Package 'AEenrich'

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Version 1.0.0

Title Adverse Event Enrichment Tests

Type Package

Description We extend existing gene enrichment tests to perform adverse
event enrichment analysis. Unlike the continuous gene expression data,
adverse event data are counts. Therefore, adverse event data has many zeros
and ties. We propose two enrichment tests. One is a modified Fisher's exact
test based on pre-selected significant adverse events, while the other is
based on a modified Kolmogorov-Smirnov statistic. ``Adverse event enrichment
tests using VAERS'' Shuoran Li, Lili Zhao (2020) <arXiv:2007.02266>.

License GPL-2

Encoding UTF-8

LazyData true

Biarch true

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biocViews

URL

BugReports

RoxygenNote 7.1.1

Suggests testthat

NeedsCompilation no

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R topics documented:

AEenrich-package   *AEenrich: Adverse Event Enrichment Tests*

Description

Adverse event (AE) enrichment analysis. Unlike the continuous gene expression data, AE data are counts. Therefore, AE data has many zeros and ties. We propose two enrichment tests. AEFisher is a modified Fisher's exact test based on pre-selected significant AEs, while AEKS is based on a modified Kolmogorov-Smirnov statistic.

Use the function enrich to fit models and inspect results.

See our [Github home page](#) or run ?enrich for examples.

Author(s)

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See Also

Useful links:

- <https://github.com/umich-biostatistics/AEenrich>

- Report bugs at <https://github.com/umich-biostatistics/AEenrich/issues>

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enrich | *Perform Adverse Event Enrichment Tests*

Description

Adverse event (AE) enrichment analysis. Unlike the continuous gene expression data, AE data are counts. Therefore, AE data has many zeros and ties. We propose two enrichment tests. AEFisher is a modified Fisher's exact test based on pre-selected significant AEs, while AEKS is based on a modified Kolmogorov-Smirnov statistic.

Usage

```
enrich(
  df,
  dd.group,
  drug.case,
  drug.control = NULL,
  method = "aeks",
  n_iter = 1000,
  q.cut = 0.1,
  or.cut = 1.5,
  seed = NULL,
  verbose = FALSE
)
```

Arguments

df	a data.frame with 3 columns. The function allows two data types. One type (data type I) consists data on the report level, including ID, Drug type and AE name. The other type (data type II) consists of aggregated data, including drug type, AE name and Count. Data should be ordered as ID, Drug type, AE name in data type I and Drug type, AE name, Count in data type II.
dd.group	a data.frame with AE name and Group name. This data.frame have the group information for each individual AE.
drug.case	a character string for the target drug of interest.
drug.control	a character string for the reference drug. If NULL(default), all other drugs combined are the reference.
method	a character string specifying the method for the enrichment test. It must take "aeks" (default) or "aefisher"; "aeks" is the rank-based enrichment test, and "aefisher" is the modified Fisher enrichment test. See details described in the paper (see reference section of this document).
n_iter	an integer value specifying the number of iterations in aeks method or the number of permutations in aefisher.
q.cut	a numerical value specifying the significance cut for q value of AEs in aefisher.

or.cut   a numerical value specifying the significance cut for odds ratio of AEs in ae-
                 fisher.

seed   a numeric seed for reproducible analysis.

verbose   logical, if TRUE, print iterations. If FALSE, silence printing to the console.
                 Default is verbose = FALSE.

Value

A list containing 2 data.frames named **Final_result** and **AE_info**.

The **Final_result** data.frame contains the following columns:

- GROUP_NAME: AE group names
- ES: enrichment score
- p_value: p value of the enrichment test
- GROUP_SIZE: number of AEs per group

The **AE_info** in 'aeks' contains the following columns:

- AE_NAME: AE names
- Ratio: reporting rate
- p_value: p value for AE-drug association

The **AE_info** in 'aefisher' contains the following columns:

- AE_NAME: AE names
- OR: Odds ratio for AE-drug association
- p_value: p value for AE-drug association

References

Li, S. and Zhao, L. (2020). Adverse event enrichment tests using VAERS. arXiv:2007.02266.

Examples

```
drug.case = 'FLUN'
drug.control = 'FLU'

# AEKS
## Input data using data Type I
KS_result1 = enrich(df = flu1, dd.group = group, drug.case = drug.case,
                    drug.control = drug.control, method = 'aeks', n_iter = 10)
## Input data using data Type II

KS_result2 = enrich(df = flu2, dd.group = group, drug.case = drug.case,
                    drug.control = drug.control, method = 'aeks', n_iter = 1000)

# AEFisher
fisher_result1 = enrich(df = flu1, dd.group = group, drug.case = drug.case,
```

```
                              drug.control = drug.control, method = 'aefisher',
                              n_iter = 1000, q.cut = 0.1, or.cut=1.5)
```

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flu1   *Flu Vaccine Adverse Event Data*

Description

Adverse event data in the long format. Each row is a single adverse event.

Usage

```
flu1
```

Format

An object of class data.frame with 12622 rows and 3 columns.

Details

- VAERS_ID Event ID
- VAX_TYPE Vaccine type
- AE_NAME Adverse event name

---

flu2   *Flu Vaccine Adverse Event Data*

Description

Adverse event data in the short format. Each row is a count of adverse events with the given name.

Usage

```
flu2
```

Format

An object of class data.frame with 1603 rows and 3 columns.

Details

- VAX_TYPE Vaccine type
- AE_NAME Adverse event name
- Count Frequency of adverse event

---

group   *Group Structure Data*

Description

Identifies which group each set of adverse events belongs.

Usage

```
group
```

Format

An object of class `data.frame` with 434 rows and 2 columns.

Details

- AE_NAME Adverse event name
- GROUP_NAME Group name

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