Package 'polypharmacy'

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Type Package

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Title Calculate several polypharmacy indicators

Description Analyse prescription drug deliveries to calculate several indicators of polypharmacy corresponding to the various definitions found in the literature.

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BugReports https://github.com/guiboucher/polypharmacy/issues

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Imports data.table (>= 1.13.0),
doParallel (>= 1.0.16),
foreach (>= 1.5.1),
itertools (>= 0.1.3),
lubridate (>= 1.7.9),
parallel (>= 4.0.3),
stringr (>= 1.4.0)

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RoxygenNote 7.1.1

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Suggests knitr,
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VignetteBuilder knitr

Depends R (>= 2.10)

Config/testthat/edition 3

R topics documented:

polypharmacy-package   *Calculate several polypharmacy indicators*

Description

This package analyse prescription drug deliveries to calculate several indicators of polypharmacy corresponding to the various definitions found in the literature.

Details

It is essential to know the concepts used to calculate the various polypharmacy indicators to adequately use this package.
The core of the package is the data_process() function that creates the data.table of drug treatments by restructuring the drug delivery records (usually extracted from a pharmacy or a health insurance information system) into continuous periods of drug availability (called drug treatments), applying user-defined arguments such as the grace periods between renewals or the longest treatment duration that an individual may accumulate through the successive renewals.

Then, each polypharmacy indicator can be computed using the corresponding function (ind_simult(), ind_stdcumul(), ind_wcumul(), ind_stdcontinuous(), ind_ucontinuous()) or using the overall function indicators() to select the desired indicator(s) to be calculated at once.

Prior to running data_process() the user may need to pre-process the table of original drug delivery records to break down combination drug into their individual components (drugs_bkdn()) and/or to overwrite some delivery durations of specified drugs with constant durations (cst_trt_dur()).

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See Also

Useful links:

- Report bugs at https://github.com/guiboucher/polypharmacy/issues

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cst_deliv_duration *Constant delivery duration drugs*

Description

Overwrites the delivery durations with constant durations for each drug code listed in a user-provided table.

Usage

```
cst_deliv_duration(
  Rx_deliv,
  Rx_drug_code,
  Rx_deliv_dur,
  Cst_deliv_dur,
  Cst_drug_code,
  Cst_duration
)
```

Arguments

Rx_deliv	Name of the table listing all prescription drugs delivered.
Rx_drug_code	Column name of Rx_deliv that contains the drug unique identifier.
Rx_deliv_dur	Column name of the constant treatment duration in the Rx_deliv table.
Cst_deliv_dur	Name of the table that contains the constant delivery durations that will overwrite that in the Rx_deliv table for the specified drug codes.
Cst_drug_code	Column name of Cst_deliv_dur that contains the drug unique identifier (same format as Rx_drug_code).
Cst_duration	Column name of the constant treatment duration in the Cst_deliv_dur table (same format as Rx_deliv_dur).

Value

data.table of the same structure as Rx_deliv.

Examples

```
Rx_dt <- data.frame(id = c(rep(1, 3), rep(2, 2)),
                    code = c("A", "B", "C", "B", "D"),
                    duration = c(rep(15, 3), 15, 90))
cst_dt <- data.frame(codes = c("A", "C", "D"),
                     dur = c(50, 100, 45))
Rx_cst <- cst_deliv_duration(Rx_deliv = Rx_dt,
                             Rx_drug_code = "code", Rx_deliv_dur = "duration",
                             Cst_deliv_dur = cst_dt,
                             Cst_drug_code = "codes", Cst_duration = "dur")
```

---

data_process   *Create the table of the drug treatments*

Description

Reads a table of successive drug delivery records (usually extracted from a pharmacy or a health insurance information system) and creates the table required for the calculation of the polypharmacy indicators by applying various user-defined arguments, incorporating hospital stays into the treatment periods and reconstruct continuous treatment periods by merging quasi continuous and/or overlapping drugs deliveries.

Usage

```
data_process(
  Rx_deliv,
  Rx_id,
  Rx_drug_code,
  Rx_drug_deliv,
  Rx_deliv_dur,
  Cohort = NULL,
  Cohort_id = NULL,
  Hosp_stays = NULL,
  Hosp_id = NULL,
  Hosp_admis = NULL,
  Hosp_discharge = NULL,
  study_start = NULL,
  study_end = NULL,
  grace_fctr = 0.5,
  grace_cst = 0,
  max_reserve = NULL,
  cores = parallel::detectCores(logical = FALSE),
  ...
)
```

Arguments

Rx_deliv	Name of the table listing all prescription drugs deliveries including the run-in period. See *Details*.
Rx_id	Column name of Rx_deliv containing individual unique identifier (any format).
Rx_drug_code	Column name of Rx_deliv that contains the drug unique identifier (any format).
Rx_drug_deliv	Column name of Rx_deliv that contains the dates of the drug delivery (Date format, see *Details*).
Rx_deliv_dur	Column name of Rx_deliv that contains the duration of the delivery (integer number).
Cohort	Name of the table providing the unique identifiers of the study cohort. Only the ids listed in both the Cohort and the Rx_deliv tables will be returned. if Cohort = NULL, all ids of the Rx_deliv table will be returned.
Cohort_id	Column name of Cohort containing individual's unique identifiers (same format as Rx_id). If Cohort is not NULL and Cohort_id is NULL, Cohort_id will take the same value as Rx_id.

`Hosp_stays`	Name of the table listing all hospital stays. (see *Details* for possible format).
`Hosp_id`	Column name of `Hosp_stays` containing individual's unique identifier (same format as `Rx_id`). If `Hosp_stays` is not `NULL` and `Hosp_id` is `NULL`, `Hosp_id` will take the same value as `Rx_id`.
`Hosp_admis`	Column name of `Hosp_stays` that contains the date of admission in hospital (Date format, see *Details*).
`Hosp_discharge`	Column name of Hosp_stays that contains the date of discharge from hospital (Date format, see *Details*).
`study_start, study_end`	
	Defines the first and last day of the study period for which the polypharmacy indicator(s) need to be calculated. All treatment periods prior to `study_start` and past `study_end` are not transcribed into the result table (Date format, see *Details*).
`grace_fctr, grace_cst`	
	Numbers ≥ 0. Two types of grace periods can be applied. One is proportional to the treatment duration of the latest delivery (`grace_fctr`) and the other is a constant number of days (`grace_cst`).
`max_reserve`	An integer number ≥ 0 or `NULL`. Longest treatment duration, in days, that can be stored from successive overlapping deliveries. When `max_reserve = NULL` no limit is applied. When `max_reserve = 0` no accumulation of extra treatment duration is accounted for.
`cores`	The number of cores to use when executing data_process(). See parallel::detectCores.

Details

Variables:

- `Rx_id`, `Cohort_id` and `Hosp_id` columns must be of the same class (integer, numeric, character, ...).
- `Rx_drug_deliv`, `Hosp_admis` and `Hosp_discharge` can be 1) `as.Date('yyyy-mm-dd')`, 2) `as.character('yyyy-mm-dd')` or 3) `as.integer()` where 0 is January 1st, 1970.

Arguments:

- `study_start` and `study_end` can be 1) `as.Date('yyyy-mm-dd')`, 2) `as.character('yyyy-mm-dd')` or 3) `as.integer()` where 0 is January 1st, 1970.

Hospital stays:

Drug availability is assumed to continue during the hospital stay as it is on the day prior admission. The patient is assumed to resume the consumption of the drugs delivered by community pharmacists (as recorded in `Rx_deliv`) the day after hosp_discharge.

Run-in period:

A run-in period is necessary to account for the medications that are available to the individuals on the day of `study_start`. It is recommended to include a run-in period of about 6 months (e.g. 7 months to account for possible delays) as some drugs are delivered for up to 6 months at once.

Grace period:

The grace period is used to determine if two successive deliveries can be considered as a continuous treatment even if there is a gap of several days for which no treatment is apparently available. Two successive deliveries of an identical drug are considered part of a single continuous treatment if the next delivery doesn't occur more than `grace_cst + (grace_fctr × Rx_deliv_dur)` days after the end of the latest drug delivery. The availability of extra drugs accumulated over the successive deliveries is accounted for prior to evaluating the duration of the gap between deliveries.

Performance

For better performance, date columns are converted to integer numbers.

...

`verif_cols=FALSE` : For better performance, you can avoid columns class checking with `verif_cols=FALSE`.
Not recommended.

Value

`data.table` with four (4) variables:

- The individual unique identifier which name is defined by `Rx_id`.

- The drug unique identifier which name is defined by `Rx_drug_code`.

- `tx_start`: The date of initiation of the reconstructed continued treatment (format as date).

- `tx_end`: The date of the last day of the reconstructed continued treatment (format as date).

Examples

```
Rx_dt1 <- data.frame(id = 1, code = 'A',
                date = c('2020-01-01', '2020-01-09', '2020-01-21', '2020-02-05', '2020-02-21'),
                     duration = 10)
Rx1 <- data_process(Rx_deliv = Rx_dt1,
                    Rx_id = 'id', Rx_drug_code = 'code',
                    Rx_drug_deliv = 'date', Rx_deliv_dur = 'duration')

## With a study cohort
Rx_dt2 <- data.frame(id = c(1, 1, 1, 2, 2), code = 'A',
                date = c('2020-01-01', '2020-01-09', '2020-01-21', '2020-02-05', '2020-02-21'),
                     duration = 10)
Cohort_dt2 = data.frame(id = 1, age = 65, sex = 'F', x1 = 'ind8', x2 = 'ex1')
Rx2 <- data_process(Rx_deliv = Rx_dt2,
                    Rx_id = 'id', Rx_drug_code = 'code',
                    Rx_drug_deliv = 'date', Rx_deliv_dur = 'duration',
                    Cohort = Cohort_dt2, Cohort_id = 'id')

## With hospital stays
Hosp_dt2 <- data.frame(id = 1,
                       start = c('2019-01-01', '2019-12-25'),
                       end = c('2019-05-20', '2019-12-31'))
Rx3 <- data_process(Rx_deliv = Rx_dt2,
                    Rx_id = 'id', Rx_drug_code = 'code',
                    Rx_drug_deliv = 'date', Rx_deliv_dur = 'duration',
                    Cohort = Cohort_dt2, Cohort_id = 'id',
                    Hosp_stays = Hosp_dt2, Hosp_id = 'id',
                    Hosp_admis = 'start', Hosp_discharge = 'end')

## With study_start not NULL
Rx3_start <- data_process(Rx_deliv = Rx_dt2,
                         Rx_id = 'id', Rx_drug_code = 'code',
                         Rx_drug_deliv = 'date', Rx_deliv_dur = 'duration',
                         Cohort = Cohort_dt2, Cohort_id = 'id',
                         Hosp_stays = Hosp_dt2, Hosp_id = 'id',
                         Hosp_admis = 'start', Hosp_discharge = 'end',
                         study_start = '2019-12-29')
```

| drug_bkdn | *Translate combination drug deliveries into single active ingredients* |

Description

Replaces each combination drug into several deliveries of elementary active ingredients according to a user-provided correspondence table.

Usage

```
drug_bkdn(Rx_deliv, Rx_drug_code, Combn_drugs, Combn_drug_code, Combn_act_code)
```

Arguments

Rx_deliv	Name of the table listing all prescription drugs deliveries.
Rx_drug_code	Column name of Rx_deliv that contains the combination drug unique identifiers (any format).
Combn_drugs	Name of the correspondence table listing all elementary active ingredients that make up each combination drug.
Combn_drug_code	
	Column name of Combn_drugs that contains the combination drug unique identifiers (same format as Rx_drug_code).
Combn_act_code	Column name of elementary active ingredients that is present in Combn_drugs (same format as Rx_drug_code).

Value

data.table of the same structure as Rx_deliv.

Examples

```
Rx_dt <- data.frame(id = c(1, 1, 2, 2, 2),
                    codeDrug = c(159, 753, 123, 456, 789))
SplitCode <- data.frame(code = c(159, 159, 456, 456, 456),
                        split_code = c(1591, 1592, 4567, 4568, 4569))
Rx_split <- drug_bkdn(Rx_deliv = Rx_dt, Rx_drug_code = "codeDrug",
                      Combn_drugs = SplitCode, Combn_drug_code = "code",
                      Combn_act_code = "split_code")
```

| indicators | *Indicators: All selected* |

Description

Wrapper function for all *Indicator* functions.

Usage

```
indicators(
 processed_tab,
 stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max"),
 method = c("ind_simult", "ind_stdcumul", "ind_wcumul", "ind_stdcontinuous",
    "ind_ucontinuous"),
 stdconti_pdays,
 simult_ind_stats = c("mean", "min", "median", "max"),
 simult_calendar = FALSE,
 stdcumul_nPeriod = 1,
 cores = parallel::detectCores()
)
```

Arguments

processed_tab   Table created by [data_process](#) function.

stats   Statistics to calculate on the drug consumption. See *Details* for possible values.

method   Indicator functions name to use.

stdconti_pdays *stdcontinuous* method: Number of days to create intervals [min; min+pdays] and [max-pdays; max] where a drug should be consumed to be counted.

simult_ind_stats
                simult method: Statistics to calculate for each drug user.

simult_calendar
                simul method: TRUE or FALSE. Create a table indicating the number of drugs consumed for each day for each user (FALSE by default).

stdcumul_nPeriod
                std_cumul method: Integer value greater or equal to 1 and lesser or equal to the total number of days in the study period. If nPeriod is greater than 1, the study period is divide in nPeriod subperiod and the total number of drugs consumption would be the average of the periods.

cores   The number of cores to use when executing ind_simult(). See [parallel::detectCores](#).

Details

stats & simult_ind_stats: Possible values are

- 'mean', 'min', 'median', 'max', 'sd';
- 'pX' where *X* is a value in]0, 100];
- 'q1' = 'p25', 'q2' = 'p50' = 'median', q3 = 'p75'.

Value

list of all indicators

ind_simult	*Indicator: Simultaneous*

Description

Descriptive statistics on daily consumption.

Usage

```
ind_simult(
  processed_tab,
  individual_stats = c("mean", "min", "median", "max"),
 stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max"),
  calendar = FALSE,
  cores = parallel::detectCores()
)
```

Arguments

processed_tab   Table created by [data_process](#) function.

individual_stats

     Statistics to calculate for each drug user. See *Details* for possible values.

stats   Statistics to calculate for each `individual_stats`. See *Details* for possible values.

calendar   `TRUE` or `FALSE`. Create a table indicating the number of drugs consumed for each day for each user (`FALSE` by default).

cores   The number of cores to use when executing ind_simult(). See [parallel::detectCores](#).

Details

`individual_stats` & `stats`: Possible values are

- `'mean'`, `'min'`, `'median'`, `'max'`, `'sd'`;
- `'pX'` where *X* is a value in]0, 100];
- `'q1'` = `'p25'`, `'q2'` = `'p50'` = `'median'`, q3 = `'p75'`.

Value

`list`:

- indic: data.table indicating each `stats` (columns) for each `individual_stats` (rows).
- stats_id: data.table indicating each `individual_stats` for each individuals (all cohort).
- min_conso: data.table indicating each `stats` for the number of days where an individual consume at least X drugs.
- calendar: If `calendar=TRUE`, data.table indicating the number of drugs consumed for each day (only for individuals who has at least 1 day with 1 drug consumption).

Examples

```
dt_process <- data_process(
  Rx_deliv = data.frame(
    ID = c(1, 1, 1, 2, 2), Code = c('A', 'B', 'C', 'D', 'E'),
    Date = c('2020-01-01', '2020-01-05', '2020-01-10', '2020-01-15', '2020-01-26'),
    Duration = c(20, 15, 10, 5, 3)
  ), Rx_id = 'ID', Rx_drug_code = 'Code', Rx_drug_deliv = 'Date', Rx_deliv_dur = 'Duration',
  cores = 1
)
dt_simult <- ind_simult(dt_process, cores = 1)
dt_calendar <- ind_simult(dt_process, calendar = TRUE, cores = 1)
```

---

ind_stdcontinuous   *Indicator: Standard Continuous*

Description

Descriptive statistics.

A drug is counted if there is a least 1 consumption in the interval [min; min+pdays] and another in [max-pdays; max]. In other words, a drug consumption is considered continuous if there is a consumption at the beginning and at the end of the period.r

Usage

```
ind_stdcontinuous(
  processed_tab,
  pdays,
  stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max")
)
```

Arguments

processed_tab	Table created by [data_process](#) function.
pdays	Number of days to create intervals [min; min+pdays] and [max-pdays; max] where a drug should be consumed to be counted.
stats	Statistics to calculate on the drug consumption. See *Details* for possible values.

Details

stats: Possible values are

- 'mean', 'min', 'median', 'max', 'sd';
- 'pX' where *X* is a value in]0, 100];
- 'q1' = 'p25', 'q2' = 'p50' = 'median', q3 = 'p75'.

Value

list:

- indic: data.table indicating each stats (columns).
- stats_id: data.table indicating the number of drugs use for each individual (all cohort).

---

ind_stdcumul *Indicator: Cumulative (multiple medication)*

Description

Descriptive statistics: Sum of different drugs consumed over a given period time.

Usage

```
ind_stdcumul(
  processed_tab,
  nPeriod = 1,
 stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max")
)
```

Arguments

processed_tab	Table created by data_process function.
nPeriod	Integer value greater or equal to 1 and lesser or equal to the total number of days in the study period. If nPeriod is greater than 1, the study period is divide in nPeriod subperiod and the total number of drugs consumption would be the average of the periods.
stats	Statistics to calculate on the drug consumption. See *Details* for possible values.

Details

stats: Possible values are

- 'mean', 'min', 'median', 'max', 'sd';

- 'pX' where *X* is a value in]0, 100];

- 'q1' = 'p25', 'q2' = 'p50' = 'median', q3 = 'p75'.

Value

list:

- indic: data.table indicating each stats (columns).

- stats_id: data.table. For each individual (all cohort), indicate the number of drug use per period (perX where X is a number between 1 and nPeriod) and the mean of the periods (nRx).

---

ind_ucontinuous   *Indicator: Uninterrupted Continuous*

Description

Descriptive statistics for drugs that are consumed every day of the study period.

Usage

```
ind_ucontinuous(
  processed_tab,
 stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max")
)
```

Arguments

processed_tab   Table created by [data_process](#) function.

stats   Statistics to calculate on the drug consumption. See *Details* for possible values.

Details

stats: Possible values are

- `'mean'`, `'min'`, `'median'`, `'max'`, `'sd'`;
- `'pX'` where *X* is a value in]0, 100];
- `'q1'` = `'p25'`, `'q2'` = `'p50'` = `'median'`, q3 = `'p75'`.

Value

list:

- indic: data.table indicating each stats (columns).
- stats_id: data.table indicating the number of drugs use for each individual (all cohort).

---

ind_wcumul   *Indicator: Weight Cumulative*

Description

Description

Usage

```
ind_wcumul(
  processed_tab,
 stats = c("mean", "sd", "min", "p5", "p10", "p25", "median", "p75", "p90", "p95",
    "max")
)
```

Arguments

processed_tab   Table created by [data_process](#) function.

stats   Statistics to calculate on the drug consumption. See *Details* for possible values.

Details

stats: Possible values are

- 'mean', 'min', 'median', 'max', 'sd';
- 'pX' where *X* is a value in]0, 100];
- 'q1' = 'p25', 'q2' = 'p50' = 'median', q3 = 'p75'.

Value

list:

- indic: data.table indicating each stats (columns).
- stats_id: data.table indicating the number of drugs use for each individual (all cohort).

Rx_processed   *Table: Processed "unprocessed table"*

Description

Table required for the calculation of the polypharmacy indicators. This table is created by using data_process() function on Rx_unprocessed data.

Usage

Rx_processed

Format

A data.table with 6792 obs and 4 variables:

id Individual unique identifier.

code Drug unique identifier.

tx_start The date of initiation of the reconstructed continued treatment (format as date).

tx_end The date of the last day of the reconstructed continued treatment (format as date).

Rx_unprocessed   *Table: Prescription drugs deliveries*

Description

Table listing all prescription drugs deliveries.

Usage

```
Rx_unprocessed
```

Format

A `data.table` with 17060 obs and 4 variables:

id Individual unique identifier

code Drug unique identifier

start Date of the drug delivery

duration Duration of the delivery

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