

# Package ‘rsq’

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**Title** R-Squared and Related Measures

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**Depends** R (>= 3.1.0)

**Imports** methods, stats, MASS, lme4, nlme, Deriv, Matrix, deming, mcr

## Description

Calculate generalized R-squared, partial R-squared, and partial correlation coefficients for generalized linear (mixed) models (including quasi models with well defined variance functions).

**License** GPL (>= 2)

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**See Also**

[rsq](#), [rsq.partial](#), [pcor](#), [singlm](#).

**Examples**

```
data(hcrabs)
summary(hcrabs)
head(hcrabs)

attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq(bnfit)
rsq(bnfit,adj=TRUE)
rsq.partial(bnfit)

quasips <- glm(num.satellites~color+spine+width+weight,family=quasipoisson)
rsq(quasips)
rsq(quasips,adj=TRUE)
rsq.partial(quasips)
```

---

hschool

*Attendance Behavior of High School Juniors*

---

**Description**

Recorded are the number of days of absence, gender, and two test scores of 316 high school juniors from two urban high schools.

**Usage**

```
data("hschool")
```

**Format**

A data frame with 316 observations on the following 5 variables.

`school` school of the two, coded 1 or 2;

`male` whether the student is male, coded 1: male; 0: female;

`math` the standardized test score for math;

`langarts` the standardized test score for language arts;

`daysabs` the number of days of absence.

**Details**

Some school administrators studied the attendance behavior of high school juniors at two schools. Predictors of the number of days of absence include gender of the student and standardized test scores in math and language arts. The original source of this data set is unknown.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**Source**

UCLA IDRE Statistical Consulting Group for data analysis.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#), [simglm](#).

**Examples**

```
data(hschool)
summary(hschool)
head(hschool)

require(MASS)
absfit <- glm.nb(daysabs~school+male+math+langarts,data=hschool)
summary(absfit)
rsq(absfit)
rsq(absfit,adj=TRUE)

rsq.partial(absfit)
```

---

lifetime

*Lifetimes in Two Different Environments.*

---

**Description**

There are 27 tests in each of the two environments.

**Usage**

```
data("lifetime")
```

**Format**

A data frame with 54 observations on the following 2 variables.

time the lifetime (x10).

env the environment of each test (kg/mm<sup>2</sup>).

**Details**

This data set is discussed by Wang et al. (1992).

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**Source**

Wang, H., Ma, B., and Shi, J. (1992). Estimation of environmental factors for the inverse gaussian distribution. *Microelectron. Reliab.*, 32: 931-934.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#), [simglm](#).

**Examples**

```
data(lifetime)
summary(lifetime)
head(lifetime)

attach(lifetime)
igfit <- glm(time~env, family=inverse.gaussian)
rsq(igfit)
rsq(igfit, adj=TRUE)
```

---

pcor

*Partial Correlation for Generalized Linear Models*


---

**Description**

Calculate the partial correlation for both linear and generalized linear models.

**Usage**

```
pcor(objF, objR=NULL, adj=FALSE, type=c('v', 'kl', 'sse', 'lr', 'n'))
```

**Arguments**

objF	an object of class "lm" or "glm", a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , or <a href="#">glm.nb</a> to fit the full model.
objR	an object of class "lm" or "glm", a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , or <a href="#">glm.nb</a> to fit the reduced model.
adj	logical; if TRUE, calculate the adjusted partial $R^2$ .
type	the type of R-squared used: 'v' (default) – variance-function-based (Zhang, 2016), calling <a href="#">rsq.v</a> ; 'kl' – KL-divergence-based (Cameron and Windmeijer, 1997), calling <a href="#">rsq.kl</a> ; 'sse' – SSE-based (Efron, 1978), calling <a href="#">rsq.sse</a> ; 'lr' – likelihood-ratio-based (Maddala, 1983; Cox and Snell, 1989; Magee, 1990), calling <a href="#">rsq.lr</a> ; 'n' – corrected version of 'lr' (Nagelkerke, 1991), calling <a href="#">rsq.n</a> .

**Details**

When the fitting object of the reduced model is not specified, the partial correlation of each covariate (excluding factor covariates with more than two levels) in the model will be calculated.

**Value**

The partial correlation coefficient is returned.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Cameron, A. C. and Windmeijer, A. G. (1997) An R-squared measure of goodness of fit for some common nonlinear regression models. *Journal of Econometrics*, 77: 329-342.

Cox, D. R. and Snell, E. J. (1989) *The Analysis of Binary Data*, 2nd ed. London: Chapman and Hall.

Efron, B. (1978) Regression and ANOVA with zero-one data: measures of residual variation. *Journal of the American Statistical Association*, 73: 113-121.

Maddala, G. S. (1983) *Limited-Dependent and Qualitative Variables in Econometrics*. Cambridge University.

Magee, L. (1990) R<sup>2</sup> measures based on Wald and likelihood ratio joint significance tests. *The American Statistician*, 44: 250-253.

Nagelkerke, N. J. D. (1991) A note on a general definition of the coefficient of determination. *Biometrika*, 78: 691-692.

Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.

**See Also**

[rsq](#), [rsq.partial](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.partial(bnfit)

bnfitr <- glm(y~color+weight,family=binomial)
rsq.partial(bnfit,bnfitr)

quasibn <- glm(y~color+spine+width+weight,family=quasibinomial)
rsq.partial(quasibn)

quasibnr <- glm(y~color+weight,family=binomial)
rsq.partial(quasibn,quasibnr)
```

---

 rsq *R-Squared for Generalized Linear (Mixed) Models*


---

**Description**

Calculate the coefficient of determination, aka  $R^2$ , for both linear and generalized linear (mixed) models.

**Usage**

```
rsq(fitObj,adj=FALSE,type=c('v','kl','sse','lr','n'))
```

**Arguments**

fitObj	an object of class "lm", "glm", "merMod", "lmerMod", "lme", "deming", or "MCRresultResampling"; usually a result of call to <a href="#">lm</a> , <a href="#">glm</a> , <a href="#">glm.nb</a> , <a href="#">lmer</a> , <a href="#">glmer</a> , <a href="#">glmer.nb</a> , <a href="#">lme</a> , <a href="#">deming</a> , or <a href="#">mcreg</a> .
adj	logical; if TRUE, calculate the adjusted $R^2$ .
type	the type of R-squared (only applicable for generalized linear models): 'v' (default) – variance-function-based (Zhang, 2017), calling <a href="#">rsq.v</a> ; 'kl' – KL-divergence-based (Cameron and Windmeijer, 1997), calling <a href="#">rsq.kl</a> ; 'sse' – SSE-based (Efron, 1978), calling <a href="#">rsq.sse</a> ; 'lr' – likelihood-ratio-based (Maddala, 1983; Cox and Snell, 1989; Magee, 1990), calling <a href="#">rsq.lr</a> ; 'n' – corrected version of 'lr' (Nagelkerke, 1991), calling <a href="#">rsq.n</a> .

**Details**

Calculate the R-squared for (generalized) linear models. For (generalized) linear mixed models, there are three types of  $R^2$  calculated on the basis of observed response values, estimates of fixed effects, and variance components, i.e., model-based  $R_M^2$  (proportion of variation explained by the model in total, including both fixed-effects and random-effects factors), fixed-effects  $R_F^2$  (proportion of variation explained by the fixed-effects factors), and random-effects  $R_R^2$  (proportion of variation explained by the random-effects factors).

**Value**

The  $R^2$  or adjusted  $R^2$ . For (generalized) linear mixed models,

$R_M^2$	proportion of variation explained by the model in total, including both fixed-effects and random-effects factors.
$R_F^2$	proportion of variation explained by the fixed-effects factors.
$R_R^2$	proportion of variation explained by the random-effects factors.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

## References

- Cameron, A. C. and Windmeijer, A. G. (1997) An R-squared measure of goodness of fit for some common nonlinear regression models. *Journal of Econometrics*, 77: 329-342.
- Cox, D. R. and Snell, E. J. (1989) *The Analysis of Binary Data*, 2nd ed. London: Chapman and Hall.
- Efron, B. (1978) Regression and ANOVA with zero-one data: measures of residual variation. *Journal of the American Statistical Association*, 73: 113-121.
- Maddala, G. S. (1983) *Limited-Dependent and Qualitative Variables in Econometrics*. Cambridge University.
- Magee, L. (1990) R<sup>2</sup> measures based on Wald and likelihood ratio joint significance tests. *The American Statistician*, 44: 250-253.
- Nagelkerke, N. J. D. (1991) A note on a general definition of the coefficient of determination. *Biometrika*, 78: 691-692.
- Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.
- Zhang, D. (2022). Coefficients of determination for mixed-effects models. *Journal of Agricultural, Biological and Environmental Statistics*, 27: 674-689.

## See Also

[rsq.partial](#), [pcor](#), [singlm](#).

## Examples

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq(bnfit)
rsq(bnfit,adj=TRUE)

quasibn <- glm(y~color+spine+width+weight,family=quasibinomial)
rsq(quasibn)
rsq(quasibn,adj=TRUE)

psfit <- glm(num.satellites~color+spine+width+weight,family=poisson)
rsq(psfit)
rsq(psfit,adj=TRUE)

quasips <- glm(num.satellites~color+spine+width+weight,family=quasipoisson)
rsq(quasips)
rsq(quasips,adj=TRUE)

# Linear mixed models
require(lme4)
lmm1 <- lmer(Reaction~Days+(Days|Subject),data=sleepstudy)
rsq(lmm1)
rsq.lmm(lmm1)
```

```
# Generalized linear mixed models
data(cbpp)
glmm1 <- glmer(cbind(incidence,size-incidence)~period+(1|herd),data=cbpp,family=binomial)
rsq(glmm1)
```

rsq.glmm

*R-Squared for Generalized Linear Mixed Models***Description**

Calculate the variance-function-based R-squared for generalized linear mixed models.

**Usage**

```
rsq.glmm(fitObj,adj=FALSE)
```

**Arguments**

`fitObj` an object of class "glmerMod", usually, a result of a call to [glmer](#) or [glmer.nb](#).  
`adj` logical; if TRUE, calculate the adjusted R<sup>2</sup>.

**Details**

There are three types of R<sup>2</sup> calculated on the basis of observed response values, estimates of fixed effects, and variance components, i.e., model-based R<sub>M</sub><sup>2</sup> (proportion of variation explained by the model in total, including both fixed-effects and random-effects factors), fixed-effects R<sub>F</sub><sup>2</sup> (proportion of variation explained by the fixed-effects factors), and random-effects R<sub>R</sub><sup>2</sup> (proportion of variation explained by the random-effects factors).

**Value**

R<sub>M</sub><sup>2</sup> proportion of variation explained by the model in total, including both fixed-effects and random-effects factors.  
R<sub>F</sub><sup>2</sup> proportion of variation explained by the fixed-effects factors.  
R<sub>R</sub><sup>2</sup> proportion of variation explained by the random-effects factors.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.  
Zhang, D. (2022). Coefficients of determination for mixed-effects models. *Journal of Agricultural, Biological and Environmental Statistics*, 27: 674-689.

**See Also**

[vresidual](#), [rsq](#), [rsq.v](#).

**Examples**

```
require(lme4)
data(cbpp)
glmm1 <- glmer(cbind(incidence, size-incidence)~period+(1|herd), data=cbpp, family=binomial)
rsq.glm(glm1)
rsq(glm1)
```

---

rsq.kl

*KL-Divergence-Based R-Squared*

---

**Description**

The Kullback-Leibler-divergence-based  $R^2$  for generalized linear models.

**Usage**

```
rsq.kl(fitObj, adj=FALSE)
```

**Arguments**

`fitObj` an object of class "lm" or "glm", usually, a result of a call to [lm](#), [glm](#), or [glm.nb](#).  
`adj` logical; if TRUE, calculate the adjusted  $R^2$ .

**Details**

This version of  $R^2$  was proposed by Cameron and Windmeijer (1997). It is extended to quasi models (Zhang, 2017) based on the quasi-likelihood function (McCullagh, 1983).

**Value**

The  $R^2$  or adjusted  $R^2$ .

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Cameron, A. C. and Windmeijer, A. G. (1997) An R-squared measure of goodness of fit for some common nonlinear regression models. *Journal of Econometrics*, 77: 329-342.  
McCullagh, P. (1983) Quasi-likelihood functions. *Annals of Statistics*, 11: 59-67.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.kl(bnfit)
rsq.kl(bnfit,adj=TRUE)

psfit <- glm(num.satellites~color+spine+width+weight,family=poisson)
rsq.kl(psfit)
rsq.kl(psfit,adj=TRUE)

# Effectiveness of Bycycle Safety Helmets in Thompson et al. (1989)
y <- matrix(c(17,218,233,758),2,2)
x <- factor(c("yes","no"))
tbn <- glm(y~x,family=binomial)
rsq.kl(tbn)
rsq.kl(tbn,adj=TRUE)
```

---

rsq.lmm

*R-Squared for Linear Mixed Models*


---

**Description**

Calculate the R-squared for linear mixed models.

**Usage**

```
rsq.lmm(fitObj,adj=FALSE)
```

**Arguments**

fitObj	an object of class "merMod" or "lmerMod" or "lme", usually, a result of a call to <a href="#">lmer</a> , or <a href="#">lme</a> .
adj	logical; if TRUE, calculate the adjusted R <sup>2</sup> .

**Details**

There are three types of R<sup>2</sup> calculated on the basis of observed response values, estimates of fixed effects, and variance components, i.e., model-based R<sub>M</sub><sup>2</sup> (proportion of variation explained by the model in total, including both fixed-effects and random-effects factors), fixed-effects R<sub>F</sub><sup>2</sup> (proportion of variation explained by the fixed-effects factors), and random-effects R<sub>R</sub><sup>2</sup> (proportion of variation explained by the random-effects factors).

**Value**

R_M^2	proportion of variation explained by the model in total, including both fixed-effects and random-effects factors.
R_F^2	proportion of variation explained by the fixed-effects factors.
R_R^2	proportion of variation explained by the random-effects factors.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2022). Coefficients of determination for mixed-effects models. *Journal of Agricultural, Biological and Environmental Statistics*, 27: 674-689.

**See Also**

[rsq](#), [rsq.v](#).

**Examples**

```
# lmer in lme4
require(lme4)
lmm1 <- lmer(Reaction~Days+(Days|Subject), data=sleepstudy)
rsq(lmm1)
rsq.lmm(lmm1)

# lme in nlme
require(nlme)
lmm2 <- lme(Reaction~Days, data=sleepstudy, random=~Days|Subject)
rsq(lmm2)
rsq.lmm(lmm2)
```

---

rsq.lr

*Likelihood-Ratio-Based R-Squared*

---

**Description**

Calculate the likelihood-ratio-based  $R^2$  for generalized linear models.

**Usage**

```
rsq.lr(fitObj, adj=FALSE)
```

**Arguments**

fitObj	an object of class "lm" or "glm", usually, a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , or <a href="#">glm.nb</a> .
adj	logical; if TRUE, calculate the adjusted $R^2$ .

**Details**

Proposed by Maddala (1983), Cox and Snell (1989), and Magee (1990), this version of  $R^2$  is defined with the likelihood ratio statistics, so it is not defined for quasi models. It reduces to the classical  $R^2$  when the variance function is constant or linear.

**Value**

The  $R^2$  or adjusted  $R^2$ .

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Cox, D. R. and Snell, E. J. (1989) *The Analysis of Binary Data*, 2nd ed. London: Chapman and Hall.

Maddala, G. S. (1983) *Limited-Dependent and Qualitative Variables in Econometrics*. Cambridge University.

Magee, L. (1990)  $R^2$  measures based on Wald and likelihood ratio joint significance tests. *The American Statistician*, 44: 250-253.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#), [rsq.n](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.lr(bnfit)
rsq.lr(bnfit,adj=TRUE)

psfit <- glm(num.satellites~color+spine+width+weight,family=poisson)
rsq.lr(psfit)
rsq.lr(psfit,adj=TRUE)

# Effectiveness of Bycycle Safety Helmets in Thompson et al. (1989)
y <- matrix(c(17,218,233,758),2,2)
x <- factor(c("yes","no"))
tbn <- glm(y~x,family=binomial)
rsq.lr(tbn)
rsq.lr(tbn,adj=TRUE)
```

---

`rsq.n`*Corrected Likelihood-Ratio-Based R-Squared*

---

**Description**

Corrected likelihood-ratio-based  $R^2$  for generalized linear models.

**Usage**

```
rsq.n(fitObj, adj=FALSE)
```

**Arguments**

`fitObj` an object of class "lm" or "glm", usually, a result of a call to [lm](#), [glm](#), or [glm.nb](#).  
`adj` logical; if TRUE, calculate the adjusted  $R^2$ .

**Details**

Nagelkerke (1991) proposed this version of  $R^2$  to correct the likelihood-ratio-statistic-based one which was proposed by Maddala (1983), Cox and Snell (1989), and Magee (1990). This corrected generalization of  $R^2$  cannot reduce to the classical  $R^2$  in case of linear models. It is not defined for quasi models.

**Value**

The  $R^2$  or adjusted  $R^2$ .

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

- Cox, D. R. and Snell, E. J. (1989) *The Analysis of Binary Data*, 2nd ed. London: Chapman and Hall.
- Maddala, G. S. (1983) *Limited-Dependent and Qualitative Variables in Econometrics*. Cambridge University.
- Magee, L. (1990)  $R^2$  measures based on Wald and likelihood ratio joint significance tests. *The American Statistician*, 44: 250-253.
- Nagelkerke, N. J. D. (1991) A note on a general definition of the coefficient of determination. *Biometrika*, 78: 691-692.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#), [rsq.lr](#).

**Examples**

```

data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.n(bnfit)
rsq.n(bnfit,adj=TRUE)

psfit <- glm(num.satellites~color+spine+width+weight,family=poisson)
rsq.n(psfit)
rsq.n(psfit,adj=TRUE)

# Effectiveness of Bycycle Safety Helmets in Thompson et al. (1989)
y <- matrix(c(17,218,233,758),2,2)
x <- factor(c("yes","no"))
tbn <- glm(y~x,family=binomial)
rsq.n(tbn)
rsq.n(tbn,adj=TRUE)

```

rsq.partial

*Partial R-Squared for Generalized Linear Models***Description**

Calculate the coefficient of partial determination, aka partial  $R^2$ , for both linear and generalized linear models.

**Usage**

```
rsq.partial(objF,objR=NULL,adj=FALSE,type=c('v','kl','sse','lr','n'))
```

**Arguments**

objF	an object of class "lm" or "glm", a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , or <a href="#">glm.nb</a> to fit the full model.
objR	an object of class "lm" or "glm", a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , or <a href="#">glm.nb</a> to fit the reduced model.
adj	logical; if TRUE, calculate the adjusted partial $R^2$ .
type	the type of R-squared: 'v' (default) – variance-function-based (Zhang, 2017), calling <a href="#">rsq.v</a> ; 'kl' – KL-divergence-based (Cameron and Windmeijer, 1997), calling <a href="#">rsq.kl</a> ; 'sse' – SSE-based (Efron, 1978), calling <a href="#">rsq.sse</a> ; 'lr' – likelihood-ratio-based (Maddala, 1983; Cox and Snell, 1989; Magee, 1990), calling <a href="#">rsq.lr</a> ; 'n' – corrected version of 'lr' (Nagelkerke, 1991), calling <a href="#">rsq.n</a> .

**Details**

When the fitting object of the reduced model is not specified, the partial  $R^2$  of each term in the model will be calculated.

**Value**

Returned values include `adjustment` and `partial.rsq`. When `objR` is not `NULL`, `variable.full` and `variable.reduced` are returned; otherwise `variable` is returned.

`adjustment`      logical; if `TRUE`, calculate the adjusted partial  $R^2$ .

`variable.full`    all covariates in the full model.

`variable.reduced`    all covariates in the reduced model.

`variable`          all covariates in the full model.

`partial.rsq`       partial  $R^2$  or the adjusted partial  $R^2$ .

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

- Cameron, A. C. and Windmeijer, A. G. (1997) An R-squared measure of goodness of fit for some common nonlinear regression models. *Journal of Econometrics*, 77: 329-342.
- Cox, D. R. and Snell, E. J. (1989) *The Analysis of Binary Data*, 2nd ed. London: Chapman and Hall.
- Efron, B. (1978) Regression and ANOVA with zero-one data: measures of residual variation. *Journal of the American Statistical Association*, 73: 113-121.
- Maddala, G. S. (1983) *Limited-Dependent and Qualitative Variables in Econometrics*. Cambridge University.
- Magee, L. (1990)  $R^2$  measures based on Wald and likelihood ratio joint significance tests. *The American Statistician*, 44: 250-253.
- Nagelkerke, N. J. D. (1991) A note on a general definition of the coefficient of determination. *Biometrika*, 78: 691-692.
- Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.

**See Also**

[rsq](#), [pcor](#).

**Examples**

```

data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.partial(bnfit)

bnfitr <- glm(y~color+weight,family=binomial)
rsq.partial(bnfit,bnfitr)

quasibn <- glm(y~color+spine+width+weight,family=quasibinomial)
rsq.partial(quasibn)

quasibnr <- glm(y~color+weight,family=binomial)
rsq.partial(quasibn,quasibnr)

```

---

rsq.sse	<i>SSE-Based R-Squared</i>
---------	----------------------------

---

**Description**

The sum-of-squared-errors-based  $R^2$  for generalized linear models.

**Usage**

```
rsq.sse(fitObj,adj=FALSE)
```

**Arguments**

`fitObj` an object of class "lm" or "glm", usually, a result of a call to [lm](#), [glm](#), or [glm.nb](#).  
`adj` logical; if TRUE, calculate the adjusted  $R^2$ .

**Details**

This version of  $R^2$  was proposed by Efron (1978). It is calculated on the basis of the formula of the classical  $R^2$ .

**Value**

The  $R^2$  or adjusted  $R^2$ .

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Efron, B. (1978) Regression and ANOVA with zero-one data: measures of residual variation. *Journal of the American Statistical Association*, 73: 113-121.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.sse(bnfit)
rsq.sse(bnfit,adj=TRUE)

psfit <- glm(num.satellites~color+spine+width+weight,family=poisson)
rsq.sse(psfit)
rsq.sse(psfit,adj=TRUE)

# Effectiveness of Bicycle Safety Helmets in Thompson et al. (1989)
y <- matrix(c(17,218,233,758),2,2)
x <- factor(c("yes","no"))
tbn <- glm(y~x,family=binomial)
rsq.sse(tbn)
rsq.sse(tbn,adj=TRUE)
```

---

rsq.v

*Variance-Function-Based R-Squared*


---

**Description**

Calculate the variance-function-based R-squared for generalized linear (mixed) models.

**Usage**

```
rsq.v(fitObj,adj=FALSE)
```

**Arguments**

<code>fitObj</code>	an object of class "lm", "glm", "lme", or "glmerMod", usually, a result of a call to <a href="#">lm</a> , <a href="#">glm</a> , <a href="#">glm.nb</a> , <a href="#">glmer</a> , or <a href="#">glmer.nb</a> .
<code>adj</code>	logical; if TRUE, calculate the adjusted R <sup>2</sup> .

**Details**

The R<sup>2</sup> relies on the variance function, and is well-defined for quasi models. It reduces to the classical R<sup>2</sup> when the variance function is constant or linear. For (generalized) linear mixed models, there are three types of R<sup>2</sup> calculated on the basis of observed response values, estimates of fixed effects, and variance components, i.e., model-based R<sub>M</sub><sup>2</sup> (proportion of variation explained by the model in total, including both fixed-effects and random-effects factors), fixed-effects R<sub>F</sub><sup>2</sup> (proportion of variation explained by the fixed-effects factors), and random-effects R<sub>R</sub><sup>2</sup> (proportion of variation explained by the random-effects factors).

**Value**

The  $R^2$  or adjusted  $R^2$ . For (generalized) linear mixed models,

$R_M^2$	proportion of variation explained by the model in total, including both fixed-effects and random-effects factors.
$R_F^2$	proportion of variation explained by the fixed-effects factors.
$R_R^2$	proportion of variation explained by the random-effects factors.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.

Zhang, D. (2020). Coefficients of determination for mixed-effects models. arXiv:2007.08675.

**See Also**

[vresidual](#), [rsq](#), [rsq.glmm](#), [rsq.partial](#), [pcor](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family=binomial)
rsq.v(bnfit)
rsq.v(bnfit,adj=TRUE)

quasibn <- glm(y~color+spine+width+weight,family=quasibinomial)
rsq.v(quasibn)
rsq.v(quasibn,adj=TRUE)

# Generalized linear mixed models
require(lme4)
data(cbpp)
glmm1 <- glmer(cbind(incidence,size-incidence)~period+(1|herd),data=cbpp,family=binomial)
rsq.v(glmm1)
```

---

`simglm`*Simulate Data from Generalized Linear Models*

---

**Description**

Simulate data from linear and generalized linear models. Only the first covariate truly affects the response variable with coefficient equal to lambda.

**Usage**

```
simglm(family=c("binomial", "gaussian", "poisson", "Gamma"), lambda=3, n=50, p=3)
```

**Arguments**

<code>family</code>	the family of the distribution.
<code>lambda</code>	size of the coefficient of the first covariate.
<code>n</code>	the sample size.
<code>p</code>	the number of covariates.

**Details**

The first covariate takes 1 in half of the observations, and 0 or -1 in the other half. When lambda gets larger, it is supposed to be easier to predict the response variable.

**Value**

Returned values include `yx` and `beta`.

<code>yx</code>	a data frame including the response <code>y</code> and covariates <code>x.1</code> , <code>x.2</code> , and so on.
<code>beta</code>	true values of the regression coefficients.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.

**See Also**

[rsq](#), [rsq.partial](#), [pcor](#).

**Examples**

```

# Poisson Models
sdata <- simglm(family="poisson",lambda=4)
fitf <- glm(y~x.1+x.2+x.3,family=poisson,data=sdata$yx)
rsq(fitf) # type='v'

fitr <- glm(y~x.2+x.3,family=poisson,data=sdata$yx)
rsq(fitr) # type='v'
rsq(fitr,type='kl')
rsq(fitr,type='lr')
rsq(fitr,type='n')

pcor(fitr) # type='v'
pcor(fitr,type='kl')
pcor(fitr,type='lr')
pcor(fitr,type='n')

# Gamma models with shape=100
n <- 50
sdata <- simglm(family="Gamma",lambda=4,n=n)
fitf <- glm(y~x.1+x.2+x.3,family=Gamma,data=sdata$yx)
rsq(fitf) # type='v'
rsq.partial(fitf) # type='v'

fitr <- glm(y~x.2,family=Gamma,data=sdata$yx)
rsq(fitr) # type='v'
rsq(fitr,type='kl')
rsq(fitr,type='lr')
rsq(fitr,type='n')

# Likelihood-ratio-based R-squared
y <- sdata$yx$y
yhatr <- fitr$fitted.values
fit0 <- update(fitr,~1)
yhat0 <- fit0$fitted.values
llr <- sum(log(dgamma(y,shape=100,scale=yhatr/100)))
ll0 <- sum(log(dgamma(y,shape=100,scale=yhat0/100)))

# Likelihood-ratio-based R-squared
1-exp(-2*(llr-ll0)/n)

# Corrected likelihood-ratio-based R-squared
(1-exp(-2*(llr-ll0)/n))/(1-exp(2*ll0/n))

```

**Description**

Simulate data from linear and generalized linear mixed models. The coefficients of the two covariate are specified by beta.

**Usage**

```
simglm(family=c("binomial", "gaussian", "poisson", "negative.binomial"),
beta=c(2, 0), tau=1, n=200, m=10, balance=TRUE)
```

**Arguments**

family	the family of the distribution.
beta	regression coefficients (excluding the intercept which is set as zero).
tau	the variance of the random intercept.
n	the sample size.
m	the number of groups.
balance	simulate balanced data if TRUE, unbalanced data otherwise.

**Details**

The first covariate takes 1 in half of the observations, and 0 or -1 in the other half. When beta gets larger, it is supposed to be easier to predict the response variable.

**Value**

Returned values include  $yx$ ,  $\beta$ , and  $u$ .

$yx$	a data frame including the response $y$ and covariates $x_1$ , $x_2$ , and so on.
$\beta$	true values of the regression coefficients.
$u$	the random intercepts.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2022). Coefficients of determination for mixed-effects models. *Journal of Agricultural, Biological and Environmental Statistics*, 27: 674-689.

**See Also**

[rsq](#), [rsq.lmm](#), [rsq.glmm](#), [simglm](#),

**Examples**

```
require(lme4)

# Linear mixed models
gdata <- simglm(family="gaussian")
lmm1 <- lmer(y~x1+x2+(1|subject), data=gdata$yx)
rsq(lmm1)
```

```
# Generalized linear mixed models
bdata <- singlmm(family="binomial",n=400,m=20)
glmm1 <- glmer(y~x1+x2+(1|subject),family="binomial",data=bdata$yx)
rsq(glmm1)
```

---

toxox

*Toxoplasmosis Test in El Salvador*

---

## Description

Recorded are the numbers of subjects testing positive for toxoplasmosis in 34 cities of El Salvador.

## Usage

```
data("toxox")
```

## Format

A data frame with the test results in 34 cities of El Salvador, including the following 4 variables.

`city` index of each city.

`positive` the number of subjects testing positive for toxoplasmosis.

`nsubs` the total number of subjects tested.

`rainfall` annual rainfall (mm) in home city of subject.

## Details

All subjects are between 11 and 15 year old. The data set was abstracted from a larger data set in Remington et al. (1970).

## Author(s)

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

## Source

Efron, B. (1978). Regression and ANOVA with zero-one data: measures of residual variation. *JASA*, 73: 113-121.

## References

Remington, J.S., Efron, B., Cavanaugh, E., Simon, H.J., and Trejos, A. (1970). Studies on toxoplasmosis in El Salvador, prevalence and incidence of toxoplasmosis as measured by the Sabin-Feldman Dye test. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 64: 252-267.

## See Also

[rsq](#), [rsq.partial](#), [pcor](#), [singlm](#).

**Examples**

```

data(toxo)
summary(toxo)
attach(toxo)

toxofit<-glm(cbind(positive, nsubs-positive)~rainfall+I(rainfall^2)+I(rainfall^3), family=binomial)

rsq(toxofit)
rsq(toxofit, adj=TRUE)
rsq.partial(toxofit)

detach(toxo)

```

---

vresidual

*Variance-Function-Based Residuals*


---

**Description**

Calculate the variance-function-based residuals for generalized linear models, which are used to calculate the variance-function-based R-squared.

**Usage**

```
vresidual(y, yfit, family=binomial(), variance=NULL)
```

**Arguments**

y	a vector of observed values.
yfit	a vector of fitted values.
family	<a href="#">family</a> of the distribution.
variance	variance function (specified by family by default).

**Details**

The calculated residual relies on the variance function, and is well-defined for quasi models. It reduces to the classical residual when the variance function is constant or linear. Note that only the variance function is required to specify, via either "family" or "variance".

**Value**

Variance-function-based residuals.

**Author(s)**

Dabao Zhang, Department of Epidemiology and Biostatistics, University of California, Irvine

**References**

Zhang, D. (2017). A coefficient of determination for generalized linear models. *The American Statistician*, 71(4): 310-316.

**See Also**

[rsq.v](#), [rsq](#).

**Examples**

```
data(hcrabs)
attach(hcrabs)
y <- ifelse(num.satellites>0,1,0)
bnfit <- glm(y~color+spine+width+weight,family="binomial")
vresidual(y,bnfit$fitted.values,family="binomial")

# Effectiveness of Bicycle Safety Helmets in Thompson et al. (1989)
y <- matrix(c(17,218,233,758),2,2)
x <- factor(c("yes","no"))
tbn <- glm(y~x,family="binomial")
yfit <- cbind(tbn$fitted.values, 1-tbn$fitted.values)
vr0 <- vresidual(matrix(0,2,1),yfit[,1],family="binomial")
vr1 <- vresidual(matrix(1,2,1),yfit[,2],family="binomial")
y[,1]*vr0+y[,2]*vr1
```

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