

Package ‘TBFmultinomial’

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Type Package

Title TBF Methodology Extension for Multinomial Outcomes

Version 0.1.3

VignetteBuilder knitr

Description Extends the test-based Bayes factor (TBF) methodology to multinomial regression models and discrete time-to-event models with competing risks. The TBF methodology has been well developed and implemented for the generalised linear model [Held et al. (2015) <doi:10.1214/14-ST510>] and for the Cox model [Held et al. (2016) <doi:10.1002/sim.7089>].

Depends VGAM, nnet, parallel, stats, stringr, plotrix, methods

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TBFmultinomial-package

Objective Bayesian variable selection for multinomial regression and discrete time-to-event models with competing risks

Description

Extension of the TBF methodology introduced by Held et al. (2015) <doi:10.1214/14-STS510> to discrete time-to-event models with competing risks (also applicable to the multinomial regression model)

Author(s)

Rachel Heyard <rachel.heyard@uzh.ch>

AIC_BIC_based_marginalLikelihood

Marginal likelihoods based on AIC or BIC

Description

This function computes the marginal likelihoods based on the AIC or on the BIC, that will later be used to calculate the TBF.

Usage

```
AIC_BIC_based_marginalLikelihood(fullModel = NULL, candidateModels = NULL,
  data, discreteSurv = TRUE, AIC = TRUE, package = "nnet", maxit = 150,
  numberCores = 1)
```

Arguments

| | |
|-----------------|---|
| fullModel | formula of the model including all potential variables |
| candidateModels | Instead of defining the full model we can also specify the candidate models whose deviance statistic and d.o.f should be computed |
| data | the data |
| discreteSurv | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| AIC | if TRUE, AIC will be used, else we use BIC |
| package | Which package should be used to fit the models; by default the nnet package is used; we could also specify to use the package 'VGAM' |
| maxit | Only needs to be specified with package nnet: maximal number of iterations |
| numberCores | How many cores should be used in parallel? |

Value

a vector with the marginal likelihoods of all candidate models

Author(s)

Rachel Heyard

Examples

```
# data extraction:
data("VAP_data")

# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here the define time as a spline with 3 knots

# now we can compute the marginal likelihoods based on the AIC f.ex:
mL_AIC <-
AIC_BIC_based_marginalLikelihood(fullModel = FULL,
                                  data = VAP_data,
                                  discreteSurv = TRUE,
                                  AIC = TRUE)
```

all_formulas

Formulas of all the candidate models

Description

This function retrieves the formulas of all the candidate models if the reference model is the null / baseline model.

Usage

```
all_formulas(fullModel, discreteSurv = TRUE)
```

Arguments

`fullModel` formula of the model including all potential variables

`discreteSurv` Boolean variable telling us whether a ‘simple’ multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed.

Value

character vector with all the formulas; the first one will be the reference model; the last element will be the full model.

Author(s)

Rachel Heyard

Examples

```
data("VAP_data")
FULL <- outcome ~ ns(day, df = 4) + male + type + SOFA
models <- TBFmultinomial:::all_formulas(fullModel = FULL,
discreteSurv = TRUE)
# models
```

as.data.frame.PMP *Convert a PMP object into a data frame*

Description

This function takes a PMP object and returns a `data.frame` summarising the information.

Usage

```
## S3 method for class 'PMP'
as.data.frame(x, ...)
```

Arguments

`x` valid [PMP](#) object

`...` arguments to be passed to `data.frame`

Value

a `data.frame` with the posterior and prior probabilities as well as the definition of the models

Author(s)

Rachel Heyard

CSVS

*Cause-specific variable selection (CSVS)***Description**

This function performs CSVS given a model fitted using the `multinom()` function of the `nnet` package or the `vglm()` function of the `VGAM` package.

Usage

```
CSVS(g, model, discreteSurv = TRUE, nbIntercepts = NULL, package = "nnet")
```

Arguments

| | |
|---------------------------|---|
| <code>g</code> | the estimated <code>g</code> , must be fixed to one value |
| <code>model</code> | the model fitted using either <code>nnet</code> or <code>VGAM</code> |
| <code>discreteSurv</code> | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| <code>nbIntercepts</code> | how many cause-specific intercepts are there? they |
| <code>package</code> | Which package has been used to fit the model, <code>nnet</code> or <code>VGAM</code> ? |

Author(s)

Rachel Heyard

Examples

```
# data extraction:
data("VAP_data")

# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here the define time as a spline with 3 knots

# we first need to fit the multinomial model:
model_full <- multinom(formula = FULL, data = VAP_data,
                       maxit = 150, trace = FALSE)

G <- 9 # let's suppose g equals to nine

# then we proceed to CSVS
CSVS_nnet <- CSVS(g = G, model = model_full,
                  discreteSurv = TRUE, package = 'nnet')
```

| | |
|--------------|--------------------------------|
| model_priors | <i>Prior model probability</i> |
|--------------|--------------------------------|

Description

This function computes the prior model probabilities of the candidate models

Usage

```
model_priors(fullModel, discreteSurv = TRUE, modelPrior = "flat")
```

Arguments

| | |
|--------------|---|
| fullModel | formula of the model including all potential variables |
| discreteSurv | Boolean var telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| modelPrior | what prior should be used on the model space? modelPrior should be included in {'flat', 'dependent'} where 'flat' means a uniform prior and 'dependent' sets a multiplicity-corrected model prior on the model space. |

Value

a numerical vector with the prior model probabilities

Author(s)

Rachel Heyard

Examples

```
# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here we define time as a spline with 3 knots

priors <- model_priors(fullModel = FULL, discreteSurv = TRUE,
                      modelPrior = 'dependent')
```

PIPs_by_landmarking *Posterior inclusion probabilities (PIPs) by landmarking*

Description

This function gives us the PIPs for each landmark.

Usage

```
PIPs_by_landmarking(fullModel, data, discreteSurv = TRUE, numberCores = 1,  
  package = "nnet", maxit = 150, prior = "flat", method = "LEB",  
  landmarkLength = 1, lastlandmark, timeVariableName)
```

Arguments

| | |
|------------------|---|
| fullModel | formula of the model including all potential variables |
| data | the data frame with all the information |
| discreteSurv | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| numberCores | How many cores should be used in parallel? |
| package | Which package should be used to fit the models; by default the nnet package is used; we could also specify to use the package 'VGAM' |
| maxit | Only needs to be specified with package nnet: maximal number of iterations |
| prior | Prior on the model space |
| method | Method for the g definition |
| landmarkLength | Length of the landmark, by default we use each day |
| lastlandmark | Where will be the last landmark? |
| timeVariableName | What is the name of the variable indicating time? |

Value

a list with the PIPs for each landmark

Author(s)

Rachel Heyard

Examples

```
# extract the data:
data("VAP_data")

# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here we define time as a spline with 3 knots

PIPs_landmark <- PIPs_by_landmarking(fullModel = FULL, data = VAP_data,
                                     discreteSurv = TRUE, numberCores = 1,
                                     package = 'nnet', maxit = 150,
                                     prior = 'flat', method = 'LEB',
                                     landmarkLength = 7, lastlandmark = 21,
                                     timeVariableName = 'day')
```

`plot_CSVS`*Plot a CSVS object*

Description

Plot a CSVS object

Usage

```
plot_CSVS(CSVSobject, namesVar = NULL, shrunken = FALSE,
          standardized = FALSE, numberIntercepts, ...)
```

Arguments

| | |
|-------------------------------|--|
| <code>CSVSobject</code> | valid CSVS object |
| <code>namesVar</code> | names of the variables |
| <code>shrunken</code> | should the coefficients be shrunken? |
| <code>standardized</code> | should the coefficients be standardized? |
| <code>numberIntercepts</code> | how many cause-specific intercepts are in the model for each outcome |
| <code>...</code> | parameters for plot |

Author(s)

Rachel Heyard

Description

This function computes the posterior probability of all candidate models

Usage

```
PMP(fullModel = NULL, candidateModels = NULL, data = NULL,
    discreteSurv = TRUE, modelPrior = NULL, method = "LEB",
    prior = "flat", package = "nnet", maxit = 150, numberCores = 1)
```

Arguments

| | |
|------------------------------|--|
| <code>fullModel</code> | formula of the model including all potential variables |
| <code>candidateModels</code> | Instead of defining the full model we can also specify the candidate models whose deviance statistic and d.o.f should be computed |
| <code>data</code> | the data frame with all the information |
| <code>discreteSurv</code> | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| <code>modelPrior</code> | optionally the model priors can be computed before if <code>candidateModels</code> is different from <code>NULL</code> . |
| <code>method</code> | tells us which method for the definition of <code>g</code> should be used. Possibilities are: <code>LEB</code> , <code>GEB</code> , <code>g=n</code> , <code>hyperG</code> , <code>ZS</code> , <code>ZSadapted</code> and <code>hyperGN</code> |
| <code>prior</code> | should a dependent or a flat prior be used on the model space? Only needed if <code>method = 'GEB'</code> . |
| <code>package</code> | Which package should be used to fit the models; by default the <code>nnet</code> package is used; we could also specify to use the package ' <code>VGAM</code> ' |
| <code>maxit</code> | Only needs to be specified with package <code>nnet</code> : maximal number of iterations |
| <code>numberCores</code> | How many cores should be used in parallel? |

Value

an object of class `TBF.ingredients`

Author(s)

Rachel Heyard

Examples

```
# extract the data:
data("VAP_data")

# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here we define time as a spline with 3 knots

# computation of the posterior model probabilities:
test <- PMP(fullModel = FULL, data = VAP_data,
            discreteSurv = TRUE, maxit = 150)
class(test)
```

PMP-class

Class for PMP objects

Description

Class for PMP objects

postInclusionProb

Posterior inclusion probability (PIP)

Description

This function computes the PIPs of all potential predictors

Usage

```
postInclusionProb(object)
```

Arguments

object An object of class PMP

Value

an named vector with all PIPs

Author(s)

Rachel Heyard

Examples

```
# extract the data:
data("VAP_data")

# the definition of the full model with three potential predictors:
FULL <- outcome ~ ns(day, df = 4) + gender + type + SOFA
# here we define time as a spline with 3 knots

# computation of the posterior model probabilities:
test <- PMP(fullModel = FULL, data = VAP_data,
            discreteSurv = TRUE, maxit = 150)
class(test)

#computation of the posterior inclusion probabilities:
postInclusionProb(test)
```

sample_multinomial *Samples from a PMP object*

Description

This function samples from a specific model inside a PMP object.

Usage

```
sample_multinomial(PMP_object, shrink = TRUE, data, which = "MPM",
                  discreteSurv = TRUE)
```

Arguments

| | |
|--------------|---|
| PMP_object | formula of the model including all potential variables |
| shrink | should the coefficients be shrunken towards their prior mean? |
| data | the (training) data frame with all the information |
| which | which model should be sampled from? either an integer, 'MPM' or 'MAP' |
| discreteSurv | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |

Value

returns an object with the model coefficients and supplementary information

Author(s)

Rachel Heyard

TBF *Test-based Bayes factor*

Description

This function computes the TBF as well as g

Usage

```
TBF(ingredients = NULL, fullModel = NULL, method = "LEB", data = NULL,
    discreteSurv = TRUE, prior = NULL, package = "nnet", maxit = 150)
```

Arguments

| | |
|---------------------------|---|
| <code>ingredients</code> | TBF_ingredients_object ingredients for the TBF (and g) calculation. |
| <code>fullModel</code> | if <code>ingredients</code> is NULL, formula of the model including all potential variables |
| <code>method</code> | tells us which method for the definition of g should be used. Possibilities are: LEB, GEB, g=n, hyperG, ZS, ZSadapted and hyperGN |
| <code>data</code> | the data frame with all the information. Only needed if <code>ingredients</code> is NULL |
| <code>discreteSurv</code> | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| <code>prior</code> | should a dependent or a flat prior be used on the model space? Only needed if <code>method = `GEB`</code> . |
| <code>package</code> | Which package should be used to fit the models; by default the <code>nnet</code> package is used; we could also specify to use the package <code>'VGAM'</code> |
| <code>maxit</code> | Only needs to be specified with package <code>nnet</code> : maximal number of iterations |

Value

A list with the TBF and the g (if it is fixed) for all the candidate models.

Author(s)

Rachel Heyard

| | |
|-----------------|---|
| TBF_ingredients | <i>Ingredients to calculate the TBF</i> |
|-----------------|---|

Description

This function calculates the ingredients needed to compute the TBFs: like the deviances with their degrees of freedom of the relevant candidate models.

Usage

```
TBF_ingredients(fullModel = NULL, data, discreteSurv = FALSE,  
  numberCores = 1, candidateModels = NULL, package = "nnet",  
  maxit = 150)
```

Arguments

| | |
|-----------------|---|
| fullModel | formula of the model including all potential variables |
| data | the data frame with all the information |
| discreteSurv | Boolean variable telling us whether a 'simple' multinomial regression is looked for or if the goal is a discrete survival-time model for multiple modes of failure is needed. |
| numberCores | How many cores should be used in parallel? |
| candidateModels | Instead of defining the full model we can also specify the candidate models whose deviance statistic and d.o.f should be computed |
| package | Which package should be used to fit the models; by default the nnet package is used; we could also specify to use the package 'VGAM' |
| maxit | Only needs to be specified with package nnet: maximal number of iterations |

Value

an object of class `TBF.ingredients`

Author(s)

Rachel Heyard

VAP_data

Data on VAP acquisition in one ICU

Description

It is a tiny subset of the OUTCOMEREA database whose only perhaps will be to test and illustrate the functions of this package.

Usage

```
data(VAP_data)
```

Format

A data frame with 1640 rows and 7 variables on 90 distinct patients:

ID distinct ID for each patient

day day of ventilation, day = 1 is the first day of ventilation

type is it a medical or a surgical patient

gender gender of the patient, 1 = male, 0 = female

SAPSadmission the SAPS 2 score at admission to the ICU

SOFA the daily SOFA score

outcome final outcome after the first observation period

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