

Package ‘epocakir’

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Title Clinical Coding of Patients with Kidney Disease

Version 0.9.7

Description Clinical coding and diagnosis of patients with kidney using clinical practice guidelines. The guidelines used are the evidence-based KDIGO guidelines, see <<https://kdigo.org/guidelines/>> for more information. This package covers acute kidney injury (AKI), anemia, and chronic liver disease (CKD).

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URL <https://github.com/alwinw/epocakir>

BugReports <https://github.com/alwinw/epocakir/issues>

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aki_bCr	<i>AKI Staging based on Baseline Serum Creatinine</i>
---------	---

Description

Using KDIGO Clinical Practice Guideline for Acute Kidney Injury Volume 2 | Issue 1 | March 2012

Usage

```
aki_bCr(...)

## S3 method for class 'data.frame'
aki_bCr(.data, SCr, bCr, ...)

## S3 method for class 'units'
```

```
aki_bCr(SCr, bCr, ...)

## S3 method for class 'numeric'
aki_bCr(SCr, bCr, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
bCr	Baseline creatinine column name, or vector of units or numeric if .data is not provided

Details

- AKI Stage 1: 1.5-1.9 times baseline
- AKI Stage 2: 2.0-2.9 times baseline
- AKI Stage 3: 3.0 times baseline

See <https://kdigo.org/guidelines/acute-kidney-injury/> for more details.

Value

(ordered factor) AKI stages

Examples

```
aki_bCr(aki_pt_data, SCr = "SCr_", bCr = "bCr_")

aki_pt_data %>%
  dplyr::mutate(aki = aki_bCr(SCr = SCr_, bCr = bCr_))
```

aki_pt_data

AKI Patient Data

Description

A sample dataset to demonstrate calculating AKI with `epocakir`

Usage

```
aki_pt_data
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 27 rows and 7 columns.

Examples

```
aki_pt_data
```

```
aki_SCr AKI Staging based on Changes in Serum Creatinine
```

Description

Using KDIGO Clinical Practice Guideline for Acute Kidney Injury Volume 2 | Issue 1 | March 2012

Usage

```
aki_SCr(...)

## S3 method for class 'data.frame'
aki_SCr(.data, SCr, dtm, pt_id, ...)

## S3 method for class 'units'
aki_SCr(SCr, dtm, pt_id, ...)

## S3 method for class 'numeric'
aki_SCr(SCr, dtm, pt_id, ...)
```

Arguments

<code>...</code>	Further optional arguments
<code>.data</code>	(data.frame) A data.frame, optional
<code>SCr</code>	Serum creatinine column name, or vector of units or numeric if <code>.data</code> is not provided
<code>dtm</code>	DateTime column name, or vector of POSIXct if <code>.data</code> is not provided
<code>pt_id</code>	Patient ID column name, or vector of characters or factors if <code>.data</code> is not provided

Details

- AKI Stage 1: ≥ 0.3 mg/dl (≥ 26.5 mmol/l) increase
- AKI Stage 2: N/A
- AKI Stage 3: ≥ 4.0 mg/dl (≥ 353.6 mmol/l)

See <https://kdigo.org/guidelines/acute-kidney-injury/> for more details.

Value

(ordered factor) AKI stages

Examples

```
aki_SCr(aki_pt_data, SCr = "SCr_", dtm = "dtm_", pt_id = "pt_id_")

aki_pt_data %>%
  dplyr::mutate(aki = aki_SCr(SCr = SCr_, dtm = dtm_, pt_id = pt_id_))
```

aki_stages	<i>AKI Stages</i>
------------	-------------------

Description

Ordered factor of AKI stages

Usage

```
aki_stages
```

Format

An object of class ordered (inherits from factor) of length 4.

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Examples

```
aki_stages
```

aki_staging	<i>Codify AKI from Serum Creatinine and/or Urine Output</i>
-------------	---

Description

Using KDIGO Clinical Practice Guideline for Acute Kidney Injury Volume 2 | Issue 1 | March 2012

Usage

```
aki_staging(...)

## S3 method for class 'data.frame'
aki_staging(
  .data,
  SCr = NULL,
  bCr = NULL,
  UO = NULL,
```

```

    dttm = NULL,
    pt_id = NULL,
    ...
)

## S3 method for class 'units'
aki_staging(SCr = NULL, bCr = NULL, UO = NULL, dttm = NULL, pt_id = NULL, ...)

## S3 method for class 'numeric'
aki_staging(SCr = NULL, bCr = NULL, UO = NULL, dttm = NULL, pt_id = NULL, ...)

```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
bCr	Baseline creatinine column name, or vector of units or numeric if .data is not provided
UO	Urine output column name, or vector of units or numeric if .data is not provided
dttm	DateTime column name, or vector of POSIXct if .data is not provided
pt_id	Patient ID column name, or vector of characters or factors if .data is not provided

Details

Provided a baseline creatinine, series of Serum Creatinine readings and/or Urine Output, `aki_staging()` calculates whether or not a patient has AKI. The staging (1, 2, 3) of AKI is returned.

When multiple columns are provided, `aki_staging()` will automatically calculate whether or not AKI has occurred using each KDIGO definition.

- `aki_bCr()`: Staging of AKI based on baseline serum creatinine
- `aki_SCr()`: Staging of AKI based on changes in serum creatinine
- `aki_UO()`: Staging of AKI based on urine output

The most severe AKI stage is then returned.

See <https://kdigo.org/guidelines/acute-kidney-injury/> for more details.

Value

(ordered factor) AKI stages

Examples

```

aki_staging(aki_pt_data, SCr = "SCr_", bCr = "bCr_", UO = "UO_", dttm = "dttm_", pt_id = "pt_id_")

aki_pt_data %>%
  dplyr::mutate(aki = aki_staging(SCr = SCr_, bCr = bCr_, UO = UO_, dttm = dttm_, pt_id = pt_id_))

```

aki_UO *AKI Staging based on Urine Output*

Description

Using KDIGO Clinical Practice Guideline for Acute Kidney Injury Volume 2 | Issue 1 | March 2012

Usage

```
aki_UO(...)

## S3 method for class 'data.frame'
aki_UO(.data, UO, dttm, pt_id, ...)

## S3 method for class 'units'
aki_UO(UO, dttm, pt_id, ...)

## S3 method for class 'numeric'
aki_UO(UO, dttm, pt_id, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
UO	Urine output column name, or vector of units or numeric if .data is not provided
dttm	DateTime column name, or vector of POSIXct if .data is not provided
pt_id	Patient ID column name, or vector of characters or factors if .data is not provided

Details

- AKI Stage 1: <0.5 ml/kg/h for 6–12 hours
- AKI Stage 2: <0.5 ml/kg/h for ≥ 12 hours
- AKI Stage 3: <0.3 ml/kg/h for ≥ 24 hours OR Anuria for ≥ 12 hours

See <https://kdigo.org/guidelines/acute-kidney-injury/> for more details.

Value

(ordered factor) AKI stages

Examples

```
aki_UO(aki_pt_data, UO = "UO_", dttm = "dttm_", pt_id = "pt_id_")

aki_pt_data %>%
  dplyr::mutate(aki = aki_UO(UO = UO_, dttm = dttm_, pt_id = pt_id_))
```

Albuminuria_stages *Albuminuria Stages*

Description

Ordered factor of Albuminuria stages

Usage

Albuminuria_stages

Format

An object of class ordered (inherits from factor) of length 4.

Details

- A1: Normal to mildly increased
- A2: Moderately increased
- A3: Severely increased

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Examples

Albuminuria_stages

Albuminuria_staging_ACR
Albuminuria Staging based on ACR

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
Albuminuria_staging_ACR(...)

## S3 method for class 'data.frame'
Albuminuria_staging_ACR(.data, ACR, ...)

## S3 method for class 'units'
Albuminuria_staging_ACR(ACR, ...)

## S3 method for class 'numeric'
Albuminuria_staging_ACR(ACR, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
ACR	Albumin-to-creatinine ratio column name, or vector of units or numeric if .data is not provided

Details

- A1: Normal to mildly increased
- A2: Moderately increased
- A3: Severely increased

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Albuminuria category

Examples

```
df <- tibble::tibble(
  ACR = units::set_units(c(-1, NA, 1, 10, 50), "mg/g")
)

Albuminuria_staging_ACR(df, "ACR")

df %>%
  dplyr::mutate(GFR_level = Albuminuria_staging_ACR(ACR))
```

Albuminuria_staging_AER

Albuminuria Staging based on AER

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
Albuminuria_staging_AER(...)

## S3 method for class 'data.frame'
Albuminuria_staging_AER(.data, AER, ...)

## S3 method for class 'units'
Albuminuria_staging_AER(AER, ...)
```

```
## S3 method for class 'numeric'
Albuminuria_staging_AER(AER, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
AER	Albumin excretion rate column name, or vector of units or numeric if .data is not provided

Details

- A1: Normal to mildly increased
- A2: Moderately increased
- A3: Severely increased

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Albuminuria category

Examples

```
df <- tibble::tibble(
  AER = units::set_units(c(-1, NA, 15, 100, 500), "mg/day")
)

Albuminuria_staging_AER(df, "AER")

df %>%
  dplyr::mutate(GFR_level = Albuminuria_staging_AER(AER))
```

anemia

Diagnosis of anemia from Hb concentration

Description

KDIGO Clinical Practice Guideline for Anemia in Chronic Kidney Disease Volume 2 | Issue 4 | August (2) 2012

Usage

```
anemia(...)  
  
## S3 method for class 'data.frame'  
anemia(.data, Hb, age, male, ...)  
  
## S3 method for class 'units'  
anemia(Hb, age, male, ...)  
  
## S3 method for class 'numeric'  
anemia(Hb, age, male, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
Hb	Hemoglobin concentration column name, or vector of units or numeric if .data is not provided
age	Age of patient column name, or vector of units or numeric if .data is not provided
male	Male or not column name, or vector of logical (TRUE/FALSE) if .data is not provided

Details

- Adults and children >15 years with CKD when the Hb concentration is <13.0 g/dl (<130 g/l) in males and <12.0 g/dl (<120 g/l) in females.
- Children with CKD if Hb concentration is <11.0 g/dl (<110 g/l) in children 0.5-5 years, <11.5 g/dl (115 g/l) in children 5-12 years, and <12.0 g/dl (120 g/l) in children 12-15 years.

See <https://kdigo.org/guidelines/anemia-in-ckd/> for more details.

Value

Anemia as logical TRUE or FALSE

Examples

```
anemia(anemia_pt_data, Hb = "Hb", age = "age", male = "male")  
  
anemia_pt_data %>%  
  dplyr::mutate(anemia = anemia(Hb = Hb, age = age, male = male))
```

anemia_pt_data	<i>Anemia Patient Data</i>
----------------	----------------------------

Description

A sample dataset to demonstrate calculating anemia with epocakir

Usage

```
anemia_pt_data
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 10 rows and 3 columns.

Examples

```
anemia_pt_data
```

as_metric	<i>Convert a measured value to metric units</i>
-----------	---

Description

Refer to [conversion_factors](#) for a full list of available conversions

Usage

```
as_metric(param = NULL, meas = NULL, ..., value_only = FALSE)
```

Arguments

param	(character) Name of measurement, e.g. <code>param = "SCr"</code>
meas	(units) Measurement or vector of measurements
...	(units) One of <code>conversion_factors\$parameter</code> , e.g. <code>SCr = units::set_units(88.4, "umol/l")</code> . Case insensitive.
value_only	(logical) Return as value only without units

Value

(units) Converted measured value or vector of measured values, unless `value_only = T`

Examples

```
as_metric(param = "scr", meas = units::set_units(88.4, "umol/l"))
as_metric("scr", units::set_units(88.4, "umol/l"))

values <- units::set_units(c(60, 70, 80), "umol/l")
as_metric(SCr = values)
```

binary2factor	<i>Convert binary data to factors based on column name</i>
---------------	--

Description

Convert binary data to factors based on column name

Usage

```
binary2factor(.data, ...)
```

Arguments

`.data` (data.frame) A data frame or data frame extension (e.g. a tibble)
`...` Name-value pairs. The names of columns to be transformed

Value

(data.frame) An object of the same type as `.data`

Examples

```
df <- data.frame(
  a = c(1, 0, NA, 1, 0),
  b = c("y", "n", NA, "Y", "n"),
  c = c("yes", "no", NA, "Yes", "No"),
  d = c(TRUE, FALSE, NA, TRUE, FALSE),
  e = c(1, 2, 3, 4, 5)
)
binary2factor(df, a, b:d)
df %>%
  binary2factor(-e)
```

clinical_obvs	<i>Clinical Patient Data</i>
---------------	------------------------------

Description

A sample dataset to demonstrate utility functions in epocakir

Usage

```
clinical_obvs
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 3 rows and 9 columns.

Examples

```
clinical_obvs
```

combine_date_time_cols	<i>Combine date and time columns into a single DateTime column</i>
------------------------	--

Description

Combine date and time columns into a single DateTime column

Usage

```
combine_date_time_cols(.data, tz = NULL)
```

Arguments

<code>.data</code>	(<code>data.frame</code>) A data frame or data frame extension (e.g. a tibble)
<code>tz</code>	(<code>character</code>) a time zone name (default: time zone of the POSIXt object <code>x</code>)

Value

(`data.frame`) An object of the same type as `.data`

Examples

```
df <- data.frame(
  date_a = as.Date(c("2020-01-01", "2020-01-02")),
  date_b = as.POSIXct(c("2020-02-01", "2020-02-02")),
  time_a = as.POSIXct(c("1900-01-01 01:01:01", "1900-01-01 02:02:02")),
  time_b = as.POSIXct(c("1900-01-01 01:01:01", "1900-01-01 02:02:02"))
)

combine_date_time_cols(df)
```

combn_changes	<i>Combinatorics changes</i>
---------------	------------------------------

Description

Compares a value with all previous values

Usage

```
combn_changes(...)
```

```
## S3 method for class 'data.frame'
combn_changes(.data, dtm, val, pt_id, ...)
```

```
## S3 method for class 'POSIXct'
combn_changes(dtm, val, pt_id, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
dtm	DateTime column name, or vector of POSIXct if .data is not provided
val	Variable column name, or vector of units or numeric if .data is not provided
pt_id	Patient ID column name, or vector of characters or factors if .data is not provided

Value

Combinatorics changes of the same type provided (numeric or units)

Examples

```
combn_changes(aki_pt_data, dtm = "dtm_", val = "SCR_", pt_id = "pt_id_")
```

```
aki_pt_data %>%
  combn_changes(dtm_, SCR_, pt_id_)
```

conversion_factors	<i>Conversion Factors</i>
--------------------	---------------------------

Description

List of conversion factors based on tables in KDIGO Clinical Practice Guidelines.

Usage

```
conversion_factors
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 21 rows and 4 columns.

Details

parameter Name of the measurement
metric_units Metric units for the parameter
mol_weight Molecular weight (where required)
description Full name

Examples

```
conversion_factors
```

dob2age	<i>Calculate age from DOB</i>
---------	-------------------------------

Description

Calculate age from DOB

Usage

```
dob2age(dob, age_on = lubridate::today(), fun = NULL, units = "years", ...)
```

Arguments

<code>dob</code>	The date or vector of dates representing date(s) of birth.
<code>age_on</code>	(Date) The date on which age is to be calculated. Defaults to today.
<code>fun</code>	(function) The function to be applied to the age, e.g. <code>floor</code> . Defaults to <code>NULL</code> .
<code>units</code>	(character) The units to measure age in, e.g. "years". Only used if <code>fun</code> is specified. Defaults to "years".
<code>...</code>	Further optional arguments that will be passed to <code>fun</code>

Value

(duration) The age as a duration.

Examples

```
dob2age(lubridate::as_date("1990-01-01"))
dob2age(
  dob = c(
    lubridate::as_date("1990-01-01"),
    lubridate::as_date("1994-01-01"),
    lubridate::as_date("1998-01-01")
  ),
  age_on = lubridate::as_date("2002-12-31"),
  fun = floor
)
```

eGFR

GFR Estimation

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR(...)

## S3 method for class 'data.frame'
eGFR(
  .data,
  SCr = NULL,
  SCysC = NULL,
  Age = NULL,
  height = NULL,
  BUN = NULL,
  male = NULL,
  black = NULL,
  pediatric = NULL,
  ...
)

## S3 method for class 'units'
eGFR(
  SCr = NULL,
  SCysC = NULL,
  Age = NULL,
  height = NULL,
```

```

    BUN = NULL,
    male = NULL,
    black = NULL,
    pediatric = NULL,
    ...
)

## S3 method for class 'numeric'
eGFR(
  SCr = NULL,
  SCysC = NULL,
  Age = NULL,
  height = NULL,
  BUN = NULL,
  male = NULL,
  black = NULL,
  pediatric = NULL,
  ...
)

```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
SCysC	Serum Cystatin C column name, or vector of units or numeric if .data is not provided
Age	Age of patient column name, or vector of units or numeric if .data is not provided
height	Height of patient column name, or vector of units or numeric if .data is not provided
BUN	Blood urea nitrogen column name, or vector of units or numeric if .data is not provided
male	Male or not column name, or vector of logical (TRUE/FALSE) if .data is not provided
black	Black race or not column name, or vector of logical (TRUE/FALSE) if .data is not provided
pediatric	(logical) Pediatric or not column name, or vector of logical (TRUE/FALSE) if .data is not provided

Details

Automatic selection of equation to estimation the Glomerular Filtration Rate (eGFR), based on input data

- [eGFR_adult_SCr\(\)](#): 2009 CKD-EPI creatinine equation

- `eGFR_adult_SCysC()`: 2012 CKD-EPI cystatin C equation
- `eGFR_adult_SCr_SCysC()`: 2012 CKD-EPI creatinine-cystatin C equation
- `eGFR_child_SCr()`: Pediatric creatinine-based equation
- `eGFR_child_SCr_BUN()`: Pediatric creatinine-BUN equation
- `eGFR_child_SCysC()`: Pediatric cystatin C-based equation

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

(units) Estimated glomerular filtration rate (eGFR) of the same type provided (numeric or units in ml/min/1.73m²)

Examples

```
eGFR(eGFR_pt_data,
     SCr = "SCr_", SCysC = "SCysC_",
     Age = "Age_", height = "height_", BUN = "BUN_",
     male = "male_", black = "black_", pediatric = "pediatric_"
)

eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR(
    SCr = SCr_, SCysC = SCysC_,
    Age = Age_, height = height_, BUN = BUN_,
    male = male_, black = black_, pediatric = pediatric_
  ))
```

eGFR_adult_SCr

eGFR 2009 CKD-EPI creatinine equation

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_adult_SCr(...)

## S3 method for class 'data.frame'
eGFR_adult_SCr(.data, SCr, Age, male, black, ...)

## S3 method for class 'units'
eGFR_adult_SCr(SCr, Age, male, black, ...)

## S3 method for class 'numeric'
eGFR_adult_SCr(SCr, Age, male, black, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
Age	Age of patient column name, or vector of units or numeric if .data is not provided
male	Male or not column name, or vector of logical (TRUE/FALSE) if .data is not provided
black	Black race or not column name, or vector of logical (TRUE/FALSE) if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_adult_SCr(eGFR_pt_data,
  SCr = "SCr_", Age = "Age_", male = "male_", black = "black_"
)

eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR_adult_SCr(
    SCr = SCr_, Age = Age_, male = male_, black = black_
  ))
```

eGFR_adult_SCr_SCysC *eGFR 2012 CKD-EPI creatinine-cystatin C equation*

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_adult_SCr_SCysC(...)

## S3 method for class 'data.frame'
eGFR_adult_SCr_SCysC(.data, SCr, SCysC, Age, male, black, ...)
```

```
## S3 method for class 'units'
eGFR_adult_SCr_SCysC(SCr, SCysC, Age, male, black, ...)
```

```
## S3 method for class 'numeric'
eGFR_adult_SCr_SCysC(SCr, SCysC, Age, male, black, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
SCysC	Serum Cystatin C column name, or vector of units or numeric if .data is not provided
Age	Age of patient column name, or vector of units or numeric if .data is not provided
male	Male or not column name, or vector of logical (TRUE/FALSE) if .data is not provided
black	Black race or not column name, or vector of logical (TRUE/FALSE) if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_adult_SCr_SCysC(eGFR_pt_data,
  SCr = "SCr_", SCysC = "SCysC_",
  Age = "Age_", male = "male_", black = "black_"
)
```

```
eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR_adult_SCr_SCysC(
    SCr = SCr_, SCysC = SCysC_,
    Age = Age_, male = male_, black = black_
  ))
```

eGFR_adult_SCysC *eGFR 2012 CKD-EPI cystatin C equation*

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_adult_SCysC(...)

## S3 method for class 'data.frame'
eGFR_adult_SCysC(.data, SCysC, Age, male, ...)

## S3 method for class 'units'
eGFR_adult_SCysC(SCysC, Age, male, ...)

## S3 method for class 'numeric'
eGFR_adult_SCysC(SCysC, Age, male, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCysC	Serum Cystatin C column name, or vector of units or numeric if .data is not provided
Age	Age of patient column name, or vector of units or numeric if .data is not provided
male	Male or not column name, or vector of logical (TRUE/FALSE) if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_adult_SCysC(eGFR_pt_data,
  SCysC = "SCysC_", Age = "Age_", male = "male_"
)

eGFR_pt_data %>%
```

```
dplyr::mutate(eGFR = eGFR_adult_SCysC(
  SCysC = SCysC_, Age = Age_, male = male_
))
```

eGFR_child_SCr

eGFR Pediatric SCr and Height

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_child_SCr(...)

## S3 method for class 'data.frame'
eGFR_child_SCr(.data, SCr, height, ...)

## S3 method for class 'units'
eGFR_child_SCr(SCr, height, ...)

## S3 method for class 'numeric'
eGFR_child_SCr(SCr, height, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
height	Height of patient column name, or vector of units or numeric if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_child_SCr(eGFR_pt_data,
  SCr = "SCr_", height = "height_"
)

eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR_child_SCr(
    SCr = SCr_, height = height_,
  ))
```

eGFR_child_SCr_BUN *eGFR Pediatric SCr, Height and BUN*

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_child_SCr_BUN(...)

## S3 method for class 'data.frame'
eGFR_child_SCr_BUN(.data, SCr, height, BUN, ...)

## S3 method for class 'units'
eGFR_child_SCr_BUN(SCr, height, BUN, ...)

## S3 method for class 'numeric'
eGFR_child_SCr_BUN(SCr, height, BUN, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCr	Serum creatinine column name, or vector of units or numeric if .data is not provided
height	Height of patient column name, or vector of units or numeric if .data is not provided
BUN	Blood urea nitrogen column name, or vector of units or numeric if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_child_SCR_BUN(eGFR_pt_data,
  SCr = "SCr_", height = "height_", BUN = "BUN_",
)
```

```
eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR_child_SCR_BUN(
    SCr = SCr_, height = height_, BUN = BUN_,
  ))
```

eGFR_child_SCysC

eGFR Pediatric SCysC

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
eGFR_child_SCysC(...)

## S3 method for class 'data.frame'
eGFR_child_SCysC(.data, SCysC, ...)

## S3 method for class 'units'
eGFR_child_SCysC(SCysC, ...)

## S3 method for class 'numeric'
eGFR_child_SCysC(SCysC, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
SCysC	Serum Cystatin C column name, or vector of units or numeric if .data is not provided

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

Estimated GFR of the same type provided (numeric or units)

Examples

```
eGFR_child_SCysC(eGFR_pt_data,
  SCysC = "SCysC_"
)

eGFR_pt_data %>%
  dplyr::mutate(eGFR = eGFR_child_SCysC(
    SCysC = SCysC_
  ))
```

eGFR_pt_data	<i>eGFR Patient Data</i>
--------------	--------------------------

Description

A sample dataset to demonstrate calculating eGFR with epocakir

Usage

```
eGFR_pt_data
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 51 rows and 10 columns.

Examples

```
eGFR_pt_data
```

GFR_stages	<i>GFR Stages</i>
------------	-------------------

Description

Ordered factor of GFR stages

Usage

```
GFR_stages
```

Format

An object of class `ordered` (inherits from `factor`) of length 6.

Details

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Examples

```
GFR_stages
```

```
GFR_staging
```

```
GFR Staging
```

Description

Using KDIGO 2012 Clinical Practice Guideline for the Evaluation and Management of Chronic Kidney Disease Volume 3 | Issue 1 | January 2013

Usage

```
GFR_staging(...)

## S3 method for class 'data.frame'
GFR_staging(.data, GFR, ...)

## S3 method for class 'units'
GFR_staging(GFR, ...)

## S3 method for class 'numeric'
GFR_staging(GFR, ...)
```

Arguments

...	Further optional arguments
.data	(data.frame) A data.frame, optional
GFR	Glomerular filtration rate column name, or vector of units or numeric if .data is not provided

Details

- G1: Normal or high GFR, ≥ 90
- G2: Mildly decreased, 60-89
- G3a: Mildly to moderately decreased, 45-59
- G3b: Moderately to severely decreased, 30-44
- G4: Severely decreased, 15-29
- G5: Kidney failure, < 15

See <https://kdigo.org/guidelines/ckd-evaluation-and-management/> for more details

Value

GFR category

Examples

```
df <- tibble::tibble(  
  eGFR = units::set_units(c(-1, NA, 100, 70, 50, 35, 20, 10), "mL/min/1.73m2")  
)  
  
GFR_staging(df, "eGFR")  
  
df %>%  
  dplyr::mutate(GFR_level = GFR_staging(eGFR))
```

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