Package 'trajMSM'

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Type Package

Title Marginal Structural Models with Latent Class Growth Analysis of Treatment Trajectories

Version 0.1.0

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Description The package trajMSM is based on the paper Marginal Structural Models with Latent Class Growth Analysis of Treatment Trajectories: https://doi.org/10.48550/arXiv.2105.12720.

License GPL-3

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown

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`trajMSM-package` *trajMSM: Marginal Structural Models with Latent Class Growth Analysis of Treatment Trajectories*

Description

The package trajMSM is based on the paper Marginal Structural Models with Latent Class Growth Analysis of Treatment Trajectories: https://doi.org/10.48550/arXiv.2105.12720.

Details

The package trajMSM is based on the paper Marginal Structural Models with Latent Class Growth Analysis of Treatment Trajectories: https://doi.org/10.48550/arXiv.2105.12720. Latent class growth analysis (LCGA) are increasingly proposed as a solution to summarize the observed longitudinal treatment in a few distinct groups. When combined with standard approaches like Cox proportional hazards models, LCGM can fail to control time-dependent confounding bias because of time-varying covariates that have a double role of confounders and mediators. We propose to use LCGA to classify individuals into a few latent classes based on their medication adherence pattern, then choose a working marginal structural model (MSM) that relates the outcome to these groups. The parameter of interest is nonparametrically defined as the projection of the true MSM onto the chosen working model. The combination of LCGA with MSM (LCGA-MSM) is a convenient way to describe treatment adherence and can effectively control time-dependent confounding. Several approaches exist to estimate the parameters of a MSM and one of the most popular is the inverse probability weighting (IPW). The IPW mimics a random assignment of the treatment by creating a pseudo-population where the treated and the untreated groups are comparable. In longitudinal settings, IPW can appropriately adjust for time-varying covariates affected by prior exposure and selection bias. In this first version, we proposed to estimate parameters of the LCGA-MSM using the IPW. Further development will include other estimators such as the g-formula and the pooled LTMLE.

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Author:	Awa Diop, Denis Talbot

`buildtraj` *Wrapper of flexmix*

Description

Call the package flexmix to construct trajectory groups

Usage

```
buildtraj(
  Rdat,
```

```
  formula = as.formula(cbind(A, 1 - A) ~ time),
  J,
  id = "id",
  family = "binomial",
  control = list(iter.max = 1000, minprior = 0),
  ...
)
```

Arguments

Rdat	sample data to build trajectory groups. These data are in long format. Each row represent a person time, column A is a binary data.
formula	designate the formula to model the longitudinal variable of interest.
J	an integer to choose the number of trajectory groups.
family	designate the type of distribution "gaussian", "binomial", "poisson" and "gamma".
control	object of class FLXcontrol.
...	to add supplementary functions.

Value

dpost	Posterior probability.
model	Fitted trajectory model.

Author(s)

Awa Diop, Denis Talbot

Examples

```
obsdata = gendatatraj()
Rdat =longtowide(obsdata = obsdata, varying = 1:5)
head(Rdat)
res.traj = buildtraj(Rdat = Rdat, k=3,formula = cbind(A,1-A) ~ time, id=id)
head(res.traj$dpost)
```

---

gendatatraj *Data Simulation for Trajectory Analysis*

Description

Example of longitudinal data with three hidden subgroups to perform LCGA/GBTM.

Usage

```
gendatatraj(
  n1 = 250,
  n2 = 350,
  n3 = 400,
  beta01 = -5,
  beta02 = -0.15,
```

```
  beta03 = -0.01,
  beta11 = -1,
  beta12 = 0.5,
  beta13 = 5,
  set.seed = 355
)
```

Arguments

n1	sample size of the first subgroup.
n2	sample size of the second subgroup.
n3	sample size of the third subgroup.
beta01	intercept for the first subgroup.
beta02	intercept for the second subgroup.
beta03	intercept for the third subgroup.
beta11	slope for the first subgroup.
beta12	slope for the second subgroup.
beta13	slope for the third subgroup.
set.seed	to add a seed.

Value

Obsdata	Wide format data.

Author(s)

Awa Diop, Denis Talbot

Examples

```
Obsdata = gendatatraj()
head(Obsdata)
```

---

gformcountermeans *Counterfactual means for g-formula.*

Description

Get the counterfactual means for the g-formula.

Usage

```
sub_gform(
  dat,
  formula = paste0("Y~", paste0("A", 1:s, collapse = "+"), "+", paste0("L", 1:s,
    collapse = "+"), "+", V, collapse = "+"),
  Y,
  A,
  L,
```

```
  V,
  s,
  time
)
```

Arguments

Y	outcome variable.
A	time-varying treatment.
L	time-varying covariates.
V	baseline covariates.
s	number of measuring times.
time	measuring times.
C	censor variable.

Value

counter_means	Counterfactual means obtained with g-formula
treatment_regimes	Liste of treatment regimes

Author(s)

Awa Diop, Denis Talbot

Examples

```
Obswidedata = longtowide(Obsdata = gendatrajMSM(n=500), idvar = "ID", timevar = "Time");
formula = paste0("Y.2013~", paste0("Statins.", c(2011:2013),collapse = "+"), "+",
paste0("BMI.", c(2011:2013),collapse = "+"),"+",
paste0("Hyper.", c(2011:2013),collapse = "+"),"+",
"Age.2011 + Sex.2011", collapse = "+")
Y = "Y.2013 "
A = "Statins."
L = c("Hyper.", "BMI.")
V = c("Age.", "Sex.")
s=3
time = c(2011,2012,2013)
res.gform = sub_gform(dat=Obswidedata, formula = formula, Y=Y, A=A,L=L,V=V,s=3, time=time)
res.gform$counter_means
```

IPW *Inverse of Probability Weighting*

Description

Compute stabilized and unstabilized with and without censor weights.

Usage

```
IPW(
  numerator = c("stabilized", "unstabilized"),
  id,
  V,
  L,
  A,
  Censor = FALSE,
  s,
  time,
  obsdata
)
```

Arguments

V	baseline covariates.
L	time-varying covariates.
A	time-varying treatment.
s	number of measuring times per interval.
time	measuring times.
obsdata	observed data in wide format.
C	Censor variable.

Value

IPW	Stabilized and unstabilized inverse of probabilities with and without censoring

Author(s)

Awa Diop, Denis Talbot

Examples

```
dat = gendatTrajMSM(n=500, Censor=FALSE)
V <- c("Age","Sex")
L <- c("Hyper","BMI")
time <- "Time"
A <- "Statins"
Censor = "C"
sw = IPW(numerator = "stabilized",id= "ID", V = c("Age","Sex"),
     L = c("Hyper","BMI"),
     time ="Time",
     A=c("Statins"),obsdata = dat)
summary(sw)
```

longtowide *Reshape from long to wide format.*

Description

To convert observed data into a wide format for the g-formula and pooled ltmle.

Usage

```
longtowide(obsdata, idvar, timevar)
```

Arguments

obsdata	the data to reshape in a long format.
varying	varying columns.

Value

long_dat	Long format data.

Author(s)

Awa Diop, Denis Talbot

Examples

```
widedata = longtowide(obsdata = gendatrajMSM(n=500), idvar = "ID", timevar = "Time")
head(widedata)
```

plotraj *plotraj*

Description

Use "ggplot2" to plot trajectory groups produced by the function "buildtraj".

Usage

```
plotraj(
  Rdat = NULL,
  dpost = NULL,
  trajdat = NULL,
  formula = as.formula(A ~ time + class),
  trt = "A",
  time = "time",
  id = "id",
  class = "class",
  FUN = "mean",
  ...
)
```

Arguments

Rdat	an object produced by the function "longtowide".
dpost	matrice contenant les probabilités a posterio et les groupes de trajectoires.
trt	name of the time-varying treatment.
time	name of the variable measurements of time.
id	name of the id variable.
class	name of the trajectory groups.
FUN	specify what statistics to display, by default calculate the mean.
...	to add supplementary functions.
Trajdat	merged datasets containing observed data in long format and trajectory groups.

Author(s)

Awa Diop, Denis Talbot

Examples

```
Obsdata = gendatatraj()
Rdat = longtowide(Obsdata = Obsdata, varying = 1:5)
head(Rdat)
res.traj = buildtraj(Rdat = Rdat, k=3,formula = cbind(A,1-A) ~ time, id="id")
dpost = res.traj$dpost
head(dpost)
plotraj(Rdat = Rdat, dpost = dpost, formula = A ~ time + class,
trt = "A",time = "time",id="id",class = "class", FUN = "mean")
```

---

predicTraj. *Predict trajectory groups for deterministic treatment regimes*

Description

function to predict trajectory groups for deterministic treatment regimes used with gformula and pooled LTMLE.

Usage

```
predicTraj(s, trajmodel, trt, time_name, id)
```

Arguments

s	number of measuring times per interval.
trajmodel	trajectory model built with the observed treatment.
time_name	name of the measuring times.
A	name of the time-varying treatment.
name	of the id column variable.

Author(s)

Awa Diop, Denis Talbot

split_data *Split Observed data into multiple subsets*

Description

function to split the data into multiple subsets of size s each one corresponding to one time-interval.

Usage

```
split_data(obsdata, K, s, A, L, Y)
```

Arguments

obsdata	observed data in wide format.
K	total length of follow-up.
s	number of measuring times per interval.
A	time-varying treatment.
L	time-varying covariates.
V	baseline covariates.

sub_pooled_LTMLE *Counterfactual means for a Pooled LTMLE*

Description

function to estimate counterfactual means for a pooled LTMLE.

Usage

```
sub_pooled_tmle(
  obsdata,
  Traj,
  formula = paste0("Y~", paste0("A", 1:s, collapse = "+"), "+", paste0("L", 1:s,
    collapse = "+"), "+", paste0("V", 1:s, collapse = "+"), collapse = "+"),
  Y,
  A,
  L,
  V,
  s,
  time,
  trt,
  time_name = time_name
)
```

Arguments

obsdata	observed data in wide format.
Y	outcome variable.
A	time-varying treatment.
L	time-varying covariates.
V	baseline covariates.
s	number of measuring times.
time	measuring times.

Value

counter_means	Counterfactual means obtained with g-formula
D	Influence functions

Author(s)

Awa Diop, Denis Talbot

Examples

```
Obsdatawide = longtowide(Obsdata = gendatrajMSM(n=500), idvar = "ID", timevar = "Time");
formula = paste0("Y.2011~", paste0("Statins.", c(2011:2013),collapse = "+"), "+",
paste0("BMI.", c(2011:2013),collapse = "+"),"+",
paste0("Hyper.", c(2011:2013),collapse = "+"),"+",
"Age.2011 + Sex.2011", collapse = "+")
Y = "Y."
A = "Statins."
L = c("Hyper.", "BMI.")
V = c("Age.2011, Sex.2011")
s=3
time = c(2011,2012,2013)
time_name = "Time"
res_pooledl_tmle <- sub_pooled_tmle(dat = Obsdata,Traj,formula = formula,Y=Y,A=A,L=L,V=V,s=3,
time=time,trt=trt, time_name = time_name)
res_pooledl_tmle$counter_means
```

---

trajHRMSM *Combination of trajectory analysis and history restricted MSM*

Description

function to estimate counterfactual means for a pooled LTMLE.

Usage

```
trajMSM(
  trajdata,
  Obsdata,
  formula1 = as.formula("Y ~ class"),
  formula2 = as.formula("Surv(Y,event) ~ class"),
  numerator = c("stabilized", "unstabilized"),
  id,
  V,
  L,
  A,
  Y,
  Censor = FALSE,
  time,
  family = c("binomial", "gaussian", "survival"),
  estimator = c("IPW", "gform", "pooledltmle")
)
```

Arguments

V	baseline covariates.
L	time-varying covariates.
A	time-varying treatment.
Y	outcome variable.
time	measuring times.
s	number of measuring times.
obsdata	observed data in wide format.

Author(s)

Awa Diop Denis Talbot

---

trajMSM *Combination of trajectory analysis and MSM*

Description

function to estimate counterfactual means for a pooled LTMLE.

Usage

```
trajMSM(
  trajdata,
  Obsdata,
  formula1 = as.formula("Y ~ class"),
  formula2 = as.formula("Surv(Y,event) ~ class"),
  numerator = c("stabilized", "unstabilized"),
  id,
  V,
```

```
  L,
  A,
  Y,
  Censor = FALSE,
  time,
  family = c("binomial", "gaussian", "survival"),
  estimator = c("IPW", "gform", "pooledltmle")
)
```

Arguments

V	baseline covariates.
L	time-varying covariates.
A	time-varying treatment.
Y	outcome variable.
time	measuring times.
s	number of measuring times.
obsdata	observed data in wide format.

---

widetolong *Reshape from wide to long format.*

Description

To convert data generated by the function gen_datatraj into a long format.

Usage

```
widetolong(obsdata, varying)
```

Arguments

obsdata	the data to reshape in a long format.
varying	varying columns.

Value

widetolong_dat	Long format data.

Author(s)

Awa Diop, Denis Talbot

Examples

```
longdata = widetolong(obsdata = gendatatraj(), varying = 1:5)
head(longdata)
```

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