Package ‘ega’

July 22, 2025

Title Error Grid Analysis

Version 2.0.0

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Description Functions for assigning Clarke or Parkes (Consensus) error grid zones to blood glucose values, and for plotting both types of error grids in both mg/mL and mmol/L units.

Depends R (>= 2.14.0)

Imports ggplot2, mgcv

Suggests knitr

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LazyData true

VignetteBuilder knitr

RoxygenNote 5.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-03-21 06:50:34 UTC

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Description

Clarke and Parkes (Consensus) error grid analysis

`getClarkeZones` *Assign Clarke error grid zones to paired glucose values*

Description

`referenceVals` and `testVals` are assumed to contain paired glucose values from a reference method and a test method, respectively. `unit` contains info on the unit of measurement. Two options exist: `"gram"` for mg/dL and `"mol"` for mmol/l with `"gram"` applied by default. The discrepancy between the two values is used to place the pair into a Clarke error grid zone according to the criteria described in the original paper by Clarke et. al. (see reference below).

Usage

```
getClarkeZones(referenceVals, testVals, unit = "gram")
```

Arguments

`referenceVals`	A vector of glucose values obtained via the reference method.
`testVals`	A vector of glucose values obtained via a non-reference method (e.g. a new meter). The values in this vector are paired with those in `referenceVals`, so the length should be the same.
`unit`	A string specifying the units of measurement. This should be either `"gram"` (the default) for `mg/dl` or `"mol"` for `mmol/l`.

Value

A character vector is returned, with each element being one of `"A"`, `"B"`, `"C"`, `"D"`, or `"E"`.

References

Clarke, W. L., D. Cox, L. A. Gonder-Frederick, W. Carter, and S. L. Pohl. "Evaluating Clinical Accuracy of Systems for Self-Monitoring of Blood Glucose." Diabetes Care 10, no. 5 (September 1, 1987): 622-28.

Examples

```
zones <- getClarkeZones (glucose_data$ref / 18, glucose_data$test / 18,
unit="mol")

# counts
table(zones)

# percentages
round (table (zones) / length (zones) * 100, digits=2)
```

`getParkesZones` *Assign Parkes (Consensus) error grid zones to paired glucose values*

Description

`referenceVals` and `testVals` are assumed to contain paired glucose values from a reference method and a test method, respectively. The discrepancy between the two values, as well as the type of error grid desired (Type 1 or Type 2 diabetes), is used to place the pair into a Parkes (Consensus) error grid zone, according to the criteria described in the second reference below. `unit` contains info on the unit of measurement. Two options exist: `"gram"` for mg/dL and `"mol"` for mmol/l with `"gram"` applied by default.

Usage

```
getParkesZones(referenceVals, testVals, type = 1, unit = "gram")
```

Arguments

`referenceVals`	A vector of glucose values obtained via the reference method.
`testVals`	A vector of glucose values obtained via a non-reference method (e.g. a new meter). The values in this vector are paired with those in `referenceVals`, so the length should be the same.
`type`	An integer (1 or 2) specifying whether to obtain zones for Type 1 or Type 2 diabetes. Defaults to 1.
`unit`	A string specifying the units of measurement. This should be either `"gram"` (the default) for `mg/dl` or `"mol"` for `mmol/l`.

Value

A character vector is returned, with each element being one of `"A"`, `"B"`, `"C"`, `"D"`, or `"E"`.

References

Parkes, J. L., S. L. Slatin, S. Pardo, and B.H. Ginsberg. "A New Consensus Error Grid to Evaluate the Clinical Significance of Inaccuracies in the Measurement of Blood Glucose." Diabetes Care 23, no. 8 (August 2000): 1143-48

Pfutzner, Andreas, David C. Klonoff, Scott Pardo, and Joan L. Parkes. "Technical Aspects of the Parkes Error Grid." Journal of Diabetes Science and Technology 7, no. 5 (September 2013): 1275-81

Examples

```
zones <- getParkesZones(glucose_data$ref, glucose_data$test)

# counts
table(zones)

# percentages
round (table (zones) / length (zones) * 100, digits=2)
```

`glucose_data` *5072 paired reference and test glucose values.*

Description

A dataset containing 5072 paired reference method and test method glucose values (in mg/dL).

Usage

```
glucose_data
```

Format

A data frame with 5072 rows and 2 variables:

ref Reference method glucose value, in mg/dL

test Test method glucose value, in mg/dL

Source

The data is from a modified clinical dataset.

`plotClarkeGrid` *Plot a Clarke Error Grid*

Description

The function uses `ggplot` to draw the Clarke error grid lines according to the criteria described in the original publication by Clarke et. al. (see reference below). If zones have not already been assigned via the `zones` parameter, the function `getClarkeZones` is called first. The values in `referenceVals` and `testVals` are then superimposed as a scatter plot. Some basic plot parameters can be specified as arguments, but the return value can also be stored and modified further before plotting (see examples and vignette).

Usage

```
plotClarkeGrid(referenceVals, testVals, title = "Clarke Error Grid",
  xlab = "", ylab = "", linesize = 0.5, linetype = "solid",
  linecolor = "black", linealpha = 0.6, pointsize = 2, pointalpha = 1,
  zones = NA, unit = "gram")
```

Arguments

`referenceVals`	A vector of glucose values obtained via the reference method.
`testVals`	A vector of glucose values obtained via a non-reference method (e.g. a new meter). The values in this vector are paired with those in `referenceVals`, so the length should be the same.
`title`	The main plot title. Defaults to "Clarke Error Grid".
`xlab`	The x-axis label. Defaults to "Reference Glucose Concentration (mg/dL)".
`ylab`	The y-axis label. Defaults to "Test Glucose Concentration (mg/dL)".
`linesize`	The size to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is 0.5.
`linetype`	The type of line to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is "solid".
`linecolor`	The color of the zone lines. The acceptable values are the same as for `geom_segment`. The default is "black".
`linealpha`	The alpha (transparency) level to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is 0.6.
`pointsize`	The size to be used when plotting the glucose data points. The acceptable values are the same as for `geom_point`. The default is 2.
`pointalpha`	The alpha (transparency) level to be used when plotting the glucose data points. The acceptable values are the same as for `geom_point`. The default is 1.
`zones`	An optional character vector specifying the Clarke zones for each paired value. If this is not supplied, `getClarkeZones` will be called to generate zone labels.
`unit`	A string specifying the units of measurement. This should be either `"gram"` (the default) for `mg/dl` or `"mol"` for `mmol/l`.

Value

A `ggplot` object is returned. If the return value is not assigned, a plot is drawn.

References

Clarke, W. L., D. Cox, L. A. Gonder-Frederick, W. Carter, and S. L. Pohl. "Evaluating Clinical Accuracy of Systems for Self-Monitoring of Blood Glucose." Diabetes Care 10, no. 5 (September 1, 1987): 622-28.

See Also

`getClarkeZones` `ggplot`

Examples

```
library(ggplot2)

# default
plotClarkeGrid(glucose_data$ref, glucose_data$test)

# with options
plotClarkeGrid(glucose_data$ref, glucose_data$test,
              pointsize=1.5,
              pointalpha=0.6,
              linetype="dashed")

# store return value and modify
ceg <- plotClarkeGrid(glucose_data$ref, glucose_data$test)

ceg + theme_gray() +
   theme(plot.title = element_text(size = rel(2), colour = "blue"))
```

`plotParkesGrid` *Plot a Parkes (Consensus) Error Grid*

Description

The function uses `ggplot` to draw the Parkes (consensus) error grid lines according to the criteria described in the publications listed in the References section (see below). If zones have not already been assigned via the `zones` parameter, the function `getParkesZones` is called first. The values in `referenceVals` and `testVals` are then superimposed as a scatter plot. Some basic plot parameters can be specified as arguments, but the return value can also be stored and modified further before plotting (see examples and vignette).

Usage

```
plotParkesGrid(referenceVals, testVals, type = 1, title = "", xlab = "",
  ylab = "", linesize = 0.5, linetype = "solid", linecolor = "black",
  linealpha = 0.6, pointsize = 2, pointalpha = 1, zones = NA,
  unit = "gram")
```

Arguments

`referenceVals`	A vector of glucose values obtained via the reference method.
`testVals`	A vector of glucose values obtained via a non-reference method (e.g. a new meter). The values in this vector are paired with those in `referenceVals`, so the length should be the same.
`type`	An integer (1 or 2) specifying whether to plot the grid for Type 1 or Type 2 diabetes. Defaults to 1.
`title`	The main plot title. Defaults to "Parkes (Consensus) Error Grid for Type [type] Diabetes".
`xlab`	The x-axis label. Defaults to "Reference Glucose Concentration (mg/dL)".
`ylab`	The y-axis label. Defaults to "Test Glucose Concentration (mg/dL)".
`linesize`	The size to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is 0.5.
`linetype`	The type of line to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is "solid".
`linecolor`	The color of the zone lines. The acceptable values are the same as for `geom_segment`. The default is "black".
`linealpha`	The alpha (transparency) level to be used when drawing the zone lines. The acceptable values are the same as for `geom_segment`. The default is 0.6.
`pointsize`	The size to be used when plotting the glucose data points. The acceptable values are the same as for `geom_point`. The default is 2.
`pointalpha`	The alpha (transparency) level to be used when plotting the glucose data points. The acceptable values are the same as for `geom_point`. The default is 1.
`zones`	An optional character vector specifying the Clarke zones for each paired value. If this is not supplied, `getClarkeZones` will be called to generate zone labels.
`unit`	A string specifying the units of measurement. This should be either `"gram"` (the default) for `mg/dl` or `"mol"` for `mmol/l`.

Value

A `ggplot` object is returned. If the return value is not assigned, a plot is drawn.

References

Parkes, J. L., S. L. Slatin, S. Pardo, and B.H. Ginsberg. "A New Consensus Error Grid to Evaluate the Clinical Significance of Inaccuracies in the Measurement of Blood Glucose." Diabetes Care 23, no. 8 (August 2000): 1143-48

Pfutzner, Andreas, David C. Klonoff, Scott Pardo, and Joan L. Parkes. "Technical Aspects of the Parkes Error Grid." Journal of Diabetes Science and Technology 7, no. 5 (September 2013): 1275-81

See Also

`getParkesZones` `ggplot`

Examples

```
library(ggplot2)

# default
plotParkesGrid(glucose_data$ref, glucose_data$test)

# with options
plotParkesGrid(glucose_data$ref, glucose_data$test,
              pointsize=2,
              pointalpha=0.5,
              linesize=2,
              linealpha=0.3,
              linetype="dotdash")

# store return value and modify
peg <- plotParkesGrid(glucose_data$ref, glucose_data$test, type=2)

peg + theme_gray() +
   theme(plot.title = element_text(size = rel(2), colour = "red"))
```

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