

Package ‘MIIPW’

May 7, 2026

Type Package

Title IPW and Mean Score Methods for Time-Course Missing Data

Version 0.1.2

Maintainer Atanu Bhattacharjee <atanustat@gmail.com>

Description Contains functions for data analysis of Repeated measurement using GEE. Data may contain missing value in response and covariates. For parameter estimation through Fisher Scoring algorithm, Mean Score and Inverse Probability Weighted method combining with Multiple Imputation are used when there is missing value in covariates/response. Reference for mean score method, inverse probability weighted method is Wang et al(2007)<[doi:10.1093/biostatistics/kx1024](https://doi.org/10.1093/biostatistics/kx1024)>.

Imports mice,Matrix,MASS

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 2.10), lme4, spatstat

RoxygenNote 7.3.2

NeedsCompilation no

Author Atanu Bhattacharjee [aut, cre, ctb],
Bhriku Kumar Rajbongshi [aut, ctb],
Gajendra K Vishwakarma [aut, ctb]

Repository CRAN

Suggests knitr, rmarkdown

VignetteBuilder knitr

Date/Publication 2025-04-21 19:10:02 UTC

Contents

AIPW	2
lmeaipw	5
lmeipw	8

lmmeanscore	11
MeanScore	14
miAIPW	16
miSIPW	19
print_ipw	21
print_meanscore	22
QICmiipw	22
SIPW	23
srdata1	26
summary_ipw	26
summary_meanscore	27
updateALpha	27
updateBeta	28
UpdatePhi	29
updateSandW	29

Index	31
--------------	-----------

AIPW

Fit a geeglm model using AIPW

Description

provides augmented inverse probability weighted estimates of parameters for GEE model of response variable using different covariance structure

Usage

```
AIPW(
  data,
  formula,
  id,
  visit,
  family,
  init.beta = NULL,
  init.alpha = NULL,
  init.phi = NULL,
  tol = 0.001,
  weights = NULL,
  corstr = "independent",
  maxit = 50,
  m = 2,
  pMat,
  method = NULL
)
```

Arguments

data	longitudinal data set where each subject's outcome has been measured at same time points and number of visits for each patient is similar. Covariance structure of the outcome variable like "unstructured","independent","AR-1" ,"exchangeable"
formula	formula for the response model
id	column name of id of subjects in the dataset
visit	column name of timepoints of visit in the dataset
family	name of the distribution for the response variable, For more information on how to use family objects, see family
init.beta	initial values for the regression coefficient of GEE model
init.alpha	initial values for the correlation structure
init.phi	initial values for the csale parameter for
tol	tolerance in calculation of coefficients
weights	A vector of weights for each observation. If an observation has weight 0, it is excluded from the calculations of any parameters. Observations with a NA anywhere (even in variables not included in the model) will be assigned a weight of 0. Weights are updated as the mentioned the details.
corstr	a character string specifying the correlation structure. It could "independence", "exchangeable", "AR-1", "unstructured"
maxit	maximum number iteration for newton-raphson
m	number of imputation used to update the missing score function value due incomplete data.
pMat	predictor matrix as obtained in mice
method	method option for mice model,for information see mice

Details**AIPW**

It uses the inverse probability weighted method to reduce the bias due to missing values in GEE model for longitudinal data. The response variable \mathbf{Y} is related to the coariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^k \sum_{j=1}^n \left(\frac{\delta_{ij}}{\pi_{ij}} S(Y_{ij}, \mathbf{X}_{ij}, \mathbf{X}'_{ij}) + \left(1 - \frac{\delta_{ij}}{\pi_{ij}}\right) \phi(\mathbf{V} = \mathbf{v}) \right) = 0$$

where $\delta_{ij} = 1$ if there is missing value in covariates and 0 otherwise, \mathbf{X} is fully observed all subjects and \mathbf{X}' is partially missing, where $\mathbf{V} = (Y, \mathbf{X})$. The missing score function values due to incomplete data are estimated using an imputation model through mice which we have considered as $\phi(\mathbf{V} = \mathbf{v})$.

Value

A list of objects containing the following objects

call details about arguments passed in the function

beta estimated regression coefficient value for the response model

niter number of iteration required

betalist list of beta values at different iteration

weight estimated weights for the observations

mu mu values according [glm](#)

phi estimated phi value for the [glm](#) model

hessian estimated hessian matrix obtained from the last iteration

betaSand sandwich estimator value for the variance covariance matrix of the beta

Author(s)

Atanu Bhattacharjee, Bhriгу Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIAB+Adiponectin+AgRP+ALCAM
pMat<-mice::make.predictorMatrix(srdata1[names(srdata1)%in%all.vars(formula)])
m1<-AIPW(data=srdata1,
formula<-formula,id='ID',
visit='Visit',family='gaussian',init.beta = NULL,
init.alpha=NULL,init.phi=1,tol=.00001,weights = NULL,
constr = 'exchangeable',maxit=50,m=3,pMat=pMat)
##

## End(Not run)
```

lmeaipw

*Fits a marginal model using AIPW***Description**

provides augmented inverse probability weighted estimates of parameters for semiparametric marginal model of response variable of interest. The augmented terms are estimated by using multiple imputation model.

Usage

```
lmeaipw(
  data,
  M = 5,
  id,
  analysis.model,
  wgt.model,
  imp.model,
  qpoints = 4,
  psiCov,
  nu,
  psi,
  sigma = NULL,
  sigmaMiss,
  sigmaR,
  dist,
  link,
  conv = 1e-04,
  maxiter,
  maxpiinv = -1,
  se = TRUE,
  verbose = FALSE
)
```

Arguments

data	longitudinal data with each subject specified discretely
M	number of imputation to be used in the estimation of augmentation term
id	column names which shows identification number for each subject
analysis.model	A formula to be used as analysis model
wgt.model	Formula for weight model, which consider subject specific random intercept
imp.model	For for missing response imputation, which consider subject specific random intercept
qpoints	Number of quadrature points to be used while evaluating the numerical integration

psiCov	working model parameter
nu	working model parameter
psi	working model parameter
sigma	working model parameter
sigmaMiss	working model parameter
sigmaR	working model parameter
dist	distribution for imputation model. Currently available options are Gaussian, Binomial
link	Link function for the mean
conv	convergence tolerance
maxiter	maximum number of iteration
maxpiinv	maximum value pi can take
se	Logical for Asymptotic SE for regression coefficient of the regression model.
verbose	logical argument

Details

lmeaipw

It uses the augmented inverse probability weighted method to reduce the bias due to missing values in response model for longitudinal data. The response variable \mathbf{Y} is related to the coariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^n \sum_{j=t_1}^{t_k} \int_{a_i} \int_{b_i} \left(\frac{\delta_{ij}}{\hat{\pi}_{ij}(a_i)} S(Y_{ij}, \mathbf{X}_{ij}; \beta) + \left(1 - \frac{\delta_{ij}}{\hat{\pi}_{ij}(a_i)}\right) \phi(\mathbf{V}_{ij}, b_i; \psi) \right) da_i db_i = 0$$

where $\delta_{ij} = 1$ if there is missing value in the response and 0 otherwise, \mathbf{X} is fully observed all subjects, where $\mathbf{V}_{ij} = (\mathbf{X}_{ij}, A_{ij})$. The missing score function values due to incomplete data are estimated using an imputation model through FCS (here we have considered a mixed effect model) which we have considered as $\phi(\mathbf{V}_{ij} = \mathbf{v}_{ij})$. The estimated value $\hat{\phi}(\mathbf{V}_{ij} = \mathbf{v}_{ij})$ is obtained through multiple imputation. The working model for imputation of missing response is

$$Y_{ij}|b_i \sim N(\mathbf{V}_{ij}\psi + b_i, \sigma); b_i \sim N(0, \sigma_{miss})$$

and for the missing data probability

$$\text{Logit}(P(\delta_{ij} = 1 | \mathbf{V}_{ij}\nu + a_i)); a_i \sim N(0, \sigma_R)$$

Value

A list of objects containing the following objects

Call details about arguments passed in the function

nr.conv logical for checking convergence in Newton Raphson algorithm

nr.iter number of iteration required

nr.diff absolute difference for roots of Newton Raphson algorithm

beta estimated regression coefficient for the analysis model

var.beta Asymptotic SE for beta

Author(s)

Atanu Bhattacharjee, Bhrigu Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
library(JMbayes2)
library(lme4)
library(insight)
library(numDeriv)
library(stats)
lmer(log(alkaline)~drug+age+year+(1|id),data=na.omit(pbc2))
data1<-pbc2
data1$alkaline<-log(data1$alkaline)
names(pbc2)
apply(pbc2,2,function(x){sum(is.na(x))})
r.ij<-ifelse(is.na(data1$alkaline)==T,0,1)
data1<-cbind.data.frame(data1,r.ij)
data1$drug<-factor(data1$drug,levels=c("placebo","D-penicil"),labels = c(0,1))
data1$sex<-factor(data1$sex,levels=c('male','female'),labels=c(1,0))
data1$drug<-as.numeric(as.character(data1$drug))
data1$sex<-as.numeric(as.character(data1$sex))
r.ij~year+age+sex+drug+serBilir+(1|id)
model.r<-glmer(r.ij~year+age+sex+drug+serBilir+(1|id),family=binomial(link='logit'),data=data1)
model.y<-lmer(alkaline~year+age+sex+drug+serBilir+(1|id),data=na.omit(data1))
nu<-model.r@beta
psi<-model.y@beta
sigma<-get_variance_residual(model.y)
sigmaR<-get_variance(model.r)$var.random
sigmaMiss<-get_variance(model.y)$var.random
m11<-lmeaipw(data=data1,id='id',
analysis.model = alkaline~year,
wgt.model=~year+age+sex+drug+serBilir+(1|id),
```

```

imp.model = ~year+age+sex+drug+serBilir+(1|id),
psiCov = vcov(model.y),nu=nu,psi=psi,
sigma=sigma,sigmaMiss=sigmaMiss,sigmaR=sigmaR,dist='gaussian',link='identity',
maxiter = 200)
m11
##

## End(Not run)

```

lmeipw

Fits a marginal model using IPW

Description

provides inverse probability weighted estimates of parameters for semiparametric marginal model of response variable of interest. The weights are computed using a generalized linear mixed effect model.

Usage

```

lmeipw(
  data,
  M = 5,
  id,
  analysis.model,
  wgt.model,
  qpoints = 4,
  nu,
  sigmaR,
  dist,
  link,
  conv = 1e-04,
  maxiter,
  maxpiinv = -1,
  se = TRUE,
  verbose = FALSE
)

```

Arguments

data	longitudinal data with each subject specified discretely
M	number of imputation to be used in the estimation of augmentation term
id	column names which shows identification number for each subject
analysis.model	A formula to be used as analysis model
wgt.model	Formula for weight model, which consider subject specific random intercept
qpoints	Number of quadrature points to be used while evaluating the numerical integration

nu	working model parameter
sigmaR	working model parameter
dist	distribution for imputation model. Currently available options are Gaussian, Binomial
link	Link function for the mean
conv	convergence tolerance
maxiter	maximum number of iteration
maxpiinv	maximum value pi can take
se	Logical for Asymptotic SE for regression coefficient of the regression model.
verbose	logical argument

Details

lmeipw

It uses the simple inverse probability weighted method to reduce the bias due to missing values in response model for longitudinal data. The response variable \mathbf{Y} is related to the covariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^n \sum_{j=t_1}^{t_k} \int_{a_i} \frac{\delta_{ij}}{\hat{\pi}_{ij}(a_i)} S(Y_{ij}, \mathbf{X}_{ij}) da_i = 0$$

where $\delta_{ij} = 1$ if there is missing no value in response and 0 otherwise. \mathbf{X} is fully observed all subjects and for the missing data probability

$$\text{Logit}(P(\delta_{ij} = 1 | \mathbf{V}_{ij}\nu + a_i)) ; a_i \sim N(0, \sigma_R)$$

; where $\mathbf{V}_{ij} = (\mathbf{X}_{ij}, A_{ij})$

Value

A list of objects containing the following objects

Call details about arguments passed in the function

nr.conv logical for checking convergence in Newton Raphson algorithm

nr.iter number of iteration required

nr.diff absolute difference for roots of Newton Raphson algorithm

beta estimated regression coefficient for the analysis model

var.beta Asymptotic SE for beta

Author(s)

Atanu Bhattacharjee, Bhriku Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW,miSIPW,miAIPW](#)

Examples

```
## Not run:
##
library(JMbayes2)
library(lme4)
library(insight)
library(numDeriv)
library(stats)
lmer(log(alkaline)~drug+age+year+(1|id),data=na.omit(pbc2))
data1<-pbc2
data1$alkaline<-log(data1$alkaline)
names(pbc2)
apply(pbc2,2,function(x){sum(is.na(x))})
r.ij<-ifelse(is.na(data1$alkaline)==T,0,1)
data1<-cbind.data.frame(data1,r.ij)
data1$drug<-factor(data1$drug,levels=c("placebo","D-penicil"),labels = c(0,1))
data1$sex<-factor(data1$sex,levels=c('male','female'),labels=c(1,0))
data1$drug<-as.numeric(as.character(data1$drug))
data1$sex<-as.numeric(as.character(data1$sex))
r.ij~year+age+sex+drug+serBilir+(1|id)
model.r<-glmer(r.ij~year+age+sex+drug+serBilir+(1|id),family=binomial(link='logit'),data=data1)
nu<-model.r@beta
sigmaR<-get_variance(model.r)$var.random
m11<-lmeipw(data=data1,id='id',
            analysis.model = alkaline~year,
            wgt.model=~year+age+sex+drug+serBilir+(1|id),
            nu=nu,sigmaR=sigmaR,dist='gaussian',link='identity',qpoints=4,
            maxiter = 200)

m11
##

## End(Not run)
```

lmemeanscore *Fits a marginal model using meanscore*

Description

provides meanscore estimates of parameters for semiparametric marginal model of response variable of interest. The augmented terms are estimated by using multiple imputation model.

Usage

```
lmemeanscore(
  data,
  M = 5,
  id,
  analysis.model,
  imp.model,
  qpoints = 4,
  psiCov,
  psi,
  sigma = NULL,
  sigmaMiss,
  dist,
  link,
  conv = 1e-04,
  maxiter,
  maxpiinv = -1,
  se = TRUE,
  verbose = FALSE
)
```

Arguments

data	longitudinal data with each subject specified discretely
M	number of imputation to be used in the estimation of augmentation term
id	cloumn names which shows identification number for each subject
analysis.model	A formula to be used as analysis model
imp.model	For for missing response imputation, which consider subject specific random intercept
qpoints	Number of quadrature points to be used while evaluating the numerical integration
psiCov	working model parameter
psi	working model parameter
sigma	working model parameter
sigmaMiss	working model parameter

dist	distribution for imputation model. Currently available options are Gaussian, Binomial
link	Link function for the mean
conv	convergence tolerance
maxiter	maximum number of iteration
maxpiinv	maximum value pi can take
se	Logical for Asymptotic SE for regression coefficient of the regression model.
verbose	logical argument

Details

Immeanscore

It uses the mean score method to reduce the bias due to missing values in response model for longitudinal data. The response variable \mathbf{Y} is related to the coariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^n \sum_{j=t_1}^{t_k} \int_{b_i} (\delta_{ij} S(Y_{ij}, \mathbf{X}_{ij}) + (1 - \delta_{ij}) \phi(\mathbf{V}_{ij}, b_i; \psi)) db_i = 0$$

where $\delta_{ij} = 1$ if there is missing value in response and 0 otherwise, \mathbf{X} is fully observed all subjects and $\mathbf{V}_{ij} = (\mathbf{X}_{ij}, A_{ij})$. The missing score function values due to incomplete data are estimated using an imputation model through mice which we have considered as

$$Y_{ij}|b_i \sim N(\mathbf{V}_{ij}\gamma + b_i, \sigma); b_i \sim N(0, \sigma_{miss})$$

through multiple imputation.

Value

A list of objects containing the following objects

Call details about arguments passed in the function

nr.conv logical for checking convergence in Newton Raphson algorithm

nr.iter number of iteration required

nr.diff absolute difference for roots of Newton Raphson algorithm

beta estimated regression coefficient for the analysis model

var.beta Asymptotic SE for beta

Author(s)

Atanu Bhattacharjee, Bhriku Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
library(JMbayes2)
library(lme4)
library(insight)
library(numDeriv)
library(stats)
lmer(log(alkaline)~drug+age+year+(1|id),data=na.omit(pbc2))
data1<-pbc2
data1$alkaline<-log(data1$alkaline)
names(pbc2)
apply(pbc2,2,function(x){sum(is.na(x))})
r.ij<-ifelse(is.na(data1$alkaline)==T,0,1)
data1<-cbind.data.frame(data1,r.ij)
data1$drug<-factor(data1$drug,levels=c("placebo","D-penicil"),labels = c(0,1))
data1$sex<-factor(data1$sex,levels=c('male','female'),labels=c(1,0))
data1$drug<-as.numeric(as.character(data1$drug))
data1$sex<-as.numeric(as.character(data1$sex))
model.y<-lmer(alkaline~year+age+sex+drug+serBilir+(1|id),data=na.omit(data1))
psi<-model.y@beta
sigma<-get_variance_residual(model.y)
sigmaMiss<-get_variance(model.y)$var.random
m11<-lmmeanscore(data=data1,id='id',
analysis.model = alkaline~year,
imp.model = ~year+age+sex+drug+serBilir+(1|id),
psiCov = vcov(model.y),psi=psi,
sigma=sigma,sigmaMiss=sigmaMiss,dist='gaussian',link='identity',qpoints = 4,
maxiter = 200)
m11
##

## End(Not run)
```

MeanScore

Fit a geeglm model using meanScore

Description

provides mean score estimates of parameters for GEE model of response variable using different covariance structure

Usage

```
MeanScore(
  data,
  formula,
  id,
  visit,
  family,
  init.beta = NULL,
  init.alpha = NULL,
  init.phi = NULL,
  tol = 0.001,
  weights = NULL,
  corstr = "independent",
  maxit = 50,
  m = 2,
  pMat,
  method = NULL
)
```

Arguments

data	longitudinal data set where each subject's outcome has been measured at same time points and number of visits for each patient is similar. Covariance structure of the outcome variable like "unstructured", "independent", "AR-1", "exchnageable"
formula	formula for the response model
id	column name of id of subjects in the dataset
visit	column name of timepoints of visit in the dataset
family	name of the distribution for the response variable, For more information on how to use family objects, see family
init.beta	initial values for the regression coefficient of GEE model
init.alpha	initial values for the correlation structure
init.phi	initial values for the scale parameter
tol	tolerance in calculation of coefficients

weights	A vector of weights for each observation. If an observation has weight 0, it is excluded from the calculations of any parameters. Observations with a NA anywhere (even in variables not included in the model) will be assigned a weight of 0. Weights are updated as the mentioned the details.
corstr	a character string specifying the correlation structure. It could "independence", "exchangeable", "AR-1", "unstructured"
maxit	maximum number iteration for newton-raphson
m	number of imputation used to update the missing score function value due incomplete data.
pMat	predictor matrix as obtained in mice
method	method option for mice model,for information see mice

Details

meanScore

It uses the mean score method to reduce the bias due to missing covariate in GEE model. The response variable \mathbf{Y} is related to the coariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^k \sum_{j=1}^n (\delta_{ij} S(Y_{ij}, \mathbf{X}_{ij}, \mathbf{X}'_{ij}) + (1 - \delta_{ij}) \phi(\mathbf{V} = \mathbf{v})) = 0$$

where $\delta_{ij} = 1$ if there is missing value in covariates and 0 otherwise, \mathbf{X} is fully observed all subjects and \mathbf{X}' is partially missing, where $\mathbf{V} = (Y, \mathbf{X})$. The missing score function values due to incomplete data are estimated using an imputation model through mice which we have considered as $\phi(\mathbf{V} = \mathbf{v})$. The estimated value $\phi(\mathbf{V} = \mathbf{v})$ is obtained through multiple imputation.

Value

A list of objects containing the following objects

call details about arguments passed in the function

beta estimated regression coefficient value for the response model

niter number of iteration required

betalist list of beta values at different iteration

weight estimated weights for the observations

mu mu values according [glm](#)

phi etsimated phi value for the glm model

hessian estimated hessian matrix obtained from the last iteration

betaSand sandwich estimator value for the variance covariance matrix of the beta

Author(s)

Atanu Bhattacharjee, Bhriku Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIAB+Adiponectin+AgRP+ALCAM
pMat<-mice::make.predictorMatrix(srdata1[names(srdata1)%in%all.vars(formula)])
m1<-MeanScore(data=srdata1,
formula<-formula,id='ID',
visit='Visit',family='gaussian',init.beta = NULL,
init.alpha=NULL,init.phi=1,tol=.00001,weights = NULL,
constr = 'exchangeable',maxit=50,m=2,pMat=pMat)
##

## End(Not run)
```

miAIPW

Fit a geeglm model using miAIPW

Description

provides augmented inverse probability weighted estimates of parameters for GEE model of response variable using different covariance structure. The augmented terms are estimated by using multiple imputation model.

Usage

```
miAIPW(
  data,
  formula,
  id,
  visit,
  family,
```

```

    init.beta = NULL,
    init.alpha = NULL,
    init.phi = NULL,
    tol = 0.001,
    weights = NULL,
    corstr = "independent",
    maxit = 50,
    m = 2,
    pMat,
    method = NULL
  )

```

Arguments

data	longitudinal data set where each subject's outcome has been measured at same time points and number of visits for each patient is similar. Covariance structure of the outcome variable like "unstructured", "independent", "AR1", "Exchangeable"
formula	formula for the response model
id	column name of id of subjects in the dataset
visit	column name of timepoints of visit in the dataset
family	name of the distribution for the response variable, For more information on how to use family objects, see family
init.beta	initial values for the regression coefficient of GEE model
init.alpha	initial values for the correlation structure
init.phi	initial values for the csale parameter for
tol	tolerance in calculation of coefficients
weights	A vector of weights for each observation. If an observation has weight 0, it is excluded from the calculations of any parameters. Observations with a NA anywhere (even in variables not included in the model) will be assigned a weight of 0. Weights are updated as the mentioned the details.
corstr	a character string specifying the correlation structure. It could "independent", "exchangeable", "AR-1", "unstructured"
maxit	maximum number iteration for newton-raphson
m	number of imputation used to update the missing score function value due in-complete data.
pMat	predictor matrix as obtained in mice
method	method option for mice model,for information see mice

Details

miAIPW

It uses the augmented inverse probability weighted method to reduce the bias due to missing values in GEE model for longitudinal data. The response variable \mathbf{Y} is related to the coariates as $g(\mu) =$

$\mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^k \sum_{j=1}^n \left(\frac{\delta_{ij}}{\pi_{ij}} S(Y_{ij}, \mathbf{X}_{ij}, \mathbf{X}'_{ij}) + \left(1 - \frac{\delta_{ij}}{\pi_{ij}}\right) \phi(\mathbf{V} = \mathbf{v}) \right) = 0$$

where $\delta_{ij} = 1$ if there is missing value in covariates and 0 otherwise, \mathbf{X} is fully observed all subjects and \mathbf{X}' is partially missing, where $\mathbf{V} = (Y, \mathbf{X})$. The missing score function values due to incomplete data are estimated using an imputation model through mice which we have considered as $\phi(\mathbf{V} = \mathbf{v})$. The estimated value $\phi(\mathbf{V} = \mathbf{v})$ is obtained through multiple imputation.

Value

A list of objects containing the following objects

call details about arguments passed in the function

beta estimated regression coefficient value for the response model

niter number of iteration required

betalist list of beta values at different iteration

weight estimated weights for the observations

mu mu values according [glm](#)

phi estimated phi value for the glm model

hessian estimated hessian matrix obtained from the last iteration

betaSand sandwich estimator value for the variance covariance matrix of the beta

Author(s)

Atanu Bhattacharjee, Bhriгу Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```

## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIAB+Adiponectin+AgRP+ALCAM
pMat<-mice::make.predictorMatrix(srdata1[names(srdata1)%in%all.vars(formula)])
m1<-miAIPW(data=srdata1,
formula<-formula,id='ID',
visit='Visit',family='gaussian',init.beta = NULL,
init.alpha=NULL,init.phi=1,tol=.00001,weights = NULL,
corstr = 'exchangeable',maxit=4,m=2,pMat=pMat)
##

## End(Not run)

```

miSIPW

*Fit a geeglm model using miSIPW***Description**

provides simple inverse probability weighted estimates of parameters for GEE model of response variable using different covariance structure, missing values in covariates are multiply imputed for those subjects whose response is observed.

Usage

```

miSIPW(
  data,
  formula,
  id,
  visit,
  family,
  init.beta = NULL,
  init.alpha = NULL,
  init.phi = NULL,
  tol = 0.001,
  weights = NULL,
  corstr = "independent",
  maxit = 50,
  m = 2,
  pMat,
  method = NULL
)

```

Arguments

data longitudinal data set where each subject's outcome has been measured at same time points and number of visits for each patient is similar. Covariance structure of the outcome variable like "unstructured","independent","AR-1" ,"exchangeable"

<code>formula</code>	formula for the response model
<code>id</code>	column name of id of subjects in the dataset
<code>visit</code>	column name of timepoints of visit in the dataset
<code>family</code>	name of the distribution for the response variable, For more information on how to use family objects, see family
<code>init.beta</code>	initial values for the regression coefficient of GEE model
<code>init.alpha</code>	initial values for the correlation structure
<code>init.phi</code>	initial values for the scale parameter
<code>tol</code>	tolerance in calculation of coefficients
<code>weights</code>	A vector of weights for each observation. If an observation has weight 0, it is excluded from the calculations of any parameters. Observations with a NA anywhere (even in variables not included in the model) will be assigned a weight of 0. Weights are updated as the mentioned the details.
<code>corstr</code>	a character string specifying the correlation structure. It could "independence", "exchangeable", "AR-1", "unstructured"
<code>maxit</code>	maximum number iteration for newton-raphson
<code>m</code>	number of imputation used to update the missing score function value due incomplete data.
<code>pMat</code>	pMat predictor matrix as obtained in mice
<code>method</code>	method option for mice model,for information see mice

Details

miSIPW

It uses the simple inverse probability weighted method to reduce the bias due to missing values in GEE model for longitudinal data. The response variable \mathbf{Y} is related to the coariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^k \sum_{j=1}^n \frac{\delta_{ij}}{\pi_{ij}} S(Y_{ij}, \mathbf{X}_{ij}, \mathbf{X}'_{ij})$$

=0 where $\delta_{ij} = 1$ if there is missing no value in covariates and 0 otherwise. \mathbf{X} is fully observed all subjects and \mathbf{X}' is partially missing.

Value

A list of objects containing the following objects

call details about arguments passed in the function

beta estimated regression coefficient value for the response model

niter number of iteration required

betalist list of beta values at different iteration

weight estimated weights for the observations

mu mu values according [glm](#)
phi estimated phi value for the [glm](#) model
hessian estimated hessian matrix obtained from the last iteration
betaSand sandwich estimator value for the variance covariance matrix of the beta

Author(s)

Atanu Bhattacharjee, Bhriгу Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[SIPW](#), [AIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIAB+Adiponectin+AgRP+ALCAM
pMat<-mice::make.predictorMatrix(srdata1[names(srdata1)%in%all.vars(formula)])
m1<-miSIPW(data=srdata1,
formula=formula,id='ID',
visit='Visit',family='gaussian',init.beta = NULL,
init.alpha=NULL,init.phi=1,tol=0.001,weights = NULL,
corstr = 'exchangeable',maxit=50,m=2,pMat=pMat)
##

## End(Not run)
```

print_ipw

print method for ipw

Description

print method for ipw

Usage

```
print_ipw(x, ...)
```

Arguments

```
x          ipw object
...        further argument can be passed
```

Value

print result for ipw object

```
print_meanscore      print method for meanscore
```

Description

print method for meanscore

Usage

```
print_meanscore(x, ...)
```

Arguments

```
x          meanscore object
...        further argument can be passed
```

Value

print result for meanscore object

```
QICmiipw      Model Selection criteria QIC
```

Description

It provides model selection criteria such as quasi-likelihood under the independence model criterion (QIC), an approximation to QIC under large sample i.e QICu and quasi likelihood

Usage

```
QICmiipw(model.R, model.indep, family)
```

Arguments

<code>model.R</code>	fitted object obtained from GEE model MeanScore, SIPW, AIPW, miSIPW, miAIPW with correlation structure other than "independent"
<code>model.indep</code>	same fitted object as in <code>model.indep</code> with "independent" correlation structure
<code>family</code>	currently we have included "poisson", "binomial", "gaussian"

Details

QICmiipw

Value

returns a list containing QIC, QICu, Quasi likelihood

References

Pan, Wei. "Akaike's information criterion in generalized estimating equations." *Biometrics* 57.1 (2001): 120-125.

Examples

```
## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIB+Adiponectin+AgRP+ALCAM
pMat<-mice::make.predictorMatrix(srdata1[names(srdata1)%in%all.vars(formula)])
m1<-MeanScore(data=srdata1,
               formula<-formula,id='ID',
               visit='Visit',family='gaussian',init.beta = NULL,
               init.alpha=NULL,init.phi=1,tol=.00001,weights = NULL,
               corstr = 'exchangeable',maxit=50,m=2,pMat=pMat)
m11<-MeanScore(data=srdata1,
               formula<-formula,id='ID',
               visit='Visit',family='gaussian',init.beta = NULL,
               init.alpha=NULL,init.phi=1,tol=.00001,weights = NULL,
               corstr = 'independent',maxit=50,m=2,pMat=pMat)
QICmiipw(model.R=m1,model.indep=m11,family="gaussian")
##

## End(Not run)
```

SIPW

Fit a geeglm model using SIPW

Description

provides simple inverse probability weighted estimates of parameters for GEE model of response variable using different covariance structure

Usage

```
SIPW(
  data,
  formula,
  id,
  visit,
  family,
  init.beta = NULL,
  init.alpha = NULL,
  init.phi = NULL,
  tol = 0.001,
  weights = NULL,
  corstr = "independent",
  maxit = 10,
  maxvisit = NULL
)
```

Arguments

<code>data</code>	longitudinal data set where each subject's outcome has been measured at same time points and number of visits for each patient is similar. Covariance structure of the outcome variable like "unstructured", "independent", "exchangeable"
<code>formula</code>	formula for the response model
<code>id</code>	column name of id of subjects in the dataset
<code>visit</code>	column name of timepoints of visit in the dataset
<code>family</code>	name of the distribution for the response variable, For more information on how to use family objects, see family
<code>init.beta</code>	initial values for the regression coefficient of GEE model
<code>init.alpha</code>	initial values for the correlation structure
<code>init.phi</code>	initial values for the scale parameter
<code>tol</code>	tolerance in calculation of coefficients
<code>weights</code>	A vector of weights for each observation. If an observation has weight 0, it is excluded from the calculations of any parameters. Observations with a NA anywhere (even in variables not included in the model) will be assigned a weight of 0. Weights are updated as the mentioned the details.
<code>corstr</code>	a character string specifying the correlation structure. It could "independence", "exchangeable", "AR-1", "unstructured"
<code>maxit</code>	maximum number of iteration
<code>maxvisit</code>	maximum number of visit

Details

SIPW

It uses the simple inverse probability weighted method to reduce the bias due to missing values in GEE model for longitudinal data. The response variable \mathbf{Y} is related to the covariates as $g(\mu) = \mathbf{X}\beta$, where g is the link function for the glm. The estimating equation is

$$\sum_{i=1}^k \sum_{j=1}^n \frac{\delta_{ij}}{\pi_{ij}} S(Y_{ij}, \mathbf{X}_{ij}, \mathbf{X}'_{ij})$$

=0 where $\delta_{ij} = 1$ if there is missing no value in covariates and 0 otherwise. \mathbf{X} is fully observed all subjects and \mathbf{X}' is partially missing.

Value

A list of objects containing the following objects

call details about arguments passed in the function

beta estimated regression coefficient value for the response model

niter number of iteration required

betalist list of beta values at different iteration

weight estimated weights for the observations

mu mu values according [glm](#)

phi estimated phi value for the glm model

hessian estimated hessian matrix obtained from the last iteration

betaSand sandwich estimator value for the variance covariance matrix of the beta

Author(s)

Atanu Bhattacharjee, Bhriku Kumar Rajbongshi and Gajendra Kumar Vishwakarma

References

Wang, C. Y., Shen-Ming Lee, and Edward C. Chao. "Numerical equivalence of imputing scores and weighted estimators in regression analysis with missing covariates." *Biostatistics* 8.2 (2007): 468-473.

Seaman, Shaun R., and Stijn Vansteelandt. "Introduction to double robust methods for incomplete data." *Statistical science: a review journal of the Institute of Mathematical Statistics* 33.2 (2018): 184.

Vansteelandt, Stijn, James Carpenter, and Michael G. Kenward. "Analysis of incomplete data using inverse probability weighting and doubly robust estimators." *Methodology: European Journal of Research Methods for the Behavioral and Social Sciences* 6.1 (2010): 37.

See Also

[AIPW](#), [miSIPW](#), [miAIPW](#)

Examples

```
## Not run:
##
formula<-C6kine~ActivinRIB+ActivinRIIA+ActivinRIIB+Adiponectin+AgRP+ALCAM
m1<-SIPW(data=srdata1,formula<-formula,id='ID',
visit='Visit',family='gaussian',corstr = 'exchangeable',maxit=5)
##

## End(Not run)
```

srdata1	<i>protein data</i>
---------	---------------------

Description

Repeated measurement dataset, for each id we have four visit observations

Usage

```
data(srdata1)
```

Format

A dataframe with 164 rows and 9 columns

ID ID of subjects

Visit Number of times observations recorded

C6kine,.....,GFRalpha4 These are covariates

Examples

```
data(srdata1)
```

summary_ipw	<i>summary method for ipw</i>
-------------	-------------------------------

Description

summary method for ipw

Usage

```
summary_ipw(object, ...)
```

Arguments

object ipw object
 ... further argument can be passed

Value

summary of ipw object

summary_meanscore *summary method for meanscore*

Description

summary method for meanscore

Usage

summary_meanscore(object, ...)

Arguments

object meanscore object
 ... further argument can be passed

Value

summary of meanscore object

updateALpha *internal function for updating alpha*

Description

internal function for updating alpha

Usage

updateALpha(y, x, vfun, mu, w, phi, corstr, ni, mv = NULL, id, visit)

Arguments

y	response value for GEE model
x	model matrix for the GEE model
vfun	variance function for the GLM
mu	mu vector for the GLM
w	weight matrix
phi	scale parameter
corstr	correlation structure
ni	list of visits per subject
mv	NULL
id	id column
visit	visit column

Details

arguments are from Fisher Scoring Algorithm

updateBeta	<i>internal function for updating beta through Fisher Scoring</i>
------------	---

Description

internal function for updating beta through Fisher Scoring

Usage

```
updateBeta(y, x, vfun, mu, w, D, Ralpha, beta)
```

Arguments

y	response value for GEE model
x	model matrix for the GEE model
vfun	variance function for the GLM
mu	mu vector for the GLM
w	weight matrix
D	derivation of the inverse link function
Ralpha	correlation matrix
beta	vector of beta value for GEE model

UpdatePhi	<i>internal function for updating scale parameter</i>
-----------	---

Description

internal function for updating scale parameter

Usage

```
UpdatePhi(y, x, vfun, mu, w)
```

Arguments

y	response value for GEE model
x	model matrix for the GEE model
vfun	variance function for the GLM
mu	mu vector for the GLM
w	weight matrix

updateSandW	<i>internal function for sandwich estimator</i>
-------------	---

Description

internal function for sandwich estimator

Usage

```
updateSandW(y, x, vfun, mu, w, D, Ralpha, beta, hessmat, blockdiag)
```

Arguments

y	response value for GEE model
x	model matrix for the GEE model
vfun	variance function for the GLM
mu	mu vector for the GLM
w	weight matrix
D	derivation of the inverse link function
Ralpha	correlation matrix
beta	vector of beta value for GEE model
hessmat	hessian matrix
blockdiag	vector containing the dim of block matrix for block diagonal matrix

Details

arguments are required for obtaining Sandwich Estimator for variance matrix of regression coefficient of GEE model

Index

* datasets

srdata1, [26](#)

AIPW, [2](#), [21](#), [25](#)

family, [3](#), [14](#), [17](#), [20](#), [24](#)

glm, [4](#), [15](#), [18](#), [21](#), [25](#)

lmeaipw, [5](#)

lmeipw, [8](#)

lmemeanscore, [11](#)

MeanScore, [14](#)

miAIPW, [4](#), [7](#), [10](#), [13](#), [16](#), [16](#), [18](#), [21](#), [25](#)

mice, [3](#), [15](#), [17](#), [20](#)

miSIPW, [4](#), [7](#), [10](#), [13](#), [16](#), [18](#), [19](#), [25](#)

print_ipw, [21](#)

print_meanscore, [22](#)

QICmiipw, [22](#)

SIPW, [4](#), [7](#), [10](#), [13](#), [16](#), [18](#), [21](#), [23](#)

srdata1, [26](#)

summary_ipw, [26](#)

summary_meanscore, [27](#)

updateAlpha, [27](#)

updateBeta, [28](#)

UpdatePhi, [29](#)

updateSandW, [29](#)