Package ‘factorplot’

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Description

Factorplot is a way to summarize and plot information from categorical predictors from linear models and GLMs. It creates all simple contrasts and analytical standard errors for those contrasts.

Details

After a linear model or GLM has been estimated, the factorplot command creates all pairwise differences among the levels (including the reference category) of the indicated factor as well as their associated standard errors to facilitate hypothesis testing directly. The print method prints the pairwise difference, standard error, p-value and Bonferroni-corrected p-value. The summary method prints the number of significant positive/negative pairwise differences. The plot method makes something akin to an upper-triangular levelplot that indicates whether differences are positive/negative and statistically significant.

Author(s)

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References


Description

This function calculates all pairwise difference from the input data. The input data can be the result of a GLM (produced with glm), a multinomial logit model (produced with multinom from the nnet package), a general linear hypothesis test (produced with glht from the multcomp package), an object of class eff from the effects package or any vector of values and a corresponding variance-covariance matrix.
Usage

```r
## S3 method for class 'glm'
factorplot(obj, adjust.method="none", order="natural",
           factor.variable=NULL, pval=.05, two.sided=TRUE, ...)
## S3 method for class 'lm'
factorplot(obj, adjust.method="none", order="natural",
           factor.variable=NULL, pval=.05, two.sided=TRUE, ...)
## S3 method for class 'glht'
factorplot(obj, adjust.method="none", pval=.05, ...)
## S3 method for class 'summary.glht'
factorplot(obj, ...)
## S3 method for class 'multinom'
factorplot(obj, adjust.method="none", order="natural",
           variable, pval = .05, two.sided=TRUE, ...)
## S3 method for class 'eff'
factorplot(obj, adjust.method="none", order="natural",
           pval=0.05, two.sided=TRUE, ordby = NULL, ...)
## Default S3 method:
factorplot(obj, adjust.method="none", order="natural",
           var, resdf, pval=0.05, two.sided=TRUE, ...)
```

Arguments

- **obj** An object of class `glm` or `lm`, `glht`, `summary.glht`, `multinom` or a vector of values (of class numeric) for which pairwise differences will be calculated.
- **factor.variable** String containing the name of the factor for which pairwise coefficient differences will be calculated (if a `glm` or `lm` class object is passed to the function).
- **variable** String containing the name of the column of the model matrix for which pairwise differences will be calculated if a `multinom` class object is passed to the function.
- **var** Variance-covariance matrix to be used if `obj` is a numeric vector. This could also be a vector of quasi/floating variances from which a diagonal variance-covariance matrix will be produced.
- **resdf** Residual degrees of freedom used as the degrees of freedom for the t-distribution from which p-values will be generated if `obj` is a numeric vector.
- **pval** The (uncorrected) Type I error probability required, default = 0.05
- **two.sided** Logical argument indicating whether the hypothesis test should be against a two-sided alternative if TRUE (default) or a one-sided alternative if FALSE.
- **order** One of ‘natural’, ‘alph’, or ‘size’ indicating how the levels of the factor should be ordered for presentation. The ‘natural’ option (the default) leaves the levels as they are in the factor contrasts. ‘alph’ sorts the levels alphabetically and ‘size’ sorts the levels by size of coefficient.
- **adjust.method** For objects of class `multinom` and numeric - one of the methods allowed by `p.adjust` in `stats` - ‘holm’, ‘hochberg’, ‘hommel’, ‘bonferroni’, ‘BH’, ‘BY’, ‘fdr’, ‘none’. See help for the `p.adjust` for more information on these different adjustment methods. For objects of class `glm`, `lm` or `glht`, additional arguments
of ‘single-step’, ‘Shaffer’, ‘Westfall’ and ‘free’ are possible. See glht from the multcomp package for details.

ordby For objects of class eff with interactions, ordby is a string indicating the variable by which the plot should be ordered.

Additional arguments to be passed to summary.glht, including, but not limited to level and alternative.

Details

This function calculates pairwise differences that can be passed to a novel plotting method that does not suffer from some of the same problems as floating/quasi confidence intervals and is easier to apprehend immediately than a compact letter display.

While the factorplot function and its print and summary methods work equally well regardless of the number of levels in the factor_variable, the plot function automatically scales the resulting graph to the appropriate size, but will be less useful as the number of contrasts gets large (e.g., > 30). If more than one factor covariate is present and the factor_variable option is NULL, the function generates a text-based menu in the R GUI that will allow the users to pick the term for which they want to calculate the results.

Value

b_diff An upper-triangular matrix of pairwise differences between row and column levels of the factor

b_sd An upper-triangular matrix of standard errors of the pairwise differences represented in b_diff

pval An upper-triangular matrix of uncorrected (one-sided) p-values corresponding to the entries of b_diff

p The p-value specified in the command

Author(s)

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References


Examples

```r
# for lm/glm
x <- as.factor(round(runif(1000, .5,5.5)))
levels(x) <- paste("lab", 1:20, sep="")
X <- model.matrix(~x)
```
\begin{verbatim}
Y <- X %%*% rnorm(ncol(X), 0, 4) + rnorm(1000)
mod <- lm(Y ~ x)
f <- factorplot(mod, factor.variable="x", pval = 0.05, order="alph")

## for glht
library(multcomp)
mod.glht <- glht(mod, linfct = mcp('x' = 'Tukey'))
f2 <- factorplot(mod.glht, adjust.method='single-step')

## for vector of values
b <- c(0, mod$coef[-])
v <- rbind(0, vcov(mod)[-1,-1])
names(b) <- colnames(v) <- rownames(v) <- mod$levels[["x"]]
f3 <- factorplot(b, var=v, resdf=mod$df.residual)

## for multinomial logit
library(nnet)
multi.mod <- multinom(vote ~ retnat + lrself + male + age, data=france)
f4 <- factorplot(multi.mod, variable="lrself")
\end{verbatim}

**Description**

A subset of data from the 1994 Eurobarometer for France

**Usage**

data(france)

**Format**

A data frame with 542 observations on the following 5 variables.

- **lrself**: respondent’s left-right self-placement on a 1(left)-10(right) scale
- **male**: a dummy variable coded 1 for males and 0 for females
- **age**: respondent’s age
- **vote**: a factor indicating vote choice with levels PCF, PS, Green, RPR and UDF
- **retnat**: a factor indicating the respondent’s retrospective national economic evaluation with levels Better, Same and Worse

**References**

plot.factorplot  

Plot method for objects of class factorplot

Description

Creates a plot akin to an upper-triangular levelplot (though using plot rather than levelplot) where the coloring of the squares represents significance and text inside the squares represents the pairwise difference and its corresponding standard error.

Usage

```r
## S3 method for class 'factorplot'
plot(x, ..., abbrev.char=10, polycol=NULL,
textcol= NULL, trans= NULL, print.sig.leg= TRUE, print.square.leg= TRUE,
scale.text= 1, space.text= 1, print.est= TRUE, print.se= TRUE)
```

Arguments

- **x**: An object of class factorplot, produced by `factorplot`.
- **abbrev.char**: The number of characters that should be used to abbreviate the levels of the factor. Set to a large value for unabbreviated names.
- **polycol**: A vector of three colors indicating the colors of polygons when the difference is significant negative, insignificant, and significant positive, in that order. Defaults to c('gray80', 'white', 'gray40').
- **textcol**: A vector of three colors indicating the text color for polygons that are significant negative, insignificant, and significant positive, in that order. Defaults to c('black', 'black', 'white').
- **trans**: A character string representing the post-hypothesis-testing transformation to be performed on the estimates. For example, if the estimates provided to the factorplot command are log-floating absolute risks, you could use the transformation 'exp'. The transformation is performed through a call to `do.call`
- **print.sig.leg**: logical indicating whether the legend identifying the meaning of the different colors should be included.
- **print.square.leg**: logical indicating whether the legend identifying the meaning of the numbers in each square should be included.
- **scale.text**: optional scale factor to be applied to text, numbers bigger than 1 make text bigger than default and numbers smaller than 1 do the opposite.
- **space.text**: optional text spacing factor, numbers bigger than 1 push text toward the extent of the boxes and numbers smaller than one bring text in toward the center.
- **print.est**: logical argument indicating whether the estimates should be printed in the boxes.
- **print.se**: logical argument indicating whether the standard errors should be printed in the boxes.
- **...**: Other arguments to be passed to plot, currently not implemented.
Value

A graph

Author(s)

Dave Armstrong (Department of Political Science, UW-Milwaukee)

See Also

factorplot

Examples

est1 <- log(c(1,0.12,1.44,1.31,1.44,1.46,0.90))
var1 <- c(0.242,0.096,0.156,0.140,0.388,0.484,0.375)^2
names(est1) <- c("Normal & superficial gastritis", "Chronic gastritis", "Chronic atrophic gastritis", "Intestinal metaplasia I", "Intestinal metaplasia II", "Intestinal metaplasia III", "Dysplasia")

plummer_fp1 <- factorplot(est1, var=var1, resdf=Inf)
plot(plummer_fp1, trans="exp", abbrev.char = 100)

print.factorplot

Print method for objects of class factorplot

Description

Prints the output from an object of class factorplot. By default, the function prints all pairwise differences along with standard errors and p-values (optionally adjusted for multiple testing). Optionally, it can print only significant differences.

Usage

## S3 method for class 'factorplot'
print(x, ..., digits = 3, sig = FALSE, trans=NULL)
Arguments

- **x**: An object of class `factorplot`.
- **digits**: The number of digits to print in each column.
- **trans**: A character string representing the post-hypothesis-testing transformation to be performed on the estimates. For example, if the estimates provided to the `factorplot` command are log-floating absolute risks, you could use the transformation `exp`. The transformation is performed through a call to `do.call`.
- **sig**: Logical indicating whether only significant differences should be printed.
- **...**: Other arguments passed to print, currently not implemented.

Author(s)

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See Also

- `factorplot`

Examples

```r
est1 <- log(c(1.00, 2.12, 1.44, 1.31, 1.44, 1.46, 0.90))
var1 <- c(0.242, 0.096, 0.156, 0.140, 0.380, 0.484, 0.375)^2
names(est1) <- c("Normal & superficial gastritis", "Chronic gastritis", "Chronic atrophic gastritis", "Intestinal metaplasia I", "Intestinal metaplasia II", "Intestinal metaplasia III", "Dysplasia")
plummer_fp1 <- factorplot(est1, var=var1, resdf=Inf)
print(plummer_fp1, trans="exp")
```

Description

An auxiliary function to plot squares, used by the `plot.factorplot` function.

Usage

```r
squares(ll, width = 1, col)
```
summary.factorplot

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ll</td>
<td>The ((x,y)) coordinate of the lower-left corner of the square</td>
</tr>
<tr>
<td>width</td>
<td>A scalar indicating how wide the squares should be</td>
</tr>
<tr>
<td>col</td>
<td>A color with which the square will be filled in</td>
</tr>
</tbody>
</table>

Details

This is a function called by `plot.factorplot` and not intended to be directly used by the user; however, it is possible that this could be of more general use as a utility. The function is simply a wrapper to `polygon` that obviates the need to specify all \((x,y)\) coordinates for the polygon.

Value

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>square</td>
<td>A square is printed on the graph, but nothing else is returned</td>
</tr>
</tbody>
</table>

Author(s)

Dave Armstrong (UW-Milwaukee, Department of Political Science)

summary.factorplot  Summary method for objects of class factorplot

Description

Summarizes the number of significant positive and negative differences for objects of class `factorplot`.

Usage

```r
## S3 method for class 'factorplot'
summary(object, ...)```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object of class <code>factorplot</code></td>
</tr>
<tr>
<td>...</td>
<td>Other arguments passed to <code>summary</code>, currently not implemented</td>
</tr>
</tbody>
</table>

Author(s)

Dave Armstrong (Department of Political Science, UW-Milwaukee)

See Also

`factorplot`
Examples

```r
x <- as.factor(round(runif(1000, .5, 5.5)))
levels(x) <- paste("lab", 1:20, sep="")
X <- model.matrix(~x)
b <- rnorm(ncol(X), 0, 4)
Y.hat <- X %*% b
Y <- Y.hat + rnorm(1000)
mod <- lm(Y ~ x)
fp <- factorplot(mod, factor.variable="x", pval=0.05, order="alph")
summary(fp)
```
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