Package ‘nbc4va’

May 9, 2026

Type Package

Title Bayes Classifier for Verbal Autopsy Data

Version 1.2

Date 2022-04-25

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Description An implementation of the Naive Bayes Classifier (NBC) algorithm used for Verbal Autopsy (VA) built on code from Miasnikof et al (2015) <DOI:10.1186/s12916-015-0521-2>.

Depends R (>= 4.0.0)

Imports graphics, methods, utils, shiny

Suggests bookdown, knitr, rmarkdown, testthat

Enhances openVA

License GPL-3

LazyData TRUE

RoxygenNote 7.1.2

Collate 'nbc4va.R' 'nbc4va_data.R' 'nbc4va_validation.R' 'nbc4va_internal.R' 'nbc4va_main.R' 'nbc4va_extra.R' 'nbc4va_utility.R' 'nbc4va_wrapper.R'

VignetteBuilder knitr

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-05-10 10:40:02 UTC

Contents

`csmf.nbc` *Calculate predicted CSMFs from a NBC model*

Description

Obtains the predicted Cause Specific Mortality Fraction (CSMF) from a result `nbc` object.

Usage

```
csmf.nbc(object)
```

Arguments

`object`	The result `nbc` object.

Value

out A numeric vector of the predicted CSMFs in which the names are the corresponding causes.

See Also

Other wrapper functions: `topCOD.nbc()`

Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]
results <- nbc(train, test)
```

```
# Obtain the predicted CSMFs
predCSMF <- csmf.nbc(results)
```

`nbc` *Train a NBC model*

Description

Performs supervised Naive Bayes Classification on verbal autopsy data.

Usage

```
nbc(train, test, known = TRUE)
```

Arguments

`train` Dataframe of verbal autopsy train data (See Data documentation).

- Columns (in order): ID, Cause, Symptom-1 to Symptom-n..
- ID (vectorof char): unique case identifiers
- Cause (vectorof char): observed causes for each case
- Symptom-n.. (vectorsof (1 OR 0)): 1 for presence, 0 for absence, other values are treated as unknown
- Unknown symptoms are imputed randomly from distributions of 1s and 0s per symptom column; if no 1s or 0s exist then the column is removed

Example:

ID	Cause	S1	S2	S3
"a1"	"HIV"	1	0	0
"b2"	"Stroke"	0	0	1
"c3"	"HIV"	1	1	0

`test` Dataframe of verbal autopsy test data in the same format as *train* except if causes are not known:

- The 2nd column (Cause) can be omitted if *known* is FALSE

`known` TRUE to indicate that the *test* causes are available in the 2nd column and FALSE to indicate that they are not known

Value

out The result nbc list object containing:

- $prob.causes (vectorof double): the probabilities for each test case prediction by case id
- $pred.causes (vectorof char): the predictions for each *test* case by case id
- Additional values:

- * indicates that the value is only available if *test* causes are known
- $train (dataframe): the input *train* data
- $train.ids (vectorof char): the ids of the *train* data
- $train.causes (vectorof char): the causes of the *train* data by case id
- $train.samples (double): the number of input *train* samples
- $test (dataframe): the input *test* data
- $test.ids (vectorof char): the ids of the *test* data
- $test.causes* (vectorof char): the causes of the *test* data by case id
- $test.samples (double): the number of input *test* samples
- $test.known (logical): whether the *test* causes are known
- $symptoms (vectorof char): all unique symptoms in order
- $causes (vectorof char): all possible unique causes of death
- $causes.train (vectorof char): all unique causes of death in the *train* data
- $causes.test* (vectorof char): all unique causes of death in the *test* data
- $causes.pred (vectorof char): all unique causes of death in the predicted cases
- $causes.obs* (vectorof char): all unique causes of death in the observed cases
- $pred (dataframe): a table of predictions for each *test* case, sorted by probability
  - Columns (in order): CaseID, TrueCause, Prediction-1 to Prediction-n..
  - CaseID (vectorof char): case identifiers
  - TrueCause* (vectorof char): the observed causes of death
  - Prediction-n.. (vectorsof char): the predicted causes of death, where Prediction1 is the most probable cause, and Prediction-n is the least probable cause

  Example:

CaseID	Prediction1	Prediction2
"a1"	"HIV"	"Stroke"
"b2"	"Stroke"	"HIV"
"c3"	"HIV"	"Stroke"

- $obs* (dataframe): a table of observed causes matching *$pred* for each *test* case
  - Columns (in order): CaseID, TrueCause
  - CaseID (vectorof char): case identifiers
  - TrueCause (vectorof char): the actual cause of death if applicable

  Example:

CaseID	TrueCause
"a1"	"HIV"
"b2"	"Stroke"
"c3"	"HIV"

- $obs.causes* (vectorof char): all observed causes of death by case id
- $prob (dataframe): a table of probabilities of each cause for each test case
  - Columns (in order): CaseID, Cause-1 to Cause-n..
  - CaseID (vectorof char): case identifiers

- Cause-n.. (vectorsof double): probabilies for each cause of death

Example:

CaseID	HIV	Stroke
"a1"	0.5	0.5
"b2"	0.3	0.7
"c3"	0.9	0.1

References

- Miasnikof P, Giannakeas V, Gomes M, Aleksandrowicz L, Shestopaloff AY, Alam D, Tollman S, Samarikhalaj, Jha P. Naive Bayes classifiers for verbal autopsies: comparison to physician-based classification for 21,000 child and adult deaths. BMC Medicine. 2015;13:286. doi:10.1186/s12916-015-0521-2.

See Also

Other main functions: `plot.nbc`(), `print.nbc_summary`(), `summary.nbc`()

Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
# Set "known" to indicate whether or not "test" causes are known
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]
results <- nbc(train, test, known=TRUE)

# Obtain the probabilities and predictions
prob <- results$prob.causes
pred <- results$pred.causes
```

`nbc4va` *nbc4va: Bayes Classifier for Verbal Autopsy Data*

Description

An implementation of the Naive Bayes Classifier (NBC) algorithm used for Verbal Autopsy (VA) built on code from Miasnikof et al (2015) <DOI:10.1186/s12916-015-0521-2>.

For documentation and help, please see:

`https://rrwen.github.io/nbc4va/`

Acknowledgements

This package was developed at the Centre for Global Health Research (CGHR) in Toronto, Ontario, Canada. The original NBC algorithm code was developed by Pierre Miaskinof and Vasily Giannakeas. The original performance metrics code was provided by Dr. Mireille Gomes whom also offered guidance in metrics implementation and user testing. Special thanks to Richard Zehang Li for providing a standard structure for the package and Patrycja Kolpak for user testing of the GUI.

Author(s)

Richard Wen <`<rrwen.dev@gmail.com>`>

References

Use `citation("nbc4va")` to view citation information for the nbc4va package.

- Miasnikof P, Giannakeas V, Gomes M, Aleksandrowicz L, Shestopaloff AY, Alam D, Tollman S, Samarikhalaj, Jha P. Naive Bayes classifiers for verbal autopsies: comparison to physician-based classification for 21,000 child and adult deaths. BMC Medicine. 2015;13:286. doi:10.1186/s12916-015-0521-2.

Examples

```
## Not run:
library(nbc4va)

# Quick start
# Follow the instructions in the web interface
nbc4vaGUI()

# View user guides for the nbc4va package
browseVignettes("nbc4va")

## End(Not run)
```

`nbc4vaData` *Example of clean data in nbc4va*

Description

A random generation of clean verbal autopsy synthetic data for use in demonstrating the nbc4va package.

Usage

```
nbc4vaData
```

Format

A dataframe with 100 rows and 102 columns:

- id (vectorof char): the case identifiers
- cause (vectorof char): the cause of death for each case
- symptom1..100 (vectorsof (1 OR 0)): whether the symptom is recorded as present (1) or not (0) for each case (row)
- Example:

id	cause	symptom1	symptom2	symptom3
"a27"	"cause10"	1	0	0
"k37"	"cause2"	0	0	1
"e57"	"cause8"	1	0	0

Source

Random generation using the `sample` function with `set.seed` set to 1.

Examples

```
library(nbc4va)
data(nbc4vaData)
```

`nbc4vaDataRaw` *Example of unclean data in nbc4va*

Description

A random generation of unclean verbal autopsy synthetic data for use in demonstrating the nbc4va package.

Usage

```
nbc4vaDataRaw
```

Format

A dataframe with 100 rows and 102 columns:

- id (vectorof char): the case identifiers
- cause (vectorof char): the cause of death for each case
- symptom1..100 (vectorsof (1 OR 0 OR 99)): whether the symptom is recorded as present (1), absent (0), or unknown (99) for each case (row)
- Example:

id	cause	symptom1	symptom2	symptom3
"a27"	"cause10"	99	0	1
"k37"	"cause2"	0	99	1
"e57"	"cause8"	1	0	99

Details

Warning: This data may produce errors depending on how you use it in the package.

Source

Random generation using the `sample` function with `set.seed` set to 1.

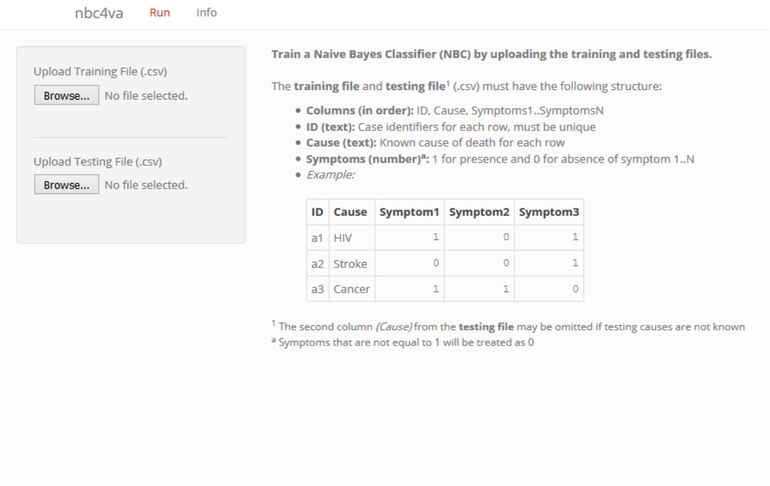
Examples

```
library(nbc4va)
data(nbc4vaDataRaw)
```

`nbc4vaGUI` *Web-based graphical user interface in nbc4va*

Description

A Graphical User Interface (GUI) for the nbc4va package using shiny.



Train a Naive Bayes Classifier (NBC) by uploading the training and testing files.

The **training file** and **testing file**[1] (.csv) must have the following structure:

- **Columns (in order):** ID, Cause, Symptoms1..SymptomsN
- **ID (text):** Case identifiers for each row, must be unique
- **Cause (text):** Known cause of death for each row
- **Symptoms (number)[a]:** 1 for presence and 0 for absence of symptom 1..N
- *Example:*

ID	Cause	Symptom1	Symptom2	Symptom3
a1	HIV	1	0	1
a2	Stroke	0	0	1
a3	Cancer	1	1	0

[1] The second column *(Cause)* from the **testing file** may be omitted if testing causes are not known
[a] Symptoms that are not equal to 1 will be treated as 0

Usage

```
nbc4vaGUI()
```

Details

This function requires the shiny package, which can be installed via:

`install.packages("shiny")`

Use *esc* in the R console to stop the GUI.

Please use a modern browser (e.g. latest firefox, chrome) for the best experience.

Value

Creates a GUI for running nbc4va in a web browser.

See Also

Other utility functions: `nbc4vaIO()`

Examples

```
## Not run:
library(nbc4va)
nbc4vaGUI()

## End(Not run)
```

`nbc4vaIO` *Run nbc4va using file input and output*

Description

Runs `nbc` and uses `summary.nbc` on input data files or dataframes to output result files or dataframes with data on predictions, probabilities, causes, and performance metrics in an easily accessible way.

Usage

```
nbc4vaIO(
  trainFile,
  testFile,
  known = TRUE,
  csmfaFile = NULL,
  saveFiles = TRUE,
  outDir = dirname(testFile),
  fileHeader = strsplit(basename(testFile), "\\.")[[1]][[1]],
  fileReader = read.csv,
  fileReaderIn = "file",
  fileReaderArgs = list(as.is = TRUE),
```

```
    fileWriter = write.csv,
    fileWriterIn = "x",
    fileWriterOut = "file",
    fileWriterArgs = list(row.names = FALSE),
    outExt = "csv"
  )
```

Arguments

`trainFile`	A character value of the path to the data to be used as the *train* argument for `nbc` or a dataframe of the *train* argument.
`testFile`	A character value of the path to the data to be used as the *test* argument for `nbc` or a dataframe of the *test* argument.
`known`	TRUE to indicate that the *test* causes are available in the 2nd column and FALSE to indicate that they are not known
`csmfaFile`	A character value of the path to the data to be used as the *csmfa.obs* argument for `summary.nbc` or a named vector of the *csmfa.obs* argument. • If (csmfaFile is char): the file must have only 1 column of the causes per case
`saveFiles`	Set to TRUE to save the return object as files or FALSE to return the actual object
`outDir`	A character value of the path to the directory to store the output results files.
`fileHeader`	A character value of the file header name to use for the output results files. • The default is to use the name of the *testFile*
`fileReader`	A function that is able to read the *trainFile* and the *testFile*. • The default is set to read csv files using `read.csv`
`fileReaderIn`	A character value of the *fileReader* argument name that accepts a file path for reading as an input.
`fileReaderArgs`	A list of the *fileReader* arguments to be called with `do.call`.
`fileWriter`	A function that is able to write `data.frame` objects to a file location. • The default is set to write csv files using `write.csv`
`fileWriterIn`	A character value of the *fileWriter* argument name that accepts a dataframe for writing.
`fileWriterOut`	A character value of the *fileWriter* argument name that accepts a file path for writing as an output.
`fileWriterArgs`	A list of arguments of the *fileWriter* arguments to be called with `do.call`.
`outExt`	A character value of the extension (without the period) to use for the result files. • The default is set to use the "csv" extension • The default is the directory of the *testFile*

Details

See Methods documentation for details on the methodology and implementation of the Naive Bayes Classifier algorithm. This function may also act as a wrapper for the main nbc4va package functions.

Value

out Vector or list of respective paths or data from the naive bayes classifier:

- If (*saveFiles* is TRUE) return a named character vector of the following:
  - Names: dir, pred, prob, causes, summary
  - dir (char): the path to the directory of the output files
  - pred (char): the path to the prediction table file, where the columns of Pred1..PredN are ordered by the prediction probability with Pred1 being the most probable cause
  - prob (char): the path to the probability table file, where the columns excluding the CaseID are the cause and each cell has a probability value
  - causes (char): the path to the cause performance metrics table file, where each column is a metric and each row is a cause
  - metrics (char): the path to the overall performance metrics table file, where each column is a metric
- If (*saveFiles* is FALSE) return a list of the following:
  - Names: pred, prob, causes, summary
  - pred (dataframe): the prediction table, where the columns of Pred1..PredN are ordered by the prediction probability with Pred1 being the most probable cause
  - prob (dataframe): the probability table, where the columns excluding the CaseID are the cause and each cell has a probability value
  - causes (dataframe): the cause performance metrics table, where each column is a metric and each row is a cause
  - metrics (dataframe): the summary table, where each column is a performance metric
  - nbc (object): the returned `nbc` object
  - nbc_summary (object): the returned `summary.nbc` object

See Also

Other utility functions: `nbc4vaGUI()`

Examples

```
library(nbc4va)
data(nbc4vaData)

# Split data into train and test sets
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]

# Save train and test data as csv in temp location
trainFile <- tempfile(fileext=".csv")
testFile <- tempfile(fileext=".csv")
write.csv(train, trainFile, row.names=FALSE)
write.csv(test, testFile, row.names=FALSE)

# Use nbc4vaIO via file input and output
# Set "known" to indicate whether test causes are known
```

```
outFiles <- nbc4vaIO(trainFile, testFile, known=TRUE)

# Use nbc4vaIO as a wrapper
out <- nbc4vaIO(train, test, known=TRUE, saveFiles=FALSE)
```

`ova2nbc` *Translate open verbal autopsy arguments to train a NBC model*

Description

A wrapper function for creating an nbc object with the parameters specified by the **openVA** package.

Usage

```
ova2nbc(symps.train, symps.test, causes.train, causes.table = NULL, ...)
```

Arguments

`symps.train` Dataframe of verbal autopsy train data.

- Columns (in order): ID, Cause, Symptom-1 to Symptom-n..
- ID (vectorof char): case identifiers
- Cause (vectorof char): observed causes for each case
- Symptom-n.. (vectorsof char): "Y" for presence, "" for absence, "." for missing

Example:

ID	Cause	S1	S2	S3
"a1"	"HIV"	"Y"	""	"."
"b2"	"Stroke"	"."	""	"Y"
"c3"	"HIV"	"Y"	"Y"	"."

`symps.test` Dataframe of verbal autopsy test data in the same format as *symps.train*.

- If (*causes.train* is (vectorof char)): *symps.test* is assumed to not have a cause column

`causes.train` The train vector or column for the causes of death to use.

- If (vectorof char): cause of death values with number of values equal to nrow(*symps.train*); it is assumed that *symps.test* has no causes of death column
- If (char): name of cause of death column from *symps.train*

`causes.table` Character list of unique causes to learn.

- If (NULL): set to unique causes of death in *symps.train*

`...` Additional arguments to be passed to avoid errors if necessary.

Value

nbc An `nbc` object with the following modifications:

- $id (vectorof char): set to test data ids
- $prob (matrixof numeric): set to a matrix of likelihood for each cause of death for the test cases
- $CSMF (vectorof char): set to the predicted CSMFs with names for the corresponding causes

References

- Li Z, McCormick T, Clark S. openVA: Automated Method for Verbal Autopsy [Internet]. 2016. [cited 2016 Apr 29]. Available from: `https://cran.r-project.org/package=openVA`

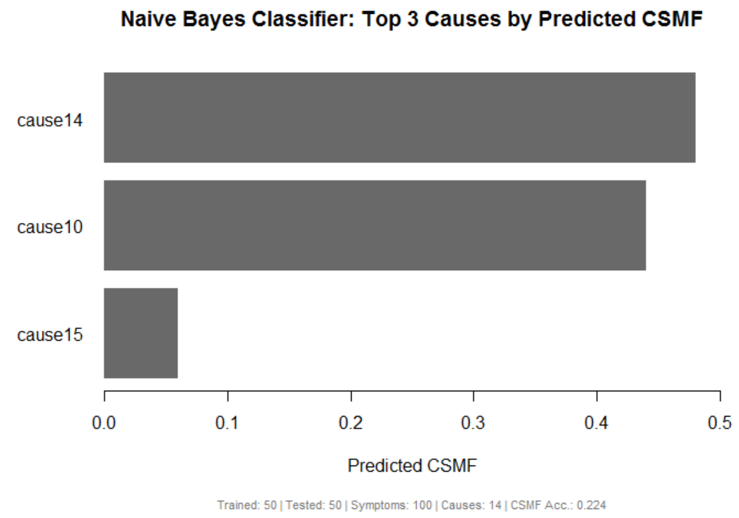
Examples

```
## Not run:
library(openVA)  # install.packages("openVA")
library(nbc4va)

# Obtain some openVA formatted data
data(RandomVA3) # cols: deathId, cause, symptoms..
train <- RandomVA3[1:100, ]
test <- RandomVA3[101:200, ]

# Run naive bayes classifier on openVA data
results <- ova2nbc(train, test, "cause")

# Obtain the probabilities and predictions
prob <- results$prob.causes
pred <- results$pred.causes

## End(Not run)
```

`plot.nbc` *Bar plot of top predicted causes from a NBC model*

Description

Plots the results from a `nbc` object as a `barplot` for a number of causes based on predicted Cause Specific Mortality Fraction (CSMF).



Usage

```
## S3 method for class 'nbc'
plot(
  x,
  top.plot = length(x$causes.pred),
  min.csmf = 0,
  csmfa.obs = NULL,
  footnote = TRUE,
  footnote.color = "gray48",
  footnote.size = 0.7,
 main = paste("Naive Bayes Classifier: Top ", top.plot, " Causes by Predicted CSMF",
    sep = ""),
  xlab = "Predicted CSMF",
  col = "dimgray",
  horiz = TRUE,
  border = NA,
  las = 1,
  ...
)
```

Arguments

`x`	A nbc object.
`top.plot`	A number that produces top k causes depending on a Cause Specific Mortality Fraction (CSMF) measure.
`min.csmf`	A number that represents the minimum CSMF measure for a cause to be included in the plot.
`csmfa.obs`	A character vector of the true causes for calculating the CSMF accuracy.

`footnote`	A boolean indicating whether to include a footnote containing details about the nbc or not.
`footnote.color`	A character specifying the color of the footnote text.
`footnote.size`	A numeric value specifying the size of the footnote text.
`main`	A character value of the title to display.
`xlab`	A character value of the x axis title.
`col`	A character value of the color to use for the plot.
`horiz`	Set to TRUE to draw bars horizontally and FALSE to draw bars vertically.
`border`	A character value of the colors to use for the bar borders. Set to NA to disable.
`las`	An integer value to determine if labels should be parallel or perpendicular to axis.
`...`	Additional arguments to be passed to `barplot`.

Details

See Methods documentation for details on CSMF and CSMF accuracy.

Value

Generates a bar plot the top predicted causes from the NBC model

See Also

`barplot`

Other main functions: `nbc()`, `print.nbc_summary()`, `summary.nbc()`

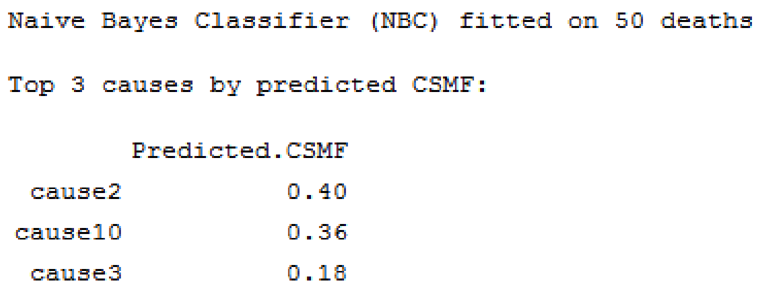
Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]
results <- nbc(train, test)

# Plot the top 3 causes by CSMF
plot(results, top.plot=3)
```

`print.nbc_summary` *Print top predicted causes from a NBC model*

Description

Prints a summary message from a `summary.nbc` object of the top causes by probability or predicted Cause Specific Mortality Fraction (CSMF).



```
Naive Bayes Classifier (NBC) fitted on 50 deaths

Top 3 causes by predicted CSMF:

          Predicted.CSMF
  cause2            0.40
 cause10            0.36
  cause3            0.18
```

Usage

```
## S3 method for class 'nbc_summary'
print(x, ...)
```

Arguments

`x`	A `summary.nbc` object.
`...`	Additional arguments to be passed if applicable.

Details

See Methods documentation for details on CSMF and probability from the Naive Bayes Classifier.

Value

Prints a summary of the top causes of death by probability for the NBC model.

See Also

Other main functions: `nbc()`, `plot.nbc()`, `summary.nbc()`

Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
train <- nbc4vaData[1:50, ]
```

```
test <- nbc4vaData[51:100, ]
results <- nbc(train, test)

# Print a summary of all the test data for the top 3 causes by predicted CSMF
brief <- summary(results, top=3)
print(brief)
```

`summary.nbc` *Summarize a NBC model with metrics*

Description

Summarizes the results from a `nbc` object. The summary can be either for a particular case or for the entirety of cases.

Usage

```
## S3 method for class 'nbc'
summary(object, top = 5, id = NULL, csmfa.obs = NULL, ...)
```

Arguments

`object`	The result `nbc` object.
`top`	A number that produces top causes depending on *id*: • If (*id* is char): provide the *top* causes of the case by probability • If (*id* is NULL): provide the *top* causes by predicted Cause Specific Mortality Fractions (CSMF)
`id`	A character representing a case id in the test data.
`csmfa.obs`	A character vector of the true causes for calculating the CSMF accuracy.
`...`	Additional arguments to be passed if applicable

Details

See Methods documentation for details on calculations and metrics.

Value

out A summary object built from a `nbc` object with modifications/additions:

- If (*id* is char):
  - Additions to a `nbc` object:
    - $id (char): the case *id* chosen by the user
    - $top (numeric): the input number of *top* causes for *id*
    - $top.prob (vectorof double): the *top* probabilities for *id*

  - The following are modified from a nbc object to be *id* specific:
    $test, $test.ids, $test.causes, $obs.causes, $prob, $prob.causes, $pred, $pred.causes
- If (*id* is NULL):
  - Additions to the `nbc` object:
    - * indicates that the item is only available if *test* causes are known
    - ** indicates that the item ignores * if *csmfa.obs* is given
    - $top.csmf.pred (vectorof double): the *top* predicted CSMFs by cause
    - $top.csmf.obs* (vectorof double): the *top* observed CSMFs by cause
    - $metrics.all** (vectorof double): a numeric vector of overall metrics.
      - Names: TruePositives, TrueNegatives, FalsePositives, FalseNegatives, Accuracy, Sensitivity, PCCC, CSMFMaxError, CSMFaccuracy
      - TruePositives* (double): total number of true positives
      - TrueNegatives* (double): total number of true negatives
      - FalsePositives* (double): total number of false positives
      - FalseNegatives* (double): total number of false negatives
      - Sensitivity* (double): the overall sensitivity
      - PCCC* (double): the partial chance corrected concordance
      - CSMFMaxError** (double): the maximum Cause Specific Mortality Fraction Error
      - CSMFaccuracy** (double): the Cause Specific Mortaliy Fraction accuracy
    - $metrics.causes (dataframe): a perfomance table of metrics by cause.
      - Columns: Cause, Sensitivity, CSMFpredicted, CSMFobserved
      - Cause (vectorof char): The unique causes from both the *obs* and *pred* inputs
      - Sensitivity* (vectorof double): the sensitivity for a cause
      - CSMFpredicted (vectorof double): the cause specific mortality fraction for a cause given the predicted deaths
      - CSMFobserved* (vectorof double): the cause specific mortality fraction for a cause given the observed deaths
      - TruePositives (vectorof double): The total number of true positives per cause
      - TrueNegatives (vectorof double): The total number of true negatives per cause
      - FalsePositives (vectorof double): The total number of false positives per cause
      - FalseNegatives (vectorof double): The total number of false negatives per cause
      - PredictedFrequency (vectorof double): The occurence of a cause in the *pred* input
      - ObservedFrequency (vectorof double): The occurence of a cause in the *obs* input
      - Example:

Cause	Sensitivity	Metric-n..
HIV	0.5	#..
Stroke	0.5	#..

See Also

Other main functions: `nbc`(), `plot.nbc`(), `print.nbc_summary`()

Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]
results <- nbc(train, test)

# Obtain a summary for the results
brief <- summary(results, top=2)  # top 2 causes by CSMF for all test data
briefID <- summary(results, id="v48")  # top 5 causes by probability for case "v48"
```

`topCOD.nbc` *Cause of death predictions from a NBC model*

Description

Obtains the top causes of deaths for each testing case from a result `nbc` object.

Usage

```
topCOD.nbc(object)
```

Arguments

`object`	The result `nbc` object.

Value

out A dataframe of the top CODs:

- Columns: ID, COD
- ID (vectorof char): The ids for each testing case
- COD (vectorof char): The top prediction for each testing case

See Also

Other wrapper functions: `csmf.nbc()`

Examples

```
library(nbc4va)
data(nbc4vaData)

# Run naive bayes classifier on random train and test data
train <- nbc4vaData[1:50, ]
test <- nbc4vaData[51:100, ]
results <- nbc(train, test)

# Obtain the top cause of death predictions for the test data
topPreds <- topCOD.nbc(results)
```

Index