

Package ‘zGPS.AO’

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Type Package

Title Zero Inflated Gamma Poisson Shrinker with Adverse Event Ontology

Version 0.1.0

Maintainer Bangyao Zhao <byzhao@umich.edu>

Description The method zGPS.AO (Zero Inflated Gamma Poisson Shrinker with AE (Adverse Event) ontology) is based on the zero-inflated negative binomial distribution.

It estimates the association between a specific vaccine and an adverse event group, as well as associations between that vaccine and individual adverse events within the adverse event group. This model handles the adverse event count data with excess zeros and over-dispersion, and it allows borrowing information from adverse event data in the same group. Details can be found in "Data Mining in Large Frequency Tables With Ontology, with an Application to the Vaccine Adverse Event Reporting System."

Bangyao Zhao, Lili Zhao (2020) <arXiv:2010.12471>.

License GPL-3

Encoding UTF-8

LazyData true

Suggests testthat, knitr, rmarkdown

Imports dplyr, pscl (>= 1.5.5), MASS, doRNG, foreach, doParallel, questionr, ggplot2, plotly, viridis, hrbrthemes, parallel

RoxygenNote 7.1.1

Depends R (>= 2.10)

VignetteBuilder knitr

NeedsCompilation no

Author Bangyao Zhao [aut, cre],
Lili Zhao [aut],
Michael Kleinsasser [aut]

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dd.meddra	<i>Medical Dictionary for Regulatory Activities (MedDRA)</i>
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Description

This example data uses the HTML level terms of MedDRA to define AE groups. AE groups may overlap slightly.

Usage

```
dd.meddra
```

Format

An object of class `data.frame` with 12482 rows and 2 columns.

Details

The data contains 2 columns

- AE_NAME Adverse event name
- GROUP_NAME AE group name

merge_list	<i>An example of merge list</i>
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Description

The function 'zinb_analysis_tool' requires users to define the vaccines of interest and which vaccines are merged in to one vaccine type. Here is an example of how to specify the parameter 'merge_list' in that function.

Usage

```
merge_list
```

Format

An object of class list of length 10.

Details

The 'merge_list' should be a list of length *i*. An element of 'merge_list' should be a list of length 2, with the first element to be an vector string containing one or several vaccine names, and the second element to be a single string of vaccine type.

For example, an element of 'merge_list' could be 'list(c('FLUN3', 'FLUN4'),'FLUN')', meaning to merge FLUN3 and FLUN4 into one vaccine type FLUN.

plotly_heatmap	<i>Generate the heatmap (Plotly)</i>
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Description

This function is an advanced visualization tool of group level RRs obtained from the 'zinb_analysis_tool'. It will generate an interactive heatmap with each cell representing the RR of an AE group with a vaccine.

Usage

```
plotly_heatmap(big_data)
```

Arguments

`big_data` The big data.frame from the 'zinb_analysis_tool' function

Value

A heatmap produced by 'plotly::plotly()'

plotly_lambdas	<i>Generate the scatter plot of lambdas (Plotly)</i>
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Description

This function is to visualize the AE level RRs in an AE group interactively.

Usage

```
plotly_lambdas(vaccine_name, AE_grp_name, big_data)
```

Arguments

vaccine_name	The vaccine type to be visualized
AE_grp_name	The AE group name to be visualized
big_data	The big data.frame from the 'zinb_analysis_tool' function

Value

A scatter plot produced by 'plotly::plotly()'

plot_heatmap	<i>Generate the heatmap</i>
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Description

This function is a visualization tool of group level RRs obtained from the 'zinb_analysis_tool'. It will generate a heatmap with each cell representing the RR of an AE group with a vaccine.

Usage

```
plot_heatmap(big_data)
```

Arguments

big_data	The big data.frame from the 'zinb_analysis_tool' function
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Value

A heatmap produced by 'ggplot2::ggplot()'

plot_lambdas	<i>Generate the scatter plot of lambdas</i>
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Description

This function is to visualize the AE level RRs in an AE group.

Usage

```
plot_lambdas(vaccine_name, AE_grp_name, big_data)
```

Arguments

vaccine_name	The vaccine type to be visualized
AE_grp_name	The AE group name to be visualized
big_data	The big data.frame from the 'zinb_analysis_tool' function

Value

A scatter plot produced by 'ggplot2::ggplot()'

vaers_data	<i>The VAERS data</i>
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Description

VAERS stands for the Vaccine Adverse Event Reporting System. This system was created by the Food and Drug Administration (FDA) and Centers for Disease Control and Prevention (CDC) to receive reports about adverse events that may be associated with vaccines.

Usage

```
vaers_data
```

Format

An object of class tbl_df (inherits from tbl, data.frame) with 1017599 rows and 3 columns.

Details

This example data contains VAERS reports from 2005-01-01 to 2018-12-31 with the patient age ranging from 2 to 49.

This are three columns in this data:

- ID The unique identifier of each report in VAERS data
- VAX_TYPE Vaccine type(s) in the report
- AE_NAME Adverse event(s) in the report

zinb_analysis_tool *Perform ZINB analysis on real data.*

Description

Perform ZINB analysis on real data.

Usage

```
zinb_analysis_tool(
  grp_data,
  pair_data,
  merge_list,
  min_freq = 15,
  min_size = 20,
  n_perm = 20,
  n_copies = round(detectCores()/2),
  seed = 1234
)
```

Arguments

grp_data	a data.frame containing the following 2 columns: <ul style="list-style-type: none"> • AE_NAME: The name of the Adverse Event (AE) • GROUP_NAME: The AE group of the AE
pair_data	a data.frame containing the following 3 columns: <ul style="list-style-type: none"> • ID: The unique identifier of the report • VAX_TYPE: The vaccines appeared in the report • AE_NAME: The AEs appeared in the report Please notice that this data reflects all the vaccine-AE combinations. If n1 AEs and n2 vaccines are mentioned in one reports, then n1*n2 pairs should be generated in the data.
merge_list,	a list with nesting lists, indicating which vaccines are of interest and which vaccines are to be merged. For example, if you are interested in vaccines FLU3 and FLU4, and you want to merge them into one vaccine FLU, you would like to add list(c('FLU3','FLU4'),'FLU') in this list
min_freq	a non-negative integer indicating the criteria for scarce AEs. If an AE appears less than 'min_freq' times in the data.frame pair_data, it will be labeled as scarce and be ignored in the study. It can be set to 0.
min_size	a positive integer indicating the criteria for small AE groups. If an AE group contains less than 'min_size' AEs, it will be label as a small AE group, and be ignored from the study.
n_perm	a positive integer that decide the number of permutations to determine the p value for observed RRs.

n_copies	a positive integer indicating the number of permutations can be done in parallel. This number is default to half of the computer's number of cores.
seed	to obtain reproducible result, you may want to set this seed.

Value

A big data.frame containing the following columns:

- y: The weighted count of the vaccine-AE cell
- E: The baseline frequency of the vaccine-AE cell
- vaccine: The vaccine type
- AE_grp: The AE group
- AE: The Adverse Event (AE)
- s: The group level RR for this vaccine
- r: The over dispersion parameter for this AE group
- p: The zero component probability of this vaccine-AE_grp combination
- beta: The log mean parameter for this vaccine-AE_grp combination
- lambda_hat: The individual AE RR (Bayes Estimator)
- s_pval: The p value for s
- lambda_pval: The p value for lambda_hat (individual AE RR)

Examples

```
data(vaers_data)
data("dd.meddra")
data("merge_list")
big_data = zinb_analysis_tool(dd.meddra[1:10000,],
                             vaers_data[1:10000,],
                             merge_list,
                             n_perm = 2,
                             n_copies = 2)
```

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