# Package 'blendedLink'

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**Type** Package

**Title** A New Link Function that Blends Two Specified Link Functions

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**Imports** stats

**Description** A new link function that equals one specified link function up to a cutover then a linear rescaling of another specified link function. For use in glm() or glm2(). The intended use is in binary regression, in which case the first link should be set to ``log" and the second to ``logit". This ensures that fitted probabilities are between 0 and 1 and that exponentiated coefficients can be interpreted as relative risks for probabilities up to the cutoff.

**License** GPL-2 | GPL-3

**LazyData** TRUE

**RoxygenNote** 5.0.1

## R topics documented:

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| blendedLink | *Link object where the link function equals a specified link function for values of the mean up to a specified cutoff, and a smooth linear-rescaling of a different link function when the mean is above the cutoff* |
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## Description

This function produces a blended object for a specified cutover and link functions for use in binary regression using glm or glm2.

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## Usage

```
blendedLink(link1, link2, cutover)
```

## Arguments

| | |
|---|---|
| link1 | Character string indicating the link function to be used up to the cutover |
| link2 | Character string indicating the link function to be used above the cutover |
| cutover | The link function switches smoothly from link1 to link2 |

## Details

This function returns a link function which which equals link function link1 for values of the fitted probability below cutover. When the fitted probability is greater than cutover, a linearly scaled user-specified linkis used. The linear scaling is such that the new link is smooth (link and first derivative both continuous). The main use of the function is to use an easily interpretable link in binary regression up to a cutoff (e.g. log), and a more traditional link which asymptotes to 1 above the cutoff (e.g. logit). The advantage is that the exponentiated regression coefficients can be interpreted as relative risks for individuals whose probability is up to cutover both with and without the risk factor. In practice this is usually the great majority of cases. The function is not normally called directly. Instead, glm or glm2 should be used (preferably the latter to avoid fitting problems), as per the example below.

## Value

An object of class "link-glm", with link name "blended".

## Examples

```
example.binary.regression <- glm(y~x1+x2 , data=loglogit.example,
    family = binomial(link=blendedLink("log","logit",0.8)))
summary(example.binary.regression)
```

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| loglogit.example | *An example data file.* |
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## Description

A dataset with 500 rows containing the values of y (a binary dependent variable equal to 0 or 1), and two covariates x1 and x2 (with continuous values ranging from -1 to 1).

## Usage

```
loglogit.example
```

## Format

An object of class data.frame with 500 rows and 3 columns.

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| pvalue.cutover | *p-value of hypothesis test that the cutover of a blended link is equal to a specific value* |
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## Description

This function calculates an asymptotic chi-square likelihood ratio hypothesis test of a specified null hypothesis for the cutover.

## Usage

```
pvalue.cutover(data, formula, link1, link2, cutover0, eps = 0.01)
```

## Arguments

| | |
|---|---|
| data | a data frame containing the variables in the model. |
| formula | an object of class formula, a symbolic description of the model to be fitted, see help(glm) |
| link1 | Character string indicating the link function to be used up to the cutover |
| link2 | Character string indicating the link function to be used above the cutover |
| cutover0 | The hypothesized value of the cutover at which the link function switches smoothly from link1 to link2. Must be strictly greater than 0 and strictly less than 1. |
| eps | A tuning parameter. The MLE of the cutover is restricted to the range eps to (1-eps). Usually eps=0 is appropriate, but occasionally a small positive value may be needed to avoid numerical problems in the maximisation of the likelihood. |

## Details

Binary regression is assumed. Not suitable when the null value is on the boundary (i.e. when cutover0 is 0 or 1).

## Value

The p-value of a test of the null hypothesis that cutover=cutover0.

## Examples

```
pvalue.cutover(y~x1+x2 , data=loglogit.example,link1="log",link2="logit",
cutover0=0.8)
```

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