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 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
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  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
**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**
```
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 `retrieved_faersxml` or `retrieved_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**

```r
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")
```

---

**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`

---

going_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**
```
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** syntax)
- `drug_pattern` (optional) a string. filter ADRs with a specific drug name pattern (**stringr** syntax)
- `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** 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

`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**

Retrieves unique drug and ADR information values from XML files.

**Description**

Retrieve unique drug and ADR information values from XML files.

**Usage**

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

**Arguments**

- `xml_address_vector`
  - Vector with XML addresses to be read
- `...`
  - Arguments to be passed to `retrieved_faersxml`

**Value**

A list with all the unique information on FAERS variables.

---

**summary_faersdata**

FAERS description.

**Description**

FAERS description.

**Usage**

```r
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.
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.

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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