Package 'InterVA4'

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Type Package

Title Replicate and analyse InterVA4

Version 1.0

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Description The package provides an R version of the InterVA4 software for coding cause of death from verbal autopsies. It also provides simple graphical representation of individual and population level statistics.

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R topics documented:

InterVA4-package	*Perform InterVA4 algorithm and provide graphical summarization of COD distribution.*

Description

Computes individual cause of death and population cause-specific mortality fractions using the InterVA4 algorithm. Provides a simple graphical representation of the result.

Details

1

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License:	GPL-2

Author(s)

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References

http://www.interva.net/

Examples

```
data(SampleInput)
sample.output<-InterVA(SampleInput, HIV = "h", Malaria = "v", directory = "VA test",
filename = "VA_result", output = "extended", append=FALSE)
```

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causetext	*Translation list of COD codes*

Description

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

Usage

```
data(causetext)
```

Format

A data frame with the translation of COD codes to their names on 68 CODs.

Examples

```
data(causetext)
```

InterVA   *Provide InterVA4 analysis on the data input.*

Description

This function implements the algorithm in the InterVA4 software. It produces individual cause of death and population cause-specific mortality fractions.

Usage

```
InterVA(Input, HIV, Malaria, directory = NULL, filename = "VA_result",
        output = "classic", append = FALSE, replicate = FALSE)
```

Arguments

Input	A matrix input, or data read from csv files in the same format as required by InterVA4. Sample input is included as data(SampleInput).
HIV	An indicator of the level of prevalence of HIV. The input should be one of the following: "h"(high),"l"(low), or "v"(very low).
Malaria	An indicator of the level of prevalence of Malaria. The input should be one of the following: "h"(high),"l"(low), or "v"(very low).
directory	The directory to store the output from InterVA4. It should either be an existing valid directory, or a new folder to be created. If no path is given, the current working directory will be used.
filename	The filename the user wish to save the output. No extension needed. The output is in .csv format by default.
output	"classic": The same deliminated output format as InterVA4; or "extended": deliminated output followed by full distribution of cause of death proability.
append	A logical value indicating whether or not the new output should be appended to the existing file.
replicate	A logical value indicating whether or not the calculation should contain a possible bug in original InterVA4 implementation. If replicate=T, then the output values will be exactly as they would be from calling the InterVA4 program.

Details

InterVA performs the same tasks as the InterVA4. The output is saved in a .csv file specified by user. The calculation is based on the conditional and prior distribution of 68 CODs. The function also could save the full probability distibution of each individual to file. All information about each individual is saved to a va class object.

Value

ID	identifier from batch (input) file
MALPREV	selected malaria prevalence
HIVPREV	selected HIV prevalence
PREGSTAT	most likely pregnancy status
PREGLIK	likelihood of PREGSTAT

PRMAT	likelihood of maternal death
INDET	indeterminate outcome
CAUSE1	most likely cause
LIK1	likelihood of 1st cause
CAUSE2	second likely cause
LIK2	likelihood of 2nd cause
CAUSE3	third likely cause
LIK3	likelihood of 3rd cause
wholeprob	full distribution of causes of death

Author(s)

Zehang Li, Tyler McCormick, Sam Clark

References

http://www.interva.net/

See Also

InterVA.plot

Examples

```
data(SampleInput)
sample.output<-InterVA(SampleInput, HIV = "h", Malaria = "l", directory = "VA test",
filename = "VA_result", output = "extended", append = FALSE, replicate = TRUE)
```

InterVA.plot	*Plot a individual level distribution of va probabilities.*

Description

The function takes input of a single va object and produces a summary plot for it.

Usage

```
InterVA.plot(va, type = "both", min.prob = 0.01, ...)
```

Arguments

va	A va object
min.prob	The minimum probability that is to be plotted in bar chart, or to be labeled in pie chart.
type	An indicator of the type of chart to plot. "pie" for pie chart; "bar" for bar chart and "both" for both.
...	Arguments to be passed to/from graphic function barplot, [pie](pie), and more graphical paramters (see [par](par)). They will affect the main title, size and font of labels, and the radius of the pie chart.

See Also

[Population.summary](#)

Examples

```
data(SampleInput)
sample.output<-InterVA(SampleInput, HIV = "h", Malaria = "v", directory = "VA test",
filename = "VA_result", output = "extended", append = FALSE)

## Individual level summary using pie chart
InterVA.plot(sample.output$VA[[7]], type ="pie", min.prob =0.01,
main = "1st sample VA analysis using pie chart", clockwise = FALSE,
radius = 0.6, cex = 0.6, cex.main = 0.8)


## Individual level summary using bar chart
InterVA.plot(sample.output$VA[[7]],type="bar",min.prob=0.01,
main = "2nd sample VA analysis using bar chart", cex.main = 0.8)
```

Population.summary   *Summarize and plot a population level distribution of va probabilities.*

Description

The function takes input of a list of va object and produces a summary plot for the population distribution.

Usage

```
Population.summary(va, type="both", min.prob = 0.01, ... )
```

Arguments

va	The list of va object to summarize.
min.prob	The minimum probability that is to be plotted in bar chart, or to be labeled in pie chart.
type	An indicator of the type of chart to plot. "pie" for pie chart; "bar" for bar chart and "both" for both.
...	Arguments to be passed to/from graphic function [barplot](#), [pie](#), and more graphical paramters (see [par](#)). They will affect the main title, size and font of labels, and the radius of the pie chart.

Value

dist.cod	The population probability of CODs.

Author(s)

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Examples

```
data(SampleInput)
sample.output<-InterVA(SampleInput, HIV = "h", Malaria = "v", directory = "VA test",
filename = "VA_result", output = "extended", append=FALSE)

## Population level summary using pie chart
population.summary <- Population.summary(sample.output$VA, type = "pie", min.prob = 0.01,
main = "population COD distribution using pie chart", clockwise = FALSE,
radius = 0.7, cex = 0.7, cex.main = 0.8)

## Population level summary using bar chart
population.summary <- Population.summary(sample.output$VA, type = "bar", min.prob = 0.01,
main = "population COD distribution using bar chart", cex.main = 1)
```

---

probbase   *Conditional probability of InterVA4*

Description

This is the table of conditional probabilities of symptoms given CODs. The values are from InterVA-4.1.

Usage

```
data(probbase)
```

Format

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

Examples

```
data(probbase)
```

SampleInput   *10 records of Sample Input*

Description

This is a dataset consisting of 10 arbitrary sample input deaths in the acceptable format of InterVA4. Any data that needs to be analyzed by this package should be in the same format. The orders of the input fields must not be changed.

Usage

```
data(SampleInput)
```

Format

10 arbitrary input records.

Examples

```
data(SampleInput)
```

Index