

Package ‘ezglm’

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Title selects significant non-additive interaction between two variables using fast GLM implementation.

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Description This package implements a simplified version of least squares, and logistic regression for efficiently selecting the significant non-additive interactions between two variables.

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URL <http://code.google.com/p/ezglm/>

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ezglm	<i>selects significant non-additive interaction between two variables using fast GLM implementation.</i>
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Description

selects significant non-additive interaction between two variables using fast GLM implementation.

Usage

```
ezglm(y, x1, x2, thr = 1, family=c("gaussian","binomial"))
```

Arguments

y	response variable, of length n. This argument should be quantitative for least squares, and a two-level factor for logistic regression.
x1	the first predictor, of length n.
x2	the second predictor, of length n.
thr	p-value tolerance. Truncate any p-value to 1 if it is larger than thr. Defaults value is 1.
family	a character string specifying the model to use, valid options are: <ul style="list-style-type: none"> • "gaussian" least squares regression (regression), • "binomial" logistic regression (classification). Default is "gaussian".

Details

Motivated by pairwise gene interaction selection in genome-wide association study (GWAS), this package implements fast and simplified least squares, and logistic regression for efficiently selecting the significant non-additive interactions between two variables. Once a user specifies a response variable y and predictors x1 and x2, for "gaussian" a least squares model $y \sim x1 + x2 + x1*x2$ is fitted; for "binomial" a logistic regression $\text{logit } \sim x1 + x2 + x1*x2$ is fitted. Users can then select significant $x1*x2$ term using returned p-value of Wald test.

Value

A matrix of coefficients.

Author(s)

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Examples

```
n = 10000
x1 = rnorm(n)
x2 = rnorm(n)
y1 = sample(c(0,1),n,rep=TRUE)
y2 = rnorm(n)

system.time(m1 <- ezglm(y1, x1, x2, 1, family = "binomial"))
m1

system.time(m2 <- glm(y1~x1+x2+x1*x2, family = binomial))
summary(m2)$coef

system.time(m3 <- ezglm(y2, x1, x2, 1, family = "gaussian"))
m3

system.time(m4 <- glm(y2~x1+x2+x1*x2, family = gaussian))
```

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summary(m4)\$coef

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