Package 'smoothy'

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Type Package

Title Automatic Estimation of the Most Likely Drug Combination using Smooth Algorithm

Version 1.0.0

Description A flexible moving average algorithm for modeling drug exposure in pharmacoepidemiology studies as presented in the article: Ouchi, D., Giner-Soriano, M., Gómez-Lumbreras, A., Vedia Urgell, C.,Torres, F., & Morros, R. (2022). ``Automatic Estimation of the Most Likely Drug Combination in Electronic Health Records Using the Smooth Algorithm : Development and Validation Study." JMIR medical informatics, 10(11), e37976. <doi:10.2196/37976>.

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Encoding UTF-8

RoxygenNote 7.2.3

Depends R (>= 4.3)

Imports dplyr, tidyr (>= 1.3.0), zoo (>= 1.8), stringr

LazyData true

Suggests knitr, rmarkdown, ggplot2, gridExtra

VignetteBuilder knitr

NeedsCompilation no

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Contents

`drugstreatment` *Drug Administration Data*

Description

This dataset contains information about drug administration. Each row represents a unique drug administration event.

Usage

```
drugstreatment
```

Format

A data frame with the following columns:

id Unique identifier for each drug administration event.

start_date The start date of drug administration.

end_date The end date of drug administration.

drug The name of the drug administered.

Examples

```
data("drugstreatment")
head(drugstreatment)
```

`smooth_algorithm` *Apply Smooth Algorithm in a Dataset*

Description

Description part

Usage

```
smooth_algorithm(id, treatment, day, N, width = 61)
```

Arguments

id	Unique identifier of the patient.
treatment	Name of the drug used.
day	Day of the treatment.
N	Number of drugs used in the treatment.
width	An integer specifying the window width (in numbers of days, 61 by default).

Value

A data.frame with the following structure:

id A character vector representing the unique identifier for each patient.

day A character vector representing the date when the treatment was administered to the patients.

treatment A character vector representing the type of treatment given to each patient.

smoothed_treatment A character vector representing the smoothed treatment given to each patient.

Examples

```
library(smoothy)
library(dplyr)

data(drugstreatment)

df <- drugstreatment |>
  filter(id == "01f13c15-d9f1-4106-a04f-976c457edd0a")

structured_df <- smooth_parse(
  id = df$id,
  start_date = df$start_date,
  end_date = df$end_date,
  drug = df$drug,
  study_from = "1970-01-01",
  study_to = "1975-01-01"
)

head(structured_df)

id = structured_df$id
treatment = structured_df$treatment
day = structured_df$day
N = structured_df$N
width = 61

smoothed <- smooth_algorithm(id = id, treatment = treatment, day = day, N = N, width = width)
head(smoothed)
```

`smooth_deparse` *Deparse*

Description

Transforms the Data with a Row by Date to a Row by Individual.

Usage

```
smooth_deparse(id, day, treatment)
```

Arguments

`id`	Unique identifier of the patient.
`day`	Day of the treatment.
`treatment`	A character vector representing the type of treatment given to each patient.

Value

A data.frame with the following structure:

id A character vector representing the unique identifier for each patient.

start_date Start date of the treatment.

end_date End date of the treatment.

treatment A character vector representing the type of treatment given to each patient.

Examples

```
library(smoothy)
library(dplyr)

data(drugstreatment)

my_data <- filter(drugstreatment, id == "01f13c15-d9f1-4106-a04f-976c457edd0a")

structured_df <- smooth_parse(
  id = my_data$id,
  start_date = my_data$start_date,
  end_date = my_data$end_date,
  drug = my_data$drug,
  study_from = "1970-01-01",
  study_to = "1975-01-01"
)

head(structured_df)

id = structured_df$id
treatment = structured_df$treatment
```

```
day = structured_df$day
N = structured_df$N
width = 61

smoothed <- smooth_algorithm(id = id, treatment = treatment, day = day, N = N, width = width)

head(smoothed)

deparsed_treatment <- smooth_deparse(smoothed$id, smoothed$day, smoothed$treatment)
deparsed_smothed <- smooth_deparse(smoothed$id, smoothed$day, smoothed$smoothed_treatment)
```

`smooth_diff` *Compute the Difference Between Initial and Smoothed Treatment*

Description

This function computes the differences between the initial treatment and the treatment when it's smoothed.

Usage

```
smooth_diff(treatment, smoothed_treatment)
```

Arguments

`treatment`	a character vector containing the original treatment data..
`smoothed_treatment`	a character vector containing the smoothed treatment return by `smooth_algorithm` function.

Value

A data.frame with three columns: diff_type , diff, change and treatment:

type A character vector representing indicating the type of difference computed.

days_changed The number of different items.

proportion_of_change The proportion of difference computed as number of diferent rows over number of rows.

treatment A character vector representing the type of treatment given to each patient.

Examples

```
library(smoothy)
library(dplyr)

data(drugstreatment)

my_data <- filter(drugstreatment, id == "01f13c15-d9f1-4106-a04f-976c457edd0a")

structured_df <- smooth_parse(
  id = my_data$id,
  start_date = my_data$start_date,
  end_date = my_data$end_date,
  drug = my_data$drug,
  study_from = "1970-01-01",
  study_to = "1975-01-01"
)

head(structured_df)

id = structured_df$id
treatment = structured_df$treatment
day = structured_df$day
N = structured_df$N
width = 61

smoothed <- smooth_algorithm(id = id, treatment = treatment, day = day, N = N, width = width)

head(smoothed)

smooth_diff(treatment = smoothed$treatment, smoothed_treatment = smoothed$smoothed_treatment)
```

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smooth_parse *Transform Data to be Used in* smooth_algorithm() *Function*

Description

This function transforms the data to obtain the daily treatment.

Usage

```
smooth_parse(
  id,
  start_date,
  end_date,
  drug,
  study_from = min(start_date),
  study_to = max(end_date)
)
```

Arguments

id	Unique identifier of the patient.
start_date	Start date of the treatment.
end_date	End date of the treatment.
drug	Name of the drug used.
study_from	A date indicating when the study start.
study_to	A date indicating when the study finish.

Value

A data.frame with the following structure:

id Unique identifier of the patient.

drug Name of the drug used.

day Day of the treatment.

N Number of drugs used in the treatment

Examples

```
library(smoothy)
library(dplyr)

data(drugstreatment)

df <- drugstreatment |>
  filter(id == "01f13c15-d9f1-4106-a04f-976c457edd0a")

structured_df <- smooth_parse(
  id = df$id,
  start_date = df$start_date,
  end_date = df$end_date,
  drug = df$drug,
  study_from = "1970-01-01",
  study_to = "1975-01-01"
)

head(structured_df)
```

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