

# Package ‘coder’

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**Type** Package

**Title** Deterministic Categorization of Items Based on External Code Data

**Version** 0.13.10

**Description** Fast categorization of items based on external code data identified by regular expressions. A typical use case considers patient with medically coded data, such as codes from the International Classification of Diseases ('ICD') or the Anatomic Therapeutic Chemical ('ATC') classification system.

Functions of the package relies on a triad of objects: (1) case data with unit id:s and possible dates of interest; (2) external code data for corresponding units in (1) and with optional dates of interest and; (3) a classification scheme ('classcodes' object) with regular expressions to identify and categorize relevant codes from (2).

It is easy to introduce new classification schemes ('classcodes' objects) or to use default schemes included in the package. Use cases includes patient categorization based on 'comorbidity indices' such as 'Charlson', 'Elixhauser', 'RxRisk V', or the 'comorbidity-polypharmacy' score (CPS), as well as adverse events after hip and knee replacement surgery.

**License** GPL-2

**Depends** R (>= 3.3)

**Suggests** covr, testthat, knitr, rmarkdown, writexl

**Imports** data.table, decoder, generics, methods, tibble

**LazyData** TRUE

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

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**BugReports** <https://github.com/ropensci/coder/issues>

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**Author** Erik Bulow [aut, cre] (<<https://orcid.org/0000-0002-9973-456X>>),  
 Emely C Zabore [rev] (Emily reviewed the package (v. 0.12.1) for  
 rOpenSci, see  
 <<https://github.com/ropensci/software-review/issues/381>>),  
 David Robinson [rev] (David reviewed the package (v. 0.12.1) for  
 rOpenSci, see  
 <<https://github.com/ropensci/software-review/issues/381>>)

**Maintainer** Erik Bulow <eriklgb@gmail.com>

**Repository** CRAN

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 ae

*Classcodes for adverse events after knee and hip arthroplasty*

---

### Description

ICD-10 group names are prefixed by two letters as given by the references. Two groups (DB and DM) are split into two due to different conditions.

**Usage**

knee\_ae

hip\_ae

**Format**

Data frame with 3 columns:

**group** Different types of adverse events (see reference section)

**icd10** regular expressions identifying ICD-10 codes for each group

**icd10\_fracture** regular expressions for fracture patients. Essentially the same as regex but with some additional codes for group "DM1 other"

**kva** regular expressions identifying KVA codes

**condition** special conditions are used, see below.

An object of class `classcodes` (inherits from `tbl_df`, `tbl`, `data.frame`) with 7 rows and 5 columns.

**Hip fractures**

Adverse events (AE) codes for hip fractures are based on codes for elective cases but with some additional codes for DM 1 (N300, N308, N309 and N390).

**Conditions**

Special conditions apply to all categories. Those require non-standard modifications of the `classcodes` data prior to categorization.

**hbdia1\_hdia** TRUE if the code was given as any type of diagnose during hospital visit for index operation, or as main diagnose for later visits, otherwise FALSE

**late\_hdia** TRUE if the code was given as main diagnose at a later visit after the index operation, otherwise FALSE

**post\_op** TRUE if the code was given at a later visit after the index operation, otherwise FALSE

**References**

Magneli M, Unbeck M, Rogmark C, Rolfson O, Hommel A, Samuelsson B, et al. Validation of adverse events after hip arthroplasty: a Swedish multi-centre cohort study. *BMJ Open*. 2019 Mar 7;9(3):e023773.

**See Also**

hip\_ae\_hailer

Other default `classcodes`: [charlson](#), [cps](#), [elixhauser](#), [hip\\_ae\\_hailer](#), [rxriskv](#)

---

all_classcodes	<i>Summary data for all default classcodes object in the package</i>
----------------	--

---

**Description**

Tabulate object names and list all related versions of implemented regular expressions and index weights.

**Usage**

```
all_classcodes()
```

**Value**

`tibble::tibble` with columns describing all default classcodes objects from the package.

**See Also**

Other classcodes: `as.data.frame.classified()`, `classcodes`, `codebook()`, `print.classcodes()`, `print.classified()`, `set_classcodes()`, `summary.classcodes()`, `visualize.classcodes()`

**Examples**

```
all_classcodes()
```

---

as.data.frame.classified	<i>Convert output from classify() to matrix/data.frame/data.table</i>
--------------------------	---

---

**Description**

Convert output from classify() to matrix/data.frame/data.table

**Usage**

```
## S3 method for class 'classified'
as.data.frame(x, ...)
```

```
## S3 method for class 'classified'
as.data.table(x, ...)
```

```
## S3 method for class 'classified'
as.matrix(x, ...)
```

**Arguments**

x                    output from `classify()`  
 ...                 ignored

**Value**

data frame/data table with:

- first column named as "id" column specified as input to `classify()` and with data from `row.names(x)`
- all columns from `classified`
- no row names

or simply the input matrix without additional attributes

**See Also**

Other classcodes: `all_classcodes()`, `classcodes`, `codebook()`, `print.classcodes()`, `print.classified()`, `set_classcodes()`, `summary.classcodes()`, `visualize.classcodes()`

**Examples**

```
x <- classify(c("C80", "I20", "invalid_code"), "elixhauser")

as.matrix(x)[, 1:3]
as.data.frame(x)[, 1:3]
data.table::as.data.table(x)[, 1:3]

# `as_tibble()` works automatically due to internal use of `as.data.frame()`.
tibble::as_tibble(x)
```

---

as.keyvalue.classcodes

*Make keyvalue object from classcodes object*

---

**Description**

S3-method for generic `decoder::as.keyvalue()`

**Usage**

```
## S3 method for class 'classcodes'
as.keyvalue(x, coding, cc_args = list(), ...)
```

**Arguments**

<code>x</code>	classcodes object
<code>coding</code>	either a vector with codes from the original classification, or a name (character vector of length one) of a keyvalue object from package "decoder" (for example "icd10cm" or "atc")
<code>cc_args</code>	List of named arguments passed to <code>set_classcodes()</code>
<code>...</code>	additional arguments passed to <code>decoder::as.keyvalue()</code>

**Value**

Object of class keyvalue where key is the subset of codes from `object$key` identified by the regular expression from `x` and where value is the corresponding `x$group`. Hence, note that the original `object$value` is not used in the output.

**Examples**

```
# List all codes with corresponding classes as recognized by the Elixhauser
# comorbidity classification according to the Swedish version of the
# international classification of diseases version 10 (ICD-10-SE)
head(decoder::as.keyvalue(elixhauser, "icd10se"))

# Similar but with the American ICD-10-CM instead
# Note that the `value` column is similar as above
# (with names from `x$group`) and not
# from `object$value`
head(decoder::as.keyvalue(elixhauser, "icd10cm"))

# Codes identified by regular expressions based on ICD-9-CM and found in
# the Swedish version of ICD-9 used within the national cancer register
# (thus, a subset of the whole classification).
head(
  decoder::as.keyvalue(
    elixhauser, "icd9",
    cc_args = list(regex = "icd9cm")
  )
)
```

---

categorize

*Categorize cases based on external data and classification scheme*


---

**Description**

This is the main function of the package, which relies of a triad of objects: (1) data with unit id:s and possible dates of interest; (2) codedata for corresponding units and with optional dates of interest and; (3) a classification scheme (`classcodes` object; `cc`) with regular expressions to identify and categorize relevant codes. The function combines the three underlying steps performed by `codify()`, `classify()` and `index()`. Relevant arguments are passed to those functions by `codify_args` and `cc_args`.

**Usage**

```

categorize(x, ...)

## S3 method for class 'data.frame'
categorize(x, ...)

## S3 method for class 'tbl_df'
categorize(x, ...)

## S3 method for class 'data.table'
categorize(x, ..., codedata, id, code, codify_args = list())

## S3 method for class 'codified'
categorize(
  x,
  ...,
  cc,
  index = NULL,
  cc_args = list(),
  check.names = TRUE,
  .data_cols = NULL
)

```

**Arguments**

x	data set with mandatory character id column (identified by argument id = "<col_name>"), and optional <a href="#">Date</a> of interest (identified by argument date = "<col_name>"). Alternatively, the output from <a href="#">codify()</a>
...	arguments passed between methods
codedata	external code data with mandatory character id column (identified by id = "<col_name>"), code column (identified by argument code = "<col_name>") and optional <a href="#">Date</a> column (identified by codify_args = list(code_date = "<col_name>")).
id	name of unique character id column found in both x and codedata. (where it must not be unique).
code	name of code column in codedata.
codify_args	Lists of named arguments passed to <a href="#">codify()</a>
cc	<a href="#">classcodes</a> object (or name of a default object from <a href="#">all_classcodes()</a> ).
index	Argument passed to <a href="#">index()</a> . A character vector of names of columns with index weights from the corresponding classcodes object (as supplied by the cc argument). See attr(cc, "indices") for available options. Set to FALSE if no index should be calculated. If NULL, the default, all available indices (from attr(cc, "indices")) are provided.
cc_args	List with named arguments passed to <a href="#">set_classcodes()</a>
check.names	Column names are based on cc\$group, which might include spaces. Those names are changed to syntactically correct names by check.names = TRUE. Syntactically invalid, but grammatically correct names might be preferred for presentation of the data as achieved by check.names = FALSE. Alternatively, if

categorize is called repeatedly, longer informative names might be created by `cc_args = list(tech_names = TRUE)`.

`.data_cols` used internally

### Value

Object of the same class as `x` with additional logical columns indicating membership of groups identified by the `classcodes` object (the `cc` argument). Numeric indices are also included if requested by the `index` argument.

### See Also

Other verbs: [classify\(\)](#), [codify\(\)](#), [index\\_fun](#)

### Examples

```
# For this example, 1 core would suffice:
old_threads <- data.table::getDTthreads()
data.table::setDTthreads(1)

# For some patient data (ex_people) and related hospital visit code data
# with ICD 10-codes (ex_icd10), add the Elixhauser comorbidity
# conditions based on all registered ICD10-codes
categorize(
  x           = ex_people,
  codedata    = ex_icd10,
  cc          = "elixhauser",
  id          = "name",
  code        = "icd10"
)

# Add Charlson categories and two versions of a calculated index
# ("quan_original" and "quan_updated").
categorize(
  x           = ex_people,
  codedata    = ex_icd10,
  cc          = "charlson",
  id          = "name",
  code        = "icd10",
  index       = c("quan_original", "quan_updated")
)

# Only include recent hospital visits within 30 days before surgery,
categorize(
  x           = ex_people,
  codedata    = ex_icd10,
  cc          = "charlson",
  id          = "name",
  code        = "icd10",
  index       = c("quan_original", "quan_updated"),
```



```

    codify_args = list(
      date      = "surgery",
      days      = c(-30, -1),
      code_date = "admission"
    )
  )

# Multiple versions -----

# We can compare categorization by according to Quan et al. (2005); "icd10",
# and Armitage et al. (2010); "icd10_rcs" (see `?charlson`)
# Note the use of `tech_names = TRUE` to distinguish the column names from the
# two versions.

# We first specify some common settings ...
ind <- c("quan_original", "quan_updated")
cd  <- list(date = "surgery", days = c(-30, -1), code_date = "admission")

# ... we then categorize once with "icd10" as the default regular expression ...
categorize(
  x           = ex_people,
  codedata    = ex_icd10,
  cc         = "charlson",
  id         = "name",
  code       = "icd10",
  index      = ind,
  codify_args = cd,
  cc_args    = list(tech_names = TRUE)
) %>%

# .. and once more with `regex = "icd10_rcs"`
categorize(
  codedata    = ex_icd10,
  cc         = "charlson",
  id         = "name",
  code       = "icd10",
  index      = ind,
  codify_args = cd,
  cc_args    = list(regex = "icd10_rcs", tech_names = TRUE)
)

# column names -----

# Default column names are based on row names from corresponding classcodes
# object but are modified to be syntactically correct.
default <-
  categorize(ex_people, codedata = ex_icd10, cc = "elixhauser",
            id = "name", code = "icd10")

```

```

# Set `check.names = FALSE` to retain original names:
original <-
  categorize(
    ex_people, codedata = ex_icd10, cc = "elixhauser",
    id = "name", code = "icd10",
    check.names = FALSE
  )

# Or use `tech_names = TRUE` for informative but long names (use case above)
tech <-
  categorize(ex_people, codedata = ex_icd10, cc = "elixhauser",
    id = "name", code = "icd10",
    cc_args = list(tech_names = TRUE)
  )

# Compare
tibble::tibble(names(default), names(original), names(tech))

# Go back to original number of threads
data.table::setDTthreads(old_threads)

```

---

charlson

*Classcodes for Charlson comorbidity based on ICD-codes*


---

## Description

Classcodes for Charlson comorbidity based on ICD-codes

## Usage

```
charlson
```

## Format

A data frame with 17 rows and 8 variables:

- `group`: comorbidity groups
- `description`: Verbal description of codes as described by Deyo et al. (1992).
- `icd10`: regular expressions identifying ICD-10 codes of each group as decoded from Quan et al. 2005. Note that this classification was not originally used with all weights! To simply use this classification table with weights other than `quan_original` and `quan_updated` might therefore lead to different results than originally intended for each index.
- `icd9cm_deyo`: Codes from table 1 column "Deyo's ICD-9-CM" in Quan et al. (2005). Procedure code 38.48 for peripheral vascular disease ignored.
- `icd9cm_enhanced`: Codes from table 1 column "Enhanced ICD-9-CM" in Quan et al. (2005).
- `icd10_rcs`: Codification by Armitage (2010). Note that Peptic ulcer disease is not included. All liver diseases (including mild) are included in "moderate or severe liver disease". All diabetes is included in "diabetes complication"

- `icd8_brusselaers`: Back translated version from ICD-10 to ICD-8 by Brusselsaers et al. (2017). "Moderate and severe liver disease" contains all liver disease and "diabetes complication" contains all diabetes.
- `icd9_brusselaers`: Back translated version from ICD-10 to ICD-9 by Brusselsaers et al. (2017). "Moderate and severe liver disease" contains all liver disease and "diabetes complication" contains all diabetes.
- `charlson`: original weights as suggested by Charlson et al. (1987)\*
- `doyo_ramano`: weights suggested by Deyo and Romano\*
- `dhoore`: weights suggested by D'Hoore\*
- `ghali`: weights suggested by Ghali\*
- `quan_original`: weights suggested by Quan (2005)
- `quan_updated`: weights suggested by Quan (2011)
  
- Weights decoded from Yurkovich et al. (2015).

## References

Armitage, J. N., & van der Meulen, J. H. (2010). Identifying co-morbidity in surgical patients using administrative data with the Royal College of Surgeons Charlson Score. *British Journal of Surgery*, 97(5), 772–781.

Brusselsaers N, Lagergren J. (2017) The Charlson Comorbidity Index in Registry-based Research. *Methods Inf Med* 2017;56:401–6.

Deyo, R. A., Cherkin, D. C., & Ciol, M. A. (1992). Adapting a clinical comorbidity index for use with ICD-9-CM administrative databases. *Journal of Clinical Epidemiology*, 45(6), 613–619.

Quan Hude et al. (2005). Coding algorithms for defining comorbidities in ICD-9-CM and ICD-10 administrative data. *Medical care*, 1130-1139.

Yurkovich, M., Avina-Zubieta, J. A., Thomas, J., Gorenchtein, M., & Lacaille, D. (2015). A systematic review identifies valid comorbidity indices derived from administrative health data. *Journal of clinical epidemiology*, 68(1), 3-14.

## See Also

Other default classcodes: [ae](#), [cps](#), [elixhauser](#), [hip\\_ae\\_hailer](#), [rxriskv](#)

---

classcodes

*Classcodes methods*

---

## Description

`classcodes` are classification schemes based on regular expression stored in data frames. These are essential to the package and constitute the third part of the triad of case data, code data and a classification scheme.

**Usage**

```

as.classcodes(x, ...)

## S3 method for class 'classcodes'
as.classcodes(
  x,
  ...,
  regex = attr(x, "regex"),
  indices = attr(x, "indices"),
  hierarchy = attr(x, "hierarchy")
)

## S3 method for class 'data.frame'
as.classcodes(
  x,
  ...,
  regex = NULL,
  indices = NULL,
  hierarchy = attr(x, "hierarchy"),
  .name = NULL
)

is.classcodes(x)

```

**Arguments**

<code>x</code>	data frame with columns described in the details section. Alternatively a <code>classcodes</code> object to be modified.
<code>...</code>	arguments passed between methods#'
<code>regex, indices</code>	character vector with names of columns in <code>x</code> containing regular expressions/indices.
<code>hierarchy</code>	named list of pairwise group names to appear as superior and subordinate for indices. To be used for indexing when the subordinate class is redundant (see the details section of <a href="#">elixhauser</a> for an example).
<code>.name</code>	used internally for name dispatch

**Details**

A `classcodes` object is a data frame with mandatory columns:

- `group`: unique and non missing class names
- At least one column with regular expressions ([regex](#) without Perl-like versions) defining class membership. Those columns can have arbitrary names (as specified by the `regex` argument). Occurrences of non unique regular expressions will lead to the same class having multiple names. This is accepted but will raise a warning. Classes do not have to be disjoint.

The object can have additional optional columns:

- `description`: description of each category

- `condition`: a class might have conditions additional to what is expressed by the regular expressions. If so, these should be specified as quoted expressions that can be evaluated within the data frame used by `classify()`
- `weights` for each class used by `index()`. Could be more than one and could have arbitrary names (as specified by the `indicesargument`).

## Value

Object of class `classcodes` (inheriting from data frame) with additional attributes:

- `code`: the coding used (for example "icd10", or "ATC"). NULL for unknown/arbitrary coding.
- `regexprs`: name of columns with regular expressions (as specified by the `regexargument`)
- `indices`: name of columns with (optional) index weights (as specified by the `indicesargument`)
- `hierarchy`: list as specified by the `hierarchy` argument.
- `name`: name as specified by the `.name` argument.

## See Also

`vignette("classcodes")` `vignette("Interpret_regular_expressions")` The package have several default `classcodes` included, see [all\\_classcodes\(\)](#).

Other `classcodes`: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [codebook\(\)](#), [print.classcodes\(\)](#), [print.classified\(\)](#), [set\\_classcodes\(\)](#), [summary.classcodes\(\)](#), [visualize.classcodes\(\)](#)

Other `classcodes`: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [codebook\(\)](#), [print.classcodes\(\)](#), [print.classified\(\)](#), [set\\_classcodes\(\)](#), [summary.classcodes\(\)](#), [visualize.classcodes\(\)](#)

## Examples

```
# The Elixhauser comorbidity classification is already a classcodes object
is.classcodes(coder::elixhauser)

# Strip its class attributes to use in examples
df <- as.data.frame(coder::elixhauser)

# Specify which columns store regular expressions and indices
# (assume no hierarchy)
elix <-
  as.classcodes(
    df,
    regex    = c("icd10", "icd10_short", "icd9cm", "icd9cm_ahrqweb", "icd9cm_enhanced"),
    indices  = c("sum_all", "sum_all_ahrq", "walraven",
                "sid29", "sid30", "ahrq_mort", "ahrq_readm"),
    hierarchy = NULL
  )
elix

# Specify hierarchy for patients with different types of cancer and diabetes
# See `?elixhauser` for details
as.classcodes(
  elix,
  hierarchy = list(
```

```

    cancer = c("metastatic cancer", "solid tumor"),
    diabetes = c("diabetes complicated", "diabetes uncomplicated")
  )
)

# Several checks are performed to not allow any erroneous classcodes object
## Not run:
as.classcodes(iris)
as.classcodes(iris, regex = "Species")

## End(Not run)

```

---

classify

*Classify codified data*

---

### Description

This is the second step of `codify()`  $\gg$  `classify()`  $\gg$  `index()`. Hence, the function takes a codified data set and classify each case based on relevant codes as identified by the classification scheme provided by a `classcodes` object.

### Usage

```

classify(codified, cc, ..., cc_args = list())

## Default S3 method:
classify(codified, cc, ..., cc_args = list())

## S3 method for class 'codified'
classify(codified, ...)

## S3 method for class 'data.frame'
classify(codified, ...)

## S3 method for class 'data.table'
classify(codified, cc, ..., id, code, cc_args = list())

```

### Arguments

<code>codified</code>	output from <code>codify()</code>
<code>cc</code>	<code>classcodes</code> object (or name of a default object from <code>all_classcodes()</code> ).
<code>...</code>	arguments passed between methods
<code>cc_args</code>	List with named arguments passed to <code>set_classcodes()</code>
<code>code, id</code>	name of code/id columns (in <code>codified</code> ).

**Value**

Object of class "classified". Inheriting from a Boolean matrix with one row for each element/row of codified and columns for each class with corresponding class names (according to the `classcodes` object). Note, however, that `print.classified()` preview this output as a tibble.

**See Also**

`as.data.frame.classified()`, `as.data.table.classified()` and `as.matrix.classified()`, `print.classified()`

Other verbs: `categorize()`, `codify()`, `index_fun`

**Examples**

```
# classify.default() -----

# Classify individual ICD10-codes by Elixhauser
classify(c("C80", "I20", "invalid_code"), "elixhauser")

# classify.codified() -----

# Prepare some codified data with ICD-10 codes during 1 year (365 days)
# before surgery
x <-
  codify(
    ex_people,
    ex_icd10,
    id      = "name",
    code    = "icd10",
    date    = "surgery",
    days    = c(-365, 0),
    code_date = "admission"
  )

# Classify those patients by the Charlson and Elixhasuer comorbidity indices
classify(x, "charlson")      # classcodes object by name ...
classify(x, coder::elixhauser) # ... or by the object itself

# -- start/stop --
# Assume that a prefix "ICD-10 = " is used for all codes and that some
# additional numbers are added to the end
x$icd10 <- paste0("ICD-10 = ", x$icd10)

# Set start = FALSE to identify codes which are not necessarily found in the
# beginning of the string
classify(x, "charlson", cc_args = list(start = FALSE))
```

```

# -- regex --
# Use a different version of Charlson (as formulated by regular expressions
# according to the Royal College of Surgeons (RCS) by passing arguments to
# `set_classcodes()` using the `cc_args` argument
y <-
  classify(
    x,
    "charlson",
    cc_args = list(regex = "icd10_rcs")
  )

# -- tech_names --
# Assume that we want to compare the results using the default ICD-10
# formulations (from Quan et al. 2005) and the RCS version and that the result
# should be put into the same data frame. We can use `tech_names = TRUE`
# to distinguish variables with otherwise similar names
cc <- list(tech_names = TRUE) # Prepare sommon settings
compare <-
  merge(
    classify(x, "charlson", cc_args = cc),
    classify(x, "charlson", cc_args = c(cc, regex = "icd10_rcs"))
  )
names(compare) # long but informative and distinguishable column names

# classify.data.frame() / classify.data.table() -----

# Assume that `x` is a data.frame/data.table without additional attributes
# from `codify()` ...
xdf <- as.data.frame(x)
xdt <- data.table::as.data.table(x)

# ... then the `id` and `code` columns must be specified explicitly
classify(xdf, "charlson", id = "name", code = "icd10")
classify(xdt, "charlson", id = "name", code = "icd10")

```

---

codebook

*codebook(s) for classcodes object*


---

## Description

`summary.classcodes()` and `visualize.classcodes()` are used to summarize/visualize classcodes in R. A codebook, on the other hand, is an exported summary saved in an Excel spreadsheet to use in collaboration with non R-users. Several codebooks might be combined into a single Excel document with several sheets (one for each codebook).



**Usage**

```
codebook(object, coding, ..., file = NULL)
```

```
## S3 method for class 'codebook'
print(x, ...)
```

```
codebooks(..., file = NULL)
```

**Arguments**

object	classcodes object
coding	either a vector with codes from the original classification, or a name (character vector of length one) of a keyvalue object from package "decoder" (for example "icd10cm" or "atc")
...	Additional arguments for each function: <ul style="list-style-type: none"> <li>• <code>codebook()</code>: arguments passed to <code>summary.classcodes()</code></li> <li>• <code>codebooks()</code>: multiple named outputs from <code>codebook()</code></li> <li>• <code>print.codebook()</code>: arguments passed to <code>tibble:::print.tbl()</code></li> </ul>
file	name/path to Excel file for data export
x	output from <code>codebook()</code>

**Value**

Functions are primarily called for their side effects (exporting data to Excel or printing to screen). In addition:

- `codebook()` returns list of data frames describing relationship between groups and individual codes
- `codebooks()` returns a concatenated list with output from `codebook()`. Only one 'README' object is kept however and renamed as such.
- `print.codebook()` returns x (invisible)

**See Also**

Other classcodes: `all_classcodes()`, `as.data.frame.classified()`, `classcodes`, `print.classcodes()`, `print.classified()`, `set_classcodes()`, `summary.classcodes()`, `visualize.classcodes()`

**Examples**

```
# codebook() -----
## Not run:
# Export codebook (to temporary file) with all codes identified by the
# Elixhauser comorbidity classification based on ICD-10-CM
codebook(elixhauser, "icd10cm", file = tempfile("codebook", fileext = ".xlsx"))

# All codes from ICD-9-CM Disease part used by Elixhauser enhanced version
codebook(elixhauser, "icd9cmd",
```

```

    cc_args = list(regex = "icd9cm_enhanced",
                  file = tempfile("codebook", fileext = ".xlsx"))
  )

# The codebook returns a list with three objects.
# Access a dictionary table with translates of each code to text:
codebook(charlson, "icd10cm")$all_codes

# print.codebook() -----

# If argument `file` is unspecified, a preview of each sheet of the codebook is
# printed to the screen
(cb <- codebook(charlson, "icd10cm"))

# The preview can be modified by arguments to the print-method
print(cb, n = 20)

# codebooks() -----

# Combine codebooks based on different versions of the regular expressions
# and export to a single (temporary) Excel file
c1 <- codebook(elixhauser, "icd10cm")
c2 <- codebook(elixhauser, "icd9cmd",
              cc_args = list(regex = "icd9cm_enhanced")
              )

codebooks(
  elix_icd10 = c1, elix_icd9cm = c2,
  file = tempfile("codebooks", fileext = ".xlsx")
)

## End(Not run)

```

---

codify

*Codify case data with external code data (within specified time frames)*


---

## Description

This is the first step of `codify()` %>% `classify()` %>% `index()`. The function combines case data from one data set with related code data from a second source, possibly limited to codes valid at certain time points relative to case dates.

## Usage

```
codify(x, codedata, ..., id, code, date = NULL, code_date = NULL, days = NULL)
```

```
## S3 method for class 'data.frame'
codify(x, ..., id, date = NULL, days = NULL)
```

```
## S3 method for class 'data.table'
codify(
  x,
  codedata,
  ...,
  id,
  code,
  date = NULL,
  code_date = NULL,
  days = NULL,
  alnum = FALSE,
  .copy = NA
)

## S3 method for class 'codified'
print(x, ..., n = 10)
```

### Arguments

x	data set with mandatory character id column (identified by argument <code>id = "&lt;col_name&gt;"</code> ), and optional <a href="#">Date</a> of interest (identified by argument <code>date = "&lt;col_name&gt;"</code> ). Alternatively, the output from <a href="#">codify()</a>
codedata	additional data with columns including case id (character), code and an optional date ( <a href="#">Date</a> ) for each code. An optional column condition might distinguish codes/dates with certain characteristics (see example).
...	arguments passed between methods
id, code, date, code_date	column names with case id (character from x and codedata), code (from x) and optional date ( <a href="#">Date</a> from x) and code_date ( <a href="#">Date</a> from codedata).
days	numeric vector of length two with lower and upper bound for range of relevant days relative to date. See "Relevant period".
alnum	Should codes be cleaned from all non alphanumeric characters?
.copy	Should the object be copied internally by <a href="#">data.table::copy()</a> ? NA (by default) means that objects smaller than 1 GB are copied. If the size is larger, the argument must be set explicitly. Set TRUE to make copies regardless of object size. This is recommended if enough RAM is available. If set to FALSE, calculations might be carried out but the object will be changed by reference. <b>IMPORTANT!</b> This might lead to undesired consequences and should only be used if absolutely necessary!
n	number of rows to preview as tibble. The output is technically a <a href="#">data.table::data.table</a> , which might be an unusual format to look at. Use <code>n = NULL</code> to print the object as is.

### Value

Object of class `codified` (inheriting from [data.table::data.table](#)). Essentially x with additional columns: `code`, `code_date`: left joined from `codedata` or NA if no match within period. `in_period`:

Boolean indicator if the case had at least one code within the specified period.

The output has one row for each combination of "id" from x and "code" from codedata. Rows from x might be repeated accordingly.

### Relevant period

Some examples for argument days:

- `c(-365, -1)`: window of one year prior to the date column of x. Useful for patient comorbidity.
- `c(1, 30)`: window of 30 days after date. Useful for adverse events after a surgical procedure.
- `c(-Inf, Inf)`: no limitation on non-missing dates.
- `NULL`: no time limitation at all.

### See Also

Other verbs: [categorize\(\)](#), [classify\(\)](#), [index\\_fun](#)

### Examples

```
# Codify all patients from `ex_people` with their ICD-10 codes from `ex_icd10`
x <- codify(ex_people, ex_icd10, id = "name", code = "icd10")
x

# Only consider codes if recorded at hospital admissions within one year prior
# to surgery
codify(
  ex_people,
  ex_icd10,
  id      = "name",
  code    = "icd10",
  date    = "surgery",
  code_date = "admission",
  days    = c(-365, 0) # admission during one year before surgery
)

# Only consider codes if recorded after surgery
codify(
  ex_people,
  ex_icd10,
  id      = "name",
  code    = "icd10",
  date    = "surgery",
  code_date = "admission",
  days    = c(1, Inf) # admission any time after surgery
)

# Dirty code data -----
# Assume that codes contain unwanted "dirty" characters
```

```

# Those could for example be a dot used by ICD-10 (i.e. X12.3 instead of X123)
dirt <- c(strsplit(c("#%&/()=?`.-_"), split = ""), recursive = TRUE)
rdirt <- function(x) sample(x, nrow(ex_icd10), replace = TRUE)
sub <- function(i) substr(ex_icd10$icd10, i, i)
ex_icd10$icd10 <-
  paste0(
    rdirt(dirt), sub(1),
    rdirt(dirt), sub(2),
    rdirt(dirt), sub(3),
    rdirt(dirt), sub(4),
    rdirt(dirt), sub(5)
  )
head(ex_icd10)

# Use `alnum = TRUE` to ignore non alphanumeric characters
codify(ex_people, ex_icd10, id = "name", code = "icd10", alnum = TRUE)

# Big data -----

# If `data` or `codedata` are large compared to available
# Random Access Memory (RAM) it might not be possible to make internal copies
# of those objects. Setting `.copy = FALSE` might help to overcome such problems

# If no copies are made internally, however, the input objects (if data tables)
# would change in the global environment
x2 <- data.table::as.data.table(ex_icd10)
head(x2) # Look at the "icd10" column (with dirty data)

# Use `alnum = TRUE` combined with `.copy = FALSE`
codify(ex_people, x2, id = "name", code = "icd10", alnum = TRUE, .copy = FALSE)

# Even though no explicit assignment was specified
# (neither for the output of codify(), nor to explicitly alter `x2`,
# the `x2` object has changed (look at the "icd10" column!):
head(x2)

# Hence, the `.copy` argument should only be used if necessary
# and if so, with caution!

# print.codify() -----

x # Preview first 10 rows as a tibble
print(x, n = 20) # Preview first 20 rows as a tibble
print(x, n = NULL) # Print as data.table (ignoring the 'classified' class)

```

**Description**

Classcodes for the comorbidity-polypharmacy score (CPS) based on ICD-10 codes

**Usage**

cps

**Format**

A data frame with 2 rows and 2 variables:

**group** comorbidity groups, either "ordinary" for most ICD-10-codes or "special" for codes beginning with "UA", "UB" and "UP"

**icd10** regular expressions identifying ICD-10 codes of each group

**only\_ordinary** index weights, 1 for ordinary and 0 for special

**References**

Stawicki, Stanislaw P., et al. "Comorbidity polypharmacy score and its clinical utility: A pragmatic practitioner's perspective." *Journal of emergencies, trauma, and shock* 8.4 (2015): 224.

**See Also**

Other default classcodes: [ae](#), [charlson](#), [elixhauser](#), [hip\\_ae\\_hailer](#), [rxriskv](#)

---

elixhauser

*Classcodes for Elixhauser based on ICD-codes*

---

**Description**

Solid tumors are subordinate to metastatic cancer. A patient with both conditions will still be classified as such but a possible (weighted) index value will only account for metastatic cancer. The same is true for "diabetes uncomplicated", which is subordinate of "diabetes complicated". See Elixhauser et al. (1998).

**Usage**

elixhauser

**Format**

A data frame with 31 rows and 8 variables:

**group** comorbidity groups

**icd10** regular expressions identifying ICD-10 codes of each group. Corresponds to column 'ICD-10' in table 2 of Quan et al. (2005).

**icd10\_short** regular expressions identifying only the first three characters of ICD-10 codes of each group. This alternative version was added only to use in emergency when only the first three digits are available. It is not an official version and we do not recommend to use it!

**icd9cm** Corresponds to column 'Elixhauser's Original ICD-9-CM' in table 2 of Quan et al. (2005).

**icd9cm\_ahrqweb** Corresponds to column 'Elixhauser AHRQ-Web ICD-9-CM' in table 2 of Quan et al. (2005).

**icd9cm\_enhanced** Corresponds to column 'Enhanced ICD-9-CM' in table 2 of Quan et al. (2005).

**sum\_all** all weights = 1 (thus no weights)

**sum\_all\_ahrq** as **sum\_all** excluding "cardiac arrhythmia. Compare to **icd9cm\_ahrqweb** which does not consider this condition.

**walraven** weights suggested by Walraven et al. (2009)

**sid29** weights suggested by Thompson et al. (2015) based on all conditions except cardiac arrhythmia

**sid30** weights suggested by Thompson et al. (2015) based on all conditions

**ahrq\_mort** weights for in-hospital mortality suggested by Moore et al. (2017)

**ahrq\_readm** weights for readmissions suggested by Moore et al. (2017)

## Details

Note that "DRG screen" as proposed in table 1 of Elixhauser et al. (1998) is not handled by the coder package. This should instead be considered as an additional pre- or post-processing step!

## References

- Elixhauser A, Steiner C, Harris DR, Coffey RM (1998). Comorbidity Measures for Use with Administrative Data. *Med Care*. 1998;36(1):8–27.
- Moore, B. J., White, S., Washington, R., Coenen, N., & Elixhauser, A. (2017). Identifying Increased Risk of Readmission and In-hospital Mortality Using Hospital Administrative Data. *Medical Care*, 55(7), 698–705.
- Quan Hude et al. (2005). Coding algorithms for defining comorbidities in ICD-9-CM and ICD-10 administrative data. *Medical care*, 1130-1139.
- Thompson, N. R., Fan, Y., Dalton, J. E., Jehi, L., Rosenbaum, B. P., Vadera, S., & Griffith, S. D. (2015). A new Elixhauser-based comorbidity summary measure to predict in-hospital mortality. *Med Care*, 53(4), 374–379.
- Walraven, C. Van, Austin, P. C., Jennings, A., Quan, H., Alan, J., Walraven, C. Van, . . . Jennings, A. (2009). A Modification of the Elixhauser Comorbidity Measures Into a Point System for Hospital Death Using Administrative Data. *Medical Care*, 47(6), 626–633.

## See Also

Other default classcodes: [ae](#), [charlson](#), [cps](#), [hip\\_ae\\_hailer](#), [rxriskv](#)

---

`ex_atc`*Example data for random ATC codes*

---

**Description**

Example data for fictive people to use for testing and in examples.

**Usage**`ex_atc`**Format**

Data frames with 100 rows and 2 variables:

**name** random person names

**atc** Random codes from the Anatomic Therapeutic Chemical classification (ATC) system.

**prescription** random dates of prescription of medications with corresponding ATC codes

**See Also**

Other example data: [ex\\_icd10](#), [ex\\_people](#)

---

`ex_icd10`*Example data for random codes assigned to random people*

---

**Description**

Example data for fictive ICD-10-diagnoses to use for testing and in examples.

**Usage**`ex_icd10`**Format**

Data frames with 1,000 rows and 4 variables:

**id** Random names corresponding to column name in dataset `ex_people`

**date** random dates corresponding to registered (comorbidity) codes

**code** ICD-10 codes from the `uranium_pathology` dataset in the `icd.data` package by Jack Wasey originating from the United States Transuranium and Uranium Registries, published in the public domain.

**hdia** boolean marker if corresponding code is the main diagnose of the hospital visit (randomly assigned to 10 percent of the codes)



**Source**

<https://github.com/jackwasey/icd.data> <https://ustur.wsu.edu/about-us/>

**See Also**

Other example data: [ex\\_atc](#), [ex\\_people](#)

---

ex_people	<i>Example data for random people</i>
-----------	---------------------------------------

---

**Description**

Example data for fictive people to use for testing and in examples.

**Usage**

```
ex_people
```

**Format**

Data frames with 100 rows and 2 variables:

**name** random person names

**surgery** random dates for a relevant event

**See Also**

Other example data: [ex\\_atc](#), [ex\\_icd10](#)

---

hip_ae_hailer	<i>Classcodes for infection and dislocation after hip arthroplasty</i>
---------------	--

---

**Description**

Classcodes for infection and dislocation after hip arthroplasty

**Usage**

```
hip_ae_hailer
```

**Format**

Data frame with 3 columns:

**group** Infection or dislocation

**icd10** regular expressions based on ICD-10

**kva** regular expressions based on NOMESCO/KVA codes

**See Also**

ae

Other default classcodes: [ae](#), [charlson](#), [cps](#), [elixhauser](#), [rxriskv](#)

index\_fun

*Calculate index based on classification scheme***Description**

This is the third step of `codify()` %>% `classify()` %>% `index()`. The function takes classified case data and calculates (weighted) index sums as specified by weights from a `classcodes` object.

**Usage**

```
index(classified, ...)

## S3 method for class 'data.frame'
index(classified, ...)

## S3 method for class 'matrix'
index(classified, index = NULL, cc = NULL, ...)
```

**Arguments**

<code>classified</code>	output from <a href="#">classify()</a>
<code>...</code>	used internally
<code>index</code>	name of column with 'weights' from corresponding <a href="#">classcodes</a> object. Can be NULL if the index is just a unweighted count of all identified groups.
<code>cc</code>	<a href="#">classcodes</a> object. Can be NULL if a <code>classcodes</code> object is already available as an attribute of <code>classified</code> (which is often the case) and/or if <code>index = NULL</code> .

**Details**

Index weights for subordinate hierarchical classes (as identified by `attr(cc, "hierarchy")`) are excluded in presence of superior classes if `index` specified with argument `index`.

**Value**

Named numeric index vector with names corresponding to `rownames(classified)`

**See Also**

Other verbs: [categorize\(\)](#), [classify\(\)](#), [codify\(\)](#)

**Examples**

```

# Prepare some codified data with ICD-10 codes during 1 year (365 days)
# before surgery
x <-
  codify(
    ex_people,
    ex_icd10,
    id      = "name",
    code    = "icd10",
    date    = "surgery",
    days    = c(-365, 0),
    code_date = "admission"
  )

# Classify those patients by the Charlson comorbidity indices
cl <- classify(x, "charlson")

# Calculate (weighted) index values
head(index(cl))           # Un-weighted sum/no of conditions for each patient
head(index(cl, "quan_original")) # Weighted index (Quan et al. 2005; see `?charlson`)
head(index(cl, "quan_updated")) # Weighted index (Quan et al. 2011; see `?charlson`)

# Tabulate index for all patients.
# As expected, most patients are healthy and have index = 0/NA,
# where NA indicates no recorded hospital visits
# found in `ex_icd10` during codification.
# In practice, those patients might be assumed to have 0 comorbidity as well.
table(index(cl, "quan_original"), useNA = "always")

# If `cl` is a matrix without additional attributes (as imposed by `codify()`)
# an explicit classcodes object must be specified by the `cc` argument
cl2 <- as.matrix(cl)
head(index(cl2, cc = "charlson"))

```

---

```
print.classcodes      Print classcodes object
```

---

**Description**

Print classcodes object

**Usage**

```
## S3 method for class 'classcodes'
print(x, n = NULL, ...)
```

**Arguments**

x                    object of type `classcodes`  
 n                    number of rows to preview (n = 0 is allowed)  
 ...                  arguments passed to print method for tibble

**See Also**

Other `classcodes`: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [classcodes](#), [codebook\(\)](#), [print.classified\(\)](#), [set\\_classcodes\(\)](#), [summary.classcodes\(\)](#), [visualize.classcodes\(\)](#)

**Examples**

```
# Default printing
elixhauser

# Print attributes data but no data preview
print(elixhauser, n = 0)

# Print all rows
print(elixhauser, n = 31)
```

---

<code>print.classified</code>	<i>Printing classified data</i>
-------------------------------	---------------------------------

---

**Description**

Preview first n rows as tibble

**Usage**

```
## S3 method for class 'classified'
print(x, ...)
```

**Arguments**

x                    output from [classify\(\)](#)  
 ...                  additional arguments passed to printing method for a tibble. n is the number of rows to preview. Set n = NULL to disable the tibble preview and print the object as is (a matrix).

**See Also**

Other `classcodes`: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [classcodes](#), [codebook\(\)](#), [print.classcodes\(\)](#), [set\\_classcodes\(\)](#), [summary.classcodes\(\)](#), [visualize.classcodes\(\)](#)

## Examples

```
# Preview all output
classify(c("C80", "I20", "invalid_code"), "elixhauser")

# Preview only the first row
print(classify(c("C80", "I20", "invalid_code"), "elixhauser"), n = 1)

# Print object as is (matrix)
print(classify(c("C80", "I20", "invalid_code"), "elixhauser"), n = NULL)
```

---

rxriskv

*Classcodes for RxRisk V based on ATC codes*

---

## Description

Note that desired implementation might differ over time and by country.

## Usage

```
rxriskv
```

## Format

Data frames with 46 rows and 6 variables:

**group** medical condition

**pratt** ATC codes from table 1 in Pratt et al. 2018 (ignoring PBS item codes and extra conditions).

**garland** Modified version by Anne Garland to resemble medical use in Sweden 2016 (Unpublished).

**caughey** From appendix 1 in Caughey et al. 2010

**pratt** Mortality weights from table 1 in Pratt et al. 2018

**sum\_all** Unweighted count of all conditions.

## References

Caughey GE, Roughead EE, Vitry AI, McDermott RA, Shakib S, Gilbert AL. Comorbidity in the elderly with diabetes: Identification of areas of potential treatment conflicts. *Diabetes Res Clin Pract* 2010;87:385–93.

Pratt NL, Kerr M, Barratt JD, Kemp-Casey A, Kalisch Ellett LM, Ramsay E, et al. The validity of the Rx-Risk Comorbidity Index using medicines mapped to the Anatomical Therapeutic Chemical (ATC) Classification System. *BMJ Open* 2018;8.

## See Also

Other default classcodes: [ae](#), [charlson](#), [cps](#), [elixhauser](#), [hip\\_ae\\_hailer](#)

---

set\_classcodes      *Set classcodes object*

---

### Description

Prepare a classcodes object by specifying the regular expressions to use for classification.

### Usage

```
set_classcodes(
  cc,
  classified = NULL,
  regex = NULL,
  start = TRUE,
  stop = FALSE,
  tech_names = NULL
)
```

### Arguments

cc	<a href="#">classcodes</a> object (or name of a default object from <a href="#">all_classcodes()</a> ).
classified	object that classcodes could be inherited from
regex	name of column with regular expressions to use for classification. NULL (default) uses <code>attr(obj, "regexr")[1]</code> .
start, stop	should codes start/end with the specified regular expressions? If TRUE, column "regex" is prefixed/suffixed by <code>^/\$</code> .
tech_names	should technical column names be used? If FALSE, colnames are taken directly from group names of cc, if TRUE, these are changed to more technical names avoiding special characters and are prefixed by the name of the classification scheme. NULL (by default) preserves previous names if cc is inherited from classified (fall backs to FALSE if not already set).

### Value

[classcodes](#) object.

### See Also

Other classcodes: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [classcodes](#), [codebook\(\)](#), [print.classcodes\(\)](#), [print.classified\(\)](#), [summary.classcodes\(\)](#), [visualize.classcodes\(\)](#)

### Examples

```
# Prepare a classcodes object for the Charlson comorbidity classification
# based on the default regular expressions
set_classcodes(charlson) # by object
set_classcodes("charlson") # by name
```

```

# Same as above but based on regular expressions for ICD-8 (see `?charlson`)
set_classcodes(charlson, regex = "icd8_brusselaers")

# Only recognize codes if no other characters are found after the relevant codes
# Hence if the code vector stops with the code
set_classcodes(charlson, stop = TRUE)

# Accept code vectors with strings which do not necessarily start with the code.
# This is useful if the code might appear in the middle of a longer character
# string or if a common prefix is used for all codes.
set_classcodes(charlson, start = FALSE)

# Use technical names to clearly describe the origin of each group.
# Note that the `cc` argument must be specified by a character string
# since this name is used as part of the column names
x <- set_classcodes("charlson", tech_names = TRUE)
x$group

```

---

summary.classcodes      *Summarizing a classcodes object*

---

## Description

Classification schemes are formalized by regular expressions within the classcodes objects. These are computationally effective but sometimes hard to interpret. Use this function to list all codes identified for each group.

## Usage

```

## S3 method for class 'classcodes'
summary(object, coding, ..., cc_args = list())

## S3 method for class 'summary.classcodes'
print(x, ...)

```

## Arguments

object	classcodes object
coding	either a vector with codes from the original classification, or a name (character vector of length one) of a keyvalue object from package "decoder" (for example "icd10cm" or "atc")
...	<ul style="list-style-type: none"> <li>summary.classcodes(): ignored</li> <li>print.summary.classcodes(): arguments passed to tibble::print.tbl()</li> </ul>
cc_args	List of named arguments passed to <a href="#">set_classcodes()</a>
x	output from summary.classcodes()

**Value**

Methods primarily called for their side effects (printing to the screen) but with additional invisible objects returned:

- `summary.classcodes()`: list with input arguments object and coding unchanged, as well as a data frame (`summary`) with columns for groups identified (`group`); the number of codes to be recognized for each group (`n`) and individual codes within each group (`codes`).
- `print.summary.classcodes()`: argument `x` unchanged

**See Also**

Other classcodes: `all_classcodes()`, `as.data.frame.classified()`, `classcodes`, `codebook()`, `print.classcodes()`, `print.classified()`, `set_classcodes()`, `visualize.classcodes()`

**Examples**

```
# summary.classcodes() -----

# Summarize all ICD-10-CM codes identified by the Elixhauser
# comorbidity classification
# See `?decoder::icd10cm` for details
summary(elixhauser, coding = "icd10cm")

# Is there a difference if instead considering the Swedish ICD-10-SE?
# See `?decoder::icd10se` for details
summary(elixhauser, coding = "icd10se")

# Which ICD-9-CM diagnostics codes are recognized by Charlson according to
# Brusseleers et al. 2017 (see `?charlson`)
summary(
  charlson, coding = "icd9cmd",
  cc_args = list(regex = "icd9_brusselaers")
)

# print.summary.classcodes() -----

# Print all 31 lines of the summarized Elixhauser classcodes object
print(
  summary(elixhauser, coding = "icd10cm"),
  n = 31
)
```



**Description**

Groups from a `classcodes` object are visualized by their regular expressions in the default web browser. The visualization does not give any details on group names, conditions or weights but might be useful both for understanding of a classification scheme in use, and during the creation and debugging of such.

**Usage**

```
## S3 method for class 'classcodes'
visualize(x, group = NULL, show = TRUE, ...)
```

**Arguments**

<code>x</code>	<code>classcodes</code> object or name of such object included in the package (see <a href="#">all_classcodes()</a> ).
<code>group</code>	names (as character vector) of groups to visualize (subset of <code>rownames(x)</code> ). (All groups if <code>NULL</code> .)
<code>show</code>	should a visualization be shown in the default web browser. Set to <code>FALSE</code> to just retrieve a URL for later use.
<code>...</code>	Arguments passed on to <a href="#">set_classcodes</a>
	<code>regex</code> name of column with regular expressions to use for classification. <code>NULL</code> (default) uses <code>attr(obj, "regexr")[1]</code> .

**Value**

URL to website with visualization (invisible)

**See Also**

Other `classcodes`: [all\\_classcodes\(\)](#), [as.data.frame.classified\(\)](#), [classcodes](#), [codebook\(\)](#), [print.classcodes\(\)](#), [print.classified\(\)](#), [set\\_classcodes\(\)](#), [summary.classcodes\(\)](#)

**Examples**

```
# The default behavior is to open a visualization in the default web browser
## Not run:

# How is depression classified according to Elixhauser?
visualize("elixhauser", "depression")

# Compare the two diabetes groups according to Charlson
visualize("charlson",
  c("diabetes without complication", "diabetes complication"))

# Is this different from the "Royal College of Surgeons classification?
# Yes, there is only one group for diabetes
visualize("charlson",
  c("diabetes without complication", "diabetes complication"),
  regex = "rcs")
```

```
)  
  
# Show all groups from Charlson  
visualize("charlson")  
  
# It is also possible to visualize an arbitrary regular expression  
# from a character string  
visualize("I2([12]|52)")  
  
## End(Not run)  
  
# The URL is always returned (invisible) but the visual display can  
# also be omitted  
url <- visualize("hip_ae", show = FALSE)  
url
```

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