Package 'hunterr'

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Type Package

Title Hunter's Useful R Functions

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Description
Some useful functions, mainly for plotting. There's also a basis expansion function in there.

License none

LazyData TRUE

RoxygenNote 5.0.0

Depends ggplot2, grid, gridExtra

R topics documented:

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get_basis_expansion   *Construct basis expansion matrices.*

Description

This function was created to avoid repeating it over and over in my research. The penalty for each marginal term is $\int \|f''(x)\|^2 dx$.

Usage

```
get_basis_expansion(df, num.knots, bases, interactions, knots.list = NULL)
```

Arguments

df	data frame for which to expand. Must already contain an intercept in column 1, and all covariates should be scaled between 0 and 1.
num.knots	a vector containing the number of knots to use for each predictor.
bases	a vector containing the bases to use for each expansion. Cubic (`cr`) and cyclic (`cc`) radial splines are supported.
interactions	logical: should two-way interactions (tensor products) be computed?
knots.list	optional list containing knots to use. Useful for predictions. If present, num.knots is ignored.

Value

A list with components:

- `C.full` a matrix containing all basis expansions, with the intercept.

- `partition` a numeric vector corresponding to group identification. `0` corresponds to the intercept.

- `nvar, pc, pz, px` scalars giving the number of total predictors (including 2-way interactions as individual predictors, if `interactions == TRUE`), total dimension of `C.full`, and the dimensions of the linear and basis expansion terms, respectively.

- `knots.list` a list of knots used for expansion. Useful for creating the same basis expansion on an independent data set (for, say, validation).

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multiplot	*Plot multiple ggplot2s in one page.*

Description

Stolen shamelessly from http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/

Usage

```
multiplot(..., plotlist = NULL, cols = 1, layout = NULL)
```

Arguments

...	plot objects for plotting.
plotlist	alternative input of plots, as list.
cols	number of columns in viewing window.
layout	layout matrix for plots.

Examples

```
rm(list=ls())

library(ggplot2)
library(hunterr)

# This example uses the ChickWeight dataset, which comes with ggplot2
# First plot
p1 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet, group=Chick)) +
 geom_line() +
 ggtitle("Growth curve for individual chicks")

# Second plot
p2 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet)) +
 geom_point(alpha=.3) +
 geom_smooth(alpha=.2, size=1) +
 ggtitle("Fitted growth curve per diet")

# Third plot
p3 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, colour=Diet)) +
 geom_density() +
 ggtitle("Final weight, by diet")

# Fourth plot
p4 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, fill=Diet)) +
 geom_histogram(colour="black", binwidth=50) +
 facet_grid(Diet ~ .) +
 ggtitle("Final weight, by diet") +
 theme(legend.position="none")         # No legend (redundant in this graph)

multiplot(p1, p2, p3, p4, cols=2)
multiplot(p1, p2, p3, p4, layout = matrix(c(1,2,3,4,4,4), nrow=2, byrow=TRUE))
```

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sharedlegendplot *Plot multiple ggplot2s in one page, with a shared legend.*

Description

Stolen shamelessly from https://github.com/hadley/ggplot2/wiki/Share-a-legend-between-two-ggplot2-graphs, with a modification to allow for custom layout.

Usage

```
sharedlegendplot(..., layout = NULL)
```

Arguments

`...`	plot objects for plotting.
`layout_mat`	layout matrix for plots.

Examples

```
rm(list=ls())

library(ggplot2)
library(hunterr)

# This example uses the ChickWeight dataset, which comes with ggplot2
# First plot
p1 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet, group=Chick)) +
 geom_line() +
 ggtitle("Growth curve for individual chicks")

# Second plot
p2 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet)) +
 geom_point(alpha=.3) +
 geom_smooth(alpha=.2, size=1) +
 ggtitle("Fitted growth curve per diet")

# Third plot
p3 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, colour=Diet)) +
 geom_density() +
 ggtitle("Final weight, by diet")

# Fourth plot
p4 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, fill=Diet)) +
 geom_histogram(colour="black", binwidth=50) +
 facet_grid(Diet ~ .) +
 ggtitle("Final weight, by diet") +
 theme(legend.position="none")          # No legend (redundant in this graph)

sharedlegendplot(p1, p2, p3, p4, layout = matrix(c(1,2,3,4,4,4), nrow=2, byrow=TRUE))
```

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