Package ‘faersquarterlydata’

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Type Package

Title FDA Adverse Event Reporting System Quarterly Data Extracting Tool

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als_faers_data

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

```r
als_faers_data
```

Format

A data frame with 200 rows and 38 columns:

Source

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")
estimate_chisq  \textit{Estimate Chi-Squared test with yates correction}

\begin{description}
\item[Description] Estimate Chi-Squared test with yates correction
\item[Usage] \texttt{estimate\_chisq(n11, n10, n01, n00)}
\item[Arguments]
\begin{itemize}
  \item \texttt{n11} Number of events of interest within the group of interest
  \item \texttt{n10} Number of events of interest from all groups
  \item \texttt{n01} Number of all events within the group of interest
  \item \texttt{n00} Number of all events from all groups
\end{itemize}
\item[Value] list with Chi-squared statistic and p-value
\item[Examples] \texttt{estimate\_chisq(n11 = 20, n10 = 10, n01 = 200, n00 = 200)}
\end{description}

estimate_infoc  \textit{Estimate Information Component}

\begin{description}
\item[Description] Estimate Information Component
\item[Usage] \texttt{estimate\_infoc(n11, n10, n01, n00)}
\item[Arguments]
\begin{itemize}
  \item \texttt{n11} Number of events of interest within the group of interest
  \item \texttt{n10} Number of events of interest from all groups
  \item \texttt{n01} Number of all events within the group of interest
  \item \texttt{n00} Number of all events from all groups
\end{itemize}
\end{description}
estimate_prr

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**

```r
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**

```r
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**

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


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
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
### retrieve_faersascii

**Read FAERS ascii files**

**Description**

Read ASCII files from a directory, removing the duplicates.

**Usage**

```r
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
**retrieve_faersxml**

**Usage**

```r
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** syntax)

**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**

```r
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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