Package 'InSilicoVA'

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Type Package

Title Probabilistic Verbal Autopsy Coding with 'InSilicoVA' Algorithm

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Depends R (>= 3.5.0), rJava, coda, ggplot2, InterVA5

Imports methods, grDevices

SystemRequirements Java (>= 7)

Description Computes individual causes of death and population cause-specific mortality fractions using the 'InSilicoVA' algorithm from McCormick et al. (2016) <DOI:10.1080/01621459.2016.1152191>. It uses data derived from verbal autopsy (VA) interviews, in a format similar to the input of the widely used 'InterVA' method. This package provides general model fitting and customization for 'InSilicoVA' algorithm and basic graphical visualization of the output.

License GPL-2

URL https://github.com/verbal-autopsy-software/InSilicoVA

BugReports https://github.com/verbal-autopsy-software/InSilicoVA/issues

RoxygenNote 7.3.2

Suggests testthat

NeedsCompilation no

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Contents

`causetext` *Translation list of COD codes*

Description

This is the translation of COD abbreviation codes into their corresponding full names.

Format

A data frame with the translation of COD codes to their names on 68 CODs (both the version of COD only and COD with group code).

Examples

```
data(causetext)
```

condprob *Conditional probability table used by InterVA-4*

Description

This is a conditional probability matrix used by InterVA-4.2. There are 60 causes and 245 symptoms. The orders of the rows and columns must not be changed.

Format

A data frame with 245 observations on 60 variables. Each observation is the conditional probability.

Examples

```
data(condprob)
```

condprobnum *Conditional probability values used by InterVA-4*

Description

This is a conditional probability matrix used by InterVA-4.2. There are 60 causes and 245 symptoms.

Format

A data frame with 245 observations on 60 variables. Each observation is the conditional probability.

Examples

```
data(condprobnum)
```

csmf.diag *Convergence test for fitted InSilico model*

Description

Produce convergence test for CSMFs from fitted "insilico" objects.

Usage

```
csmf.diag(
  csmf,
  conv.csmf = 0.02,
  test = c("gelman", "heidel")[2],
  verbose = TRUE,
  autoburnin = FALSE,
  which.sub = NULL,
  ...
)
```

Arguments

csmf	It could be either fitted "insilico" object, a list of fitted "insilico" object from different chains of the same length but different starting values, i.e., different seed. Or it could be the matrix of CSMF obtained by insilico, or the list of matrices of CSMF. All CSMF could contain more than one subpopulations, but should be in the same format and order. And notice if the raw CSMF is used instead of the "insilico" object, external causes might need to be removed manually by user is external.sep is TRUE when fitting the model.
conv.csmf	The minimum mean CSMF to be checked. Default to be 0.02, which means any causes with mean CSMF lower than 0.02 will not be tested.
test	Type of test. Currently supporting Gelman and Rubin's test (test = "gelman") for multi-chain test, and Heidelberger and Welch's test (test = "heidel") for single-chain test.
verbose	Logical indicator to return the test detail instead of one logical outcome for Heidelberger and Welch's test. Default to be TRUE.
autoburnin	Logical indicator of whether to omit the first half of the chain as burn in. Default to be FALSE since insilico return only the iterations after burnin by default.
which.sub	the name of the sub-population to test when there are multiple in the fitted object.
...	Arguments to be passed to heidel.diag or gelman.diag

Details

The tests are performed using heidel.diag and gelman.diag functions in coda package. The function takes either one or a list of output from insilico function, or only the iteration by CSMF matrix. Usually in practice, many causes with very tiny CSMF are hard to converge based on standard tests,

thus it is suggested to check convergence for only causes with mean CSMF over certain threshold by setting proper `conv.csmf`.

Note for Gelman and Rubin's test, all chains should have the same length. If the chains are sampled with automatically length determination, they might not be comparable by this test.

Author(s)

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

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Brooks, Stephen P., and Andrew Gelman. General methods for monitoring convergence of iterative simulations. *Journal of computational and graphical statistics* 7.4 (1998): 434-455.

Heidelberger, Philip, and Peter D. Welch. A spectral method for confidence interval generation and run length control in simulations. *Communications of the ACM* 24.4 (1981): 233-245.

Heidelberger, Philip, and Peter D. Welch. Simulation run length control in the presence of an initial transient. *Operations Research* 31.6 (1983): 1109-1144.

Schruben, Lee W. Detecting initialization bias in simulation output. *Operations Research* 30.3 (1982): 569-590.

See Also

`insilico`, `summary.insilico`

Examples

```
# load sample data together with sub-population list
data(RandomVA2)
## Not run:
# extract InterVA style input data
data <- RandomVA2
# extract sub-population information.
subpop <- RandomVA2$sex

# run without sub-population
fit1a<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 1,
              auto.length = FALSE)
fit1b<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 2,
              auto.length = FALSE)
fit1c<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 3,
```

```
              auto.length = FALSE)
# single chain check
csmf.diag(fit1a)

# multiple chains check
csmf.diag(list(fit1a, fit1b, fit1c), test = "gelman")


# with sub-populations
fit2a<- insilico( data, subpop = subpop,
              Nsim = 400, burnin = 200, thin = 10 , seed = 1,
              auto.length = FALSE)
fit2b<- insilico( data, subpop = subpop,
              Nsim = 400, burnin = 200, thin = 10 , seed = 2,
              auto.length = FALSE)
fit2c<- insilico( data, subpop = subpop,
              Nsim = 400, burnin = 200, thin = 10 , seed = 3,
              auto.length = FALSE)
# single chain check
csmf.diag(fit2a)

# multiple chains check
csmf.diag(list(fit2a, fit2b, fit2c), test = "gelman", which.sub = "Men")

## End(Not run)
```

`extract.prob` *Obtain conditional probabilities from training data*

Description

This is the function internally used in `insilico.train` function.

Usage

```
extract.prob(
  train,
  gs,
  gstable,
  thre = 0.95,
  type = c("quantile", "fixed", "empirical")[1],
  isNumeric = FALSE,
  impute = TRUE
)
```

Arguments

train	Training data, it should be in the same format as the testing data and contains one additional column (see cause below) specifying known cause of death. The first column is also assumed to be death ID.
gs	the name of the column in train that contains cause of death.
gstable	The list of causes of death used in training data.
thre	a numerical value between 0 to 1. It specifies the maximum rate of missing for any symptoms to be considered in the model. Default value is set to 0.95, meaning if a symptom has more than 95% missing in the training data, it will be removed.
type	Three types of learning conditional probabilities are provided: "quantile" or "fixed". Since InSilicoVA works with ranked conditional probabilities P(S|C), "quantile" means the rankings of the P(S|C) are obtained by matching the same quantile distributions in the default InterVA P(S|C), and "fixed" means P(S|C) are matched to the closest values in the default InterVA P(S|C) table. Empirically both types of rankings produce similar results. The third option "empirical" means no rankings are calculated, only the raw P(S|C) values are returned.
isNumeric	Indicator if the input is already in numeric form. If the input is coded numerically such that 1 for "present", 0 for "absent", and -1 for "missing", this indicator could be set to True to avoid conversion to standard InterVA format.
impute	Indicator for whether to impute 1. P(S|C) with P(S) if symptom S does not exist more than the threshold of fractions within death due to C; and 2. values of exact 0 or 1.

Value

cond.prob	raw P(S|C) matrix
cond.prob.alpha	ranked P(S|C) matrix
table.alpha	list of ranks used
table.num	list of median numerical values for each rank
symps.train	training data after removing symptoms with too high missing rate.

---

get.indiv *Get individual COD probabilities from InSilicoVA Model Fits*

Description

This function calculates individual probabilities for each death and provide posterior credible intervals for each estimates. The default set up is to calculate the 95

Usage

```
get.indiv(
  object,
  data = NULL,
  CI = 0.95,
  is.aggregate = FALSE,
  by = NULL,
  is.sample = FALSE,
  java_option = "-Xmx1g",
  ...
)
```

Arguments

object	Fitted "insilico" object.
data	data for the fitted "insilico" object. The first column of the data should be the ID that matches the "insilico" fitted model.
CI	Credible interval for posterior estimates.
is.aggregate	logical indicator for constructing aggregated distribution rather than individual distributions.
by	list of column names to group by.
is.sample	logical indicator for returning the posterior samples of individual probabilities instead of posterior summaries.
java_option	Option to initialize java JVM. Default to "-Xmx1g", which sets the maximum heap size to be 1GB.
...	Not used.

Value

mean	individual mean COD distribution matrix.
median	individual median COD distribution matrix.
lower	individual lower bound for each COD probability.
upper	individual upper bound for each COD probability.

Author(s)

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, updateIndiv, plot.insilico

Examples

```
## Not run:
data(RandomVA1)
fit1<- insilico(RandomVA1, subpop = NULL,
                Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
                auto.length = FALSE)
summary(fit1, id = "d199")

# Calculate aggregated COD distributions
agg.csmf <- get.indiv(data = RandomVA1, fit1, CI = 0.95,
                      is.aggregate = TRUE, by = NULL)
head(agg.csmf)

agg.by.sex.age <- get.indiv(data = RandomVA1, fit1, CI = 0.95,
                            is.aggregate = TRUE, by = list("sex", "age"))
head(agg.by.sex.age$mean)

# Obtain individual level P(Y|X) posterior draws (N by C by Nitr array)
prob <- get.indiv(data = RandomVA1, fit1, is.sample = TRUE)
dim(prob)

## End(Not run)
```

---

indivplot *plot aggregated COD distribution*

Description

Produce a bar plot of the aggregated COD distribution as approximate CSMFs for a fitted "insilico" object.

Usage

```
indivplot(
  x,
  type = c("errorbar", "bar")[1],
  top = 10,
  causelist = NULL,
  which.plot = NULL,
  xlab = "Causes",
  ylab = "COD distribution",
  title = "COD distributions for the top causes",
  horiz = TRUE,
  angle = 60,
```

```
  fill = "lightblue",
  err_width = 0.4,
  err_size = 0.6,
  point_size = 2,
  border = "black",
  bw = FALSE,
  ...
)
```

Arguments

x	object from get.indiv function.
type	An indicator of the type of chart to plot. "errorbar" for line plots of only the error bars on single population; "bar" for bar chart with error bars on single population.
top	The number of top causes to plot. If multiple sub-populations are to be plotted, it will plot the union of the top causes in all sub-populations.
causelist	The list of causes to plot. It could be a numeric vector indicating the position of the causes in the InterVA cause list (see causetext), or a vector of character string of the cause names. The argument supports partial matching of the cause names. e.g., "HIV/AIDS related death" could be abbreviated into "HIV"; "Other and unspecified infect dis" could be abbreviated into "Other and unspecified infect".
which.plot	Specification of which group to plot if there are multiple.
xlab	Labels for the causes.
ylab	Labels for the CSMF values.
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
fill	The color to fill the bars when type is set to "bar".
err_width	Size of the error bars.
err_size	Thickness of the error bar lines.
point_size	Size of the points.
border	The color to color the borders of bars when type is set to "bar".
bw	Logical indicator for setting the theme of the plots to be black and white.
...	Not used.

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, summary.insilico

Examples

```
## Not run:
# Toy example with 1000 VA deaths
data(RandomVA1)
fit1<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              auto.length = FALSE)
summary(fit1, id = "d199")

# update credible interval for individual probabilities to 90%
indiv.new <- get.indiv(fit1, CI = 0.9)
fit1$indiv.prob.lower <- indiv.new$lower
fit1$indiv.prob.upper <- indiv.new$upper
fit1$indiv.CI <- 0.9
summary(fit1, id = "d199")


# get empirical aggregated COD distribution
agg.csmf <- get.indiv(data = RandomVA2, fit1, CI = 0.95,
                      is.aggregate = TRUE, by = NULL)
head(agg.csmf)

# aggregate individual COD distribution by sex and age
# note the model was fitted assuming the same CSMF for all deaths
# this aggregation provides an approximate CSMF for each sub-groups
agg.by.sex.age <- get.indiv(data = RandomVA2, fit1, CI = 0.95,
                        is.aggregate = TRUE, by = list("sex", "age"))
head(agg.by.sex.age$mean)

# plot of aggregated individual COD distribution
# 0. plot for all data
indivplot(agg.csmf, top = 10)
# 1. plot for specific one group
indivplot(agg.by.sex.age, which.plot = "Men 60-", top = 10)
# 2. comparing multiple groups
indivplot(agg.by.sex.age, which.plot = list("Men 60+", "Men 60-"),
                          top = 5)
# 3. comparing multiple groups on selected causes
indivplot(agg.by.sex.age, which.plot = list("Men 60-", "Women 60-"),
                          top = 0, causelist = c(
                            "HIV/AIDS related death",
                            "Pulmonary tuberculosis",
```

```
                              "Other and unspecified infect dis",
                              "Other and unspecified NCD"))

## End(Not run)
```

`insilico` *Implement InSilicoVA methods*

Description

This function implements InSilicoVA model. The InSilicoVA model is fitted with MCMC implemented in Java. For more detail, see the paper on https://arxiv.org/abs/1411.3042.

Usage

```
insilico(
  data,
  data.type = c("WHO2012", "WHO2016")[2],
  sci = NULL,
  isNumeric = FALSE,
  updateCondProb = TRUE,
  keepProbbase.level = TRUE,
  CondProb = NULL,
  CondProbNum = NULL,
  datacheck = TRUE,
  datacheck.missing = TRUE,
  warning.write = FALSE,
  directory = NULL,
  external.sep = TRUE,
  Nsim = 4000,
  thin = 10,
  burnin = 2000,
  auto.length = TRUE,
  conv.csmf = 0.02,
  jump.scale = 0.1,
  levels.prior = NULL,
  levels.strength = 1,
  trunc.min = 1e-04,
  trunc.max = 0.9999,
  subpop = NULL,
  java_option = "-Xmx1g",
  seed = 1,
  phy.code = NULL,
  phy.cat = NULL,
  phy.unknown = NULL,
  phy.external = NULL,
  phy.debias = NULL,
```

```
  exclude.impossible.cause = c("subset2", "subset", "all", "InterVA", "none")[1],
  impossible.combination = NULL,
  no.is.missing = FALSE,
  indiv.CI = NULL,
  groupcode = FALSE,
  known_labels = NULL,
  ...
)
```

Arguments

data	The original data to be used. It is suggested to use similar input as InterVA4, with the first column being death IDs and 245 symptoms. The only difference in input is InsilicoVA takes three levels: "present", "absent", and "missing (no data)". Similar to InterVA software, "present" symptoms takes value "Y"; "absent" symptoms take take value "NA" or "". For missing symptoms, e.g., questions not asked or answered in the original interview, corrupted data, etc., the input should be coded by "." to distinguish from "absent" category. The order of the columns does not matter as long as the column names are correct. It can also include more unused columns than the standard InterVA4 input. But the first column should be the death ID. For example input data format, see `RandomVA1` and `RandomVA2`.
data.type	Type of questionnaire. "WHO2012" corresponds to the standard input of InterVA4, and "WHO2016" corresponds to the standard input of InterVA5.
sci	A data frame that contains the symptom-cause-information (aka Probbase) that InterVA uses to assign a cause of death.
isNumeric	Indicator if the input is already in numeric form. If the input is coded numerically such that 1 for "present", 0 for "absent", and -1 for "missing", this indicator could be set to True to avoid conversion to standard InterVA format.
updateCondProb	Logical indicator. If FALSE, then fit InSilicoVA model without re-estimating conditional probabilities.
keepProbbase.level	Logical indicator when `updateCondProb` is FALSE. If TRUE, then only estimate the InterVA's conditional probability interpretation table; if FALSE, estimate the whole conditional probability matrix. Default to TRUE.
CondProb	Customized conditional probability matrix to use.It should be strict the same configuration as InterVA-4 software. That is, it should be a matrix of 245 rows of symptoms and 60 columns of causes, arranged in the same order as in InterVA-4 specification. The elements in the matrix should be the conditional probability of corresponding symptom given the corresponding cause, represented in alphabetic form indicating levels. For example input, see `condprob`
CondProbNum	Customized conditional probability matrix to use if specified fully by numerical values between 0 and 1. If it is specified, re-estimation of conditional probabilities will not be performed, i.e., `updateCondProb` will be set to FALSE.
datacheck	Logical indicator for whether to check the data satisfying InterVA rules. Default set to be TRUE. If `warning.write` is set to true, the inconsistent input

will be logged in file warning_insilico.txt and errorlog_insilico.txt. It's strongly suggested to be set to TRUE.

`datacheck.missing`
: Logical indicator for whether to perform data check before deleting complete missing symptoms. Default to TRUE.

`warning.write`
: Logical indicator for whether to save the changes made to data input by `datacheck`. If set to TRUE, the changes will be logged in file warning_insilico.txt and errorlog_insilico.txt in current working directory.

`directory`
: The directory to store the output from. It should be an valid existing directory or a folder to be created.

`external.sep`
: Logical indicator for whether to separate out external causes first. Default set to be TRUE. If set to TRUE, the algorithm will estimate external causes, e.g., traffic accident, accidental fall, suicide, etc., by checking the corresponding indicator only without considering other medical symptoms. It is strongly suggested to set to be TRUE.

`Nsim`
: Number of iterations to run. Default to be 4000.

`thin`
: Proportion of thinning for storing parameters. For example, if thin = k, the output parameters will only be saved every k iterations. Default to be 10

`burnin`
: Number of iterations as burn-in period. Parameters sampled in burn-in period will not be saved.

`auto.length`
: Logical indicator of whether to automatically increase chain length if convergence not reached.

`conv.csmf`
: Minimum CSMF value to check for convergence if auto.length is set to TRUE. For example, under the default value 0.02, all causes with mean CSMF at least 0.02 will be checked for convergence.

`jump.scale`
: The scale of Metropolis proposal in the Normal model. Default to be 0.1.

`levels.prior`
: Vector of prior expectation of conditional probability levels. They do not have to be scaled. The algorithm internally calibrate the scale to the working scale through `levels.strength`. If NULL the algorithm will use InterVA table as prior.

`levels.strength`
: Scaling factor for the strength of prior beliefs in the conditional probability levels. Larger value constrain the posterior estimates to be closer to prior expectation. Defult value 1 scales `levels.prior` to a suggested scale that works empirically.

`trunc.min`
: Minimum possible value for estimated conditional probability table. Default to be 0.0001

`trunc.max`
: Maximum possible value for estimated conditional probability table. Default to be 0.9999

`subpop`
: This could be the column name of the variable in data that is to be used as sub-population indicator, or a list of column names if more than one variable are to be used. Or it could be a vector of sub-population assignments of the same length of death records. It could be numerical indicators or character vectors of names.

java_option
: Option to initialize java JVM. Default to "-Xmx1g", which sets the maximum heap size to be 1GB. If R produces "java.lang.OutOfMemoryError: Java heap space" error message, consider increasing heap size using this option, or one of the following: (1) decreasing `Nsim`, (2) increasing `thin`, or (3) disabling `auto.length`.

seed
: Seed used for initializing sampler. The algorithm will produce the same outcome with the same seed in each machine.

phy.code
: A matrix of physician assigned cause distribution. The physician assigned causes need not be the same as the list of causes used in InSilicoVA and InterVA-4. The cause list used could be a higher level aggregation of the InSilicoVA causes. See `phy.cat` for more detail. The first column of `phy.code` should be death ID that could be matched to the symptom dataset, the following columns are the probabilities of each cause category used by physicians.

phy.cat
: A two column matrix describing the correspondence between InSilicoVA causes and the physician assigned causes. Note each InSilicoVA cause (see `causetext`) could only correspond to one physician assigned cause. See `SampleCategory` for an example. 'Unknown' category should not be included in this matrix.

phy.unknown
: The name of the physician assigned cause that correspond to unknown COD.

phy.external
: The name of the physician assigned cause that correspond to external causes. This will only be used if `external.sep` is set to TRUE. In that case, all external causes should be grouped together, as they are assigned deterministically by the corresponding symptoms.

phy.debias
: Fitted object from physician coding debias function (see `physician_debias`) that overwrites `phy.code`.

exclude.impossible.cause
: option to exclude impossible causes at the individual level. The following rules are implemented: `subset`: Causes with 0 probability given the age group and gender of the observation, according to the InterVA conditional probabilities, are removed; `subset2`: In addition to the same rules as `subset`, also remove Prematurity for baby born during at least 37 weeks of pregnancy, remove Birth asphyxia for baby not born during at least 37 weeks of pregnancy, and remove pregnancy-related deaths for deaths without pregnancy; `all`: Causes with 0 probability given any symptom of the observation, according to the InterVA conditional probabilities, are removed; `interVA`: Causes with 0 probability given any positive indicators according to the InterVA conditional probabilities, are removed; and `none`: no causes are removed. `subset2` is the default.

impossible.combination
: matrix indicating additional impossible symptom-cause combinations in addition to the ones specified by `exlcude.impossible.cause`. It should be a matrix of three columns, where each row is one rule of impossible combination. In each row, the first column specify the name of the symptom (as in the input data column names, e.g., "i079o"), the second column specify the name of the cause (as in the probbase column name, i.e., "b_0101"), and the third column specifying either 0 or 1, indicating the cause is impossible when the symptom takes the specified value.

no.is.missing
: logical indicator to treat all absence of symptoms as missing. Default to FALSE. If set to TRUE, InSilicoVA will perform calculations similar to InterVA-4 w.r.t

	treating absent symptoms. It is highly recommended to set this argument to FALSE.
indiv.CI	credible interval for individual probabilities. If set to NULL, individual COD distributions will not be calculated to accelerate model fitting time. See get.indiv for details of updating the C.I. later after fitting the model.
groupcode	logical indicator of including the group code in the output causes
known_labels	a data frame with two columns: the first column is the death ID and the second column is the known cause of death (need to match the cause list for the given data format). When it is provided for some causes, they will be used as partial labels in the input data. Any unmatched observations (unmatched by either ID or cause) will not contribute to partial labels. Default to be NULL
...	not used

Details

For Windows user, this function will produce a popup window showing the progress. For Mac and Unix user, this function will print progress messages on the console. Special notice for users using default R GUI for mac, the output will not be printed on console while the function is running, and will only be printed out after it is completed. Thus if you use a Mac, we suggest using either RStudio for mac, or running R from terminal.

The chains could be set to run automatically longer. If set auto.length to be TRUE, the chain will assess convergence after finishing the length K chain input by user using Heidelberger and Welch's convergence diagnostic. If convergence is not reached, the chain will run another K iterations and use the first K iterations as burn-in. If the chain is still not converged after 2K iterations, it will proceed to another 2K iterations and again use the first 2K iterations as burn-in. If convergence is still not reached by the end, it will not double the length again to avoid heavy memory use. A warning will be given in that case. The extended chains will be thinned in the same way.

For more detail of model specification, see the paper on https://arxiv.org/abs/1411.3042.

Value

id	A vector of death ID. Note the order of the ID is in general different from the input file. See report for organizing the report.
data	Cleaned numerical data.
indiv.prob	Matrix of individual mean cause of death distribution. Each row corresponds to one death with the corresponding ID.
csmf	Matrix of CSMF vector at each iterations after burn-in and thinning. Each column corresponds to one cause.
conditional.probs	If the model is estimated with keepProbbase.level = TRUE, this value gives a matrix of each conditional probability at each level at each iterations. Each column corresponds to one level of probability. If keepProbbase.level = FALSE, this value gives a three-dimensional array. If updateCondProb = FALSE, the value will be set to NULL. See report for more analysis.
missing.symptoms	Vector of symptoms missing from all input data.

`external` Logical indicator of whether the model is fitted with external causes separated calculated.

`impossible.causes` Impossible cause-symptom pairs, if any.

`indiv.CI` The posterior credible interval to compute for individual COD probability distributions. If set to NULL, only the posterior mean of the individual COD probabilities will be produced. Default to be 0.95.

`indiv.prob.median` median probability of each cause of death for each individual death.

`indiv.prob.lower` lower CI bound for the probability of each cause of death for each individual death.

`indiv.prob.upper` upper CI bound for the probability of each cause of death for each individual death.

`errors` Logs of deleted observations and reasons of deletion.

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark(2014) *Probabilistic cause-of-death assignment using verbal autopsies*, https://arxiv.org/abs/1411.3042
Working paper no. 147, Center for Statistics and the Social Sciences, University of Washington

See Also

`plot.insilico`, `summary.insilico`, `physician_debias`

Examples

```
## Not run:
data(RandomVA1)
fit0<- insilico(RandomVA1, subpop = NULL,
                Nsim = 20, burnin = 10, thin = 1 , seed = 1,
 auto.length = FALSE)
summary(fit0)
summary(fit0, id = "d199")

##
## Scenario 1: standard input without sub-population specification
##
fit1<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
   auto.length = FALSE)
```

```
summary(fit1)
plot(fit1)

##
## Scenario 2: standard input with sub-population specification
##
data(RandomVA2)
fit2<- insilico(RandomVA2, subpop = list("sex"),
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
   auto.length = FALSE)
summary(fit2)
plot(fit2, type = "compare")
plot(fit2, which.sub = "Men")

##
## Scenario 3: standard input with multiple sub-population specification
##
fit3<- insilico(RandomVA2, subpop = list("sex", "age"),
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
   auto.length = FALSE)
summary(fit3)

##
## Scenario 3: standard input with multiple sub-population specification
##
fit3<- insilico(RandomVA2, subpop = list("sex", "age"),
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
   auto.length = FALSE)
summary(fit3)

##
## Scenario 5 - 7 are special situations rarely needed in practice,
##   but included here for completeness.
##   The below examples use no sub-population or physician codes,
##   but specifying sub-population is still possible as in Scenario 2 - 4.
##

##
## Scenario 5: skipping re-estimation of conditional probabilities
##
# Though in practice the need for this situation is very unlikely,
# use only the default conditional probabilities without re-estimation
fit5<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              updateCondProb = FALSE,
   auto.length = FALSE)
summary(fit5)

##
## Scenario 6: modify default conditional probability matrix
##
# Load the default conditional probability matrix
data(condprob)
```

```
# The conditional probabilities are given in levels such as I, A+, A, A-, etc.
condprob[1:5, 1:5]
# To modify certain cells
new_cond_prob <- condprob
new_cond_prob["elder", "HIV/AIDS related death"] <- "C"
# or equivalently
new_cond_prob[1, 3] <- "C"

fit6<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              CondProb = new_cond_prob,
   auto.length = FALSE)
# note: compare this with fit1 above to see the change induced
#  by changing Pr(elder | HIV) from "C+" to "C".
summary(fit6)

##
## Scenario 7: modify default numerical values in conditional probabilities directly
##
# Load the default conditional probability matrix
data(condprobnum)
# The conditional probabilities are given in numerical values in this dataset
condprobnum[1:5, 1:5]
# To modify certain cells, into any numerical values you want
new_cond_prob_num <- condprobnum
new_cond_prob_num["elder", "HIV/AIDS related death"] <- 0.004
# or equivalently
new_cond_prob_num[1, 3] <- 0.005

fit7<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              CondProbNum = new_cond_prob_num,
   auto.length = FALSE)
# note: compare this with fit1, fit5, and fit6
summary(fit7)

##
## Scenario 8: physician coding
## see also the examples in physician_debias() function section
##
# Load sample input for physicians
data(RandomPhysician)
# The symptom section looks the same as standard input
head(RandomPhysician[, 1:5])
# At the end of file, including a few more columns of physician id and coded cause
head(RandomPhysician[, 245:250])

# load Cause Grouping (if physician-coded causes are in larger categories)
data(SampleCategory)
head(SampleCategory)

# existing doctor codes in the sample dataset
doctors <- paste0("doc", c(1:15))
```

```
causelist <- c("Communicable", "TB/AIDS", "Maternal",
               "NCD", "External", "Unknown")
phydebias <- physician_debias(RandomPhysician,
phy.id = c("rev1", "rev2"), phy.code = c("code1", "code2"),
phylist = doctors, causelist = causelist,
tol = 0.0001, max.itr = 100)

fit8 <- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              phy.debias = phydebias,
              phy.cat = SampleCategory,
              phy.external = "External", phy.unknown = "Unknown",
   auto.length = FALSE)
summary(fit8)

# example to fit WHO2016 data
data(RandomVA5)
fit1a <- insilico(RandomVA5, data.type="WHO2016", subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
   auto.length = FALSE)
summary(fit1a)
plot(fit1)

# example to change directory for error files
fit1b <- insilico(RandomVA5[1:50, ], data.type="WHO2016",
Nsim = 1000, burnin = 500, thin = 10 ,
seed = 1, auto.length=F)
fit1c <- insilico(RandomVA5[1:50, ], data.type="WHO2016",
Nsim = 1000, burnin = 500, thin = 10 ,
seed = 1, auto.length=F)

 # similarly for WHO 2012 version
fit1<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
         auto.length = FALSE)


## End(Not run)
```

`insilico.fit` *Implement InSilicoVA methods with more flexible customization*

Description

This function implements InSilicoVA model. This is the lower level core function of InSilicoVA with more flexibility in customized input. For more detail of model specification, see the paper on https://arxiv.org/abs/1411.3042 and the default function insilico.

Usage

```
insilico.fit(
  data,
  data.type = c("WHO2012", "WHO2016")[1],
  sci = NULL,
  isNumeric = FALSE,
  updateCondProb = TRUE,
  keepProbbase.level = TRUE,
  CondProb = NULL,
  CondProbNum = NULL,
  datacheck = TRUE,
  datacheck.missing = TRUE,
  warning.write = FALSE,
  directory = NULL,
  external.sep = TRUE,
  Nsim = 4000,
  thin = 10,
  burnin = 2000,
  auto.length = TRUE,
  conv.csmf = 0.02,
  jump.scale = 0.1,
  levels.prior = NULL,
  levels.strength = 1,
  trunc.min = 1e-04,
  trunc.max = 0.9999,
  subpop = NULL,
  java_option = "-Xmx1g",
  seed = 1,
  phy.code = NULL,
  phy.cat = NULL,
  phy.unknown = NULL,
  phy.external = NULL,
  phy.debias = NULL,
  exclude.impossible.cause = c("subset2", "subset", "all", "InterVA", "none")[1],
  impossible.combination = NULL,
  no.is.missing = FALSE,
  customization.dev = FALSE,
  Probbase_by_symp.dev = FALSE,
  probbase.dev = NULL,
  table.dev = NULL,
  table.num.dev = NULL,
  gstable.dev = NULL,
  nlevel.dev = NULL,
  indiv.CI = NULL,
  groupcode = FALSE,
  known_labels = NULL,
  ...
)
```

Arguments

data	see insilico
data.type	see insilico
sci	see insilico
isNumeric	see insilico
updateCondProb	see insilico
keepProbbase.level	see insilico
CondProb	see insilico
CondProbNum	see insilico
datacheck	see insilico
datacheck.missing	see insilico
warning.write	see insilico
directory	see insilico
external.sep	see insilico
Nsim	see insilico
thin	see insilico
burnin	see insilico
auto.length	see insilico
conv.csmf	see insilico
jump.scale	see insilico
levels.prior	see insilico
levels.strength	see insilico
trunc.min	see insilico
trunc.max	see insilico
subpop	see insilico
java_option	see insilico
seed	see insilico
phy.code	see insilico
phy.cat	see insilico
phy.unknown	see insilico
phy.external	see insilico
phy.debias	see insilico
exclude.impossible.cause	see insilico
impossible.combination	see insilico.train

`no.is.missing`	see `insilico`
`customization.dev`	Logical indicator for customized variables
`Probbase_by_symp.dev`	Not tested yet.
`probbase.dev`	The customized conditional probabilities of symptoms given causes, which could be in a different format than InterVA default, but it should consist of `nlevel.dev` levels rather than numerical values.
`table.dev`	The table of level names in `probbase.dev`. Default to be NULL
`table.num.dev`	The corresponding prior numerical values for each level in `probbase.dev`, in the same order as `table.dev`. Default to be NULL
`gstable.dev`	Table of gold standard causes for each death. Default to be NULL
`nlevel.dev`	number of levels in `probbase.dev`. Default to be NULL
`indiv.CI`	credible interval for individual probabilities
`groupcode`	logical indicator of including the group code in the output causes
`known_labels`	a data frame with two columns: the first column is the death ID and the second column is the known cause of death (need to match the cause list for the given data format). When it is provided for some causes, they will be used as partial labels in the input data. Any unmatched observations (unmatched by either ID or cause) will not contribute to partial labels. Default to be NULL
`...`	unused arguments

Value

a insilico fit object, see see `insilico` for more detail.

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

Maintainer: Zehang Li <lizehang@uw.edu>

References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark(2014) *Probabilistic cause-of-death assignment using verbal autopsies*, https://arxiv.org/abs/1411.3042
Working paper no. 147, Center for Statistics and the Social Sciences, University of Washington

See Also

`plot.insilico`, `summary.insilico`

`insilico.train` *Modified InSilicoVA methods with training data*

Description

This function implements InSilicoVA model with non-InterVA4 input data.

Usage

```
insilico.train(
  data,
  train,
  cause,
  causes.table = NULL,
  thre = 0.95,
  type = c("quantile", "fixed", "empirical")[1],
  isNumeric = FALSE,
  updateCondProb = TRUE,
  keepProbbase.level = TRUE,
  CondProb = NULL,
  CondProbNum = NULL,
  datacheck = TRUE,
  datacheck.missing = TRUE,
  warning.write = FALSE,
  external.sep = TRUE,
  Nsim = 4000,
  thin = 10,
  burnin = 2000,
  auto.length = TRUE,
  conv.csmf = 0.02,
  jump.scale = 0.1,
  levels.prior = NULL,
  levels.strength = NULL,
  trunc.min = 1e-04,
  trunc.max = 0.9999,
  subpop = NULL,
  java_option = "-Xmx1g",
  seed = 1,
  phy.code = NULL,
  phy.cat = NULL,
  phy.unknown = NULL,
  phy.external = NULL,
  phy.debias = NULL,
  exclude.impossible.cause = TRUE,
  impossible.combination = NULL,
  indiv.CI = NULL,
  CondProbTable = NULL,
```

```
  known_labels = NULL,
  ...
)
```

Arguments

data	The original data to be used. It is suggested to use similar input as InterVA4, with the first column being death IDs and 245 symptoms. The only difference in input is InsilicoVA takes three levels: "present", "absent", and "missing (no data)". Similar to InterVA software, "present" symptoms takes value "Y"; "absent" symptoms take take value "NA" or "". For missing symptoms, e.g., questions not asked or answered in the original interview, corrupted data, etc., the input should be coded by "." to distinguish from "absent" category. The order of the columns does not matter as long as the column names are correct. It can also include more unused columns than the standard InterVA4 input. But the first column should be the death ID. For example input data format, see `RandomVA1` and `RandomVA2`.
train	Training data, it should be in the same format as the testing data and contains one additional column (see `cause` below) specifying known cause of death. The first column is also assumed to be death ID.
cause	the name of the column in `train` that contains cause of death.
causes.table	The list of causes of death used in training data.
thre	a numerical value between 0 to 1. It specifies the maximum rate of missing for any symptoms to be considered in the model. Default value is set to 0.95, meaning if a symptom has more than 95% missing in the training data, it will be removed.
type	Three types of learning conditional probabilities are provided: "empirical", "quantile" or "fixed". Since InSilicoVA works with ranked conditional probabilities P(S|C), "quantile" means the rankings of the P(S|C) are obtained by matching the same quantile distributions in the default InterVA P(S|C), and "fixed" means P(S|C) are matched to the closest values in the default InterVA P(S|C) table. Empirically both types of rankings produce similar results. "empirical", on the other hand, means no ranking is calculated, but use the empirical conditional probabilities directly. If "empirical", `updateCondProb` will be forced to be FALSE.
isNumeric	Indicator if the input is already in numeric form. If the input is coded numerically such that 1 for "present", 0 for "absent", and -1 for "missing", this indicator could be set to True to avoid conversion to standard InterVA format.
updateCondProb	Logical indicator. If FALSE, then fit InSilicoVA model without re-estimating conditional probabilities.
keepProbbase.level	see `insilico` for more detail.
CondProb	see `insilico` for more detail.
CondProbNum	see `insilico` for more detail.
datacheck	Not Implemented.
datacheck.missing	Not Implemented.

`warning.write` Not Implemented.

`external.sep` Not Implemented.

`Nsim` see `insilico` for more detail.

`thin` see `insilico` for more detail.

`burnin` see `insilico` for more detail.

`auto.length` see `insilico` for more detail.

`conv.csmf` see `insilico` for more detail.

`jump.scale` see `insilico` for more detail.

`levels.prior` see `insilico` for more detail.

`levels.strength` see `insilico` for more detail.

`trunc.min` see `insilico` for more detail.

`trunc.max` see `insilico` for more detail.

`subpop` see `insilico` for more detail.

`java_option` see `insilico` for more detail.

`seed` see `insilico` for more detail.

`phy.code` see `insilico` for more detail.

`phy.cat` see `insilico` for more detail.

`phy.unknown` see `insilico` for more detail.

`phy.external` see `insilico` for more detail.

`phy.debias` see `insilico` for more detail.

`exclude.impossible.cause` Whether to include impossible causes

`impossible.combination` a matrix of two columns, first is the name of symptoms, and the second is the name of causes. Each row corresponds to a combination of impossible symptom (that exists) and cause.

`indiv.CI` see `insilico` for more detail.

`CondProbTable` a data frame of two columns: one alphabetic level of the CondProb argument and one numerical value corresponding to the numerical value of each level. Only used when only conditional probabilities are provided instead of training data.

`known_labels` a data frame with two columns: the first column is the death ID and the second column is the known cause of death (need to match the cause list for the given data format). When it is provided for some causes, they will be used as partial labels in the input data. Any unmatched observations (unmatched by either ID or cause) will not contribute to partial labels. Default to be NULL

`...` not used

Details

Please see `insilico` for more details about choosing chain length and OS system differences. This function implements InSilico with customized input format and training data.

For more detail of model specification, see the paper on https://arxiv.org/abs/1411.3042.

Value

`insilico` object

`mapICD` *Map ICD-10 codes into the WHO 2016 cause list*

Description

Map ICD-10 codes into the WHO 2016 cause list

Usage

```
mapICD(x)
```

Arguments

`x`	a character object or a vector of ICD-10 codes

Examples

```
mapICD("A90")
mapICD(c("A90", "C30"))
```

`physician_debias` *Implement physician debias algorithm*

Description

This function implements physician debias algorithm proposed in Salter-Townshend and Murphy (2013).

Usage

```
physician_debias(
  data,
  phy.id,
  phy.code,
  phylist,
  causelist,
  tol = 1e-04,
  max.itr = 5000,
  verbose = FALSE
)
```

Arguments

data	The original data to be used. It is suggested to use similar input as InterVA4, with the first column being death IDs. The only difference in input is InsilicoVA takes three levels: "present", "absent", and "missing (no data)". Similar to InterVA software, "present" symptoms takes value "Y"; "absent" symptoms take take value "NA" or "". For missing symptoms, e.g., questions not asked or answered in the original interview, corrupted data, etc., the input should be coded by "." to distinguish from "absent" category. The order of the columns does not matter as long as the column names are correct. Currently it cannot other non-symptom columns such as subpopulation. And the first column should be the death ID. Everything other than the death ID, physician ID, and physician codes should be symptoms.
phy.id	vector of column names for physician ID
phy.code	vector of column names for physician code
phylist	vector of physician ID used in physician ID columns
causelist	vector of causes used in physician code columns
tol	tolerance of the EM algorithm
max.itr	maximum iteration to run
verbose	logical indicator for printing out likelihood change

Value

code.debias	Individual cause likelihood distribution
csmf	Cause specific distribution in the sample
phy.bias	Bias matrix for each physician
cond.prob	Conditional probability of symptoms given causes

References

M. Salter-Townshend and T. B. Murphy (2013).*Sentiment analysis of online media*. *In Algorithms from and for Nature and Life, pages 137-145, Springer.*

Examples

```
data(RandomPhysician)
head(RandomPhysician[, 1:10])
## Not run:
causelist <- c("Communicable", "TB/AIDS", "Maternal",
               "NCD", "External", "Unknown")
phydebias <- physician_debias(RandomPhysician, phy.id = c("rev1", "rev2"),
phy.code = c("code1", "code2"), phylist = paste0("doc", c(1:15)),
causelist = causelist, tol = 0.0001, max.itr = 5000)

# see the first physician's bias matrix
round(phydebias$phy.bias[[1]], 2)

## End(Not run)
```

`plot.insilico` *plot CSMF from a "insilico" object*

Description

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

Usage

```
## S3 method for class 'insilico'
plot(
  x,
  type = c("errorbar", "bar", "compare")[1],
  top = 10,
  causelist = NULL,
  which.sub = NULL,
  xlab = "Causes",
  ylab = "CSMF",
  title = "Top CSMF Distribution",
  horiz = TRUE,
  angle = 60,
  fill = "lightblue",
  err_width = 0.4,
  err_size = 0.6,
  point_size = 2,
  border = "black",
  bw = TRUE,
  ...
)
```

Arguments

x	fitted "insilico" object
type	An indicator of the type of chart to plot. "errorbar" for line plots of only the error bars on single population; "bar" for bar chart with error bars on single population; "compare" for line charts on multiple sub-populations.
top	The number of top causes to plot. If multiple sub-populations are to be plotted, it will plot the union of the top causes in all sub-populations.
causelist	The list of causes to plot. It could be a numeric vector indicating the position of the causes in the InterVA cause list (see causetext), or a vector of character string of the cause names. The argument supports partial matching of the cause names. e.g., "HIV/AIDS related death" could be abbreviated into "HIV"; "Other and unspecified infect dis" could be abbreviated into "Other and unspecified infect".
which.sub	Specification of which sub-population to plot if there are multiple and type is set to "bar".
xlab	Labels for the causes.
ylab	Labels for the CSMF values.
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
fill	The color to fill the bars when type is set to "bar".
err_width	Size of the error bars.
err_size	Thickness of the error bar lines.
point_size	Size of the points.
border	The color to color the borders of bars when type is set to "bar".
bw	Logical indicator for setting the theme of the plots to be black and white.
...	Not used.

Details

To-do

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

Maintainer: Zehang Li <lizehang@uw.edu>

References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, summary.insilico

Examples

```
## Not run:
data(RandomVA1)
##
## Scenario 1: without sub-population specification
##
fit1<- insilico(RandomVA1, subpop = NULL,
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              auto.length = FALSE)
# basic line plot
plot(fit1)
# basic bar plot
plot(fit1, type = "bar")
# line plot with customized look
plot(fit1, top = 15, horiz = FALSE, fill = "gold",
           bw = TRUE, title = "Top 15 CSMFs", angle = 70,
           err_width = .2, err_size = .6, point_size = 2)

##
## Scenario 2: with sub-population specification
##
data(RandomVA2)
fit2<- insilico(RandomVA2, subpop = list("sex"),
              Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
              auto.length = FALSE)
summary(fit2)
# basic side-by-side line plot for all sub-populations
plot(fit2, type = "compare", main = "Top 5 causes comparison")
# basic line plot for specific sub-population
plot(fit2, which.sub = "Women", main = "Top 5 causes for women")
# customized plot with only specified causes
# the cause names need not be exact as InterVA cause list
# substrings in InterVA cause list is enough for specification
# e.g. the following two specifications are the same
some_causes_1 <- c("HIV/AIDS related death", "Pulmonary tuberculosis")
some_causes_2 <- c("HIV", "Pulmonary")
plot(fit2, type = "compare", horiz = FALSE,  causelist = some_causes_1,
              title = "HIV and TB fractions in two sub-populations",
              angle = 20)

## End(Not run)
```

---

print.insilico *Print method for summarizing InSilicoVA Model Fits*

Description

This function is the print method for class `insilico`.

Usage

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

Arguments

`x`	`insilico` object.
`...`	not used

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

`summary.insilico`

Examples

```
## Not run:
# load sample data together with sub-population list
data(RandomVA1)
# extract InterVA style input data
data <- RandomVA1$data
# extract sub-population information.
# The groups are "HIV Positive", "HIV Negative" and "HIV status unknown".
subpop <- RandomVA1$subpop

# run without subpopulation
fit1<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 1,
              external.sep = TRUE, keepProbbase.level = TRUE)
fit1

## End(Not run)
```

print.insilico_summary *Print method for summarizing InSilicoVA Model Fits*

Description

This function is the print method for class `insilico_summary`.

Usage

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

Arguments

`x`	`insilico_summary` object.
`...`	not used

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

Maintainer: Zehang Li <lizehang@uw.edu>

References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

`summary.insilico`

Examples

```
## Not run:
# load sample data together with sub-population list
data(RandomVA1)
# extract InterVA style input data
data <- RandomVA1$data
# extract sub-population information.
# The groups are "HIV Positive", "HIV Negative" and "HIV status unknown".
subpop <- RandomVA1$subpop

# run without subpopulation
fit1<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 1,
              external.sep = TRUE, keepProbbase.level = TRUE)
```

```
summary(fit1)
summary(fit1, top = 10)

# save individual COD distributions to files
summary(fit1, file = "results.csv")

## End(Not run)
```

---

probbase *Conditional probability of InterVA4*

Description

This is the table of conditional probabilities of symptoms given CODs, together with the data check rules. The values are from InterVA-4.2.

Format

A data frame with 246 observations on 81 variables.

Examples

```
data(probbase)
```

---

probbase3 *Conditional probability of InterVA4.03*

Description

This is the table of conditional probabilities of symptoms given CODs. The values are from InterVA-4.03.

Format

A data frame with 246 observations on 81 variables. Each observation is the conditional probability.

Examples

```
data(probbase)
```

RandomPhysician — *100 records of Sample Input together with two simulated physician codes*

Description

This is the same dataset as in RandomVA2 with additional columns specifying physician ID and codes.

Format

100 arbitrary input records.

Examples

```
data(RandomPhysician)
head(RandomPhysician[, 1:10])
```

RandomVA1 — *1000 records of Sample Input*

Description

This is a dataset consisting of 1000 arbitrary sample input deaths in the default format of InSilicoVA, i.e., the same input format as in InterVA-4 software and R package.

Format

1000 arbitrary input records.

Examples

```
data(RandomVA1)
dim(RandomVA1)
head(RandomVA1)
```

RandomVA2 *100 records of Sample Input*

Description

This is a dataset consisting of 1000 arbitrary sample input deaths in the default format of InSilicoVA with additional columns specifying age and sex, which could be served as characteristics in sub-population estimation.

Format

100 arbitrary input records.

Examples

```
data(RandomVA2)
dim(RandomVA2)
head(RandomVA2)
```

SampleCategory *Correspondence between InterVA causes and the physician coded cause categories*

Description

This is the matrix explaining the correspondence between InterVA causes and the physician coded cause categories.

Format

matrix of 2 columns

Examples

```
data(SampleCategory)
head(SampleCategory)
```

SamplePhysician *100 records of Sample debiased physician codes*

Description

This is in the same format of the output running physician_debias. It is a data frame of 100 rows, and column represents ID and probability of the cause in each category.

Format

100 arbitrary input records.

Examples

```
data(SamplePhysician)
head(SamplePhysician)
```

stackplot *plot grouped CSMF from a "insilico" object*

Description

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

Usage

```
stackplot(
  x,
  grouping = NULL,
  type = c("stack", "dodge")[1],
  order.group = NULL,
  order.sub = NULL,
  err = TRUE,
  CI = 0.95,
  sample.size.print = FALSE,
  xlab = "Group",
  ylab = "CSMF",
  ylim = NULL,
  title = "CSMF by broader cause categories",
  horiz = FALSE,
  angle = 60,
  err_width = 0.4,
  err_size = 0.6,
  point_size = 2,
  border = "black",
  bw = FALSE,
  ...
)
```

Arguments

x	fitted "insilico" object
grouping	C by 2 matrix of grouping rule. If set to NULL, make it default.
type	type of the plot to make
order.group	list of grouped categories. If set to NULL, make it default.
order.sub	Specification of the order of sub-populations to plot
err	indicator of inclusion of error bars
CI	confidence interval for error bars.
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.
point_size	Size of the points.
border	The color for the border of the bars.
bw	Logical indicator for setting the theme of the plots to be black and white.
...	Not used.

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

Maintainer: Zehang Li <lizehang@uw.edu>

References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, summary.insilico

Examples

```
## Not run:
  data(RandomVA1)
  ##
  ## Scenario 1: without sub-population specification
  ##
  fit1<- insilico(RandomVA1, subpop = NULL,
                Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
                auto.length = FALSE)
  # stack bar plot for grouped causes
  # the default grouping could be seen from
  data(SampleCategory)
  stackplot(fit1, type = "dodge", xlab = "")

  ##
  ## Scenario 2: with sub-population specification
  ##
  data(RandomVA2)
  fit2<- insilico(RandomVA2, subpop = list("sex"),
                Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
                auto.length = FALSE)
  stackplot(fit2, type = "stack", angle = 0)
  stackplot(fit2, type = "dodge", angle = 0)
  # Change the default grouping by separating TB from HIV
  data(SampleCategory)
  SampleCategory[c(3, 9), ]
  SampleCategory[3, 2] <- "HIV/AIDS"
  SampleCategory[9, 2] <- "TB"
  stackplot(fit2, type = "stack", grouping = SampleCategory,
            sample.size.print = TRUE, angle = 0)
  stackplot(fit2, type = "dodge", grouping = SampleCategory,
            sample.size.print = TRUE, angle = 0)

  # change the order of display for sub-population and cause groups
  groups <- c("HIV/AIDS", "TB", "Communicable", "NCD", "External",
              "Maternal", "causes specific to infancy")
  subpops <- c("Women", "Men")
  stackplot(fit2, type = "stack", grouping = SampleCategory,
            order.group = groups, order.sub = subpops,
            sample.size.print = TRUE, angle = 0)

## End(Not run)
```

`summary.insilico` *Summarizing InSilicoVA Model Fits*

Description

This function is the summary method for class `insilico`.

Usage

```
## S3 method for class 'insilico'
summary(
  object,
  CI.csmf = 0.95,
  CI.cond = 0.95,
  file = NULL,
  top = 10,
  id = NULL,
  ...
)
```

Arguments

object	Fitted "insilico" object.
CI.csmf	Confidence interval for CSMF estimates.
CI.cond	Confidence interval for conditional probability estimates
file	Optional .csv file to write to. If it is specified, individual cause of death distribution will be saved to the file.
top	Number of top causes to display on screen.
id	ID of specific death to display on screen.
...	Not used.

Details

summary.insilico formats some basic information about the InSilicoVA fitted object on screen and show the several top CSMFs of user's choice. See below for more detail.

Value

id.all	all IDs of the deaths.
indiv	individual Cause of Death distribution matrix.
csmf	CSMF distribution and confidence interval for each cause.
csmf.ordered	CSMF distribution and confidence interval for each cause, ordered by mean.
condprob	Conditional probability matrix and confidence intervals.
updateCondProb	Component of "insilico" object.
keepProbbase.level	Component of "insilico" object.
datacheck	Component of "insilico" object.
Nsim	Component of "insilico" object.
thin	Component of "insilico" object.
burnin	Component of "insilico" object.
jump.scale	Component of "insilico" object.

levels.prior	Component of "insilico" object.
levels.strength	Component of "insilico" object.
trunc.min	Component of "insilico" object.
trunc.max	Component of "insilico" object.
subpop_counts	Component of "insilico" object.
showTop	Component of "insilico" object.

Author(s)

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References

Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, plot.insilico

Examples

```
## Not run:
# load sample data together with sub-population list
data(RandomVA1)
# extract InterVA style input data
data <- RandomVA1$data
# extract sub-population information.
# The groups are "HIV Positive", "HIV Negative" and "HIV status unknown".
subpop <- RandomVA1$subpop

# run without subpopulation
fit1<- insilico( data, subpop = NULL,
              Nsim = 400, burnin = 200, thin = 10 , seed = 1,
              external.sep = TRUE, keepProbbase.level = TRUE)
summary(fit1)
summary(fit1, top = 10)

# save individual COD distributions to files
summary(fit1, file = "results.csv")

## End(Not run)
```

updateIndiv *Update individual COD probabilities from InSilicoVA Model Fits*

Description

This function updates individual probabilities for each death and provide posterior credible intervals for each estimates.

Usage

```
updateIndiv(object, CI = 0.95, java_option = "-Xmx1g", ...)
```

Arguments

object	Fitted "insilico" object.
CI	Credible interval for posterior estimates.
java_option	Option to initialize java JVM. Default to "-Xmx1g", which sets the maximum heap size to be 1GB.
...	Not used.

Value

object Updated "insilico" object.

Author(s)

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Maintainer: Zehang Li <lizehang@uw.edu>

References

#' Tyler H. McCormick, Zehang R. Li, Clara Calvert, Amelia C. Crampin, Kathleen Kahn and Samuel J. Clark Probabilistic cause-of-death assignment using verbal autopsies, *Journal of the American Statistical Association* (2016), 111(515):1036-1049.

See Also

insilico, get.indiv

Examples

```
## Not run:
data(RandomVA1)
fit1a<- insilico(RandomVA1, subpop = NULL,
                 Nsim = 1000, burnin = 500, thin = 10 , seed = 1,
                 auto.length = FALSE)
summary(fit1a, id = "d199")
```

```
# The following script updates credible interval for individual
fit1b <- updateIndiv(fit1a, CI = 0.95)
summary(fit1b, id = "d199")

## End(Not run)
```

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