Package 'MedxR'

January 14, 2026

Type Package

Title Access Drug Regulatory Data via FDA and Health Canada APIs

Version 0.1.1

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Description Provides functions to access drug regulatory data from public RESTful APIs including the 'FDA Open API' and the 'Health Canada Drug Product Database API', retrieving real-time or historical information on drug approvals, adverse events, recalls, and product details. Additionally, the package includes a curated collection of open datasets focused on drugs, pharmaceuticals, treatments, and clinical studies. These datasets cover diverse topics such as treatment dosages, pharmacological studies, placebo effects, drug reactions, misuses of pain relievers, and vaccine effectiveness. The package supports reproducible research and teaching in pharmacology, medicine, and healthcare by integrating reliable international APIs and structured datasets from public, academic, and government sources.
For more information on the APIs, see:
'FDA API' <https://open.fda.gov/apis/> and
'Health Canada API' <https://health-products.canada.ca/api/documentation/dpd-documentation-en.html>.

License GPL-3

Language en

URL https://github.com/lightbluetitan/medxr,
https://lightbluetitan.github.io/medxr/

BugReports https://github.com/lightbluetitan/medxr/issues

Encoding UTF-8

LazyData true

Depends R (>= 4.1.0)

Imports utils, httr, jsonlite, dplyr, memoise

Suggests ggplot2, testthat (>= 3.0.0), knitr, rmarkdown

RoxygenNote 7.3.2

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-01-14 09:30:02 UTC

Contents

`aspirin_infarction_df` *Aspirin after Myocardial Infarction*

Description

This dataset, aspirin_infarction_df, is a data frame containing results from a meta-analysis on the use of aspirin to prevent death after myocardial infarction. It includes binary outcome data comparing aspirin and placebo groups.

Usage

```
data(aspirin_infarction_df)
```

Format

A data frame with 7 observations and 6 variables:

study Character variable identifying each study

year Integer variable indicating the publication year

d.asp Integer variable for the number of deaths in the aspirin group

n.asp Integer variable for the total number of patients in the aspirin group

d.plac Integer variable for the number of deaths in the placebo group

n.plac Integer variable for the total number of patients in the placebo group

Details

The dataset name has been kept as 'aspirin_infarction_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the package meta version 8.2-1

ATC_code_tbl_df *Drug Related ATC Codes*

Description

This dataset, ATC_code_tbl_df, is a tibble containing ATC (Anatomical Therapeutic Chemical) classification codes assigned to drugs by the World Health Organization. The classification system categorizes drugs into different levels of anatomical and chemical structure.

Usage

```
data(ATC_code_tbl_df)
```

Format

A tibble with 50 observations and 10 variables:

atc_code Character variable representing the ATC code assigned to the drug

level_1 Character variable indicating the anatomical main group

code_1 Character variable indicating the code of level 1

level_2 Character variable indicating the therapeutic subgroup

code_2 Character variable indicating the code of level 2

level_3 Character variable indicating the pharmacological subgroup

code_3 Character variable indicating the code of level 3

level_4 Character variable indicating the chemical subgroup

code_4 Character variable indicating the code of level 4

drugbank-id Character variable with the corresponding DrugBank identifier

Details

The dataset name has been kept as 'ATC_code_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble. The original content has not been modified in any way.

Source

Data taken from the package covid19dbcand version 0.1.1

BCG_vaccine_df *BCG Vaccine Effectiveness Studies*

Description

This dataset, BCG_vaccine_df, is a data frame containing results from 13 studies evaluating the effectiveness of the Bacillus Calmette-Guerin (BCG) vaccine against tuberculosis. The dataset includes trial metadata and outcome counts for treatment and control groups.

Usage

```
data(BCG_vaccine_df)
```

Format

A data frame with 13 observations and 9 variables:

trial Integer variable identifying each trial

author Character variable with the name of the study author

year Integer variable indicating the publication year of the study

tpos Integer variable indicating the number of TB-positive cases in the treatment group

tneg Integer variable indicating the number of TB-negative cases in the treatment group

cpos Integer variable indicating the number of TB-positive cases in the control group

cneg Integer variable indicating the number of TB-negative cases in the control group

ablat Integer variable indicating the absolute latitude of the study location

alloc Character variable indicating the allocation type

Details

The dataset name has been kept as 'BCG_vaccine_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the package metadat version 1.4-0

binding_df *Antibiotic Binding in Cows*

Description

This dataset, binding_df, is a data frame containing the binding rate of antibiotics to serum protein in cows. The study measured the extent to which antibiotics bind to protein in the bloodstream, which can reduce the medical effectiveness of the drug. Twelve cows were given one of three antibiotics: chloramphenicol, erythromycin, or tetracycline.

Usage

```
data(binding_df)
```

Format

A data frame with 12 observations and 2 variables:

antibiotic Factor variable indicating the type of antibiotic administered

binding Numeric variable representing the measured binding rate to serum protein

Details

The dataset name has been kept as 'binding_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the isdals package version 3.0.1

caffeine_matrix *The Effects of Caffeine*

Description

This dataset, caffeine_matrix, is a matrix containing data from Henson et al. [1996] investigating caffeine's effect on short-term visual memory. High school students (9 eighth-graders, 10 tenth-graders, 9 twelfth-graders) were tested twice: once after drinking caffeinated Coke and once after decaffeinated Coke. Students had 10 seconds to memorize 20 common objects, then 1 minute to recall them. The study examined whether students remembered more objects with decaffeinated versus caffeinated Coke.

Usage

```
data(caffeine_matrix)
```

Format

A numeric matrix with 28 rows and 3 columns:

Grade Numeric values indicating the grade level of the student (8, 10, or 12)

Without Number of objects remembered after drinking decaffeinated Coke

With Number of objects remembered after drinking caffeinated Coke

Details

The dataset name has been kept as 'caffeine_matrix' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'matrix' indicates that the dataset is stored as a matrix object. The original content has not been modified in any way.

Source

Data taken from the msos package version 1.2.0

---

copd_drug_therapy_df *Pharmacologic Treatments for COPD*

Description

This dataset, copd_drug_therapy_df, is a data frame containing results from 39 trials examining pharmacologic treatments for chronic obstructive pulmonary disease (COPD). It includes study identifiers, treatment groups, number of exacerbations, and sample sizes.

Usage

```
data(copd_drug_therapy_df)
```

Format

A data frame with 94 observations and 6 variables:

study Character variable identifying each study

year Integer variable indicating the publication year

id Integer variable representing the study ID

treatment Character variable describing the treatment group

exac Integer variable indicating the number of COPD exacerbations

total Integer variable for the total number of patients in the group

Details

The dataset name has been kept as 'copd_drug_therapy_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the package metadat version 1.4-0

---

dosage_tbl_df *Treatment Dosages Defined by EUCAST*

Description

This dataset, dosage_tbl_df, is a tibble containing treatment dosage information for antimicrobial agents as defined by EUCAST. The dosages are used to support interpretive breakpoints in antimicrobial susceptibility testing.

Usage

```
data(dosage_tbl_df)
```

Format

A tibble with 759 observations and 9 variables:

ab Antimicrobial ID

name Name of the antimicrobial agent

type Type of dosage scheme

dose Dose amount

dose_times Number of doses per day

administration Route of administration

notes Additional clinical notes

original_txt Original EUCAST dosage description

eucast_version EUCAST guideline version number

Details

The dataset name has been kept as 'dosage_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble. The original content has not been modified in any way.

Source

Data taken from the AMR package version 3.0.0

`drugsmisuse_tbl_df` *Pain Relievers Misuse in the US*

Description

This dataset, drugsmisuse_tbl_df, is a tibble containing information about the use of pain relievers for non-medical purposes in the United States. It includes individual-level data for 100 cases, detailing misuse patterns across various opioid-based medications.

Usage

```
data(drugsmisuse_tbl_df)
```

Format

A tibble with 100 observations and 8 variables:

caseid Character variable representing the unique case identifier

hydrocd Integer variable indicating hydrocodone misuse (1 = Yes, 0 = No)

oxycodp Integer variable indicating oxycodone misuse (1 = Yes, 0 = No)

codeine Integer variable indicating codeine misuse (1 = Yes, 0 = No)

tramadl Integer variable indicating tramadol misuse (1 = Yes, 0 = No)

morphin Integer variable indicating morphine misuse (1 = Yes, 0 = No)

methdon Integer variable indicating methadone misuse (1 = Yes, 0 = No)

vicolor Integer variable indicating Vicodin or similar misuse (1 = Yes, 0 = No)

Details

The dataset name has been kept as 'drugsmisuse_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble. The original content has not been modified in any way.

Source

Data taken from the package lay version 0.1.3

drug_prices_tbl_df *Unit Drug Prices*

Description

This dataset, drug_prices_tbl_df, is a tibble containing information on unit prices for various pharmaceutical products. Each record includes a description, currency, cost per unit, unit type, and a parent key identifier.

Usage

```
data(drug_prices_tbl_df)
```

Format

A tibble with 208 observations and 5 variables:

description Character variable describing the drug or product

currency Character variable indicating the currency in which the price is expressed

cost Numeric variable indicating the unit cost of the drug

unit Character variable representing the measurement unit (e.g., tablet, mL)

parent_key Character variable serving as a linking identifier to related records

Details

The dataset name has been kept as 'drug_prices_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble data frame. The original content has not been modified in any way.

Source

Data taken from the covid19dbcand package version 0.1.1

get_fda_adverse_events *Search Adverse Events by Drug Name in FDA Adverse Event Reporting System*

Description

Retrieves adverse event reports from the FDA Adverse Event Reporting System (FAERS) that match a specific drug name using the RESTful API endpoint `/drug/event.json?search=<drug_name>`.

This includes details such as the safety report ID, receive date, serious status, patient information, drug details, and adverse reactions for each reported adverse event related to pharmaceutical products.

Usage

```
get_fda_adverse_events(drug_name)
```

Arguments

drug_name	A character string representing the name of the drug.

Details

This function sends a GET request to the FDA openFDA API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails, returns no matches, or returns an error status code, the function returns NULL with an informative message.

Value

A tibble with the following columns:

- report_id: Unique identifier for the adverse event report
- date_received: Date FDA received the report
- country: Country where event occurred
- serious: Is it serious? ("Yes", "No", or original API value / NA)
- adverse_reactions: List of adverse reactions reported (separated by semicolons) or NA
- patient_sex: Patient sex ("Male", "Female", "Unknown", original API value, or NA)
- patient_age: Patient age at onset (as returned by API) or NA

Note

Requires an internet connection.

Source

FDA Adverse Event Reporting System (FAERS) via openFDA: https://open.fda.gov/apis/drug/event/

See Also

GET, fromJSON, as_tibble

Examples

```
# Esta función requiere conexión a internet y descarga datos de la FDA
get_fda_adverse_events("aspirin")
```

`get_fda_drugs_approved` *Search FDA-Approved Drugs by Drug Name*

Description

Retrieves information about FDA-approved drug products from the official Drugs at FDA database that match a specific drug name using the RESTful API endpoint `/drug/drugsfda.json?search=<drug_name>`.

This includes details such as the application number, sponsor name, approval dates, product information, application type (NDA, ANDA, BLA), and submission details for brand name drugs, generic drugs, and therapeutic biological products approved by the FDA since 1939.

Usage

```
get_fda_drugs_approved(drug_name)
```

Arguments

`drug_name`	A character string representing the name of the drug (brand name or generic name).

Details

This function sends a GET request to the FDA openFDA API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

The Drugs at FDA database contains information about drug products approved since 1939. The majority of labels, approval letters, and reviews are available for products approved since 1998. This database includes brand name drugs, generic drugs, and therapeutic biological products.

If the API request fails, returns no matches, or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with the following columns:

- `application_number`: FDA application number (NDA, ANDA, or BLA)
- `sponsor`: Name of the company that holds the application
- `brand`: Brand or trade name of the approved product
- `generic`: Generic (non-proprietary) name of the active ingredient
- `type`: Application type (NDA, ANDA, BLA)
- `approval_date`: Date the product was approved by FDA
- `strength`: Dosage strength of the product
- `form`: Pharmaceutical dosage form
- `route`: Route of administration

Note

Requires an internet connection.

Source

FDA Drugs at FDA Database via openFDA: https://open.fda.gov/apis/drug/drugsfda/

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from FDA
get_fda_drugs_approved("aspirin")
get_fda_drugs_approved("lipitor")
```

---

get_fda_drug_labels *Search Drug Labels by Drug Name in FDA Drug Labeling Database*

Description

Retrieves drug label information from the FDA Drug Labeling Database that match a specific drug name using the RESTful API endpoint `/drug/label.json?search=<drug_name>`.

This includes details such as the product ID, brand name, generic name, indications and usage, dosage and administration, warnings, drug interactions, and other prescribing information from FDA-approved drug labels.

Usage

```
get_fda_drug_labels(drug_name)
```

Arguments

drug_name	A character string representing the name of the drug.

Details

This function sends a GET request to the FDA openFDA API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails, returns no matches, or returns an error status code, the function returns NULL with an informative message.

Value

A tibble with the following columns:

- `product_id`: Unique identifier for the product
- `brand_name`: Brand or trade name of the product
- `generic_name`: Generic name of the active ingredient
- `manufacturer`: Name of the manufacturer
- `product_type`: Type of drug product
- `route`: Route of administration
- `indications`: Approved indications for use
- `warnings`: Important warnings and precautions

Note

Requires an internet connection.

Source

FDA Drug Labeling Database via openFDA: https://open.fda.gov/apis/drug/label/

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from FDA
get_fda_drug_labels("aspirin")
```

---

get_fda_ndc_directory *Search National Drug Code (NDC) Directory by Drug Name*

Description

Retrieves National Drug Code (NDC) information from the FDA NDC Directory that match a specific drug name using the RESTful API endpoint `/drug/ndc.json?search=<drug_name>`.

This includes details such as the NDC product code, brand name, generic name, labeler information, product type, dosage form, route of administration, marketing status, and active ingredients for pharmaceutical products marketed in the United States.

Usage

```
get_fda_ndc_directory(drug_name)
```

Arguments

drug_name	A character string representing the name of the drug (brand name or generic name).

Details

This function sends a GET request to the FDA openFDA API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

The NDC Directory contains information on final marketed drugs submitted to FDA in SPL (Structured Product Labeling) electronic listing files. Assignment of an NDC number does not denote FDA approval of the product.

If the API request fails, returns no matches, or returns an error status code, the function returns NULL with an informative message.

Value

A tibble with the following columns:

- ndc: National Drug Code (NDC) product identifier
- brand: Brand or proprietary name of the drug product
- generic: Generic (non-proprietary) name of the drug
- ingredients: List of active ingredients with strengths
- form: Pharmaceutical dosage form (e.g., TABLET, CAPSULE)
- route: Route of administration (e.g., ORAL, INTRAVENOUS)
- labeler: Name of the company that labels/markets the product
- type: Type of drug product (e.g., HUMAN PRESCRIPTION DRUG)
- status: Current marketing status (e.g., Prescription)

Note

Requires an internet connection. The NDC Directory is updated daily by FDA.

Source

FDA National Drug Code Directory via openFDA: https://open.fda.gov/apis/drug/ndc/

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from FDA
get_fda_ndc_directory("aspirin")
get_fda_ndc_directory("ibuprofen")
```

`get_hc_active_ingredients` *Get Active Ingredients from Health Canada Drug Product Database*

Description

Retrieves detailed information on all active ingredients listed in the Health Canada Drug Product Database (DPD) through the RESTful API endpoint `/drug/activeingredient`.

Each record corresponds to a specific active ingredient within a registered drug product, including concentration, unit, and dosage details (if available).

Usage

```
get_hc_active_ingredients()
```

Details

The function sends a GET request to the Health Canada DPD API. It uses memoisation via the **memoise** package to cache results and includes a rate limit delay between API requests.

Missing values are retained as empty strings (`""`), preserving the original schema of the API.

Value

A tibble with the following columns:

- `dosage_unit`: Unit of dosage form (e.g., "ML", "
- `dosage_value`: Numeric dosage quantity (e.g., "100")
- `drug_code`: Unique code identifying the drug product
- `ingredient_name`: Name of the active ingredient
- `strength`: Strength or concentration value (e.g., "50", "0.05")
- `strength_unit`: Unit of the strength (e.g., "MG", "G", "

Note

Requires an active internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

`GET`, `fromJSON`, `as_tibble`

Examples

```
# This function requires an internet connection and downloads data from Health Canada
get_hc_active_ingredients()
```

`get_hc_companies` *Get Companies from Health Canada Drug Product Database*

Description

Retrieves information on all pharmaceutical companies listed in the Health Canada Drug Product Database (DPD) using the RESTful API endpoint `/drug/company`.

This includes details such as the company code, company name, address, city, province, postal code, and country. Each record corresponds to a company associated with one or more approved or discontinued drug products.

Usage

```
get_hc_companies()
```

Details

This function sends a GET request to the Health Canada Drug Product Database API. It supports caching via the **memoise** package to avoid redundant calls, and includes a small rate limit delay between successive API requests.

The columns `post_office_box` and `suite_number` are automatically removed as they generally contain incomplete or irrelevant information.

If the API request fails or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with the following columns:

- `company_code`: Unique identifier for the company
- `company_name`: Official registered name of the company
- `company_type`: Type of company (e.g., "DIN OWNER", "Manufacturer")
- `city_name`: City where the company is located
- `province_name`: Province or territory (if applicable)
- `country_name`: Country name
- `postal_code`: Postal code or ZIP code
- `street_name`: Street address

Note

Requires an active internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from Health Canada
get_hc_companies()
```

---

get_hc_din *Get All DINs from Health Canada Drug Product Database*

Description

Retrieves all Drug Identification Numbers (DINs) from the Health Canada Drug Product Database (DPD) using the RESTful API endpoint `/drug/drugproduct`.

Only the DIN column is returned, renamed as `din` for convenience.

Usage

```
get_hc_din()
```

Details

This function sends a GET request to the Health Canada Drug Product Database API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with a single column:

- `din`: The Drug Identification Number

Note

Requires an internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble, rename

Examples

```
# This function requires an internet connection and downloads data from Health Canada
get_hc_din()
```

---

get_hc_drug_by_din *Get a Drug Product by DIN from Health Canada Drug Product Database*

Description

Retrieves detailed information for a specific drug product listed in the Health Canada Drug Product Database (DPD) using the RESTful API endpoint `/drug/drugproduct?din=<DIN>`.

This includes details such as the Drug Identification Number (DIN), product name, class, number of active ingredients, company name, and update date.

Usage

```
get_hc_drug_by_din(din)
```

Arguments

din	A character or numeric string representing the Drug Identification Number (DIN) of the product to retrieve.

Details

Sends a GET request to the Health Canada Drug Product Database API. Supports caching via the **memoise** package and enforces a rate limit between successive API requests.

If the DIN does not exist or the API returns an error, the function returns NULL with an informative message.

The function fails gracefully when internet resources are unavailable, including SSL certificate errors, network timeouts, or server issues.

Value

A tibble with the following columns:

- `drug_code`: Unique code identifying the drug product
- `class_name`: Class of drug (e.g., Human, Veterinary)
- `din`: DIN assigned by Health Canada
- `brand_name`: Brand or trade name of the product
- `number_of_ais`: Number of active ingredients
- `ai_group_no`: Active ingredient group number
- `company_name`: Manufacturer name
- `last_update_date`: Date of last update in the database

Returns `NULL` if the resource is unavailable or if an error occurs.

Note

Requires an internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from Health Canada
result <- get_hc_drug_by_din("02456789")
if (!is.null(result)) {
  print(result)
}
```

---

get_hc_drug_products *Retrieve Drug Products from Health Canada Drug Product Database*

Description

Retrieves information on all drug products listed in the Health Canada Drug Product Database (DPD) using the RESTful API endpoint `/drug/drugproduct`.

Optionally, a partial product name can be provided to filter the results to products that contain the search term in their brand name.

Usage

```
get_hc_drug_products(name = NULL)
```

Arguments

name	Optional. A character string representing a partial or complete name of the drug product to filter results. If omitted, returns all available products.

Details

This function sends a GET request to the Health Canada Drug Product Database API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails, returns no matches, or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with the following columns:

- `drug_code`: Unique code identifying the drug product
- `class_name`: Class of drug (e.g., Human, Veterinary)
- `din`: Drug Identification Number (DIN)
- `brand_name`: Brand or trade name of the product
- `number_of_ais`: Number of active ingredients
- `ai_group_no`: Active ingredient group number
- `company_name`: Manufacturer name
- `last_update_date`: Date of last update in the database

Note

Requires an internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from Health Canada

# Retrieve all products
get_hc_drug_products()

# Retrieve products matching a partial name
get_hc_drug_products("acetaminophen")
```

`get_hc_forms` *Get Pharmaceutical Forms from Health Canada Drug Product Database*

Description

Retrieves information on all pharmaceutical dosage forms listed in the Health Canada Drug Product Database (DPD) using the RESTful API endpoint `/drug/form`.

This includes details such as the drug code, form code, and the pharmaceutical form name (e.g., tablet, capsule, solution).

Usage

```
get_hc_forms()
```

Details

This function sends a GET request to the Health Canada Drug Product Database API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with the following columns:

- `drug_code`: Unique code identifying the drug product.
- `pharm_form_code`: Code representing the pharmaceutical form.
- `pharm_form_desc`: Description of the pharmaceutical form (e.g., Tablet, Capsule, Solution).

Note

Requires an internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from Health Canada
get_hc_forms()
```

`get_hc_search_drug` *Search Drug Products by Brand Name in Health Canada Drug Product Database*

Description

Retrieves drug products from the Health Canada Drug Product Database (DPD) that match a specific brand (commercial) name using the RESTful API endpoint `/drug/drugproduct?search=<brand_name>`.

This includes details such as the Drug Identification Number (DIN), product name, class, number of active ingredients, company name, and update date for each approved or discontinued pharmaceutical product.

Usage

```
get_hc_search_drug(brand_name)
```

Arguments

`brand_name`	A character string representing the commercial name of the drug.

Details

This function sends a GET request to the Health Canada Drug Product Database API. It supports caching via the **memoise** package to avoid redundant calls, and respects a rate limit between successive API requests.

If the API request fails, returns no matches, or returns an error status code, the function returns `NULL` with an informative message.

Value

A tibble with the following columns:

- `drug_code`: Unique code identifying the drug product
- `class_name`: Class of drug (e.g., Human, Veterinary)
- `din`: Drug Identification Number (DIN)
- `brand_name`: Brand or trade name of the product
- `number_of_ais`: Number of active ingredients
- `ai_group_no`: Active ingredient group number
- `company_name`: Manufacturer name
- `last_update_date`: Date of last update in the database

Note

Requires an internet connection.

Source

Health Canada Drug Product Database (DPD) API: https://health-products.canada.ca/api/documentation/dpd-documentation-en.html

See Also

GET, fromJSON, as_tibble

Examples

```
# This function requires an internet connection and downloads data from Health Canada
get_hc_search_drug("NEMBUTAL")
```

---

histamine_matrix *Histamine in Dogs*

Description

This dataset, histamine_matrix, is a matrix containing data on blood histamine levels in dogs after drug treatment. Sixteen dogs were used to assess morphine and trimethaphan effects on blood histamine concentration. Dogs were divided into four groups: two received morphine, two received trimethaphan (both intravenous). In each drug pair, one group had histamine depleted prior to treatment, the other retained normal levels. Values of "0.10" indicate originally missing data, arbitrarily imputed with that value.

Usage

```
data(histamine_matrix)
```

Format

A numeric matrix with 16 rows and 4 columns:

Before Blood histamine levels measured before drug administration

After1 Histamine levels measured after 1 minute

After3 Histamine levels measured after 3 minutes

After5 Histamine levels measured after 5 minutes

Details

The dataset name has been kept as 'histamine_matrix' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'matrix' indicates that the dataset is stored as a matrix object. The original content has not been modified in any way.

Source

Data taken from the msos package version 1.2.0

---

naoh_digest_df *Digestibility of Straw Treated with NaOH*

Description

This dataset, naoh_digest_df, is a data frame containing digestibility coefficients for six horses that were fed straw. Each horse was tested under two conditions: once after being fed ordinary straw and once after being fed straw treated with sodium hydroxide (NaOH).

Usage

```
data(naoh_digest_df)
```

Format

A data frame with 6 observations and 3 variables:

horse Integer identifier for each horse

ordinary Numeric variable representing digestibility after consuming ordinary straw

naoh Numeric variable representing digestibility after consuming NaOH-treated straw

Details

The dataset name has been kept as 'naoh_digest_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the isdals package version 3.0.1

`oilvitaminA_df` *Utilization of Vitamin A in Rats*

Description

This dataset, oilvitaminA_df, is a data frame containing vitamin A concentrations in the livers of rats after being fed vitamin A dissolved in different types of oil. Twenty rats were divided into two groups: one received vitamin A in corn oil and the other in castor oil (American oil). After three days of feeding, vitamin A concentration in the liver was measured on the fourth day.

Usage

```
data(oilvitaminA_df)
```

Format

A data frame with 20 observations and 2 variables:

type Factor variable indicating the oil type used to deliver vitamin A (corn or castor oil)

avit Integer variable representing the measured vitamin A concentration in the liver

Details

The dataset name has been kept as 'oilvitaminA_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the isdals package version 3.0.1

`oral_anticoagulants_df` *Oral Anticoagulants in Coronary Artery Disease*

Description

This dataset, oral_anticoagulants_df, is a data frame containing results from 34 studies evaluating the effectiveness of oral anticoagulants in patients with coronary artery disease. The dataset includes study metadata and outcome counts for treatment and control groups, as well as intensity classifications.

Usage

```
data(oral_anticoagulants_df)
```

Format

A data frame with 34 observations and 9 variables:

study Character variable identifying each study

year Integer variable indicating the publication year

intensity Character variable describing treatment intensity

asp.t Integer variable indicating the number of aspirin users in the treatment group

asp.c Integer variable indicating the number of aspirin users in the control group

ai Integer variable indicating the number of adverse events in the treatment group

n1i Integer variable for the sample size of the treatment group

ci Integer variable indicating the number of adverse events in the control group

n2i Integer variable for the sample size of the control group

Details

The dataset name has been kept as 'oral_anticoagulants_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the package metadat version 1.4-0

parkinsons_list *Dopamine Agonists in Parkinson's Disease*

Description

This dataset, parkinsons_list, is a list containing information from 7 studies investigating the effect of dopamine agonists as adjunct therapy in patients with Parkinson's disease. The dataset includes placebo and four active drugs coded from 2 to 5, measuring outcomes such as lost work-time reduction.

Usage

```
data(parkinsons_list)
```

Format

A list with 5 elements:

Outcomes Numeric vector representing the reduction in lost work-time for each treatment arm

SE Numeric vector indicating the standard error of each observation

Treat Character vector identifying the treatment type (placebo or drug)

Study Numeric vector indicating the study each observation belongs to

Treat.order Character vector listing the treatment names in the order of coding

Details

The dataset name has been kept as 'parkinsons_list' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'list' indicates that the dataset is a list. The original content has not been modified in any way.

Source

Data taken from the package bnma version 1.6.1

pharmacy_tbl_df *Pharmacy Client Attendance*

Description

This dataset, pharmacy_tbl_df, is a tibble containing hourly client attendance data in a pharmacy located in Geneva, Switzerland. The dataset spans two years, recording the number of clients per hour alongside the date and weekday.

Usage

```
data(pharmacy_tbl_df)
```

Format

A tibble with 17,520 observations and 4 variables:

date Date variable indicating the calendar date

hours Character variable representing the hour of observation

weekday Character variable representing the day of the week

attendance Numeric variable indicating the number of clients observed

Details

The dataset name has been kept as 'pharmacy_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble. The original content has not been modified in any way.

Source

Data taken from the package idarps version 0.0.5

---

placebos_df *Placebos and Pain Relief*

Description

This dataset, placebos_df, is a data frame containing pain relief data from both analgesics and placebos. It presents observations over time comparing the effects of different treatments including placebo, aspirin (Asp), and codis (a combination analgesic), along with calculated placebo reduction.

Usage

```
data(placebos_df)
```

Format

A data frame with 7 observations and 6 variables:

Time Integer variable indicating the time point of observation

Placebo Numeric variable indicating the measured effect of the placebo

Distr Numeric variable indicating the measured effect of a distractor treatment

Asp Numeric variable indicating the measured effect of aspirin

Codis Numeric variable indicating the measured effect of codis

PlaceboRed Numeric variable indicating the reduction attributed to the placebo

Details

The dataset name has been kept as 'placebos_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the package SRMData version 1.0.2

---

products_drug_tbl_df *Drug Product Records*

Description

This dataset, products_drug_tbl_df, is a tibble containing detailed information on 3,764 commercially available pharmaceutical products in Canada and the United States. Each record includes identifiers such as NDC and DPD codes, marketing start and end dates, strength, dosage form, administration route, approval status, and source agency.

Usage

```
data(products_drug_tbl_df)
```

Format

A tibble with 3,764 observations and 19 variables:

name Character variable with the commercial name of the drug product

labeller Character variable indicating the name of the pharmaceutical company

ndc-id Character variable with the U.S. National Drug Code (NDC) identifier

ndc-product-code Character variable for the product-level NDC code

dpd-id Character variable for the Canadian Drug Product Database (DPD) ID

ema-product-code Character variable for the European Medicines Agency product code

ema-ma-number Character variable with the EMA marketing authorization number

started-marketing-on Character variable indicating marketing start date

ended-marketing-on Character variable indicating marketing end date

dosage-form Character variable representing the drug's dosage form

strength Character variable with the dosage strength

route Character variable describing the route of administration

fda-application-number Character variable for the FDA application number

generic Character variable indicating if the product is a generic formulation

over-the-counter Character variable indicating OTC availability

approved Character variable specifying whether the product is approved

country Character variable indicating the country of approval (Canada/US)

source Character variable with the originating regulatory body

parent_key Character variable linking to related records

Details

The dataset name has been kept as 'products_drug_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble data frame. The original content has not been modified in any way.

Source

Data taken from the covid19dbcand package version 0.1.1

---

ratliver_df *Drug Concentration in Rat Livers*

Description

This dataset, ratliver_df, is a data frame containing results from an experiment investigating drug absorption in the livers of rats. Nineteen rats were weighed, given an oral dose of approximately 40 mg of drug per kilogram of body weight, and sacrificed after a fixed period. Liver weight and the percentage of the administered dose found in the liver were recorded.

Usage

```
data(ratliver_df)
```

Format

A data frame with 19 observations and 4 variables:

BodyWt Integer variable indicating body weight of the rat (in grams)

LiverWt Numeric variable representing the weight of the liver (in grams)

Dose Numeric variable representing the total dose administered (in mg)

DoseInLiver Numeric variable representing the percentage of the dose found in the liver

Details

The dataset name has been kept as 'ratliver_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'df' indicates that the dataset is a data frame. The original content has not been modified in any way.

Source

Data taken from the isdals package version 3.0.1

`reactions_drug_tbl_df` *Drug Reactions*

Description

This dataset, reactions_drug_tbl_df, is a tibble containing detailed information on 69 biochemical reactions involving drug molecules. It includes enzyme-mediated transformations, pharmacological activity of drug metabolites, and mappings between substrates and products as described by DrugBank identifiers.

Usage

```
data(reactions_drug_tbl_df)
```

Format

A tibble with 69 observations and 6 variables:

sequence Numeric variable indicating the order of the metabolic reaction

left_drugbank_id Character variable with the DrugBank ID of the input compound

left_drugbank_name Character variable with the name of the input compound

right_drugbank_id Character variable with the DrugBank ID of the resulting metabolite

right_drugbank_name Character variable with the name of the resulting metabolite

parent_key Character variable for linking to external reference records

Details

The dataset name has been kept as 'reactions_drug_tbl_df' to avoid confusion with other datasets in the R ecosystem. This naming convention helps distinguish this dataset as part of the MedxR package and assists users in identifying its specific characteristics. The suffix 'tbl_df' indicates that the dataset is a tibble data frame. The original content has not been modified in any way.

Source

Data taken from the covid19dbcand package version 0.1.1

`view_datasets_MedxR` *View Available Datasets in MedxR*

Description

This function lists all datasets available in the 'MedxR' package. If the 'MedxR' package is not loaded, it stops and shows an error message. If no datasets are available, it returns a message and an empty vector.

Usage

```
view_datasets_MedxR()
```

Value

A character vector with the names of the available datasets. If no datasets are found, it returns an empty character vector.

Examples

```
if (requireNamespace("MedxR", quietly = TRUE)) {
  library(MedxR)
  view_datasets_MedxR()
}
```

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