Package ‘openVA’

February 3, 2021

Type Package
Title Automated Method for Verbal Autopsy
Version 1.0.12
Date 2021-02-02
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Depends R (>= 3.1)
Imports InterVA5 (>= 1.0.1), InSilicoVA (>= 1.1.3), InterVA4 (>= 1.7.3), Tariff (>= 1.0.1), ggplot2, crayon, cli, methods
Suggests nbc4va, testthat
License GPL-2
URL https://github.com/verbal-autopsy-software/openVA
BugReports https://github.com/verbal-autopsy-software/openVA/issues
RoxygenNote 7.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2021-02-03 16:40:08 UTC
codeVA

Running automated method on VA data

Description

Running automated method on VA data

Usage

codeVA(
  data,
  data.type = c("WHO2012", "WHO2016", "PHMRC", "customize")[1],
  data.train = NULL,
  causes.train = NULL,
  causes.table = NULL,
  model = c("InSilicoVA", "InterVA", "Tariff", "NBC")[1],
  Nchain = 1,
  Nsim = 10000,
  version = c("4.02", "4.03", "5")[2],
  HIV = "h",
  Malaria = "h",
  phmrc.type = c("adult", "child", "neonate")[1],
  convert.type = c("quantile", "fixed", "empirical")[1],
  ...
)
Arguments

data: Input VA data, see data.type below for more information about the format.
data.type: There are four data input types currently supported by codeVA function as below.
  • WHO2012: InterVA-4 input format using WHO 2012 questionnaire. For example see data(RandomVA1). The first column should be death ID.
  • WHO2016: InterVA-5 input format using WHO 2016 questionnaire. For example see data(RandomVA5). The first column should be death ID.
  • PHMRC: PHMRC data format. For example see ConvertData.phmrc
  • customized: Any dichotomized dataset with “Y” denote “presence”, “” denote “absence”, and “.” denote “missing”. The first column should be death ID.
data.train: Training data with the same columns as data, except for an additional column specifying cause-of-death label. It is not used if data.type is “WHO” and model is “InterVA” or “InSilicoVA”. The first column also has to be death ID for “WHO” and “customized” types.
causes.train: the column name of the cause-of-death assignment label in training data.
causes.table: list of causes to consider in the training data. Default to be NULL, which uses all the causes present in the training data.
model: Currently supports four models: “InSilicoVA”, “InterVA”, “Tariff”, and “NBC”.
Nchain: Parameter specific to “InSilicoVA” model. Currently not used.
Nsim: Parameter specific to “InSilicoVA” model. Number of iterations to run the sampler.
version: Parameter specific to “InterVA” model. Currently supports “4.02”, “4.03”, and “5”. For InterVA-4, “4.03” is strongly recommended as it fixes several major bugs in “4.02” version. “4.02” is only included for backward compatibility. “5” version implements the InterVA-5 model, which requires different data input format.
HIV: Parameter specific to “InterVA” model. HIV prevalence level, can take values “h” (high), “l” (low), and “v” (very low).
Malaria: HIV Parameter specific to “InterVA” model. Malaria prevalence level, can take values “h” (high), “l” (low), and “v” (very low).
phmrc.type: Which PHMRC data format is used. Currently supports only “adult” and “child”, “neonate” will be supported in the next release.
convert.type: type of data conversion when calculating conditional probability (probability of each symptom given each cause of death for InterVA and InSilicoVA models. Both “quantile” and “fixed” usually give similar results empirically.
  • quantile: the rankings of the P(S|C) are obtained by matching the same quantile distributions in the default InterVA P(S|C)
  • fixed: P(S|C) are matched to the closest values in the default InterVA P(S|C) table.
  • empirical: no ranking is calculated, but use the empirical conditional probabilities directly, which will force updateCondProb to be FALSE for InSilicoVA algorithm.
other arguments passed to \texttt{insilico}, \texttt{InterVA}, \texttt{interVA.train}, \texttt{tariff}, and \texttt{nbc} function in the nbc4va package. See respective package documents for details.

\textbf{Value}

a fitted object

\textbf{References}


http://www.interva.net/


\textbf{See Also}

\texttt{insilico}, \texttt{InterVA}, \texttt{interVA.train}, \texttt{tariff}, and \texttt{nbc} function in the nbc4va package.

\textbf{Examples}

```r
data(RandomVA3)
test <- RandomVA3[1:200, ]
train <- RandomVA3[201:400, ]
fit1 <- codeVA(data = test, data.type = "customize", model = "InSilicoVA",
data.train = train, causes.train = "cause",
Nsim=1000, auto.length = FALSE)

fit2 <- codeVA(data = test, data.type = "customize", model = "InterVA",
data.train = train, causes.train = "cause", write=FALSE,
version = "4.02", HIV = "h", Malaria = "l")

fit3 <- codeVA(data = test, data.type = "customize", model = "Tariff",
data.train = train, causes.train = "cause",
nboot.sig = 100)
```
Convert Data

Converting Input data with different coding scheme to standard format

Usage

ConvertData(
  input,
  yesLabel = NULL,
  noLabel = NULL,
  missLabel = NULL,
  data.type = c("WHO2012", "WHO2016")[1]
)

Arguments

  input     matrix input, the first column is ID, the rest of the columns each represent one symptom
  yesLabel  The value(s) coding "Yes" in the input matrix.
  noLabel   The value(s) coding "No" in the input matrix.
  missLabel The value(s) coding "Missing" in the input matrix.
  data.type The coding scheme of the output. This can be either "WHO2012" or "WHO2016".

Value

  a data frame coded as follows. For WHO2012 scheme: "Y" for yes, "" for No, and "." for missing.
  For WHO2016 scheme: "y" for yes, "n" for No, and "-" for missing.

Examples

  # make up a fake 2 by 3 dataset with 2 deaths and 3 symptoms
  id <- c("d1", "d2")
  x <- matrix(c("Yes", "No", "Don't know",
                "Yes", "Refused to answer", "No"),
              byrow = TRUE, nrow = 2, ncol = 3)
  x <- cbind(id, x)
  colnames(x) <- c("ID", "S1", "S2", "S3")
  # see possible raw data (or existing data created for other purpose)
  x
  new <- ConvertData(x, yesLabel = "Yes", noLabel = "No",
                     missLabel = c("Don't know", "Refused to answer"))
  new
ConvertData.phmrc

Convert standard PHMRC data into binary indicator format

Description
The PHMRC data and the description of the format could be found at https://ghdx.healthdata.org/record/ihme-data/population-health-metrics-research-consortium-gold-standard-verbal-autopsy-data-2005-2011. This function converts the symptoms into binary indicators of three levels: Yes, No, and Missing. The health care experience (HCE) and free-text columns, i.e., columns named "word_****", are not considered in the current version of data conversion.

Usage
ConvertData.phmrc(
  input,
  input.test = NULL,
  cause = NULL,
  phmrc.type = c("adult", "child", "neonate")[1],
  cutoff = c("default", "adapt")[1],
  ...
)

Arguments
input standard PHMRC data format
input.test standard PHMRC data format to be transformed in the same way as input
cause the column name for the cause-of-death variable to use. For example, "va34", "va46", or "va55". It is used if adaptive cut-offs are to be calculated for continuous variables. See below for details.
phmrc.type which data input format it is. The three data formats currently available are "adult", "child", and "neonate".
cutoff This determines how the cut-off values are to be set for continuous variables. "default" sets the cut-off values proposed in the original paper published with the dataset. "adapt" sets the cut-off values using the rules described in the original paper, which calculates the cut-off as being two median absolute deviations above the median of the mean durations across causes. However, we are not able to replicate the default cut-offs following this rule. So we suggest users to use this feature with caution.
...
not used

Value
converted dataset with only ID and binary symptoms. Notice that when applying this function to the raw PHMRC data, the returned ID variable corresponds to the row index of the raw PHMRC data (i.e., cleaned data with ID = 10 correspond to the 10th row of the raw dataset), and does not correspond to the "newid" column in the PHMRC data.
getCSMF

Obtain CSMF from fitted model

Description

Obtain CSMF from fitted model

Usage

getCSMF(x, CI = 0.95, interVA.rule = TRUE)
Arguments

x  a fitted object from codeVA.
CI  For insilico object only, specifying the credible interval to return. Default value to be 0.95.
interVA.rule  Logical indicator for interVA object only. If TRUE, it means only up to top 3 causes for each death are used to calculate CSMF and the rest are categorized as "undetermined"

Value

a vector or matrix of CSMF for all causes.

Examples

```r
## Not run:
library(InSilicoVA)
data(RandomVA1)
# for illustration, only use interVA on 100 deaths
fit <- codeVA(RandomVA1[1:100, ], data.type = "WHO2012", model = "InterVA",
              version = "4.03", HIV = "h", Malaria = "l", write=FALSE)
getCSMF(fit)
library(InterVA5)
data(RandomVA5)
fit <- codeVA(RandomVA5[1:100, ], data.type = "WHO2016", model = "InterVA",
              version = "5", HIV = "h", Malaria = "l", write=FALSE)
getCSMF(fit)
## End(Not run)
```

---

**getCSMF_accuracy**  
*Calculate CSMF accuracy*

---

**Description**

Calculate CSMF accuracy

**Usage**

```r
getCSMF_accuracy(csmf, truth, undet = NULL)
```

**Arguments**

- **csmf**  a CSMF vector from getCSMF or a InSilicoVA fitted object.
- **truth**  a CSMF vector of the true CSMF.
- **undet**  name of the category denoting undetermined causes. Default to be NULL.
Value

a number (or vector if input is InSilicoVA fitted object) of CSMF accuracy as 1 - \( \frac{\text{sum}(\text{abs}(	ext{CSMF} - \text{CSMF} \_\text{true}))}{2 \times (1 - \text{min}(	ext{CSMF} \_\text{true}))} \).

Examples

csmf1 <- c(0.2, 0.3, 0.5)
csmf0 <- c(0.3, 0.3, 0.4)
acc <- getCSMF_accuracy(csmf1, csmf0)

getIndivProb

Extract individual distribution of cause of death

Description

Extract individual distribution of cause of death

Usage

getIndivProb(x, CI = NULL, ...)

Arguments

x a fitted object from codeVA.
CI Credible interval for posterior estimates. If CI is set to TRUE, a list is returned instead of a data frame.
... additional arguments that can be passed to get.indiv from InSilicoVA package.

Value

a data frame of COD distribution for each individual specified by row names.

Examples

data(RandomVA1)
# for illustration, only use interVA on 100 deaths
fit <- codeVA(RandomVA1[1:100, ], data.type = "WHO", model = "InterVA",
version = "4.02", HIV = "h", Malaria = "l", write=FALSE)
probs <- getIndivProb(fit)
getPHMRC_url

Get the URL to the PHMRC dataset

Description
Get the URL to the PHMRC dataset

Usage
getPHMRC_url(type)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>adult, child, or neonate</td>
</tr>
</tbody>
</table>

Value
URL of the corresponding dataset

Examples

```r
link <- getPHMRC_url("adult")
summary(link)$description
```

getTopCOD

Extract the most likely cause of death

Description
Extract the most likely cause of death

Usage
getTopCOD(x, interVA.rule = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>a fitted object from codeVA.</td>
</tr>
<tr>
<td>interVA.rule</td>
<td>Logical indicator for interVA object only. If TRUE, only the InterVA reported first cause is extracted.</td>
</tr>
</tbody>
</table>

Value
a data frame of ID and most likely cause assignment.
Examples

data(RandomVA1)
# for illustration, only use interVA on 100 deaths
fit <- codeVA(RandomVA1[1:100, ], data.type = "WHO", model = "InterVA",
version = "4.02", HIV = "h", Malaria = "l", write=FALSE)
getTopCOD(fit)

interVA.train

Extended InterVA method for non-standard input

Description

Extended InterVA method for non-standard input

Usage

interVA.train(
data,
train,
causes.train,
causes.table = NULL,
thre = 0.95,
type = c("quantile", "fixed", "empirical")[1],
prior = c("uniform", "train")[1],
...)

Arguments

data A matrix input, or data read from csv files. Sample input is included as data(RandomVA3).

train A matrix input, or data read from csv files in the same format as data, but with an additional column specifying cause-of-death. Sample input is included as data(RandomVA3).

causes.train the column name of the cause-of-death assignment label in training data.

causes.table list of causes to consider in the training data. Default to be NULL, which uses all the causes present in the training data.

thre numerical number between 0 and 1. Symptoms with missing rate higher than thre in the training data will be dropped from both training and testing data.

type type of data conversion when calculating conditional probability (probability of each symptom given each cause of death) for InterVA and InSilicoVA models. Both “quantile” and “fixed” usually give similar results empirically.

- quantile: the rankings of the P(S/C) are obtained by matching the same quantile distributions in the default InterVA P(S/C)
The prior distribution of CSMF. “uniform” uses no prior information, i.e., 1/C for all C causes and “train” uses the CSMF in the training data as prior distribution of CSMF.

Value

fitted interVA object

References


Examples

data(RandomVA3)
test <- RandomVA3[1:200,]
train <- RandomVA3[201:400,]
out <- interVA.train(data = test, train = train, causes.train = "cause",
                    prior = "train", type = "quantile")
openVA_update

Examples

## Not run:
openVA_status()

## End(Not run)

---

openVA_update  Update openVA packages

Description

This will check to see if all openVA packages (and optionally, their dependencies) are up-to-date, and will install after an interactive confirmation.

Usage

openVA_update()

Examples

## Not run:
openVA_update()

## End(Not run)

---

plotVA  Plot top CSMF for a fitted model

Description

Plot top CSMF for a fitted model

Usage

plotVA(object, top = 10, title = NULL, ...)

Arguments

- object: a fitted object using codeVA
- top: number of top causes to plot
- title: title of the plot
- ...: additional arguments passed to plot.insilico, plot.tariff, CSMF, or plot.nbc function in the nbc4va package.
See Also

plot.insilico, plot.tariff, CSMF

Examples

data(RandomVA3)
test <- RandomVA3[1:200, ]
train <- RandomVA3[201:400, ]
fit1 <- codeVA(data = test, data.type = "customize", model = "InSilicoVA",
data.train = train, causes.train = "cause",
Nsim=1000, auto.length = FALSE)

fit2 <- codeVA(data = test, data.type = "customize", model = "InterVA",
data.train = train, causes.train = "cause",
version = "4.02", HIV = "h", Malaria = "l")

fit3 <- codeVA(data = test, data.type = "customize", model = "Tariff",
data.train = train, causes.train = "cause",
nboot.sig = 100)

plotVA(fit1)
plotVA(fit2)
plotVA(fit3)

stackplotVA

plot grouped CSMF from a "insilico" object

Description

Produce bar plot of the CSMFs for a fitted "insilico" object in broader groups.

Usage

stackplotVA(
x,
  grouping = NULL,
type = c("stack", "dodge")[1],
group_order = NULL,
err = TRUE,
CI = 0.95,
sample_size_print = FALSE,
xlab = "",
ylab = "CSMF",
ylim = NULL,
title = "CSMF by broader cause categories",
horiz = FALSE,
angle = 0,
err_width = 0.4,
err_size = 0.6,
border = "black",
bw = FALSE,
filter_legend = FALSE,
...)

Arguments

x one or a list of fitted object from codeVA function
grouping C by 2 matrix of grouping rule. If set to NULL, make it default.
type type of the plot to make
group_order list of grouped categories. If set to NULL, make it default.
err indicator of inclusion of error bars
CI Level of posterior credible intervals.
sample_size_print Logical indicator for printing also the sample size for each sub-population labels.
xlab Labels for the causes.
ylab Labels for the CSMF values.
ylim Range of y-axis.
title Title of the plot.
horiz Logical indicator indicating if the bars are plotted horizontally.
angle Angle of rotation for the texts on x axis when horiz is set to FALSE
err_width Size of the error bars.
err_size Thickness of the error bar lines.
border The color for the border of the bars.
bw Logical indicator for setting the theme of the plots to be black and white.
filter_legend Logical indicator for including all broad causes in the plot legend (default; FALSE) or filtering to only the broad causes in the data being plotted
...

Author(s)

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Examples

data(RandomVA3)
test <- RandomVA3[1:200, ]
train <- RandomVA3[201:400, ]
fit1 <- codeVA(data = test, data.type = "customize", model = "InSilicoVA",
data.train = train, causes.train = "cause",
Nsim=1000, auto.length = FALSE)

fit2 <- codeVA(data = test, data.type = "customize", model = "InterVA",
data.train = train, causes.train = "cause", write=FALSE,
version = "4.02", HIV = "h", Malaria = "l")

fit3 <- codeVA(data = test, data.type = "customize", model = "Tariff",
data.train = train, causes.train = "cause",
nboot.sig = 100)

data(SampleCategory)
stackplotVA(fit1, grouping = SampleCategory, type = "dodge",
ylim = c(0, 1), title = "InSilicoVA")
stackplotVA(fit2, grouping = SampleCategory, type = "dodge",
ylim = c(0, 1), title = "InterVA4.02")
stackplotVA(fit3, grouping = SampleCategory, type = "dodge",
ylim = c(0, 1), title = "Tariff")
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