Package ‘geepack’

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Title Generalized Estimating Equation Package

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Description Generalized estimating equations solver for parameters in
mean, scale, and correlation structures, through mean link,
scale link, and correlation link. Can also handle clustered
categorical responses. See e.g. Halekoh and Højsgaard, (2005,
<doi:10.18637/jss.v015.i02>), for details.

Encoding UTF-8

LazyData true

License GPL (>= 3)

NeedsCompilation yes

Depends R (>= 3.5.0), methods

Imports MASS, broom, magrittr

RoxygenNote 7.1.1

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compCoef

Description

Comparing regression coefficients between models when one model is nested within another for clustered data.

Usage

compCoef(fit0, fit1)

Arguments

fit0 a fitted object of class geese
fit1 another fitted object of class geese

Value

a list of two components:

delta estimated difference in the coefficients of common covariates from fit0 and fit1
variance estimated variance matrix of delta

Author(s)

Jun Yan <jyan.stat@gmail.com>
References


Examples

```r
gendat <- function(ncl, clsz) {
  ## ncl: number of clusters
  ## clsz: cluster size (all equal)
  id <- rep(1:ncl, each = clsz)
  visit <- rep(1:clsz, ncl)
  n <- ncl * clsz
  x1 <- rbinom(n, 1, 0.5) ## within cluster varying binary covariate
  x2 <- runif(n, 0, 1) ## within cluster varying continuous covariate
  ## the true correlation coefficient rho for an ar(1)
  ## correlation structure is 2/3
  rho <- 2/3
  rhomat <- rho ^ outer(1:4, 1:4, function(x, y) abs(x - y))
  chol.u <- chol(rhomat)
  noise <- as.vector(sapply(1:ncl, function(x) chol.u %*% rnorm(clsz)))
  y <- 1 + 3 * x1 - 2 * x2 + noise
  dat <- data.frame(y, id, visit, x1, x2)
  dat
}

simdat <- gendat(100, 4)
fit0 <- geese(y ~ x1, id = id, data = simdat, corstr = "un")
fit1 <- geese(y ~ x1 + x2, id = id, data = simdat, corstr = "un")
compCoef(fit0, fit1)
```

---

dietox

*Growth curves of pigs in a 3x3 factorial experiment*

Description

The dietox data frame has 861 rows and 7 columns.

Usage

dietox
Format

This data frame contains the following columns:

- **Weight**: Weight in Kg
- **Feed**: Cumulated feed intake in Kg
- **Time**: Time (in weeks) in the experiment
- **Pig**: Factor; id of each pig
- **Evit**: Factor; vitamin E dose; see 'details'.
- **Cu**: Factor, copper dose; see 'details'
- **Start**: Start weight in experiment, i.e. weight at week 1.
- **Litter**: Factor, id of litter of each pig

Details

Data contains weight of slaughter pigs measured weekly for 12 weeks. Data also contains the startweight (i.e. the weight at week 1). The treatments are 3 different levels of Evit = vitamin E (dose: 0, 100, 200 mg dl-alpha-tocopheryl acetat /kg feed) in combination with 3 different levels of Cu = copper (dose: 0, 35, 175 mg/kg feed) in the feed. The cumulated feed intake is also recorded. The pigs are littermates.

Source


Examples

```r
data(dietox)
head(dietox)
## Not run:
if (require(ggplot2)){
  qplot(Time, Weight, data=dietox, col=Pig) + geom_line() +
  theme(legend.position = "none") + facet_grid(Evit~Cu)
} else {
  coplot(Weight ~ Time | Evit * Cu, data=dietox)
}
## End(Not run)
```
**fixed2Zcor**  

*Construct zcor vector*

**Description**

Construct zcor vector (of fixed correlations) from a fixed working correlation matrix, a specification of clusters and a specification of waves.

**Usage**

```r
fixed2Zcor(cor.fixed, id, waves)
```

**Arguments**

- `cor.fixed`: Matrix
- `id`: Clusters
- `waves`: Vector giving the ordering of observations within clusters.

**Value**

A vector which can be passed as the zcor argument to `geeglm`.

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**See Also**

- `genZcor`
- `geeglm`

**Examples**

```r
timeorder <- rep(1:5, 6)
tvar <- timeorder + rnorm(length(timeorder))
idvar <- rep(1:6, each=5)
uuu <- rep(rnorm(6), each=5)
yvar <- 1 + 2*tvar + uuu + rnorm(length(tvar))
simdat <- data.frame(idvar, timeorder, tvar, yvar)
head(simdat, 12)
simdatPerm <- simdat[sample(nrow(simdat)),]
simdatPerm <- simdatPerm[order(simdatPerm$idvar),]
head(simdatPerm)
cor.fixed <- matrix(c(1 , 0.5 , 0.25, 0.125, 0.125,  
                      0.5 , 1 , 0.25, 0.125, 0.125,  
                      0.25, 0.25, 1 , 0.5 , 0.125,  
                      0.125, 0.125, 0.5 , 1 , 0.125,  
                      0.125, 0.125, 0.5 , 1 , 0.125,  
                      0.125, 0.125, 0.5 , 1 , 0.125),  
                      nrow=5, ncol=5, byrow=FALSE)

```

cor.fixed

zcor <- fixed2Zcor(cor.fixed, id=simdatPerm$idvar, waves=simdatPerm$timeorder)

mod4 <- geeglm(yvar~tvar, id=idvar, data=simdatPerm, corstr="fixed", zcor=zcor)
mod4

---

**geeglm**  
*Fit Generalized Estimating Equations (GEE)*

**Description**

The geeglm function fits generalized estimating equations using the 'geese.fit' function of the 'geepack' package for doing the actual computations. geeglm has a syntax similar to glm and returns an object similar to a glm object. An important feature of geeglm, is that an anova method exists for these models.

**Usage**

```
geeglm(
  formula,
  family = gaussian,
  data = parent.frame(),
  weights, subset, 
  na.action, start = NULL, etastart, 
  mustart, offset, 
  control = geese.control(...),
  method = "glm.fit",
  contrasts = NULL, 
  id, waves = NULL, 
  zcor = NULL, 
  corstr = "independence", 
  scale.fix = FALSE, 
  scale.value = 1, 
  std.err = "san.se",
  ...
)
```
Arguments

- **formula**: See corresponding documentation to glm
- **family**: See corresponding documentation to glm
- **data**: See corresponding documentation to glm
- **weights**: See corresponding documentation to glm
- **subset**: See corresponding documentation to glm
- **na.action**: No action is taken. Indeed geeglm only works on complete data.
- **start**: See corresponding documentation to glm
- **etastart**: See corresponding documentation to glm
- **mustart**: See corresponding documentation to glm
- **offset**: See corresponding documentation to glm
- **control**: See corresponding documentation to glm
- **method**: See corresponding documentation to glm
- **contrasts**: See corresponding documentation to glm
- **id**: a vector which identifies the clusters. The length of ‘id’ should be the same as the number of observations. Data are assumed to be sorted so that observations on each cluster appear as contiguous rows in data. If data is not sorted this way, the function will not identify the clusters correctly. If data is not sorted this way, a warning will be issued. Please consult the package vignette for details.
- **waves**: Variable specifying the ordering of repeated measurements on the same unit. Also used in connection with missing values. Please consult the package vignette for details.
- **zcor**: Used for entering a user defined working correlation structure.
- **corstr**: a character string specifying the correlation structure. The following are permitted: "'independence'", "'exchangeable'", "'ar1'", "'unstructured'" and "'userdefined'"
- **scale.fix**: a logical variable; if true, the scale parameter is fixed at the value of 'scale.value'.
- **scale.value**: numeric variable giving the value to which the scale parameter should be fixed; used only if 'scale.fix = TRUE'.
- **std.err**: Type of standard error to be calculated. Default 'san.se' is the usual robust estimate. Other options are 'jack': if approximate jackknife variance estimate should be computed. 'j1s': if 1-step jackknife variance estimate should be computed. 'fij': logical indicating if fully iterated jackknife variance estimate should be computed.
- **...**: further arguments passed to or from other methods.

Details

In the case of corstr="fixed" one must provide the zcor vector if the clusters have unequal sizes. Clusters with size one must not be represented in zcor.
**Value**

An object of type 'geeglm'

**Warning**

Use "unstructured" correlation structure only with great care. (It may cause R to crash).

**Note**

See the documentation for the 'geese' function for additional information. geeglm only works for complete data. Thus, if there are NA's in data you can specify data=na.omit(mydata).

**Author(s)**

Søren Højsgaard, <sorenh@math.aau.dk>

**References**


**See Also**

geese, glm, anova.geeglm

**Examples**

data(dietox)
dietox$Cu <- as.factor(dietox$Cu)
mf <- formula(Weight ~ Cu * (Time + I(Time^2) + I(Time^3)))
gee1 <- geeglm(mf, data=dietox, id=Pig, family=poisson("identity"), corstr="ar1")
coef(gee1)
vcov(gee1)
summary(gee1)
coef(summary(gee1))

mf2 <- formula(Weight ~ Cu * Time + I(Time^2) + I(Time^3))
gee2 <- geeglm(mf2, data=dietox, id=Pig, family=poisson("identity"), corstr="ar1")
anova(gee2)
Function to fit a Generalized Estimating Equation Model

Description

Produces an object of class ‘geese’ which is a Generalized Estimating Equation fit of the data.

Usage

geese(
  formula = formula(data),
  sformula = ~1,
  id,
  waves = NULL,
  data = parent.frame(),
  subset = NULL,
  na.action = na.omit,
  contrasts = NULL,
  weights = NULL,
  zcor = NULL,
  corp = NULL,
  control = geese.control(...),
  b = NULL,
  alpha = NULL,
  gm = NULL,
  family = gaussian(),
  mean.link = NULL,
  variance = NULL,
  cor.link = "identity",
  sca.link = "identity",
  link.same = TRUE,
  scale.fix = FALSE,
  scale.value = 1,
  corstr = "independence",
  ...
)

Arguments

formula a formula expression as for glm, of the form response ~ predictors. See the documentation of lm and formula for details. As for glm, this specifies the linear predictor for modeling the mean. A term of the form offset(expression) is allowed.

sformula a formula expression of the form ~ predictor, the response being ignored. This specifies the linear predictor for modeling the dispersion. A term of the form offset(expression) is allowed.
id a vector which identifies the clusters. The length of ‘id’ should be the same as the number of observations. Data are assumed to be sorted so that observations on a cluster are contiguous rows for all entities in the formula.

waves an integer vector which identifies components in clusters. The length of waves should be the same as the number of observation. components with the same waves value will have the same link functions.

data an optional data frame in which to interpret the variables occurring in the formula, along with the id and n variables.

subset expression saying which subset of the rows of the data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

na.action a function to filter missing data. For gee only na.omit should be used here.

contrasts a list giving contrasts for some or all of the factors appearing in the model formula. The elements of the list should have the same name as the variable and should be either a contrast matrix (specifically, any full-rank matrix with as many rows as there are levels in the factor), or else a function to compute such a matrix given the number of levels.

weights an optional vector of weights to be used in the fitting process. The length of weights should be the same as the number of observations. This weights is not (yet) the weight as in sas proc genmod, and hence is not recommended to use.

zcor a design matrix for correlation parameters.

corp known parameters such as coordinates used for correlation coefficients.

control a list of iteration and algorithmic constants. See geese.control for their names and default values. These can also be set as arguments to geese itself.

b an initial estimate for the mean parameters.

alpha an initial estimate for the correlation parameters.

gm an initial estimate for the scale parameters.

family a description of the error distribution and link function to be used in the model, as for glm.

mean.link a character string specifying the link function for the means. The following are allowed: "identity", "logit", "probit", "cloglog", "log", and "inverse". The default value is determined from family.

variance a character string specifying the variance function in terms of the mean. The following are allowed: "gaussian", "binomial", "poisson", and "gamma". The default value is determined from family.

cor.link a character string specifying the link function for the correlation coefficients. The following are allowed: "identity", and "fisherz".

sca.link a character string specifying the link function for the scales. The following are allowed: "identity", and "log".

link.same a logical indicating if all the components in a cluster should use the same link.

scale.fix a logical variable; if true, the scale parameter is fixed at the value of scale.value.
geese

scale.value numeric variable giving the value to which the scale parameter should be fixed; used only if scale.fix == TRUE.

corstr a character string specifying the correlation structure. The following are permitted: "independence", "exchangeable", "ar1", "unstructured", "userdefined", and "fixed".

... further arguments passed to or from other methods.

Details

when the correlation structure is fixed, the specification of Zcor should be a vector of length sum(clusz * (clusz -1)) / 2.

Value

An object of class "geese" representing the fit.

Author(s)

Jun Yan <jyan.stat@gmail.com>

References


See Also

glm, lm, ordgee.

Examples

data(seizure)
## Diggle, Liang, and Zeger (1994) pp166-168, compare Table 8.10
seiz.l <- reshape(seizure,
v.names="y", times=0:4, direction="long")
seiz.l <- seiz.l[order(seiz.l$id, seiz.l$time),]
seiz.l$t <- ifelse(seiz.l$time == 0, 8, 2)
seiz.l$x <- ifelse(seiz.l$time == 0, 0, 1)
m1 <- geese(y ~ offset(log(t)) + x + trt + x:trt, id = id,
data=seiz.l, corstr="exch", family=poisson)
summary(m1)
m2 <- geese(y ~ offset(log(t)) + x + trt + x:trt, id = id,
data = seiz.l, subset = id!=49,
corstr = "exch", family=poisson)
summary(m2)
## Using fixed correlation matrix
cor.fixed <- matrix(c(1, 0.5, 0.25, 0.125, 0.125,
0.5, 1, 0.25, 0.125, 0.125,
0.25, 0.25, 1, 0.5, 0.125,
cor.fixed
zcor <- rep(cor.fixed[lower.tri(cor.fixed)], 59)
m3 <- geese(y ~ offset(log(t)) + x + trt + x:trt, id = id,
           data = seiz.l, family = poisson,
           corstr = "fixed", zcor = zcor)
summary(m3)

data(ohio)
fit <- geese(resp ~ age + smoke + age:smoke, id=id, data=ohio,
             family=binomial, corstr="exch", scale.fix=TRUE)
summary(fit)
fit.ar1 <- geese(resp ~ age + smoke + age:smoke, id=id, data=ohio,
                 family=binomial, corstr="ar1", scale.fix=TRUE)
summary(fit.ar1)

#### simulated data
## a function to generate a dataset
gendat <- function() {
id <- gl(50, 4, 200)
visit <- rep(1:4, 50)
x1 <- rbinom(200, 1, 0.6) ## within cluster varying binary covariate
x2 <- runif(200, 0, 1) ## within cluster varying continuous covariate
phi <- 1 + 2 * x1 ## true scale model
## the true correlation coefficient for an ar(1) mode
rhomat <- 0.667 ^ outer(1:4, 1:4, function(x, y) abs(x - y))
chol.u <- chol(rhomat)
noise <- as.vector(sapply(1:50, function(x) chol.u %*% rnorm(4)))
e <- sqrt(phi) * noise
y <- 1 + 3 * x1 - 2 * x2 + e
dat <- data.frame(y, id, visit, x1, x2)
dat
}
dat <- gendat()
fit <- geese(y ~ x1 + x2, id = id, data = dat, sformula = ~ x1,
             corstr = "ar1", jack = TRUE, j1s = TRUE, fij = TRUE)
summary(fit)

#### create user-defined design matrix of unstructured correlation.
#### in this case, zcor has 4*3/2 = 6 columns, and 50*5*6 = 150 rows
zcor <- genZcor(clusz = rep(4, 50), waves = dat$visit, "unstr")
zfit <- geese(y ~ x1 + x2, id = id, data = dat, sformula = ~ x1,
              corstr = "userdefined", zcor = zcor,
              jack = TRUE, j1s = TRUE, fij = TRUE)
summary(zfit)

#### Now, suppose that we want the correlation of 1-2, 2-3, and 3-4
to be the same. Then zcor should have 4 columns.
z2 <- matrix(NA, 300, 4)
z2[,2:4] <- zcor[, c(2, 3, 5)]
summary(geese(y ~ x1 + x2, id = id, data = dat, sformula = ~ x1,
            corstr = "userdefined", zcor = z2,
            jack = TRUE, j1s = TRUE, fij = TRUE))

### Next, we introduce non-constant cluster sizes by
### randomly selecting 60 percent of the data
good <- sort(sample(1:nrow(dat), .6 * nrow(dat)))
mdat <- dat[good,]
summary(geese(y ~ x1 + x2, id = id, data = mdat, waves = visit,
               sformula = ~ x1, corstr="ar1",
               jack = TRUE, j1s = TRUE, fij = TRUE))

---

**geese.control**

*Auxiliary for Controlling GEE Fitting*

**Description**

Auxiliary function as user interface for `gee` fitting. Only used when calling `geese` or `geese.fit`.

**Usage**

```r
geese.control(
  epsilon = 1e-04,
  maxit = 25,
  trace = FALSE,
  scale.fix = FALSE,
  jack = FALSE,
  j1s = FALSE,
  fij = FALSE
)
```

**Arguments**

- **epsilon**: positive convergence tolerance epsilon; the iterations converge when the absolute value of the difference in parameter estimate is below epsilon.
- **maxit**: integer giving the maximal number of Fisher Scoring iteration.
- **trace**: logical indicating if output should be produced for each iteration.
- **scale.fix**: logical indicating if the scale should be fixed.
- **jack**: logical indicating if approximate jackknife variance estimate should be computed.
- **j1s**: logical indicating if 1-step jackknife variance estimate should be computed.
- **fij**: logical indicating if fully iterated jackknife variance estimate should be computed.
Details

When ‘trace’ is true, output for each iteration is printed to the screen by the c++ code. Hence, ‘options(digits = *)’ does not control the precision.

Value

A list with the arguments as components.

Author(s)

Jun Yan <jyan.stat@gmail.com>

See Also

‘geese.fit’, the fitting procedure used by ‘geese’.

description

constructs the design matrix for the correlation structures: independence, exchangeable, ar1 and unstructured. The user will need this function only as a basis to construct a user defined correlation structure: use genZcor to get the design matrix $Z$ for the unstructured correlation and define the specific correlation structure by linear combinations of the columns of $Z$.

Usage

genZcor(clusz, waves, corstrv)

Arguments

clusz integer vector giving the number of observations in each cluster
waves integer vector, observations in the same cluster with values of wave i and j have the correlation $latex$
corstrv correlation structures: 1=independence, 2=exchangeable, 3=ar1, 4=unstructured

Value

the design matrix for the correlation structure

Author(s)

Jun Yan <jyan.stat@gmail.com>

See Also

fixed2Zcor
Examples

# example to construct a Toeplitz correlation structure
#
# sigma_ij=sigma|i-j|

# data set with 5 clusters and maximally 4 observations (visits) per cluster
gendat <- function() {
  id <- gl(5, 4, 20)
  visit <- rep(1:4, 5)
  y <- rnorm(id)
  dat <- data.frame(y, id, visit)[c(-2,-9),]
}

set.seed(88)
dat<-gendat()

# generating the design matrix for the unstructured correlation
zcor <- genZcor(clusz = table(dat$id), waves = dat$visit, corstrv=4)
# defining the Toeplitz structure
zcor.toep<-matrix(NA, nrow(zcor),3)
zcor.toep[,1]<-apply(zcor[,c(1,4,6)],1,sum)
zcor.toep[,2]<-apply(zcor[,c(2,5)],1,sum)
zcor.toep[,3]<-zcor[,3]

zfit1 <- geese(y ~ 1,id = id, data = dat,
               corstr = "userdefined", zcor = zcor.toep)

zfit2 <- geeglm(y ~ 1,id = id, data = dat,
                corstr = "userdefined", zcor = zcor.toep)

---

koch

**Ordinal Data from Koch**

### Description

The koch data frame has 288 rows and 4 columns.

### Usage

koch

### Format

This data frame contains the following columns:

- **trt** a numeric vector
day  a numeric vector
y  an ordered factor with levels: 1 < 2 < 3
id  a numeric vector

Examples

data(koch)
fit <- ordgee(ordered(y) ~ trt + as.factor(day), id=id, data=koch, corstr="exch")
summary(fit)

---

muscatine  Data on Obesity from the Muscatine Coronary Risk Factor Study.

Description
The data are from the Muscatine Coronary Risk Factor (MCRF) study, a longitudinal survey of school-age children in Muscatine, Iowa. The MCRF study had the goal of examining the development and persistence of risk factors for coronary disease in children. In the MCRF study, weight and height measurements of five cohorts of children, initially aged 5-7, 7-9, 9-11, 11-13, and 13-15 years, were obtained biennially from 1977 to 1981. Data were collected on 4856 boys and girls. On the basis of a comparison of their weight to age-gender specific norms, children were classified as obese or not obese.

Usage
muscatine

Format
A dataframe with 14568 rows and 7 variables:

id  identifier of child.
gender  gender of child
base_age  baseline age
age  current age
occasion  identifier of occasion of recording
obese  'yes' or 'no'
umobese  obese in numerical form: 1 corresponds to 'yes' and 0 corresponds to 'no'.

Source
https://content.sph.harvard.edu/fitzmaur/ala2e/muscatine.txt

Examples

```r
muscatin$age <- muscatine$age - 12
muscatin$cage2 <- muscatine$cage^2

f1 <- numobese ~ gender
f2 <- numobese ~ gender + cage + cage2 +
    gender:cage + gender:cage2

gee1 <- geeglm(formula = f1, id = id,
    waves = occasion, data = muscatine, family = binomial(),
    corstr = "independence")

gee2 <- geeglm(formula = f2, id = id,
    waves = occasion, data = muscatine, family = binomial(),
    corstr = "independence")

tidy(gee1)
tidy(gee2)
QIC(gee1)
QIC(gee2)
```

Description

The `ohio` data frame has 2148 rows and 4 columns. The dataset is a subset of the six-city study, a longitudinal study of the health effects of air pollution.

Usage

`ohio`

Format

This data frame contains the following columns:

- `resp` an indicator of wheeze status (1=yes, 0=no)
- `id` a numeric vector for subject id
- `age` a numeric vector of age, 0 is 9 years old
- `smoke` an indicator of maternal smoking at the first year of the study

References

Examples

data(ohio)

fit.ex <- geeglm(resp ~ age + smoke + age:smoke, id=id, data=ohio, 
    family=binomial, corstr="exch", scale.fix=TRUE)
QIC(fit.ex)

fit.ar <- geeglm(resp ~ age + smoke + age:smoke, id=id, data=ohio, 
    family=binomial, corstr="ar1", scale.fix=TRUE)
QIC(fit.ex)

Description

Produces an object of class ‘geese’ which is a Generalized Estimating Equation fit of the clustered ordinal data.

Usage

ordgee(
    formula = formula(data),
    ooffset = NULL,
    id,
    waves = NULL,
    data = parent.frame,
    subset = NULL,
    na.action = na.omit,
    contrasts = NULL,
    weights = NULL,
    z = NULL,
    mean.link = "logit",
    corstr = "independence",
    control = geese.control(...),
    b = NA,
    alpha = NA,
    scale.fix = TRUE,
    scale.val = 1,
    int.const = TRUE,
    rev = FALSE,
    ...
)
Arguments

- **formula**: a formula expression as for `glm`, of the form `response ~ predictors`. See the documentation of `lm` and `formula` for details. As for `glm`, this specifies the linear predictor for modelling the mean. A term of the form `offset(expression)` is allowed.

- **ooffset**: vector of offset for the odds ratio model.

- **id**: a vector which identifies the clusters. The length of ‘id’ should be the same as the number of observations. Data are assumed to be sorted so that observations on a cluster are contiguous rows for all entities in the formula.

- **waves**: an integer vector which identifies components in clusters. The length of waves should be the same as the number of observation. components with the same waves value will have the same link functions.

- **data**: an optional data frame in which to interpret the variables occurring in the formula, along with the id and n variables.

- **subset**: expression saying which subset of the rows of the data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

- **na.action**: a function to filter missing data. For `gee` only `na.omit` should be used here.

- **contrasts**: a list giving contrasts for some or all of the factors appearing in the model formula. The elements of the list should have the same name as the variable and should be either a contrast matrix (specifically, any full-rank matrix with as many rows as there are levels in the factor), or else a function to compute such a matrix given the number of levels.

- **weights**: an optional vector of weights to be used in the fitting process. The length of weights should be the same as the number of observations.

- **z**: a design matrix for the odds ratio model. The number of rows of z is

\[ c^2 \sum n_i(n_i - 1)/2, \]

where \( n_i \) is the cluster size, and \( c \) is the number of categories minus 1.

- **mean.link**: a character string specifying the link function for the means. The following are allowed: "logit", "probit", and "cloglog".

- **corstr**: a character string specifying the log odds. The following are allowed: "independence", "exchangeable", "unstructured", and "userdefined".

- **control**: a list of iteration and algorithmic constants. See `geese.control` for their names and default values. These can also be set as arguments to `geese` itself.

- **b**: an initial estimate for the mean parameters.

- **alpha**: an initial estimate for the odds ratio parameters.

- **scale.fix**: a logical variable indicating if scale is fixed; it is set at TRUE currently (it can not be FALSE yet!).

- **scale.val**: this argument is ignored currently.
int.const  a logical variable; if true, the intercepts are constant, and if false, the intercepts are different for different components in the response.

rev a logical variable. For example, for a three level ordered response $Y = 2$, the accumulated indicator is coded as $(1, 0, 0)$ if true and $(0, 1, 1)$ if false.

... further arguments passed to or from other methods.

Value
An object of class "geese" representing the fit.

Author(s)
Jun Yan <jyan.stat@gmail.com>

References

See Also
glm, lm, geese.

Examples

data(respdis)
resp.l <- reshape(respdis, varying = list(c("y1", "y2", "y3", "y4")),
  v.names = "resp", direction = "long")
resp.l <- resp.l[order(resp.l$id, resp.l$time),]
fit <- ordgee(ordered(resp) ~ trt, id=id, data=resp.l, int.const=FALSE)
summary(fit)

data(ohio)
ohio$resp <- ordered(as.factor(ohio$resp))
fit <- ordgee(resp ~ age + smoke + age:smoke, id = id, data=ohio)
summary(fit)

QIC.geeglm Quasi Information Criterion

Description
Function for calculating the quasi-likelihood under the independence model information criterion (QIC), quasi-likelihood, correlation information criterion (CIC), and corrected QIC for one or several fitted geeglm model object from the geepack package.
Usage

```r
## S3 method for class 'geeglm'
QIC(object, tol = .Machine$double.eps, ...)

## S3 method for class 'ordgee'
QIC(object, tol = .Machine$double.eps, ...)

## S3 method for class 'geekin'
QIC(object, tol = .Machine$double.eps, ...)
QIC(object, tol = .Machine$double.eps, ...)
```

Arguments

- `object`: a fitted GEE model from the geepack package. Currently only works on `geeglm` objects
- `tol`: the tolerance used for matrix inversion
- `...`: optionally more fitted `geeglm` model objects

Details

QIC is used to select a correlation structure. The QICu is used to compare models that have the same working correlation matrix and the same quasi-likelihood form but different mean specifications. CIC has been suggested as a more robust alternative to QIC when the model for the mean may not fit the data very well and when models with different correlation structures are compared.

Models with smaller values of QIC, CIC, QICu, or QICC are preferred.

If the MASS package is loaded then the `ginv` function is used for matrix inversion. Otherwise the standard `solve` function is used.

Value

A vector or matrix with the QIC, QICu, quasi likelihood, CIC, the number of mean effect parameters, and the corrected QIC for each GEE object

Author(s)

Claus Ekstrom <claus@rprimer.dk>

References

See Also

ggee

Examples

library(geepack)
data(ohio)
fit <- geeglm(resp ~ age + smoke + age:smoke, id=id, data=ohio,
              family=binomial, corstr="exch", scale.fix=TRUE)
QIC(fit)

relRisk

Fit a Relative Risk Model for Binary data with Log Link

Description

Fit a Relative Risk Model for Binary data with Log Link using the COPY method.

Usage

relRisk(
  formula, 
  id, 
  waves = NULL, 
  data = parent.frame(),  
  subset = NULL, 
  contrasts = NULL, 
  na.action = na.omit, 
  corstr = "indep", 
  ncopy = 1000, 
  control = geese.control(), 
  b = NULL, 
  alpha = NULL
)

Arguments

  formula same as in geese
  id same as in geese
  waves same as in geese
  data same as in geese

relRisk

subset          same as in geese
contrasts       same as in geese
na.action       same as in geese
corstr          same as in geese
ncopy           the number of copies of the original data in constructing weight.
control         same as in geese
b               initial values for regression coefficients as in geese but more difficult to obtain due to the log link.
alpha           same as in geese

Value
An object of class "geese" representing the fit.

Author(s)
Jun Yan <jyan.stat@gmail.com>

References

Examples

## this example was used in Yu and Yan (2010, techreport)
data(respiratory)
respiratory$treat <- relevel(respiratory$treat, ref = "P")
respiratory$sex <- relevel(respiratory$sex, ref = "M")
respiratory$center <- as.factor(respiratory$center)
## 1 will be the reference level

fit <- relRisk(outcome ~ treat + center + sex + age + baseline + visit,
id = id, corstr = "ar1", data = respiratory, ncopy=10000)
summary(fit)
## fit <- relRisk(outcome ~ treat + center + sex + age + baseline + visit,
## id = id, corstr = "ex", data = respiratory)
## summary(fit)
## fit <- relRisk(outcome ~ treat + center + sex + age + baseline + visit,
## id = id, corstr = "indep", data = respiratory)
## summary(fit)
Respdis
Clustered Ordinal Respiratory Disorder

Description
The respdis data frame has 111 rows and 3 columns. The study described in Miller et. al. (1993) is a randomized clinical trial of a new treatment of respiratory disorder. The study was conducted in 111 patients who were randomly assigned to one of two treatments (active, placebo). At each of four visits during the follow-up period, the response status of each patients was classified on an ordinal scale.

Usage
respdis

Format
This data frame contains the following columns:

- **y1, y2, y3, y4** ordered factor measured at 4 visits for the response with levels, 1 < 2 < 3, 1 = poor, 2 = good, and 3 = excellent
- **trt** a factor for treatment with levels, 1 = active, 0 = placebo.

References

Examples
```r
data(respdis)
resp.l <- reshape(respdis, varying = list(c("y1", "y2", "y3", "y4")),
  v.names = "resp", direction = "long")
resp.l <- resp.l[order(resp.l$id, resp.l$time),]
fit <- ordgee(ordered(resp) ~ trt, id = id, data = resp.l, int.const = FALSE)
summary(fit)
z <- model.matrix(~ trt - 1, data = respdis)
ind <- rep(1:111, 4*3/2 * 2^2)
zmat <- z[ind,,drop=FALSE]
fit <- ordgee(ordered(resp) ~ trt, id = id, data = resp.l, int.const = FALSE,
  z = zmat, corstr = "exchangeable")
summary(fit)
```
Description

The data are from a clinical trial of patients with respiratory illness, where 111 patients from two different clinics were randomized to receive either placebo or an active treatment. Patients were examined at baseline and at four visits during treatment. The respiratory status (categorized as 1 = good, 0 = poor) was determined at each visit.

Usage

respiratory

Format

A data frame with 444 observations on the following 8 variables.

- **center** a numeric vector
- **id** a numeric vector
- **treat** treatment or placebo
- **sex** M or F
- **age** in years at baseline
- **baseline** respiratory status at baseline
- **visit** id of each of four visits
- **outcome** respiratory status at each visit

Examples

data(respiratory)
data(respiratory, package="geepack")
respiratory$center <- factor(respiratory$center)
head(respiratory)

m1 <- glm(outcome ~ center + treat + age + baseline, data=respiratory,
          family=binomial())
gee.ind <- geeglm(outcome ~ center + treat + age + baseline, data=respiratory, id=id,
                   family=binomial(), corstr="independence")
gee.exc <- geeglm(outcome ~ center + treat + age + baseline, data=respiratory, id=id,
                   family=binomial(), corstr="exchangeable")
gee.uns <- geeglm(outcome ~ center + treat + age + baseline, data=respiratory, id=id,
                   family=binomial(), corstr="unstructured")
gee.ar1 <- geeglm(outcome ~ center + treat + age + baseline, data=respiratory, id=id,
                   family=binomial(), corstr="ar1"
seizure <- list(gee.ind, gee.exc, gee.uns, gee.ar1)
do.call(rbind, lapply(mlist, QIC))
lapply(mlist, tidy)

seizure

<table>
<thead>
<tr>
<th>Epilptic Seizures</th>
</tr>
</thead>
</table>

### Description

The seizure data frame has 59 rows and 7 columns. The dataset has the number of epileptic seizures in each of four two-week intervals, and in a baseline eight-week interval, for treatment and control groups with a total of 59 individuals.

### Usage

seizure

### Format

This data frame contains the following columns:

- **y1** the number of epileptic seizures in the 1st 2-week interval
- **y2** the number of epileptic seizures in the 2nd 2-week interval
- **y3** the number of epileptic seizures in the 3rd 2-week interval
- **y4** the number of epileptic seizures in the 4th 2-week interval
- **trt** an indicator of treatment
- **base** the number of epileptic seizures in a baseline 8-week interval
- **age** a numeric vector of subject age

### Source


### References

Examples

data(seizure)
## Diggle, Liang, and Zeger (1994) pp166-168, compare Table 8.10
seiz.l <- reshape(seizure,
    varying=list(c("base","y1","y2","y3","y4")),
    v.names="y", times=0:4, direction="long")
seiz.l <- seiz.l[order(seiz.l$id, seiz.l$time),]
seiz.l$t <- ifelse(seiz.l$time == 0, 8, 2)
seiz.l$x <- ifelse(seiz.l$time == 0, 0, 1)
m1 <- geese(y ~ offset(log(t)) + x + trt + x:trt, id = id,
    data=seiz.l, corstr="exch", family=poisson)
summary(m1)
m2 <- geese(y ~ offset(log(t)) + x + trt + x:trt, id = id,
    data = seiz.l, subset = id!=49,
    corstr = "exch", family=poisson)
summary(m2)

## Thall and Vail (1990)
seiz.l <- reshape(seizure, varying=list(c("y1","y2","y3","y4")),
    v.names="y", direction="long")
seiz.l <- seiz.l[order(seiz.l$id, seiz.l$time),]
seiz.l$base <- log(seiz.l$base / 4)
seiz.l$age <- log(seiz.l$age)
seiz.l$v4 <- ifelse(seiz.l$time == 4, 1, 0)
m3 <- geese(y ~ lbase + trt + lbase:trt + lage + v4,
    sformula = ~ as.factor(time) - 1, id = id,
    data = seiz.l, corstr = "exchangeable", family=poisson)
## compare to Model 13 in Table 4, noticeable difference
summary(m3)

## set up a design matrix for the correlation
z <- model.matrix(~ age, data = seizure) # data is not seiz.l
## just to illustrate the scale link and correlation link
m4 <- geese(y ~ lbase + trt + lbase:trt + lage + v4,
    sformula = ~ as.factor(time)-1, id = id,
    data = seiz.l, corstr = "ar1", family = poisson,
    zcor = z, cor.link = "fisherz", sca.link = "log")
summary(m4)

sitka89

Growth of Sitka Spruce Trees

Description

Impact of ozone on the growth of sitka spruce trees.

Usage

sitka89
Format

A dataframe

size: size of the tree measured in \( \log(\text{height} \times \text{diameter}^2) \)

time: days after the 1st january, 1988

tree: id number of a tree

treat: ozone: grown under ozone environment, control: ozone free

Examples

data(sitka89)

Description

The spruce data frame has 1027 rows and 6 columns. The data consists of measurements on 79 sitka spruce trees over two growing seasons. The trees were grown in four controlled environment chambers, of which the first two, containing 27 trees each, were treated with introduced ozone at 70 ppb whilst the remaining two, containing 12 and 13 trees, were controls.

Usage

spruce

Format

This data frame contains the following columns:

chamber  a numeric vector of chamber numbers

ozone  a factor with levels enriched and normal

id  a numeric vector of tree id

time  a numeric vector of the time when the measurements were taken, measured in days since Jan. 1, 1988

wave  a numeric vector of the measurement number

logsize  a numeric vector of the log-size

Source

Examples

data(spruce)
spruce$contr <- ifelse(spruce$zone=="enriched", 0, 1)
sitka88 <- spruce[spruce$wave <= 5,]
sitka89 <- spruce[spruce$wave > 5,]
fit.88 <- geese(logsize ~ as.factor(wave) + contr +
               I(time/100*contr) - 1,
               id=id, data=sitka88, corstr="ar1")
summary(fit.88)

fit.89 <- geese(logsize ~ as.factor(wave) + contr - 1,
               id=id, data=sitka89, corstr="ar1")
summary(fit.89)
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