Package 'itlt'

October 27, 2019

Title Interaction tree for longitudinal trajectories

Version 0.0.0.9000

Description What the package does (one paragraph).

Depends R (>= 3.1.0), lme4, nlme, splines, partykit (>= 1.0-4)

License What license it uses

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

R topics documented:

---

bslme | *Calculate test statistic using mixed effects model (LRT based model)*

Description

Mixed effects based model tests trajectories by testing model fitting. Trajectories are assumed to follow mixed effects models. Under the null hypothesis there are only one treatment effect curve for both nodes. Under the alternative, separate treatment effect curves are assumed for both nodes

Usage

```
bslme(D.traj, D.cov, tf, nknot = 5, p.value = 0.05, degree = 3)
```

Arguments

`D.traj`	dataset of purely longitudinal observations in wide format
`D.cov`	covariate matrix of intercept, treat, grp, treat * grp
`tf`	time frame
`nknot`	knot number
`p.value`	significance value required for a node to be splitted, default is 1
`degree`	degree of spline coefficients, default is 3

Value

(LRT) chi^2 test statistic of df(nknot) under the mixed effects model

---

`Chi2Normalize`	*Nomalizing a chi^2 square statistic from df(n) to df(1)*

Description

The pruning procedure is proposed under the assumption that test statistics at each node are chi^2(1) distributed.

Usage

```
Chi2Normalize(t, n)
```

Arguments

`t`	original test statistic
`n`	original degree of freedom

Value

chi^2 test statistic of df(1) with the same significance level

Examples

```
Chi2Normalize(3, 5)
```

ItltSimulation1 *Simulation for longitudinal datasets*

Description

Simulation for longitudinal datasets

Usage

```
ItltSimulation1(N, tf, e = 0.05, p = 0, asigma = 0.1,
  seed = "1234", type = 1)
```

Arguments

N	sample size
tf	time frame
e	error standard deviation
p	missing value probability
asigma	sd of subject specific random effect
seed	seed for random number
type	simulation setting (1: non-linearity, 2: periodicity, 3: non-linearity, 4: no heterogeneity in treatment effect)

Value

a simulated longitudinal dataset

Examples

```
sample <- ItltSimulation1(250, 1:12)
```

ItltTree *Implement tree structured subgroup identification on longitudinal datasets*

Description

Methods implemented include: mixed effects based method (LRT based method), GEE based method, multiple test based method, multivariate multiple regression (mmp) based method. mixed effects and GEE are for regular longitudinal datasets and multiple test based and mmp based method are for intensive longitudinal datasets. This function is based on partynode package. Also interaction trees by scalar based methods (avg, last-k) are also implemented.But the scalar based method needs to have the same data format (see data, fm, tf for details), otherwise regular code for interaction tree could be used

Usage

```
ItltTree(data, fm, tf, split.covs, nknot = 5, p.value = 1,
  delta = 0.1, nCutpoints = 20, minsplit = 20, size.limit = 10,
  maxdepth = 3, details = "TRUE", alpha = 2.5, model = "bslme")
```

Arguments

`data`	dataset in wide format, please see fm and time frame for column name restrictions. Also data must have a column named "id", otherwise the first column will be specified to be "id"
`fm`	formula of the form "response name ~ treatment name". data must contain column names of the response with all its time frames. For instance, if fm = "y~treatment", tf = 1:12, then columns names in the dataset must include y1, y2,..., y12. And these longitudinal observations will be used as reponse for subgroup identfication
`tf`	time frame
`split.covs`	splitting covariates, vector of strings
`nknot`	knot numbers, for multiple test based and mmp based methods, nknot <= 0 means automatic selection of knot numbers using GCV
`p.value`	significance level for a node to be considered, default is 1
`delta`	lower bound of the ratio of the size of the child node and the parent node, default is 0.1
`nCutpoints`	number of cutoff points for a continuous splitting covariate, default is 20
`minsplit`	minimum number of samples for a node to be considered for splitting, default is 30
`size.limit`	minimum size for a node, default is delta * minsplit
`maxdepth`	maximum depth of the tree, default is 4
`details`	whether details in the treee building process will be printed, default is FALSE
`alpha`	tuning parametering in the selection of knot numbers using smoothing splines, specific for multiple test based method and MMP based method, default is 2
`model`	method to be implemented.

Value

identified tree of partynode type

Examples

```
library(itlt)
data <- ItltSimulation1(250, 1:12, type = 2)
ItltTree(data, as.formula(y~treatment), 1:12, paste0("X", 1:10))
```

---

knot.select	*Selection of number of knots in multiple test base and mmp based methods*

Description

For intensive longitudinal dataset (multiple test based method and mmp based method), a preprocessing step using smoothing splines is used.Generalized cross validation (GCV) is used for knot number selection.

Usage

```
knot.select(D.traj, tf, alpha = 2)
```

Arguments

D.traj	dataset consists purely of longitudinal observations
tf	time frame
alpha	penalization term in GCV

Value

mean and standard deviation of GCV of each possible knot number

---

spline.preprocess   *Use smoothing spline to preprocess original longitudinal data*

Description

For multiple test based and MMP based methods, preprocess using smoothing splines are the first step

Usage

```
spline.preprocess(D.traj, tf, nknot, alpha)
```

Arguments

D.traj	dataset consists purely of original longitudinal observations
tf	time frame
nknot	knot number
alpha	penalization term in GCV

Value

new longitudinal dataset with fitted spline coefficients

Index