

# Package ‘socialrisk’

February 15, 2023

**Type** Package

**Title** Identifying Patient Social Risk from Administrative Health Care Data

**Version** 0.5.1

**Description** Social risks are increasingly becoming a critical component of health care research. One of the most common ways to identify social needs is by using ICD-10-CM “Z-codes.” This package identifies social risks using varying taxonomies of ICD-10-CM Z-codes from administrative health care data. The conceptual taxonomies come from:

Centers for Medicare and Medicaid Services (2021) <<https://www.cms.gov/files/document/zcodes-infographic.pdf>>,

Reidhead (2018) <<https://web.mhanet.com/>>,

A Arons, S DeSilvey, C Fichtenberg, L Gottlieb (2018) <<https://sirenetwork.ucsf.edu/tools-resources/resources/>

[compendium-medical-terminology-codes-social-risk-factors](https://sirenetwork.ucsf.edu/tools-resources/resources/compendium-medical-terminology-codes-social-risk-factors)>.

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

**Imports** dplyr, magrittr, stringr, rlang, tidyselect, tidyr,

**URL** <https://github.com/WYATTBENSKEN/multimorbidity>

**BugReports** <https://github.com/WYATTBENSKEN/multimorbidity/issues>

**Suggests** rmarkdown, knitr

**VignetteBuilder** knitr

**Depends** R (>= 3.5.0)

**NeedsCompilation** no

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**Repository** CRAN

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clean_data	<i>Prepare our administrative data for analysis</i>
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### Description

clean\_data returns a dataset which has been transformed and cleaned for subsequent functions in this package.

### Usage

```
clean_data(dat = NULL, style = "long", id = NULL, prefix_dx = "dx")
```

### Arguments

dat	dataset
style	long, the default, is one diagnosis column per row whereas wide is multiple diagnosis columns
id	unique patient identifier variable name
prefix_dx	the variable prefix for the diagnosis columns (defaults to "dx"), in quotes

### Details

This function takes our raw administrative data, in a number of different forms, and prepares it in a way which allows the other functions in this package to easily work with it. It is recommended to run this package on all data regardless of setup.

### Value

dataframe with multiple rows per patient, which has re-structured their administrative data

### Examples

```
clean_data(dat = i10_wide, id = patient_id, style = "wide", prefix_dx = "dx")
```

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`i10_wide`*Example administrative data.*

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**Description**

A dataset with fake patient data for 5 patients with ICD-10 diagnosis codes.

**Usage**

```
data(i10_wide)
```

**Format**

A data frame with 29 rows and 11 variables:

**patient\_id** patient\_id

**sex** patient's sex (male or female)

**date\_of\_serv** the date of service for the fake claim

**dx1** first diagnosis

**dx2** second diagnosis

**dx3** third diagnosis

**dx4** fourth diagnosis

**dx5** fifth diagnosis

**visit\_type** inpatient (ip) or outpatient(ot)

**hcpcs** HCPCS code

**icd\_version** Which version of ICD the row is. 9 = ICD-9, 0 = ICD-10

**Source**

This was created by the package author.

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`socialrisk`*Social Risk*

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**Description**

`socialrisk` returns a summary dataset containing indicators of social risk, which vary based on the taxonomy command, for each patient.

**Usage**

```
socialrisk(dat = NULL, id = NULL, dx = "dx", taxonomy = "cms")
```

**Arguments**

<code>dat</code>	dataset which has been properly prepared in long format
<code>id</code>	variable of the unique patient identifier
<code>dx</code>	the column with the diagnoses (defaults to 'dx')
<code>taxonomy</code>	the taxonomy one wishes to use for social risk, with options of "cms" (default), "mha", and "siren"

**Details**

This function uses data which has been properly prepared to identify and flag social risks.

**Value**

dataframe with one row per patient, a column for their patient id, a column with whether they have any social risk, a column with the number of social risk domains, and columns with indicator variables for each social risk

**Examples**

```
data <- clean_data(dat = i10_wide, id = patient_id, style = "wide", prefix_dx = "dx")
socialrisk(dat = data, id = patient_id, dx = dx, taxonomy = "cms")
```

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