Package ‘icdcomorbid’

August 20, 2024

Type Package

Title Mapping ICD Codes to Comorbidity

Version 1.0.0

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Description Provides tools for mapping International Classification of Diseases codes to comorbidity, enabling the identification and analysis of various medical conditions within healthcare data.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports jsonlite

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

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-08-20 14:30:03 UTC

Contents

add_decimal *Insert decimals to the ICD codes*

Description

This is a preprocessing step to standardize the icd codes to have decimals.

Usage

```
add_decimal(df, icd_cols, places = 3)
```

Arguments

df	The dataframe to be converted.
icd_cols	A character vector specifying the names of the columns containing ICD codes.
places	An numeric value specifying the number of decimal places. Default is 3 decimal places.

Value

A dataframe in wide format where each row represents a unique identifier (ID), and each column contains a variable associated with that ID.

Examples

```
df <- data.frame(
  id = c(1, 2, 3),
  icd_1 = c("C509", "D633", "I210"),
  icd_2 = c("D509", "E788", "N183")
)
add_decimal(df, icd_cols = c("icd_1", "icd_2"), places = 3)
```

episode_of_care *Identify Episodes of Care*

Description

This function identifies episodes of care for patients based on their visit and discharge dates from two different data sources (DAD and NACRS).

Usage

```
episode_of_care(
  dad_df,
  nacrs_df,
  patient_id_col,
  dad_visit_date_col,
  dad_exit_date_col,
  nacrs_visit_date_col,
  nacrs_exit_date_col
)
```

Arguments

dad_df DataFrame containing DAD data.

nacrs_df DataFrame containing NACRS data.

patient_id_col String representing the column name for patient ID.

dad_visit_date_col
String representing the column name for visit date in DAD data.

dad_exit_date_col
String representing the column name for exit date in DAD data.

nacrs_visit_date_col
String representing the column name for visit date in NACRS data.

nacrs_exit_date_col
String representing the column name for exit date in NACRS data.

Value

A DataFrame with episodes of care identified and a unique record ID for each row.

Examples

```
# Sample DAD data
dad_df <- data.frame(
  patient_id = c("A001", "A001", "A002", "A002", "A003"),
  admit_dt = c("01Dec2023:10:00:00", "03Jan2024:12:00:00",
  "05Jan2024:09:00:00", "07Jan2024:14:00:00", "12Jan2024:12:00:00"),
  discharge_dt = c("02Dec2023:10:00:00", "04Jan2024:10:00:00",
  "06Jan2024:10:00:00", "08Jan2024:10:00:00", "15Jan2024:08:00:00")
)

# Sample NACRS data
nacrs_df <- data.frame(
  patient_id = c("A001", "A002", "A003", "A003", "A004"),
  visit_dt = c("03Jan2024:09:00:00", "07Feb2024:15:00:00",
  "10Jan2024:09:00:00", "11Jan2024:10:00:00", "12Jan2024:11:00:00"),
  disp_dt = c("03Jan2024:11:00:00", "07Feb2024:17:00:00",
  "10Jan2024:10:00:00", "12Jan2024:12:00:00", "13Jan2024:13:00:00")
)
```

```
episode_of_care(dad_df, nacrs_df, "patient_id", "admit_dt", "discharge_dt", "visit_dt", "disp_dt")
```

`icd10_to_comorbid` *Find Comorbidities from ICD_10 Codes*

Description

This function maps ICD_10 codes to comorbidities based on a provided mapping in order to indicate whether each comorbidity is present for each ID.

Usage

```
icd10_to_comorbid(df, idx, icd_cols, mapping, batch_size = 1000)
```

Arguments

`df` The dataframe containing the data.

`idx` The name of the column representing the patient identifiers.

`icd_cols` A character vector of the columns containing ICD codes.

`mapping` The mapping of comorbidities to ICD codes (e.g., quan_elixhauser10, charlson10, custom list).

`batch_size` An optional integer specifying the number of rows to process per batch. Default is 1000.

Details

This function assumes that the input dataframe is in wide format, where each row represents a unique identifier (ID), and each column contains a variable associated with that ID. The function maps the ICD_10 codes in the specified columns to comorbidities based on the provided mapping.

The mapping can be one of the following:

- Pre-defined mappings such as "quan_elixhauser10" or "charlson10", which are based on established comorbidity indices.

- Custom mappings (list), where each key represents a comorbidity and its value is a vector of ICD-9 codes associated with that comorbidity. The custom mapping codes may include up to 2 decimal places.

Value

A dataframe with comorbidities as columns and IDs as rows, with True or False values indicating whether each comorbidity is present for each ID.

References

1. Quan, H., Sundararajan, V., Halfon, P., Fong, A., Burnand, B., Luthi, J. C., ... & Ghali, W. A. (2005). Coding algorithms for defining comorbidities in ICD-9-CM and ICD-10 administrative data. Medical care, 43(11), 1130-1139. 2. ICD: Python library for working with International Classification of Diseases (ICD) codes. Available online: https://github.com/mark-hoffmann/icd

Examples

```
df <- data.frame(ID = c(1, 2, 3),
                 icd_1 = c("I21.0", "I50.3", "J45.1"),
                 icd_2 = c("I63.38", "I10.2", "I25.2"))
# Using pre-existing mapping (e.g., charlson10 or quan_elixhauser10)
mapping <- "charlson10"
icd10_to_comorbid(df, "ID", c("icd_1", "icd_2"), mapping)

# Using custom mapping
custom_mapping <- list("Myocardial Infarction" = c("I21.x", "I22.x", "I25.2"),
                       "Congestive Heart Failure" = c("I43.x", "I50.x", "I09.9"))
icd10_to_comorbid(df, "ID", c("icd_1", "icd_2"), custom_mapping, batch_size = 2)
```

`icd9_to_comorbid` *Find Comorbidities from ICD_9 Codes*

Description

This function maps ICD_9 codes to comorbidities based on a provided mapping in order to indicate whether each comorbidity is present for each ID.

Usage

```
icd9_to_comorbid(df, idx, icd_cols, mapping, batch_size = 1000)
```

Arguments

`df`	The dataframe containing the data.
`idx`	The name of the column representing the patient identifiers.
`icd_cols`	A character vector of the columns containing ICD codes.
`mapping`	The mapping of comorbidities to ICD codes (e.g., quan_elixhauser9, charlson9, custom list).
`batch_size`	An optional integer specifying the number of rows to process per batch. Default is 1000.

Details

This function assumes that the input dataframe is in wide format, where each row represents a unique identifier (ID), and each column contains a variable associated with that ID. The function maps the ICD_9 codes in the specified columns to comorbidities based on the provided mapping.

The mapping can be one of the following:

- Pre-defined mappings such as "quan_elixhauser9" or "charlson9", which are based on established comorbidity indices.

- Custom mappings (list), where each key represents a comorbidity and its value is a vector of ICD-9 codes associated with that comorbidity. The custom mapping codes may include up to 2 decimal places.

Value

A dataframe with comorbidities as columns and IDs as rows, with True or False values indicating whether each comorbidity is present for each ID.

References

1. Quan, H., Sundararajan, V., Halfon, P., Fong, A., Burnand, B., Luthi, J. C., ... & Ghali, W. A. (2005). Coding algorithms for defining comorbidities in ICD-9-CM and ICD-10 administrative data. Medical care, 43(11), 1130-1139. 2. ICD: Python library for working with International Classification of Diseases (ICD) codes. Available online: https://github.com/mark-hoffmann/icd

Examples

```
df <- data.frame(ID = c(1, 2, 3),
                 icd_1 = c("410.x", "428.0", "496"),
                 icd_2 = c("428.33", "401.9", "493.90"))
# Using pre-existing mapping (e.g., charlson9 or quan_elixhauser9)
mapping <- "charlson9"
icd9_to_comorbid(df, "ID", c("icd_1", "icd_2"), mapping)

# Using custom mapping
custom_mapping <- list("Myocardial Infarction" = c("410.x", "412.x"),
                       "Congestive Heart Failure" = c("398.91", "402.01",
                       "402.11", "402.91", "404.01", "404.03",
                       "404.11", "404.13", "404.91", "404.93", "425.4",
                       "425.5", "425.6", "425.7", "425.8", "425.9", "428.x"))
icd9_to_comorbid(df, "ID", c("icd_1", "icd_2"), custom_mapping, batch_size = 2)
```

`long_to_wide` *Reshape Long Format Data to Wide Format*

Description

This is a preprocessing step to transform a dataframe from long to wide format to use with icd_to_comorbid function.

Usage

```
long_to_wide(df, idx, icd_cols, batch_size = 1000)
```

Arguments

`df` The dataframe to be converted.

`idx` The name of the column containing the unique identifier (ID).

`icd_cols` A character vector specifying the names of the columns containing ICD codes.

`batch_size` An optional integer specifying the number of rows to process per batch. Default is 1000.

Value

A dataframe in wide format where each row represents a unique identifier (ID), and each column contains a variable associated with that ID.

References

ICD: Python library for working with International Classification of Diseases (ICD) codes. Available online: https://github.com/mark-hoffmann/icd

Examples

```
df <- data.frame( ID = c(1, 1, 2, 2, 3, 3, 3),
                 icd_1 = c("I10.2", "E03.9", "E11.9", "N18.9", "A04.7", NA, NA),
                 icd_2 = c("I11.9", "E78.5", "E78.2", "E14.9","A04.7", "E11.9", NA))
long_to_wide(df, "ID", c("icd_1", "icd_2"), batch_size = 1000)
```

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