
center.cex	Size of the plotting character for the bivariate ridge estimates
digits	Number of digits to be displayed as the (min, max) values in the diagonal panels
diag.cex	Character size for predictor labels in diagonal panels
diag.panel	Function to draw diagonal panels. Not yet implemented: just uses internal panel.label to write the variable name and ranges.
fill	Logical vector: Should the covariance ellipsoids be filled? Recycled as necessary.
fill.alpha	Numeric vector: alpha transparency value(s) for filled ellipsoids. Recycled as necessary.
...	Other arguments passed down

Value

None. Used for its side effect of plotting.

Author(s)

Michael Friendly

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

See Also

ridge for details on ridge regression as implemented here

plot.ridge, traceplot for other plotting methods

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

pairs(lridge, radius=0.5, diag.cex=1.75)

data(prostate)
py <- prostate[, "lpsa"]
pX <- data.matrix(prostate[, 1:8])
pridge <- ridge(py, pX, df=8:1)

pairs(pridge)
```

---

pca *Transform Ridge Estimates to PCA Space*

Description

The function pca.ridge transforms a ridge object from parameter space, where the estimated coefficients are β_k with covariance matrices Σ_k, to the principal component space defined by the right singular vectors, V, of the singular value decomposition of the scaled predictor matrix, X.

In this space, the transformed coefficients are $V\beta_k$, with covariance matrices

$$V\Sigma_k V^T$$

.

This transformation provides alternative views of ridge estimates in low-rank approximations. In particular, it allows one to see where the effects of collinearity typically reside — in the smallest PCA dimensions.

Usage

```
pca(x, ...)
```

Arguments

x	A ridge object, as fit by ridge
...	Other arguments passed down. Not presently used in this implementation.

Value

An object of class `c("ridge", "pcaridge")`, with the same components as the original `ridge` object.

Author(s)

Michael Friendly

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

See Also

ridge

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

plridge <- pca(lridge)
traceplot(plridge)
pairs(plridge)
# view in space of smallest singular values
plot(plridge, variables=5:6)
```

`plot.precision` *Plot Shrinkage vs. Variance for Ridge Precision*

Description

This function uses the results of `precision` to plot a measure of shrinkage of the coefficients in ridge regression against a selected measure of their estimated sampling variance, so as to provide a direct visualization of the tradeoff between bias and precision.

Usage

```
## S3 method for class 'precision'
plot(
  x,
  xvar = "norm.beta",
  yvar = c("det", "trace", "max.eig"),
  labels = c("lambda", "df"),
  label.cex = 1.25,
  label.prefix,
  criteria = NULL,
  pch = 16,
  cex = 1.5,
  col,
  main = NULL,
  xlab,
  ylab,
  ...
)
```

Arguments

`x`	A data frame of class "precision" resulting from `precision` called on a "ridge" object. Named `x` only to conform with the `plot` generic.
`xvar`	The character name of the column to be used for the horizontal axis. Typically, this is the normalized sum of squares of the coefficients ("norm.beta") used as a measure of shrinkage / bias.
`yvar`	The character name of the column to be used for the vertical axis. One of `c("det", "trace", "max.eig")`. See `precision` for definitions of these measures.
`labels`	The character name of the column to be used for point labels. One of `c("lambda", "df")`.
`label.cex`	Character size for point labels.
`label.prefix`	Character or expression prefix for the point labels.
`criteria`	The vector of optimal shrinkage criteria from the `ridge` call to be added as points in the plot.
`pch`	Plotting character for points
`cex`	Character size for points
`col`	Point colors
`main`	Plot title
`xlab`	Label for horizontal axis
`ylab`	Label for vertical axis
`...`	Other arguments passed to `plot`.

Value

Returns nothing. Used for the side effect of plotting.

Author(s)

Michael Friendly

See Also

ridge for details on ridge regression as implemented here. precision for definitions of the measures

Examples

```
lambda <- c(0, 0.001, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(Employed ~ GNP + Unemployed + Armed.Forces +
                  Population + Year + GNP.deflator,
                data=longley, lambda=lambda)

criteria <- lridge$criteria |> print()

pridge <- precision(lridge) |> print()

plot(pridge)
# also show optimal criteria
plot(pridge, criteria = criteria)

# use degrees of freedom as point labels
plot(pridge, labels = "df")
plot(pridge, labels = "df", label.prefix="df:")
# show the trace measure
plot(pridge, yvar="trace")
```

---

plot.ridge *Bivariate Ridge Trace Plots*

Description

The bivariate ridge trace plot displays 2D projections of the covariance ellipsoids for a set of ridge regression estimates indexed by a ridge tuning constant.

The centers of these ellipses show the bias induced for each parameter, and also how the change in the ridge estimate for one parameter is related to changes for other parameters.

The size and shapes of the covariance ellipses show directly the effect on precision of the estimates as a function of the ridge tuning constant.

plot.pcaridge does these bivariate ridge trace plots for "pcaridge" objects, defaulting to plotting the two smallest components.

Usage

```
## S3 method for class 'ridge'
plot(
  x,
  variables = 1:2,
  radius = 1,
  which.lambda = 1:length(x$lambda),
  labels = lambda,
  pos = 3,
  cex = 1.2,
  lwd = 2,
  lty = 1,
  xlim,
  ylim,
  col = c("black", "red", "darkgreen", "blue", "darkcyan", "magenta", "brown",
    "darkgray"),
  center.pch = 16,
  center.cex = 1.5,
  fill = FALSE,
  fill.alpha = 0.3,
  ref = TRUE,
  ref.col = gray(0.7),
  ...
)

## S3 method for class 'pcaridge'
plot(x, variables = (p - 1):p, labels = NULL, ...)
```

Arguments

`x`	A `ridge` object, as fit by `ridge`
`variables`	Predictors in the model to be displayed in the plot: an integer or character vector of length 2, giving the indices or names of the variables. Defaults to the first two predictors for `ridge` objects or the *last* two dimensions for `pcaridge` objects.
`radius`	Radius of the ellipse-generating circle for the covariance ellipsoids. The default, `radius=1` gives a standard "unit" ellipsoid. Typically, values `radius<1` gives less cluttered displays.
`which.lambda`	A vector of indices used to select the values of `lambda` for which ellipses are plotted. The default is to plot ellipses for all values of `lambda` in the `ridge` object.
`labels`	A vector of character strings or expressions used as labels for the ellipses. Use `labels=NULL` to suppress these.
`pos, cex`	Scalars or vectors of positions (relative to the ellipse centers) and character size used to label the ellipses
`lwd, lty`	Line width and line type for the covariance ellipsoids. Recycled as necessary.
`xlim, ylim`	X, Y limits for the plot, each a vector of length 2. If missing, the range of the covariance ellipsoids is used.

`col`	A numeric or character vector giving the colors used to plot the covariance ellipsoids. Recycled as necessary.
`center.pch`	Plotting character used to show the bivariate ridge estimates. Recycled as necessary.
`center.cex`	Size of the plotting character for the bivariate ridge estimates
`fill`	Logical vector: Should the covariance ellipsoids be filled? Recycled as necessary.
`fill.alpha`	Numeric vector: alpha transparency value(s) in the range (0, 1) for filled ellipsoids. Recycled as necessary.
`ref`	Logical: whether to draw horizontal and vertical reference lines at 0.
`ref.col`	Color of reference lines.
`...`	Other arguments passed down to `plot.default`, e.g., `xlab`, `ylab`, and other graphic parameters.

Value

None. Used for its side effect of plotting.

Author(s)

Michael Friendly

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

See Also

`ridge` for details on ridge regression as implemented here; `pairs.ridge`, `traceplot`, for basic plots.

`pca.ridge` for transformation of ridge regression estimates to PCA space. `biplot.pcaridge` and `plot3d.ridge` for other plotting methods

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lambdaf <- c("", ".005", ".01", ".02", ".04", ".08")
lridge <- ridge(longley.y, longley.X, lambda=lambda)

op <- par(mfrow=c(2,2), mar=c(4, 4, 1, 1)+ 0.1)
for (i in 2:5) {
plot(lridge, variables=c(1,i), radius=0.5, cex.lab=1.5)
text(lridge$coef[1,1], lridge$coef[1,i], expression(~widehat(beta)^OLS),
```

```
     cex=1.5, pos=4, offset=.1)
if (i==2) text(lridge$coef[-1,1:2], lambdaf[-1], pos=3, cex=1.25)
}
par(op)

data(prostate)
py <- prostate[, "lpsa"]
pX <- data.matrix(prostate[, 1:8])
pridge <- ridge(py, pX, df=8:1)

plot(pridge)
plot(pridge, fill=c(TRUE, rep(FALSE,7)))
```

`plot3d` *3D Ridge Trace Plots*

Description

The 3D ridge trace plot displays 3D projections of the covariance ellipsoids for a set of ridge regression estimates indexed by a ridge tuning constant.

The centers of these ellipses show the bias induced for each parameter, and also how the change in the ridge estimate for one parameter is related to changes for other parameters.

The size and shapes of the covariance ellipsoids show directly the effect on precision of the estimates as a function of the ridge tuning constant.

`plot3d.ridge` and `plot3d.pcaridge` differ only in the defaults for the variables plotted.

Usage

```
plot3d(x, ...)

## S3 method for class 'pcaridge'
plot3d(x, variables = (p - 2):p, ...)

## S3 method for class 'ridge'
plot3d(
  x,
  variables = 1:3,
  radius = 1,
  which.lambda = 1:length(x$lambda),
  lwd = 1,
  lty = 1,
  xlim,
  ylim,
  zlim,
  xlab,
```

```
  ylab,
  zlab,
  col = c("black", "red", "darkgreen", "blue", "darkcyan", "magenta", "brown",
    "darkgray"),
  labels = lambda,
  ref = TRUE,
  ref.col = gray(0.7),
  segments = 40,
  shade = TRUE,
  shade.alpha = 0.1,
  wire = FALSE,
  aspect = 1,
  add = FALSE,
  ...
)
```

Arguments

`x`	A `ridge` object, as fit by `ridge` or a `pcaridge` object as transformed by `pca.ridge`
`...`	Other arguments passed down
`variables`	Predictors in the model to be displayed in the plot: an integer or character vector of length 3, giving the indices or names of the variables. Defaults to the first three predictors for `ridge` objects or the *last* three dimensions for `pcaridge` objects.
`radius`	Radius of the ellipse-generating circle for the covariance ellipsoids. The default, `radius=1` gives a standard "unit" ellipsoid. Typically, `radius<1` gives less cluttered displays.
`which.lambda`	A vector of indices used to select the values of `lambda` for which ellipsoids are plotted. The default is to plot ellipsoids for all values of `lambda` in the `ridge` object.
`lwd, lty`	Line width and line type for the covariance ellipsoids. Recycled as necessary.
`xlim, ylim, zlim`	X, Y, Z limits for the plot, each a vector of length 2. If missing, the range of the covariance ellipsoids is used.
`xlab, ylab, zlab`	Labels for the X, Y, Z variables in the plot. If missing, the names of the predictors given in `variables` is used.
`col`	A numeric or character vector giving the colors used to plot the covariance ellipsoids. Recycled as necessary.
`labels`	A numeric or character vector giving the labels to be drawn at the centers of the covariance ellipsoids.
`ref`	Logical: whether to draw horizontal and vertical reference lines at 0. This is not yet implemented.
`ref.col`	Color of reference lines.
`segments`	Number of line segments used in drawing each dimension of a covariance ellipsoid.

shade	a logical scalar or vector, indicating whether the ellipsoids should be rendered with shade3d. Recycled as necessary.
shade.alpha	a numeric value in the range [0,1], or a vector of such values, giving the alpha transparency for ellipsoids rendered with shade=TRUE.
wire	a logical scalar or vector, indicating whether the ellipsoids should be rendered with wire3d. Recycled as necessary.
aspect	a scalar or vector of length 3, or the character string "iso", indicating the ratios of the x, y, and z axes of the bounding box. The default, aspect=1 makes the bounding box display as a cube approximately filling the display. See aspect3d for details.
add	if TRUE, add to the current rgl plot; the default is FALSE.

Value

None. Used for its side-effect of plotting

Note

This is an initial implementation. The details and arguments are subject to change.

Author(s)

Michael Friendly

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

See Also

plot.ridge, pairs.ridge, pca.ridge

Examples

```
lmod <- lm(Employed ~ GNP + Unemployed + Armed.Forces + Population +
                      Year + GNP.deflator, data=longley)
longley.y <- longley[, "Employed"]
longley.X <- model.matrix(lmod)[,-1]

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lambdaf <- c("0", ".005", ".01", ".02", ".04", ".08")
lridge <- ridge(longley.y, longley.X, lambda=lambda)


plot3d(lridge, var=c(1,4,5), radius=0.5)

# view in SVD/PCA space
plridge <- pca(lridge)
```

```
plot3d(plridge, radius=0.5)
```

`precision` *Measures of Precision and Shrinkage for Ridge Regression*

Description

The goal of `precision` is to allow you to study the relationship between shrinkage of ridge regression coefficients and their precision directly by calculating measures of each.

Three measures of (inverse) precision based on the "size" of the covariance matrix of the parameters are calculated. Let $V_k \equiv \text{Var}(\beta_k)$ be the covariance matrix for a given ridge constant, and let $\lambda_i, i = 1, \ldots p$ be its eigenvalues. Then the variance (= 1/precision) measures are:

1. `"det"`: $\log |V_k| = \log \prod \lambda$ (with `det.fun = "log"`, the default) or $|V_k|^{1/p} = (\prod \lambda)^{1/p}$ (with `det.fun = "root"`) measures the linearized volume of the covariance ellipsoid and corresponds conceptually to Wilks' Lambda criterion
2. `"trace"`: $\text{trace}(V_k) = \sum \lambda$ corresponds conceptually to Pillai's trace criterion
3. `"max.eig"`: $\lambda_1 = \max(\lambda)$ corresponds to Roy's largest root criterion.

Two measures of shrinkage are also calculated:

- `norm.beta`: the root mean square of the coefficient vector $\|\beta_k\|$, normalized to a maximum of 1.0 if `normalize == TRUE` (the default).
- `norm.diff`: the root mean square of the difference from the OLS estimate $\|\beta_{\text{OLS}} - \beta_k\|$. This measure is inversely related to `norm.beta`

A plot method, `plot.precision` facilitates making graphs of these quantities.

Usage

```
precision(object, det.fun, normalize, ...)
```

Arguments

`object`	An object of class `ridge` or `lm`
`det.fun`	Function to be applied to the determinants of the covariance matrices, one of `c("log","root")`.
`normalize`	If `TRUE` the length of the coefficient vector β_k is normalized to a maximum of 1.0.
`...`	Other arguments (currently unused)

Value

An object of class `c("precision", "data.frame")` with the following columns:

`lambda`	The ridge constant
`df`	The equivalent effective degrees of freedom
`det`	The `det.fun` function of the determinant of the covariance matrix
`trace`	The trace of the covariance matrix
`max.eig`	Maximum eigen value of the covariance matrix
`norm.beta`	The root mean square of the estimated coefficients, possibly normalized
`norm.diff`	The root mean square of the difference between the OLS solution (`lambda = 0`) and ridge solutions

Note

Models fit by `lm` and `ridge` use a different scaling for the predictors, so the results of `precision` for an `lm` model will not correspond to those for `ridge` with ridge constant = 0.

Author(s)

Michael Friendly

See Also

`ridge`, `plot.precision`

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

# same, using formula interface
lridge <- ridge(Employed ~ GNP + Unemployed + Armed.Forces + Population + Year + GNP.deflator,
data=longley, lambda=lambda)

clr <- c("black", rainbow(length(lambda)-1, start=.6, end=.1))
coef(lridge)

(pdat <- precision(lridge))
# plot log |Var(b)| vs. length(beta)
with(pdat, {
plot(norm.beta, det, type="b",
cex.lab=1.25, pch=16, cex=1.5, col=clr, lwd=2,
xlab='shrinkage: ||b|| / max(||b||)',
ylab='variance: log |Var(b)|')
text(norm.beta, det, lambda, cex=1.25, pos=c(rep(2,length(lambda)-1),4))
text(min(norm.beta), max(det), "Variance vs. Shrinkage", cex=1.5, pos=4)
```

```
})

# plot trace[Var(b)] vs. length(beta)
with(pdat, {
plot(norm.beta, trace, type="b",
cex.lab=1.25, pch=16, cex=1.5, col=clr, lwd=2,
xlab='shrinkage: ||b|| / max(||b||)',
ylab='variance: trace [Var(b)]')
text(norm.beta, trace, lambda, cex=1.25, pos=c(2, rep(4,length(lambda)-1)))
# text(min(norm.beta), max(det), "Variance vs. Shrinkage", cex=1.5, pos=4)
})
```

---

prostate *Prostate Cancer Data*

Description

Data to examine the correlation between the level of prostate-specific antigen and a number of clinical measures in men who were about to receive a radical prostatectomy.

Format

A data frame with 97 observations on the following 10 variables.

lcavol log cancer volume

lweight log prostate weight

age in years

lbph log of the amount of benign prostatic hyperplasia

svi seminal vesicle invasion

lcp log of capsular penetration

gleason a numeric vector

pgg45 percent of Gleason score 4 or 5

lpsa response

train a logical vector

Details

This data set came originally from the (now defunct) ElemStatLearn package.

The last column indicates which 67 observations were used as the "training set" and which 30 as the test set, as described on page 48 in the book.

Note

There was an error in this dataset in earlier versions of the package, as indicated in a footnote on page 3 of the second edition of the book. As of version 2012.04-0 this was corrected.

Source

Stamey, T., Kabalin, J., McNeal, J., Johnstone, I., Freiha, F., Redwine, E. and Yang, N (1989) Prostate specific antigen in the diagnosis and treatment of adenocarcinoma of the prostate II. Radical prostatectomy treated patients, *Journal of Urology*, **16**: 1076–1083.

Examples

```
data(prostate)
str( prostate )
cor( prostate[,1:8] )
prostate <- prostate[, -10]

prostate.mod <- lm(lpsa ~ ., data=prostate)
vif(prostate.mod)

py <- prostate[, "lpsa"]
pX <- data.matrix(prostate[, 1:8])
pridge <- ridge(py, pX, df=8:1)
pridge

# univariate ridge trace plots
traceplot(pridge)
traceplot(pridge, X="df")

# bivariate ridge trace plots
plot(pridge)
pairs(pridge)
```

`ridge` *Ridge Regression Estimates*

Description

The function `ridge` fits linear models by ridge regression, returning an object of class `ridge` designed to be used with the plotting methods in this package.

It is also designed to facilitate an alternative representation of the effects of shrinkage in the space of uncorrelated (PCA/SVD) components of the predictors.

The standard formulation of ridge regression is that it regularizes the estimates of coefficients by adding small positive constants λ to the diagonal elements of $\mathbf{X}^\top\mathbf{X}$ in the least squares solution to achieve a more favorable tradeoff between bias and variance (inverse of precision) of the coefficients.

$$\widehat{\beta}^{\mathrm{RR}}_k = (\mathbf{X}^\top\mathbf{X} + \lambda\mathbf{I})^{-1}\mathbf{X}^\top\mathbf{y}$$

Ridge regression shrinkage can be parameterized in several ways.

- If a vector of `lambda` values is supplied, these are used directly in the ridge regression computations.
- Otherwise, if a vector `df` can be supplied the equivalent values for effective degrees of freedom corresponding to shrinkage, going down from the number of predictors in the model.

In either case, both `lambda` and `df` are returned in the `ridge` object, but the `rownames` of the coefficients are given in terms of `lambda`.

`coef` extracts the estimated coefficients for each value of the shrinkage factor

`vcov` extracts the estimated $p \times p$ covariance matrices of the coefficients for each value of the shrinkage factor.

`best` extracts the optimal shrinkage values according to several criteria: HKB: Hoerl et al. (1975); LW: Lawless & Wang (1976); GCV: Golub et al. (1975)

Usage

```
ridge(y, ...)

## S3 method for class 'formula'
ridge(formula, data, lambda = 0, df, svd = TRUE, contrasts = NULL, ...)

## Default S3 method:
ridge(y, X, lambda = 0, df, svd = TRUE, ...)

## S3 method for class 'ridge'
coef(object, ...)

## S3 method for class 'ridge'
print(x, digits = max(5, getOption("digits") - 5), ...)

## S3 method for class 'ridge'
vcov(object, ...)

best(object, ...)

## S3 method for class 'ridge'
best(object, ...)
```

Arguments

`y`	A numeric vector containing the response variable. NAs not allowed.
`...`	Other arguments, passed down to methods
`formula`	For the `formula` method, a two-sided formula.
`data`	For the `formula` method, data frame within which to evaluate the formula.
`lambda`	A scalar or vector of ridge constants. A value of 0 corresponds to ordinary least squares.
`df`	A scalar or vector of effective degrees of freedom corresponding to `lambda`

`svd`	If `TRUE` the SVD of the centered and scaled `X` matrix is returned in the `ridge` object.
`contrasts`	a list of contrasts to be used for some or all of factor terms in the formula. See the `contrasts.arg` of `model.matrix.default`.
`X`	A matrix of predictor variables. NA's not allowed. Should not include a column of 1's for the intercept.
`x, object`	An object of class `ridge`
`digits`	For the `print` method, the number of digits to print.

Details

If an intercept is present in the model, its coefficient is not penalized. (If you want to penalize an intercept, put in your own constant term and remove the intercept.)

The predictors are centered, but not (yet) scaled in this implementation.

A number of the methods in the package assume that `lambda` is a vector of shrinkage constants increasing from `lambda[1] = 0`, or equivalently, a vector of `df` decreasing from p.

Value

A list with the following components:

`lambda`	The vector of ridge constants
`df`	The vector of effective degrees of freedom corresponding to `lambda`
`coef`	The matrix of estimated ridge regression coefficients
`scales`	scalings used on the X matrix
`kHKB`	HKB estimate of the ridge constant
`kLW`	L-W estimate of the ridge constant
`GCV`	vector of GCV values
`kGCV`	value of `lambda` with the minimum GCV
`criteria`	Collects the criteria `kHKB`, `kLW`, and `kGCV` in a named vector

If `svd==TRUE` (the default), the following are also included:

`svd.D`	Singular values of the `svd` of the scaled X matrix
`svd.U`	Left singular vectors of the `svd` of the scaled X matrix. Rows correspond to observations and columns to dimensions.
`svd.V`	Right singular vectors of the `svd` of the scaled X matrix. Rows correspond to variables and columns to dimensions.

A data.frame with one row for each of the HKB, LW, and GCV criteria

Author(s)

Michael Friendly

References

Hoerl, A. E., Kennard, R. W., and Baldwin, K. F. (1975), "Ridge Regression: Some Simulations," *Communications in Statistics*, 4, 105-123.

Lawless, J.F., and Wang, P. (1976), "A Simulation Study of Ridge and Other Regression Estimators," *Communications in Statistics*, 5, 307-323.

Golub G.H., Heath M., Wahba G. (1979) Generalized cross-validation as a method for choosing a good ridge parameter. *Technometrics*, **21**:215–223. doi:10.2307/1268518

See Also

`lm.ridge` for other implementations of ridge regression

`traceplot`, `plot.ridge`, `pairs.ridge`, `plot3d.ridge`, for 1D, 2D, 3D plotting methods

`pca.ridge`, `biplot.ridge`, `biplot.pcaridge` for views in PCA/SVD space

`precision.ridge` for measures of shrinkage and precision

Examples

```
#\donttest{
# Longley data, using number Employed as response
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

# same, using formula interface
lridge <- ridge(Employed ~ GNP + Unemployed + Armed.Forces + Population + Year + GNP.deflator,
data=longley, lambda=lambda)


coef(lridge)

# standard trace plot
traceplot(lridge)
# plot vs. equivalent df
traceplot(lridge, X="df")
pairs(lridge, radius=0.5)
#}


data(prostate)
py <- prostate[, "lpsa"]
pX <- data.matrix(prostate[, 1:8])
pridge <- ridge(py, pX, df=8:1)
pridge

plot(pridge)
pairs(pridge)
```

```
traceplot(pridge)
traceplot(pridge, X="df")


# Hospital manpower data from Table 3.8 of Myers (1990)
data(Manpower)
str(Manpower)

mmod <- lm(Hours ~ ., data=Manpower)
vif(mmod)
# ridge regression models, specified in terms of equivalent df
mridge <- ridge(Hours ~ ., data=Manpower, df=seq(5, 3.75, -.25))
vif(mridge)

# univariate ridge trace plots
traceplot(mridge)
traceplot(mridge, X="df")


# bivariate ridge trace plots
plot(mridge, radius=0.25, labels=mridge$df)
pairs(mridge, radius=0.25)

# 3D views
# ellipsoids for Load, Xray & BedDays are nearly 2D
plot3d(mridge, radius=0.2, labels=mridge$df)
# variables in model selected by AIC & BIC
plot3d(mridge, variables=c(2,3,5), radius=0.2, labels=mridge$df)

# plots in PCA/SVD space
mpridge <- pca(mridge)
traceplot(mpridge, X="df")
biplot(mpridge, radius=0.25)
```

`traceplot` *Univariate Ridge Trace Plots*

Description

The `traceplot` function extends and simplifies the univariate ridge trace plots for ridge regression provided in the `plot` method for `lm.ridge`

Usage

```
traceplot(
  x,
  X = c("lambda", "df"),
```

```
    col = c("black", "red", "darkgreen", "blue", "darkcyan", "magenta", "brown",
      "darkgray"),
    pch = c(15:18, 7, 9, 12, 13),
    xlab,
    ylab = "Coefficient",
    xlim,
    ylim,
    ...
)
```

Arguments

x	A ridge object, as fit by ridge
X	What to plot as the horizontal coordinate, one of c("lambda", "df")
col	A numeric or character vector giving the colors used to plot the ridge trace curves. Recycled as necessary.
pch	Vector of plotting characters used to plot the ridge trace curves. Recycled as necessary.
xlab	Label for horizontal axis
ylab	Label for vertical axis
xlim, ylim	x, y limits for the plot. You may need to adjust these to allow for the variable labels.
...	Other arguments passed to matplot

Details

For ease of interpretation, the variables are labeled at the side of the plot (left, right) where the coefficient estimates are expected to be most widely spread. If xlim is not specified, the range of the X variable is extended slightly to accommodate the variable names.

Value

None. Used for its side effect of plotting.

Author(s)

Michael Friendly

References

Friendly, M. (2013). The Generalized Ridge Trace Plot: Visualizing Bias *and* Precision. *Journal of Computational and Graphical Statistics*, **22**(1), 50-68, doi:10.1080/10618600.2012.681237, https://www.datavis.ca/papers/genridge-jcgs.pdf

Hoerl, A. E. and Kennard R. W. (1970). "Ridge Regression: Applications to Nonorthogonal Problems", *Technometrics*, 12(1), 69-82.

See Also

ridge for details on ridge regression as implemented here

plot.ridge, pairs.ridge for other plotting methods

Examples

```
longley.y <- longley[, "Employed"]
longley.X <- data.matrix(longley[, c(2:6,1)])

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(longley.y, longley.X, lambda=lambda)

traceplot(lridge)
#abline(v=lridge$kLW, lty=3)
#abline(v=lridge$kHKB, lty=3)
#text(lridge$kLW, -3, "LW")
#text(lridge$kHKB, -3, "HKB")

traceplot(lridge, X="df")
```

---

trans.colors *Make Colors Transparent*

Description

Takes a vector of colors (as color names or rgb hex values) and adds a specified alpha transparency to each.

Usage

```
trans.colors(col, alpha = 0.5, names = NULL)
```

Arguments

col	A character vector of colors, either as color names or rgb hex values
alpha	alpha transparency value(s) to apply to each color (0 means fully transparent and 1 means opaque)
names	optional character vector of names for the colors

Details

Colors (col) and alpha need not be of the same length. The shorter one is replicated to make them of the same length.

Value

A vector of color values of the form "#rrggbbaa"

Author(s)

Michael Friendly

See Also

col2rgb, rgb,

Examples

```
trans.colors(palette(), alpha=0.5)

# alpha can be vectorized
trans.colors(palette(), alpha=seq(0, 1, length=length(palette())))

# lengths need not match: shorter one is repeated as necessary
trans.colors(palette(), alpha=c(.1, .2))

trans.colors(colors()[1:20])

# single color, with various alphas
trans.colors("red", alpha=seq(0,1, length=5))
# assign names
trans.colors("red", alpha=seq(0,1, length=5), names=paste("red", 1:5, sep=""))
```

---

vif.ridge *Variance Inflation Factors for Ridge Regression*

Description

The function vif.ridge calculates variance inflation factors for the predictors in a set of ridge regression models indexed by the tuning/shrinkage factor, returning one row for each value of the λ parameter.

Variance inflation factors are calculated using the simplified formulation in Fox & Monette (1992).

The plot.vif.ridge method plots variance inflation factors for a "vif.ridge" object in a similar style to what is provided by traceplot. That is, it plots the VIF for each coefficient in the model against either the ridge λ tuning constant or it's equivalent effective degrees of freedom.

Usage

```
## S3 method for class 'ridge'
vif(mod, ...)

## S3 method for class 'vif.ridge'
print(x, digits = max(4, getOption("digits") - 5), ...)

## S3 method for class 'vif.ridge'
plot(
  x,
  X = c("lambda", "df"),
  Y = c("vif", "sqrt"),
  col = c("black", "red", "darkgreen", "blue", "darkcyan", "magenta", "brown",
    "darkgray"),
  pch = c(15:18, 7, 9, 12, 13),
  xlab,
  ylab,
  xlim,
  ylim,
  ...
)
```

Arguments

mod	A "ridge" object computed by ridge
...	Other arguments passed to methods
x	A ridge object, as fit by ridge
digits	Number of digits to display in the print method
X	What to plot as the horizontal coordinate, one of c("lambda", "df")
Y	What to plot as the vertical coordinate, one of c("vif", "sqrt"), where the latter plots $\sqrt{VIF}$.
col	A numeric or character vector giving the colors used to plot the ridge trace curves. Recycled as necessary.
pch	Vector of plotting characters used to plot the ridge trace curves. Recycled as necessary.
xlab	Label for horizontal axis
ylab	Label for vertical axis
xlim, ylim	x, y limits for the plot. You may need to adjust these to allow for the variable labels.

Value

vif returns a "vif.ridge" object, which is a list of four components

vif	a data frame of the same size and shape as coef{mod}. The columns correspond to the predictors in the model and the rows correspond to the values of lambda in ridge estimation.

`lambda`	the vector of ridge constants from the original call to `ridge`
`df`	the vector of effective degrees of freedom corresponding to `lambda`
`criteria`	the optimal values of `lambda`

Author(s)

Michael Friendly

References

Fox, J. and Monette, G. (1992). Generalized collinearity diagnostics. *JASA*, **87**, 178-183, doi:10.1080/01621459.1992.10475190.

See Also

`vif`, `precision`

Examples

```
data(longley)
lmod <- lm(Employed ~ GNP + Unemployed + Armed.Forces + Population +
                      Year + GNP.deflator, data=longley)
vif(lmod)

lambda <- c(0, 0.005, 0.01, 0.02, 0.04, 0.08)
lridge <- ridge(Employed ~ GNP + Unemployed + Armed.Forces +
                           Population + Year + GNP.deflator,
             data=longley, lambda=lambda)

coef(lridge)

# get VIFs for the shrunk estimates
vridge <- vif(lridge)
vridge
names(vridge)



# plot VIFs
pch <- c(15:18, 7, 9)
clr <- c("black", rainbow(5, start=.6, end=.1))

plot(vridge,
     col=clr, pch=pch, cex = 1.2,
     xlim = c(-0.02, 0.08))

plot(vridge, X = "df",
     col=clr, pch=pch, cex = 1.2,
     xlim = c(4, 6.5))

# Better to plot sqrt(VIF). Plot against degrees of freedom
```

```
plot(vridge, X = "df", Y="sqrt",
     col=clr, pch=pch, cex = 1.2,
     xlim = c(4, 6.5))
```

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