

# Package: epocakir (via r-universe)

September 18, 2024

**Title** Clinical Coding of Patients with Kidney Disease

**Version** 0.9.9

**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 kidney disease (CKD).

**License** MIT + file LICENSE

**URL** <https://github.com/alwinw/epocakir>,  
<https://alwinw.github.io/epocakir/>

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

**Depends** R (>= 3.5.0)

**Imports** dplyr (>= 1.0.1), tidyr (>= 1.1.1), tibble (>= 3.0.1),  
ellipsis, rlang (>= 0.4.0), units (>= 0.7), lubridate (>= 1.7.0), magrittr (>= 2.0.1),

**Suggests** usethis, testthat, covr, knitr, rmarkdown, vctrs,

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**Language** en-US

**Repository** <https://alwinw.r-universe.dev>

**RemoteUrl** <https://github.com/alwinw/epocakir>

**RemoteRef** HEAD

**RemoteSha** 2cd74293da1771c2fef5a8decab8d82ae99e1447

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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, dttm, pt_id, ...)

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

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

**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
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:  $\geq 0.3$  mg/dl ( $\geq 26.5$  mmol/l) increase
- AKI Stage 2: N/A
- AKI Stage 3:  $\geq 4.0$  mg/dl ( $\geq 353.6$  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  $\geq 12$  hours
- AKI Stage 3: <0.3 ml/kg/h for  $\geq 24$  hours OR Anuria for  $\geq 12$  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. param = "SCr"
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 = TRUE`

**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/1.73m<sup>2</sup>)

### 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

*eGFR Patient Data*

---

**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

*GFR Stages*

---

**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,  $\geq 90$
- 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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