

# Package ‘linERR’

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**Type** Package

**Title** Linear Excess Relative Risk Model

**Version** 1.0

**Date** 2016-02-23

**Encoding** UTF-8

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**Description** Fits a linear excess relative risk model by maximum likelihood, possibly including several variables and allowing for lagged exposures.

**Depends** R (>= 3.1.1), survival, stats4

**License** GPL (>= 2)

**NeedsCompilation** yes

**Repository** CRAN

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linERR-package

*Fits the linear excess relative risk model***Description**

Usual approaches to the analysis of cohort and case control data often follow from risk-set sampling designs, where at each failure time a new risk set is defined, including the index case and all the controls that were at risk at that time. That kind of sampling designs are usually related to the Cox proportional hazards model, available in most standard statistical packages but limited to log-linear models (except *Epicure*, (Preston et al., 1993)) of the form  $\log(\phi(z, \beta)) = \beta_1 \cdot z_1 + \dots + \beta_k \cdot z_k$ , where  $z$  is a vector of explanatory variables and  $\phi$  is the rate ratio. This implies exponential dose-response trends and multiplicative interactions, which may not be the best exposure-response representation in some cases, such as radiation exposures. One model of particular interest, especially in radiation environmental and occupational epidemiology is the ERR model,  $\phi(z, \beta) = 1 + \alpha \cdot f(\text{dose})$ . The ERR model represents the excess relative rate per unit of exposure and  $z_1, \dots, z_k$  are covariates. Estimation of a dose-response trend under a linear relative rate model implies that for every 1-unit increase in the exposure metric, the rate of disease increases (or decreases) in an additive fashion. The modification of the effect of exposure in linear relative rate models by a study covariate  $m$  can be assessed by including a log-linear subterm for the linear exposure effect (Preston et al., 2003; Ron et al., 1995), implying a model of the form  $\phi(z, \beta) = e^{\beta_0 + \beta_1 \cdot z_1 + \dots + \beta_k \cdot z_k} (1 + \alpha \cdot f(\text{dose}))$ .

**Details**

Package:	linERR
Type:	Package
Version:	1.0
Date:	2016-02-23
License:	GPL version 2 or newer
LazyLoad:	yes

**Author(s)**

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**References**

B. Langholz and D. B. Richardson. Fitting general relative risk models for survival time and matched case-control analysis. *American journal of epidemiology*, 171(3):377-383, 2010. D. L. Preston, J. H. Lubin, D. A. Pierce, and M. E. McConney. *Epicure: User's Guide*. HiroSoft International Corporation, Seattle, WA, 1993. E. Ron, J. H. Lubin, R. E. Shore, K. Mabuchi, B. Modan, L. M. Pottern, A. B. Schneider, M. A. Tucker, and J. D. Boice Jr. Thyroid Cancer after Exposure

to External Radiation: A Pooled Analysis of Seven Studies. *Radiation Research*, 141(3):259-277, 1995.

### See Also

[fit.linERR](#), [ERRci](#)

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cohort1	<i>Simulated cohort data</i>
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### Description

This data corresponds to a simulated cohort with a follow-up of 32 years, including the annual radiation dose received by each subject.

### Usage

```
cohort1
```

### Format

A data frame with 1000 rows and 70 columns.

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ERRci	<i>Profile likelihood based confidence intervals</i>
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### Description

The standard procedure for computing a confidence interval for a parameter  $\beta$  (Wald-type CI), based on  $\hat{\beta} \pm z_{1-\frac{\alpha}{2}} SE(\hat{\beta})$  may work poorly if the distribution of the parameter estimator is markedly skewed or if the standard error is a poor estimate of the standard deviation of the estimator. Profile likelihood confidence intervals doesn't assume normality of the estimator and perform better for small sample sizes or skewed estimates than Wald-type confidence intervals.

### Usage

```
ERRci(object, prob=0.95)
```

### Arguments

object	An object of class <code>fit.linERR</code> .
prob	Level of confidence, defaults to 0.95.

### Value

A numeric vector containing the *prob* profile likelihood based confidence interval.

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**References**

B. Langholz and D. B. Richardson. Fitting general relative risk models for survival time and matched case-control analysis. *American journal of epidemiology*, 171(3):377-383, 2010. D. L. Preston, J. H. Lubin, D. A. Pierce, and M. E. McConney. *Epicure: User's Guide*. HiroSoft International Corporation, Seattle, WA, 1993. E. Ron, J. H. Lubin, R. E. Shore, K. Mabuchi, B. Modan, L. M. Pottern, A. B. Schneider, M. A. Tucker, and J. D. Boice Jr. Thyroid Cancer after Exposure to External Radiation: A Pooled Analysis of Seven Studies. *Radiation Research*, 141(3):259-277, 1995.

**See Also**

[ERRci](#), [linERR-package](#)

**Examples**

```
data(cohort1)
fit.1 <- fit.linERR(Surv(entryage, exitage, leu)~sex|dose1+dose2+dose3+dose4+dose5+dose6+
  dose7+dose8+dose9+dose10+dose11+dose12+dose13+dose14+dose15+dose16+
  dose17+dose18+dose19+dose20+dose21+dose22+dose23+dose24+dose25+dose26+
  dose27+dose28+dose29+dose30+dose31+dose32, data=cohort1, beta=NULL,
  ages=cohort1[, 7:38], lag=2)
ERRci(fit.1, prob=0.9)
```

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fit.linERR

*Fits linear ERR model*

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**Description**

Usual approaches to the analysis of cohort and case control data often follow from risk-set sampling designs, where at each failure time a new risk set is defined, including the index case and all the controls that were at risk at that time. That kind of sampling designs are usually related to the Cox proportional hazards model, available in most standard statistical packages but limited to log-linear models (except *Epicure*, (Preston et al., 1993)) of the form  $\log(\phi(z, \beta)) = \beta_1 \cdot z_1 + \dots + \beta_k \cdot z_k$ , where  $z$  is a vector of explanatory variables and  $\phi$  is the rate ratio. This implies exponential dose-response trends and multiplicative interactions, which may not be the best exposure-response representation in some cases, such as radiation exposures. One model of particular interest, especially in radiation environmental and occupational epidemiology is the ERR model,  $\phi(z, \beta) = 1 + \alpha \cdot f(\text{dose})$ . The ERR model represents the excess relative rate per unit of exposure and  $z_1, \dots, z_k$  are covariates. Estimation of a dose-response trend under a linear relative rate model implies that for every 1-unit increase in the exposure metric, the rate of disease increases (or decreases) in an additive fashion. The modification of the effect of exposure in linear relative rate models by a study covariate  $m$  can be assessed by including a log-linear subterm for the linear exposure effect (Preston et al., 2003; Ron et al., 1995), implying a model of the form  $\phi(z, \beta) = e^{\beta_0 + \beta_1 \cdot z_1 + \dots + \beta_k \cdot z_k} (1 + \alpha \cdot f(\text{dose}))$ .

**Usage**

```
fit.linERR(formula, beta = NULL, data, ages, lag = 0)
```

**Arguments**

formula	An object of class formula (or one that can be coerced to that class), i.e. a symbolic description of the model to be fitted. The response must be a survival object as returned by the <code>Surv()</code> function, and the log-linear and linear terms are separated by the character “ ”. Stratum are defined using the <code>strata()</code> function.
beta	Starting values for parameter estimates. Its default value is <code>NULL</code> .
data	Data frame that contains the cohort.
ages	Age at each exposure.
lag	Lag to be applied. Its default value is zero.

**Value**

An object of class `fit.linERR`, essentially a named list. The elements of this list are detailed below

lowb	Low boundary of the parameter in the linear part.
beta	Initial values for the estimates.
max.exp	Maximum number of exposures.
covariates1	Covariates in the loglinear part.
data_2	Original data restructured as a list.
rsets_2	Risk sets restructured as a list.
doses_2	Doses at each exposure restructured as a list.
ages_2	Ages at each exposure restructured as a list.
vcov	Variance-covariance matrix.
aic	Akaike’s Information Criteria.
Call	Call to the function.
llike	Maximum log-likelihood.
deviance	Deviance of the model.

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**References**

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**See Also**

[ERRci](#), [linERR-package](#)

**Examples**

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fit.1 <- fit.linERR(Surv(entryage, exitage, leu)~sex|dose1+dose2+dose3+dose4+dose5+dose6+
  dose7+dose8+dose9+dose10+dose11+dose12+dose13+dose14+dose15+dose16+
  dose17+dose18+dose19+dose20+dose21+dose22+dose23+dose24+dose25+dose26+
  dose27+dose28+dose29+dose30+dose31+dose32, data=cohort1, beta=NULL,
  ages=cohort1[, 7:38], lag=2)
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