

Package: multipleOutcomes (via r-universe)

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Title Asymptotic Covariance Matrix of Regression Models for Multiple Outcomes

Version 0.4

Description Regression models can be fitted for multiple outcomes simultaneously. This package computes estimates of parameters across fitted models and returns the matrix of asymptotic covariance. Various applications of this package, including CUPED (Controlled Experiments Utilizing Pre-Experiment Data), multiple comparison adjustment, are illustrated.

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Encoding UTF-8

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Imports dplyr, momentfit, numDeriv, stringr, survival

Suggests asaur, coin, ggplot2, iBST, invGauss, JM, joint.Cox, knitr, mvtnorm, pec, randomForestSRC, rmarkdown, survminer, tidyr

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| | |
|------|--|
| actg | <i>ACTG 320 Clinical Trial Dataset</i> |
|------|--|

Description

actg dataset from Hosmer et al.

Format

A data frame

id Identification Code

time Time to AIDS diagnosis or death (days).

cancel Event indicator. 1 = AIDS defining diagnosis, 0 = Otherwise.

time_d Time to death (days)

cancel_d Event indicator for death (only). 1 = Death, 0 = Otherwise.

tx Treatment indicator. 1 = Treatment includes IDV, 0 = Control group.

txgrp Treatment group indicator. 1 = ZDV + 3TC. 2 = ZDV + 3TC + IDV. 3 = d4T + 3TC. 4 = d4T + 3TC + IDV.

strat2 CD4 stratum at screening. 0 = CD4 <= 50. 1 = CD4 > 50.

sex 0 = Male. 1 = Female.

raceth Race/Ethnicity. 1 = White Non-Hispanic. 2 = Black Non-Hispanic. 3 = Hispanic. 4 = Asian, Pacific Islander. 5 = American Indian, Alaskan Native. 6 = Other/unknown.

ivdrug IV drug use history. 1 = Never. 2 = Currently. 3 = Previously.

hemophil Hemophiliac. 1 = Yes. 0 = No.

karnof Karnofsky Performance Scale. 100 = Normal; no complaint no evidence of disease. 90 = Normal activity possible; minor signs/symptoms of disease. 80 = Normal activity with effort; some signs/symptoms of disease. 70 = Cares for self; normal activity/active work not possible.

cd4 Baseline CD4 count (Cells/Milliliter).

priorzdv Months of prior ZDV use (months).

age Age at Enrollment (years).

Source

ftp://ftp.wiley.com/public/sci_tech_med/survival

References

Hosmer, D.W. and Lemeshow, S. and May, S. (2008) Applied Survival Analysis: Regression Modeling of Time to Event Data: Second Edition, John Wiley and Sons Inc., New York, NY

Examples

```
data(actg)
```

coef.multipleOutcomes *Extract Model Coefficients*

Description

coef is a generic function.

Usage

```
## S3 method for class 'multipleOutcomes'  
coef(object, model_index = NULL, ...)
```

Arguments

| | |
|-------------|--|
| object | an object returned by multipleOutcomes(). |
| model_index | NULL if displaying coefficients of all fitted models; otherwise, an integer indicating the fitted model. |
| ... | for debugging only |

Value

a vector of coefficient estimates

| | |
|------------------|---|
| multipleOutcomes | <i>Fitting Regression Models for Multiple Outcomes and Returning the Matrix of Covariance</i> |
|------------------|---|

Description

multipleOutcomes can fit different types of models for multiple outcomes simultaneously and return model parameters and variance-covariance matrix for further analysis.

Usage

```
multipleOutcomes(..., family, data, data_index = NULL, score_epsilon = 1e-06)
```

Arguments

| | |
|---------------|---|
| ... | formulas of models to be fitted, or moment functions for gmm. |
| family | a character vector of families to be used in the models. Currently only gaussian, binomial, coxph and gmm are supported. long for longitudinal data may be supported in the future. family can be of length 1 if all models are fitted in the same family; otherwise family should be specified for each of the models in ... |
| data | a data frame if all models are fitted on the same dataset; otherwise a list of data frames for fitting models in ... Note that a dataset can be used to fit multiple models, thus, length(data) is unnecessary to be equal to the number of models in ... The row names in a data frame are treated as sample IDs. Consequently, for any two records in different data frames that correspond to the same sample, their row names should be consistent. |
| data_index | NULL if data is a data frame; otherwise, a vector in integer specifying mapping a model in ... to a data frame in data (a list). |
| score_epsilon | whatever. |

Value

It returns an object of class "multipleOutcomes", which is a list containing the following components:

| | |
|-----------------------|--|
| coefficients | an unnamed vector of coefficients of all fitted models. Use id_map for variable mapping. |
| mcov | a unnamed matrix of covariance of coefficients. Use id_map for variable mapping. |
| id_map | a list mapping the elements in coefficients and mcov to variable names. |
| n_shared_sample_sizes | a matrix of shared sample sizes between datasets being used to fit the models. |
| call | the matched call. |

Examples

```

## More examples can be found in the vignettes.
library(mvtnorm)
genData <- function(seed = NULL){

  set.seed(seed)
  n <- 400
  sigma <- matrix(c(1, .6, .6, 1), 2)
  x <- rmvnorm(n, sigma = sigma)
  gam <- c(.1, -.2)
  z <- rbinom(n, 1, plogis(1-1/(1+exp(-.5+x%*gam+.1*rnorm(n)))))

  bet <- c(-.2,.2)
  #y <- rbinom(n, 1, plogis(1-1/(1+exp(-.5+x%*bet + .2*z-.3*rnorm(n)))))
  y <- -.5+x%*bet + .2*z-.3*rnorm(n)

  data.frame(y = y, z = z, x1 = x[, 1], x2 = x[, 2])

}

dat <- genData(123456)
dat1 <- head(dat,200)
dat2 <- tail(dat,200)
## fitting four models simultaneously.
fit <-
  multipleOutcomes(
    y ~ z + x1 - 1,
    z ~ x1 + x2,
    z ~ x1 - 1,
    y ~ x2,
    ## z can be fitted with a linear or logistic regression
    family = c('gaussian', 'binomial', 'gaussian','gaussian'),
    data = list(dat1, dat2),
    ## each dataset is used to fit two models
    data_index = c(1, 1, 2, 2)
  )

## unnamed coefficients of all model parameters
coef(fit)

## named coefficients of a specific model
coef(fit, 2)

## unnamed covariance matrix of all model parameters
vcov(fit)

## named covariance matrix of a specific model
vcov(fit, 1)

## summary of all parameter estimates
summary(fit)

```

```
## summary of parameters in a specific model
summary(fit, 4)
```

pated

Prognostic Variables Assisted Treatment Effect Detection

Description

pated is a wrapper function of `multipleOutcomes` for testing treatment effect in randomized clinical trials. It assumes that prognostic variables are fully randomized. This assumption can help enhancing statistical power of conventional approaches in detecting the treatment effect. Specifically, the sensitivity of the conventional models specified in . . . are improved by pated.

Usage

```
pated(..., family, data)
```

Arguments

| | |
|--------|--|
| ... | formulas of models to be fitted, or moment functions for <code>gmm</code> . |
| family | a character vector of families to be used in the models. Currently only <code>gaussian</code> , <code>binomial</code> , <code>coxph</code> and <code>gmm</code> are supported. <code>long</code> for longitudinal data may be supported in the future. <code>family</code> can be of length 1 if all models are fitted in the same family; otherwise <code>family</code> should be specified for each of the models in |
| data | a data frame if all models are fitted on the same dataset; otherwise a list of data frames for fitting models in Note that a dataset can be used to fit multiple models, thus, <code>length(data)</code> is unnecessary to be equal to the number of models in The row names in a data frame are treated as sample IDs. Consequently, for any two records in different data frames that correspond to the same sample, their row names should be consistent. |

Value

a data frame of testing results.

Examples

```
# see vignettes
```

```
print.summary.multipleOutcomes
```

Title Summarize an Analysis of Multiple Outcomes.

Description

Summarize an analysis of multiple outcomes.

Usage

```
## S3 method for class 'summary.multipleOutcomes'  
print(x, ...)
```

Arguments

x an object returned by multipleOutcomes().
... for debugging only.

Value

an invisible object.

Examples

```
## no example
```

```
summary.multipleOutcomes
```

Object Summaries

Description

summary method for class multipleOutcomes.

Usage

```
## S3 method for class 'multipleOutcomes'  
summary(object, model_index = NULL, ...)
```

Arguments

object an object returned by multipleOutcomes().
model_index NULL if displaying summary of all fitted models; otherwise, an integer indicating the fitted model.
... for debugging only

Value

a list

vcov.multipleOutcomes *Calculate Variance-Covariance Matrix for a Fitted Model Object*

Description

Returns the variance-covariance matrix of the main parameters of fitted model objects. The "main" parameters of models correspond to those returned by `coef`.

Usage

```
## S3 method for class 'multipleOutcomes'  
vcov(object, model_index = NULL, ...)
```

Arguments

| | |
|--------------------------|---|
| <code>object</code> | an object returned by <code>multipleOutcomes()</code> . |
| <code>model_index</code> | NULL if displaying covariance matrix of all fitted models; otherwise, an integer indicating the fitted model. |
| <code>...</code> | for debugging only |

Value

a matrix of covariance of all estimates

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