Package 'faersquarterlydata'

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Type Package

Title FDA Adverse Event Reporting System Quarterly Data Extracting Tool

Version 1.2.0

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Description

An easy framework to read FDA Adverse Event Reporting System XML/ASCII files <https://www.fda.gov/drugs/questions-and-answers-fdas-adverse-event-reporting-system-faers/fda-adverse-event-reporting-system-faers-latest-quarterly-data-files>.

License GPL (>= 3)

Imports data.table, tibble, xml2, tableone, tidyr, dplyr, stringr, stats, utils

Encoding UTF-8

LazyData true

Depends R (>= 3.5.0)

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.2.3

NeedsCompilation no

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Repository CRAN

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als_faers_data   *List ASCII data example*

Description

A list containing data from FDA website. The list only contains safety reports which the ADR
primary suspect drug was indicated for ALS. List originated from retrieve_faersascii

Usage

```
als_faers_data
```

Format

A data frame with 200 rows and 38 columns:

Source

<https://www.fda.gov/drugs/questions-and-answers-fdas-adverse-event-reporting-system-faers/fda-adverse-event-reporting-system-faers-latest-quarterly-data-files>

`als_faers_data_unified`

Tabular ASCII data example

Description

A subset of data from FAERS data. One row corresponds to one adverse drug reaction. All the ADR in this subset have a primary suspect drug indicated for ALS. Data frame originated from [unify_tabular_ascii](#)

Usage

```
als_faers_data_unified
```

Format

A data frame with 1635 rows and 40 columns.

`arrange_date`

Convert a date string into a date format

Description

Convert a date string into a date format

Usage

```
arrange_date(date_string)
```

Arguments

date_string   A string vector with multiple formats (8, 6 or 4 digits)

Value

A converted Date

Examples

```
arrange_date("2020")
arrange_date("202006")
arrange_date("20200601")
```

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estimate_chisq   *Estimate Chi-Squared test with yates correction*

Description

Estimate Chi-Squared test with yates correction

Usage

```
estimate_chisq(n11, n10, n01, n00)
```

Arguments

n11	Number of events of interest within the group of interest
n10	Number of events of interest from all groups
n01	Number of all events within the group of interest
n00	Number of all events from all groups

Value

list with Chi-squared statistic and p-value

Examples

```
estimate_chisq(n11 = 20, n10 = 10, n01 = 200, n00 = 200)
```

---

estimate_infoc   *Estimate Information Component*

Description

Estimate Information Component

Usage

```
estimate_infoc(n11, n10, n01, n00)
```

Arguments

n11	Number of events of interest within the group of interest
n10	Number of events of interest from all groups
n01	Number of all events within the group of interest
n00	Number of all events from all groups

Value

List with Information Component estimate and its 0.95 IC

Examples

```
estimate_infoc(n11 = 20, n10 = 10, n01 = 200, n00 = 200)
```

---

estimate_prr *Estimate Proportional Reporting Odds Ratio*

Description

Estimate Proportional Reporting Odds Ratio

Usage

```
estimate_prr(n11, n10, n01, n00, ic_range = 0.95)
```

Arguments

n11	Number of events of interest within the group of interest
n10	Number of events of interest from all groups
n01	Number of all events within the group of interest
n00	Number of all events from all groups
ic_range	Confidence Interval range

Value

Proportional Reporting Odds Ratio

Examples

```
estimate_prr(n11 = 20, n10 = 10, n01 = 200, n00 = 200)
```

---

estimate_ror *Estimate Reporting Odds Ratio*

Description

Estimate Reporting Odds Ratio

Usage

```
estimate_ror(n11, n10, n01, n00, ic_range = 0.95)
```

Arguments

n11	Number of events of interest within the group of interest
n10	Number of events of interest from all groups
n01	Number of all events within the group of interest
n00	Number of all events from all groups
ic_range	Confidence Interval range

Value

list with ROR estimate and a vector with the IC boundaries

Examples

```
estimate_ror(n11 = 20, n10 = 10, n01 = 200, n00 = 200, ic_range = 0.90)
```

---

estimate_ror_bygroup *Estimate Measures of Association*

Description

Estimate Measures of Association

Usage

```
estimate_ror_bygroup(
  tabular_faers_data,
  group_of_interest_col = NULL,
  group_of_interest_ref = NULL,
  rename_vector = NULL,
  event_of_interest_col = NULL,
  ...
)
```

Arguments

tabular_faers_data

> FAERS tabular format. Output of function retrieve_faersxml or retrieve_faersxml_all

group_of_interest_col

> a string, specifying the group of interest. Must me a column name of 'tabular_faers_data', and this columns should only contain two unique values.

group_of_interest_ref

> a string, specifying the group of interest reference. Must me a value from the group of interest column.

rename_vector   optional. named vector to rename the group of interest, in order to show up in a

event_of_interest_col

> a string, specifying the event of interest. Must me a column name of 'tabular_faers_data'.

...   arguments passed to 'estimate_ror' like 'ic_range'.

Value

tibble with the event of interest counts, group of interest counts and the respective estimated measures of association (ROR and its IC, PRR and its IC, Information Component and Chi-squared statisti with Yates correction.

Examples

```
estimate_ror_bygroup(tabular_faers_data = dplyr::filter(als_faers_data_unified,
sex %in% c("M", "F") ),
group_of_interest_col = "sex",
group_of_interest_ref = "M",
event_of_interest_col = "pt")
```

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faersxml_to_r   *Convert FAERS xml to an R list*

Description

Convert FAERS xml to an R list

Usage

```
faersxml_to_r(xml_address)
```

Arguments

xml_address   XML address file

Value

a list containing all the elements from 'xml_address'

---

get_duplicate_caseids   *Get duplicated caseIDs*

Description

Retrieve the duplicated caseIDs to remove from the analysis.

Usage

```
get_duplicate_caseids(duplicates_dir = NULL)
```

Arguments

duplicates_dir   directory path where the text files with the duplicates information are.

Value

an integer vector with all the caseids to be removed

---

products_fda   *List of approved products by FDA*

Description

List of approved products by FDA

Usage

```
products_fda
```

Format

A data frame.

Source

<https://www.fda.gov/drugs/drug-approvals-and-databases/drugsfda-data-files>

retrieve_faersascii	*Read FAERS ascii files*

Description

Read ASCII files from a directory, removing the duplicates.

Usage

```
retrieve_faersascii(
  ascii_dir,
  cache_path = NULL,
  drug_indication_pattern = NULL,
  drug_pattern = NULL,
  primary_suspect = TRUE,
  ...
)
```

Arguments

ascii_dir	directory path where ascii files are
cache_path	(optional) a string. Must have a ".Rdata" extension to save the read tabular formats in each loop.
drug_indication_pattern	
	(optional) a string.filter ADRs with a specific drug indication pattern (**stringr** sintax)
drug_pattern	(optional) a string. filter ADRs with a specific drug name pattern (**stringr** sintax)
primary_suspect	
	(optional) a string.
...	directory with duplicate information to be passed to get_duplicate_caseids

Value

A list with binded tibbles retrieved from files.

retrieve_faersxml	*Convert FAERS xml to tabular format*

Description

Convert FAERS xml to tabular format

Usage

```
retrieve_faersxml(
  xml_address,
  reaction_wise = TRUE,
  drug_wise = FALSE,
  drug_indication_pattern = NULL
)
```

Arguments

xml_address   XML address to be read

reaction_wise   each row corresponds to a reaction (if TRUE, drug_wise cannot be TRUE)

drug_wise   each row corresponds to a drug (if TRUE, reaction_wise cannot be TRUE)

drug_indication_pattern

                filter by ADR with a specific drug indication pattern (**stringr** sintax)

Value

A tibble corresponding to the XML file

---

   retrieve_faersxml_all   *Convert FAERS a number of xml files to tabular format*

Description

Convert FAERS a number of xml files to tabular format

Usage

```
retrieve_faersxml_all(xml_address_vector, ..., cache_path = NULL)
```

Arguments

xml_address_vector

                Vector with XML addresses to be read

...   arguments to be passed to retrieve_faersxml

cache_path   a string. Must have a ".Rdata" extension to save the read tabular formats in each
                loop.

Value

A binded tibble with all the tibbles returned from 'retrieve_faersxml'

---

retrieve_unique_info *Retrieve unique drug and ADR information values from XML files*

Description

Retrieve unique drug and ADR information values from XML files

Usage

```
retrieve_unique_info(xml_address_vector, ...)
```

Arguments

xml_address_vector

> Vector with XML addresses to be read

...   arguments to be passed to [retrieve_faersxml](#)

Value

A list with all the unique information on FAERS variables

---

summary_faersdata *FAERS description*

Description

FAERS description

Usage

```
summary_faersdata(tabular_faers_data)
```

Arguments

tabular_faers_data

> a tibble corresponding to the unified FAERS tabular format. Output of function [unify_tabular_ascii](#)

Value

A list with a findings summary

Examples

```
summary_faersdata(als_faers_data_unified)
```

---

unify_tabular_ascii   *Unify the list to a tabular format*

Description

Turn the list elements returned from retrieve_faersascii into a tabular format

Usage

```
unify_tabular_ascii(ascii_list)
```

Arguments

ascii_list   list from retrieve_faersascii

Value

A data frame representing FAERS data, with all components from the list joined.

Examples

```
unify_tabular_ascii(ascii_list = als_faers_data)
```

---

unzip_faerszip   *Unzip FAERS zip folders*

Description

Unzip FAERS zip folders

Usage

```
unzip_faerszip(zip_folders_dir, ex_dir)
```

Arguments

zip_folders_dir

        directory containing FAERS zip folders

ex_dir   directory to be exported the unzipped files

Value

None. Just unzips the folders to a specified location.

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