Package ‘visae’

January 16, 2021

Type  Package
Title  Visualization of Adverse Events
Version  0.1.0
Description  Implementation of Shiny app to visualize adverse events based on the Common Terminology Criteria for Adverse Events using stacked correspondence analysis as described in Diniz et. al (2021) <arXiv:2101.03454>.

BugReports  https://github.com/dnzmarcio/visae/issues
License  GPL (>= 2)
Depends  shiny (>= 1.4.0), dplyr (>= 1.0.0), ggplot2 (>= 3.3.0), magrittr (>= 1.5.0)
Imports  shinyjs (>= 1.1), ca (>= 0.71), tidyr (>= 1.1.0), ggrepel (>= 0.8.2), rlang (>= 0.4.6), DT (>= 0.13)
Encoding  UTF-8
LazyData  true
RoxygenNote  7.1.1
NeedsCompilation  no
Author  Marcio A. Diniz [aut, cre, cph],
        Michael Luu [aut]
Maintainer  Marcio A. Diniz <marcio.diniz@cshs.org>
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R topics documented:

ca_ae ................................................................. 2
run_ca ................................................................. 3
Index  5
Correspondence Analysis of Adverse Events

Usage

```r
correspondence_analysis_of_adverse_events(
    data,
    id,
    group,
    ae_class,
    label = "AE",
    contr_indicator = TRUE,
    mass_indicator = TRUE,
    contr_threshold = NULL,
    mass_threshold = NULL
)
```

Arguments

data: data.frame or tibble object.
id: unquoted expression indicating the variable name in data that corresponds to the id variable.
group: unquoted expression indicating the variable name in data that corresponds to the group variable.
ae_class: unquoted expression indicating the variable name in data that corresponds to AE class.
label: character value indicating the column name of AE class in resulting tables.
contr_indicator: logical value indicating the use of color intensity to represent the maximum contribution of each ae_class.
mass_indicator: logical value indicating the use of dot size to represent the overall relative frequency of each ae_class.
contr_threshold: numerical value between 0 and 1 filtering ae_class with contribution greater than contr_threshold.
mass_threshold: numerical value between 0 and 1 filtering ae_class with mass greater than mass_threshold.
**run_ca**

**Value**

- a list of
  - `tab_abs`: a tibble showing absolute frequency of `ae_class` by group;
  - `tab_rel`: a tibble showing percent of `ae_class` by group;
  - `total_inertia`: a numerical value indicating the total inertia;
  - `tab_inertia`: a tibble showing inertia broken down by dimension and the percent relative to the total inertia;
  - `asymmetric_plot`: a contribution biplot.

**References**


**Examples**

```r
library(magrittr)
library(dplyr)

id <- rep(1:50, each = 2)
group <- c(rep("A", 50), rep("B", 50))
ae_grade <- sample(1:5, size = 100, replace = TRUE)
ae_domain <- sample(c("D", "E"), size = 100, replace = TRUE)
ae_term <- sample(c("F", "G", "H", "I"), size = 100, replace = TRUE)
df <- tibble(id = id, trt = group,
  ae_g = ae_grade, ae_d = ae_domain, ae_t = ae_term)
test <- df %>% ca_ae(. , id = id, group = trt, ae = ae_g, label = "AE",
  contr_indicator = TRUE, mass_indicator = TRUE,
  contr_threshold = 0.01, mass_threshold = 0.01)
```

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**run_ca**  
*Shiny App for Correspondence Analysis of Adverse Events*

**Description**

Shiny App for Correspondence Analysis of Adverse Events

**Usage**

```r
run_ca(
  data,
  id,
  group,
  ae_grade = NULL,
)```
```r
run_ca

  ae_domain = NULL,
  ae_term = NULL,
  ae_cycle = NULL

Arguments

data  data.frame or tibble object.
id    unquoted expression indicating the variable name in data that corresponds to the id variable.
group unquoted expression indicating the variable name in data that corresponds to the group variable.
ae_grade unquoted expression indicating the variable name in data that corresponds to AE grade class.
ae_domain unquoted expression indicating the variable name in data that corresponds to AE domain class.
ae_term unquoted expression indicating the variable name in data that corresponds to AE term class.
ae_cycle unquoted expression indicating the variable name in data that corresponds to AE cycle.

Value

an interactive web application to perform correspondence analysis for adverse event data.

Examples

## Not run:
library(magrittr)
library(dplyr)
patient_id <- 1:100
group <- c(rep("A", 50), rep("B", 50))
ae_grade <- sample(1:5, size = 100, replace = TRUE)
ae_domain <- sample(c("C", "D"), size = 100, replace = TRUE)
ae_term <- sample(c("E", "F", "G", "H"), size = 100, replace = TRUE)
dt <- tibble(patient_id = patient_id, trt = group,
             ae_g = ae_grade, ae_d = ae_domain, ae_t = ae_term)
dt %>% run_ca(., group = trt,
             id = patient_id,
             ae_grade = ae_g,
             ae_domain = ae_d,
             ae_term = ae_t)

## End(Not run)
```
Index

c_a_ae, 2
run_ca, 3