

# Package ‘faersquarterlydata’

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**Type** Package

**Title** FDA Adverse Event Reporting System Quarterly Data Extracting Tool

**Version** 1.3.0

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**Description** An easy framework to read FDA Adverse Event Reporting System XML/ASCII 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** 7.3.2

**NeedsCompilation** no

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**Repository** CRAN

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als_faers_data	<i>List ASCII data example</i>
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### 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/fdas-adverse-event-reporting-system-faers/fda-adverse-event-reporting-system-faers-latest-quarterly-data-files/>>

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als_faers_data_unified	<i>Tabular ASCII data example</i>
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### 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.

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arrange_date	<i>Convert a date string into a date format</i>
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**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	<i>Estimate Chi-Squared test with yates correction</i>
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**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)
```

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estimate_infoc	<i>Estimate Information Component</i>
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**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)
```

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estimate_prr	<i>Estimate Proportional Reporting Odds Ratio</i>
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**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)
```

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estimate_ror	<i>Estimate Reporting Odds Ratio</i>
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**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)
```

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estimate\_ror\_bygroup *Estimate Measures of Association*

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**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 be a column name of 'tabular\_faers\_data', and this column should only contain two unique values.

`group_of_interest_ref` a string, specifying the group of interest reference. Must be 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 be 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 statistic 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	<i>Convert FAERS xml to an R list</i>
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**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'

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get_duplicate_caseids	<i>Get duplicated caseIDs</i>
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**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

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products_fda	<i>List of approved products by FDA</i>
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**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	<i>Read FAERS ascii files</i>
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**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.

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retrieve_faersxml	<i>Convert FAERS xml to tabular format</i>
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### 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*

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### 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 <a href="#">retrieve_faersxml</a>
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*

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### 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 <a href="#">retrieve_faersxml</a>

### Value

A list with all the unique information on FAERS variables

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summary_faersdata	<i>FAERS description</i>
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**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)
```

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unify_tabular_ascii	<i>Unify the list to a tabular format</i>
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**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)
```

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unzip_faerszip	<i>Unzip FAERS zip folders</i>
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**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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