Package 'mgee2'

May 1, 2021

Title Marginal Analysis of Misclassified Longitudinal Ordinal Data

Version 0.2

Description Three estimating equation methods are provided in this package for marginal analysis of longitudinal ordinal data with misclassified responses and covariates.
The naive analysis which is solely based on the observed data without adjustment may lead to bias.
The corrected generalized estimating equations (GEE2) method which is unbiased requires the misclassification parameters to be known beforehand.
The corrected generalized estimating equations (GEE2) with validation subsample method estimates the misclassification parameters based on a given validation set. This package is an implementation of Chen (2013) <doi:10.1002/bimj.201200195>.

Depends R (>= 3.6.0)

License GPL (>= 2)

Encoding UTF-8

Imports MASS, ggplot2

LazyData true

RoxygenNote 7.1.1

Suggests R.rsp

VignetteBuilder R.rsp

NeedsCompilation yes

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heart   *heart: preprocessed Framingham Heart Study Teaching data*

Description

heart: preprocessed Framingham Heart Study Teaching data

Usage

    heart

Format

a dataframe with 1830 rows and 42 variables, a total of 915 participants.

RANDID individual id number

HBP a factor variable derived from SYSBP. HBP=0 indicates SBP below 140 mmHg, HBP=1 indicates SBP between 140 mmHg and 159 mmHg, and HBP=2 indicates SBP larger than 160 mmHg

chol a factor variable derived from TOTCHOL. 0=normal (less than 200 mg/dL), 1=borderline high (200-239mg/dL), 2=hypercholesterolemia (greater than 240 mg/dL)

exam3 a factor variable. 1 if the observation belongs to exam 3, 0 otherwise.

For all other variables, please refer to https://biolincc.nhlbi.nih.gov/media/teachingstudies/FHS_Teaching_Longitudinal 03-17_16:09:25.977880, The full teaching data set can be requested from https://biolincc.nhlbi.nih.gov/teaching/

Details

The authors thank Boston University and the National Heart, Lung, and Blood Institute (NHLBI) for providing the data set from the Framingham Heart Study (No. N01-HC-25195) in the illustration. The Framingham Heart Study is conducted and supported by the NHLBI in collaboration with Boston University. This package was not prepared in collaboration with investigators of the Framingham Heart Study and does not necessarily reflect the opinions or views of the Framingham Heart Study, Boston University, or NHLBI.

References

Z. Chen, G. Y. YI, and C. WU. (2011) Marginal methods for correlated binary data with misclassified responses. *Biometrika* 98(3):647-662, 2011

Z. Chen, G. Y. Yi, and C. Wu. (2014) Marginal analysis of longitudinal ordinal data with misclassification inboth response and covariates. *Biometrical Journal*, 56(1):69-85, Oct. 2014

Carroll, R.J., Ruppert, D., Stefanski, L.A. and Crainiceanu, C. (2006) Measurement error in nonlinear models: A modern perspective., Second Edition. London: Chapman and Hall.

Examples

```
{
    data(heart)
    #Example 1:
    heart$chol = as.factor(heart$chol)
    heart$exam3 = as.factor(heart$exam3)
    ## set misclassification parameters to be known.
    varphiMat <- gamMat <- log( cbind(0.04/0.95, 0.01/0.95,
                                      0.95/0.03, 0.02/0.03,
                                      0.04/0.01, 0.95/0.01) )
    mgee2k.fit = mgee2k(formula = HBP~chol+AGE+CURSMOKE+exam3, id = "RANDID",
                        data = heart,
                        corstr = "exchangeable", misvariable = "chol",
                        gamMat = gamMat,
                        varphiMat = varphiMat)
    summary(mgee2k.fit)

    #Example 2:
    naigee.fit = ordGEE2(formula = HBP~chol+AGE+CURSMOKE+exam3, id = "RANDID",
    data = heart, corstr = "exchangeable")
    summary(naigee.fit)
    }
```

---

mgee2k	*mgee2k*

Description

Corrected GEE2 for ordinal data. This method yields unbiased estimators, but the misclassification parameters are required to known.

Usage

```
mgee2k(
  formula,
  id,
  data,
  corstr = "exchangeable",
  misvariable,
```

```
    gamMat,
    varphiMat,
    maxit = 50,
    tol = 0.001
)
```

Arguments

formula	a formula object which specifies the relationship between the response and covariates for the observed data.
id	a character object which records individual id in the data.
data	a dataframe or matrix object for the observed data set.
corstr	a character object. The default value is "exchangeable", corresponding to the structure where the association between two paired responses is considered to be a constant. The other option is "log-linear" which indicates the log-linear association between two paired responses.
misvariable	a character object which names the error-prone covariate W.
gamMat	a matrix object which records the misclassification parameter gamma for response Y.
varphiMat	a matrix object which records the misclassification parameter phi for covariate X.
maxit	an integer which specifies the maximum number of iterations. The default is 50.
tol	a numeric object which indicates the tolerance threshold. The default is 1e-3.

Details

mgee2k implements the misclassification adjustment method outlined in Chen et al.(2014) where the misclassification parameters are known. In this case, validation data are not required, and only the observed data of the outcome and covariates are needed for the implementation.

Value

A list with component

beta	the coefficients in the order as those specified in the formula for the response and covariates.
alpha	the oefficients for paired responses global odds ratios. The number of alpha coefficients corresponds to the paired responses odds ratio structure selected in corstr. When corstr="exchangeable", only one baseline alpha is fitted. When corstr="log-linear", baseline, first order, second order (interaction) terms are fitted.
variance	variance-covariance matrix of the estimator of all parameters.
convergence	a logical variable; TRUE if the model converges.
iteration	the number of iterations for the estimates of the model parameters to converge.
differ	a list of difference of estimation for convergence
call	Function called

References

Z. Chen, G. Y. Yi, and C. Wu. Marginal analysis of longitudinal ordinal data with misclassification inboth response and covariates. *Biometrical Journal*, 56(1):69-85, Oct. 2014

Examples

```
if(0){
data(obs1)
obs1$visit <- as.factor(obs1$visit)
obs1$treatment <- as.factor(obs1$treatment)
obs1$S <- as.factor(obs1$S)
obs1$W <- as.factor(obs1$W)
## set misclassification parameters to be known.
varphiMat <- gamMat <- log( cbind(0.04/0.95, 0.01/0.95,
                                  0.95/0.03, 0.02/0.03,
                                  0.04/0.01, 0.95/0.01) )
mgee2k.fit = mgee2k(formula = S~W+treatment+visit, id = "ID", data = obs1,
                corstr = "exchangeable", misvariable = "W", gamMat = gamMat,
                varphiMat = varphiMat)
}
```

---

mgee2v   *mgee2v*

Description

Corrected GEE2 for ordinal data, with validation subsample

Usage

```
mgee2v(
  formula,
  id,
  data,
  corstr = "exchangeable",
  misvariable = "W",
  valid.sample.ind = "delta",
  y.mcformula,
  x.mcformula,
  maxit = 50,
  tol = 0.001
)
```

Arguments

formula   a formula object which specifies the relationship between the response and co-
              variates for the observed data.

id   a character object which records individual id in the data.

data	a dataframe or matrix object for the observed data set.
corstr	a character object. The default value is "exchangeable", corresponding to the structure where the association between two paired responses is considered to be a constant. The other option is "log-linear" which indicates the log-linear association between two paired responses.
misvariable	a character object which names the error-prone covariate W.
valid.sample.ind	
	a string object which names the indicator variable delta. When a data point belongs to the validation set, delta = 1; otherwise 0.
y.mcformula	a string object which indicates the misclassification formula between true response Y and surrogate(observed) response S.
x.mcformula	a string object which indicates the misclassification formula between true error-prone covariate X and surrogate W.
maxit	an integer which specifies the maximum number of iterations. The default is 50.
tol	a numeric object which indicates the tolerance threshold. The default is 1e-3.

Details

The function *mgee2v* does not require the misclassification parameters to be known, but require the availability of validation data. Similar to *mgee2k*, the function *mgee2v* needs the data set to be structured by individual id, i=1,...,n, and visit time, j_i=1,...,m_i. The data set should contain the observed response and covariates S and W. To indicate whether or not a subject is in the validation set, an indicator variable *delta* should be added in the data set, and we use a column named *valid.sample.ind* for this purpose. The column name of the error-prone covariate W should also be specified in *misvariable*.

Value

A list with component

beta	the coefficients in the order of 1) all non-baseline levels for response, 2) covariates - same order as specified in the formula
alpha	the coefficients for paired responses global odds ratios. Number of alpha coefficients corresponds to the paired responses odds ratio structure selected in "corstr"; when corstr="exchangeable", only one baseline alpha is fitted.
variance	variance-covariance matrix of all fitted parameters
convergence	a logical variable, TRUE if the model converges
iteration	number of iterations for the model to converge
call	Function called

References

Z. Chen, G. Y. Yi, and C. Wu. Marginal analysis of longitudinal ordinal data with misclassification inboth response and covariates. *Biometrical Journal*, 56(1):69-85, Oct. 2014

Examples

```
if(0){
data(obs1)
obs1$Y <- as.factor(obs1$Y)
obs1$X <- as.factor(obs1$X)
obs1$visit <- as.factor(obs1$visit)
obs1$treatment <- as.factor(obs1$treatment)
obs1$S <- as.factor(obs1$S)
obs1$W <- as.factor(obs1$W)
mgee2v.fit = mgee2v(formula = S~W+treatment+visit, id = "ID", data = obs1,
                    y.mcformula = "S~1", x.mcformula = "W~1", misvariable = "W",
                    valid.sample.ind = "delta",
                    corstr = "exchangeable")
}
```

---

mgee2_pkg   *A list of external packages and functions used in mgee2*

Description

A list of external packages and functions used in mgee2

---

obs1   *obs1: simulated observed data*

Description

obs1: simulated observed data

Usage

```
obs1
```

Format

a dataframe with 3000 rows and 8 variables

ID individual id number

Y true response, factor variable

X true error-prone covariate, factor variable

treatment error-free covariate

visit serial number of each visit

S observed response, same as Y when in the validation set(delta=1)

W observed error-prone covariate, same as X when in the validation set (delta=1)

delta indicator variable, 1 if in the validation set, 0 if not.

---

ordGEE2	*ordGEE2*

Description

This function provides a naive approach to estimate the data without any correction or misclassification parameters. This may lead to biased estimation for response parameters.

Usage

```
ordGEE2(formula, id, data, corstr = "exchangeable", maxit = 50, tol = 0.001)
```

Arguments

formula	a formula object: a symbolic description of the model with error-prone response, error-prone covariates and other covariates.
id	a character object which records individual id in the data.
data	a dataframe or matrix of the observed data, including id, error-prone ordinal response error-prone ordinal covaritaes, other covariates.
corstr	a character object. The default value is "exchangeable", corresponding to the structure where the association between two paired responses is considered to be a constant. The other option is "log-linear" which indicates the log-linear association between two paired responses.
maxit	an integer which specifies the maximum number of iterations. The default is 50.
tol	a numeric object which indicates the tolerance threshold. The default is 1e-3.

Details

In addition to developing the package *mgee2* to implement the methods of Chen et al.(2014) which accommodate misclassification effects in inferential procedures, we also implement the naive method of ignoring the feature of misclassification, and call the resulting function *ordGEE2*. This function can be used together with the precedingly described *mgee2k* or *mgee2v* to evaluate the impact of not addressing misclassification effects

Value

A list with component

beta	the coefficients in the order of 1) all non-baseline levels for response, 2) covariates - same order as specified in the formula
alpha	the coefficients for paired responses global odds ratios. Number of alpha coefficients corresponds to the paired responses odds ratio structure selected in "corstr"; when corstr="exchangeable", only one baseline alpha is fitted.
variance	variance-covariance matrix of all fitted parameters
convergence	a logical variable, TRUE if the model converges

iteration	number of iterations for the model to converge
differ	a list of difference of estimation for convergence
##	
call	Function called

References

Z. Chen, G. Y. Yi, and C. Wu. Marginal analysis of longitudinal ordinal data with misclassification inboth response and covariates. *Biometrical Journal*, 56(1):69-85, Oct. 2014

Examples

```
data(obs1)
obs1$Y <- as.factor(obs1$Y)
obs1$X <- as.factor(obs1$X)
obs1$visit <- as.factor(obs1$visit)
obs1$treatment <- as.factor(obs1$treatment)
obs1$S <- as.factor(obs1$S)
obs1$W <- as.factor(obs1$W)
naigee.fit = ordGEE2(formula = S~W+treatment+visit, id = "ID",
                     data = obs1, corstr = "exchangeable")
```

---

plot_model	*plot_model*

Description

This function gives plot of the odds ratio or shows the iteration for convergence.

Usage

```
plot_model(x, conv = FALSE)
```

Arguments

x	results from the fitted model.
conv	defulated for odds ratio plot, otherwise show the iteration plot.

Value

plot odds ratio with CIs or plot of the iterations.

Examples

```
beta=c(0.1,0.2,0.3)
alpha=c(0.4,0.5)
variance=c(0.8,0.5,0.7,0.3,0.4)
x=list(beta,alpha,variance)
names(x)=c("beta","alpha","variance")
plot_model(x)
```

---

print.summary.mgee2   *print.summary.mgee2*

Description

print.summary.mgee2

Usage

```
## S3 method for class 'summary.mgee2'
print(x, ...)
```

Arguments

x   the summary results

...   Other parameters

Value

a table of summary statistics

---

summary.mgee2   *summary.mgee2*

Description

summary.mgee2

Usage

```
## S3 method for class 'mgee2'
summary(object, ...)
```

Arguments

object   The fitted model

...   Other parameters summary function for mgee2 method output

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