Package: rspiro (via r-universe)

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Title Implementation of Spirometry Equations

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Description Implementation of various spirometry equations in R, currently the GLI-2012 (Global Lung Initiative; Quanjer et al. 2012 <doi:10.1183/09031936.00080312>), the race-neutral GLI global 2022 (Global Lung Initiative; Bowerman et al. 2023 <doi:10.1164/rccm.202205-0963OC>), the NHANES3 (National Health and Nutrition Examination Survey; Hankinson et al. 1999 <doi:10.1164/ajrccm.159.1.9712108>) and the JRS 2014 (Japanese Respiratory Society; Kubota et al. 2014 <doi:10.1016/j.resinv.2014.03.003>) equations. Also the GLI-2017 diffusing capacity equations <doi:10.1183/13993003.00010-2017> are implemented. Contains user-friendly functions to calculate predicted and LLN (Lower Limit of Normal) values for different spirometric parameters such as FEV1 (Forced Expiratory Volume in 1 second), FVC (Forced Vital Capacity), etc, and to convert absolute spirometry measurements to percent (%) predicted and z-scores.

License GPL (>=2)

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`rspiro-package` *rspiro: Brief overview of the package*

Description

R package **rspiro** implements multiple spirometry equations: currently the GLI-2012 (Quanjer), GLI global 2022, JRS-2014, NHANES III (Hankinson), as well as the GLI-2017 diffusing capacity equations (Stanojevic et al). More may be added later. It offers a convenient interface to calculate predicted or LLN (Lower Limit of Normal) values given demographic data, or to convert absolute values to percent (predicted or z-scores.

Details

To ensure a consistent interface, package functions are named with a prefix indicating the functionality and a suffix indicating the spirometric equations used, for example `LLN_GLI` calculates Lower Limits of Normal using the GLI-2012 equations. The suffix is currently one of 'GLI', 'GLIgl', 'JRS', 'NHANES3' or 'GLIdiff'. The prefix is one of 'LLN_', 'pred_', 'pctpred_' or 'zscore_'.

Functions prefixed 'LLN_' or 'pred_' accept as input demographic information (age, gender, height, ethnicity) and calculate the Lower Limit of Normal and the predicted value, respectively, for a given spirometry parameter (FEV1, FVC, etc). Functions prefixed 'pctpred_' or 'zscore_' accept absolute spirometry values (plus demographics) and convert those to percent (z-scores, respectively. Please note the difference between 'pred_' and 'pctpred_' above.

For detailed information, refer to the respective function documentations.

The development version of **rspiro** is available on GitHub `https://github.com/thlytras/rspiro`. To report problems and bugs, or to request a feature, please go there and open an issue. Alternatively, send an email to Theodore Lytras <`thlytras@gmail.com`>.

Author(s)

Theodore Lytras <`thlytras@gmail.com`>.

`LLN_GLI` *Calculate LLN of spirometry parameters using GLI-2012 equations*

Description

This function calculates LLNs (Lower Limits of Normal) for the various spirometry parameters, using the GLI-2012 equations. It accepts as input age, height, gender and ethnicity.

Usage

```
LLN_GLI(age, height, gender = 1, ethnicity = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = NE Asian, 4 = SE Asian, 5 = Other/mixed). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC", "FEF2575", "FEF75", "FEV075", "FEV075FVC"

Details

Arguments age, `height`, `gender` and `ethnicity` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find LLN of FEV1 and FVC for Caucasian women aged 20 to 70 and with a height of 1.70 meters.
LLN_GLI(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`LLN_GLIdiff` *Calculate LLN of diffusing capacity parameters using GLI (2017) equations*

Description

This function calculates LLNs (Lower Limits of Normal) for TLCO (transfer factor of the lung for carbon monoxide), KCO (transfer coefficient of the lung for carbon monoxide) and VA (alveolar volume) using the GLI (2017) equations. It accepts as input age, height, gender.

Usage

```
LLN_GLIdiff(age, height, gender = 1, param = "TLCO", SI = TRUE)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "TLCO", "KCO" or "VA"
`SI`	(default TRUE) Use SI (mmol/min/kPa) or traditional (ml/min/mmHg) units?

Details

Arguments age, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find LLN of TLCO and VA for women aged 20 to 70 and with a height of 1.70 meters.
LLN_GLIdiff(20:70, 1.7, 2, param=c("TLCO","VA"))
```

`LLN_GLIgl` *Calculate LLN of spirometry parameters using GLI global (2022) equations*

Description

This function calculates LLNs (Lower Limits of Normal) for the various spirometry parameters, using the GLI global (2022) equations. It accepts as input age, height, gender.

Usage

```
LLN_GLIgl(age, height, gender = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC"

Details

Arguments `age`, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find LLN of FEV1 and FVC for women aged 20 to 70 and with a height of 1.70 meters.
LLN_GLIgl(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`LLN_JRS` *Calculate LLN of spirometry parameters using JRS (2014) equations*

Description

This function calculates LLNs (Lower Limits of Normal) for the various spirometry parameters, using the JRS (Japanese Respiratory Society 2014) equations. It accepts as input age, height, gender.

Usage

```
LLN_JRS(age, height, gender = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "VC", "FEV1FVC"

Details

Arguments `age`, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find LLN of FEV1 and FVC for Japanese women aged 20 to 70 and with a height of 1.70 meters.
LLN_JRS(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`LLN_NHANES3` *Calculate predicted values of spirometry parameters using NHANES III equations*

Description

This function calculates LLNs (Lower Limits of Normal) for the various spirometry parameters, using the NHANES III equations. It accepts as input age, height, gender and ethnicity.

Usage

```
LLN_NHANES3(age, height, gender = 1, ethnicity = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = Mexican-American). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC", "PEF", "FEF2575", "FEV6", "FEV1FEV6"

Details

Arguments `age`, `height`, `gender` and `ethnicity` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find LLN of FEV1 and FVC for Caucasian women aged 20 to 70 and with a height of 1.70 meters.
LLN_NHANES3(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`pctpred_GLI` *Convert spirometric values to % predicted using GLI-2012 equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, etc) in lt plus demographic data (age, height, gender and ethnicity) and converts them to percent (%) predicted based on the GLI-2012 equations.

Usage

```
pctpred_GLI(
  age,
  height,
  gender = 1,
  ethnicity = 1,
  FEV1 = NULL,
  FVC = NULL,
  FEV1FVC = NULL,
  FEF2575 = NULL,
  FEF75 = NULL,
  FEV075 = NULL,
  FEV075FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = NE Asian, 4 = SE Asian, 5 = Other/mixed). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC ratio
`FEF2575`	Forced Expiratory Flow between 25% and 75% of FVC (lt/s)
`FEF75`	Forced Expiratory Flow at 75% of FVC (lt/s)
`FEV075`	Forced Expiratory Volume in 0.75 sec (lt)
`FEV075FVC`	FEV0.75 / FVC ratio

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, `gender` and `ethnicity` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
pctpred_GLI(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`pctpred_GLIdiff` *Convert diffusing capacity values to % predicted using GLI (2017) equations*

Description

This function takes absolute diffusing capacity measurements (TLCO, KCO and VA) plus demographic data (age, height, gender) and converts them to percent (%) predicted based on the GLI (2017) equations.

Usage

```
pctpred_GLIdiff(
  age,
  height,
  gender = 1,
  TLCO = NULL,
  KCO = NULL,
  VA = NULL,
  SI = TRUE
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.

`TLCO`	Transfer factor of the lung for carbon monoxide (in mmol/min/kPa if `SI=TRUE` or ml/min/mmHg if `SI=FALSE`)
`KCO`	Transfer coefficient of the lung for carbon monoxide (in mmol/min/kPa/lt if `SI=TRUE` or ml/min/mmHg/lt if `SI=FALSE`)
`VA`	Alveolar volume (in lt)
`SI`	(default TRUE) Use SI (mmol/min/kPa) or traditional (ml/min/mmHg) units?

Details

At least one of the diffusing capacity measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the diffusing capacity measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one diffusing capacity argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (TLCO)
pctpred_GLIdiff(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), TLCO=c(7.8, 8.8, 7.5, 8.5))
```

`pctpred_GLIgl` *Convert spirometric values to % predicted using GLI global (2022) equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC or FEV1FVC) in lt plus demographic data (age, height, gender) and converts them to percent (%) predicted based on the GLI global (2022) equations.

Usage

```
pctpred_GLIgl(age, height, gender = 1, FEV1 = NULL, FVC = NULL, FEV1FVC = NULL)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.

`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC ratio

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
pctpred_GLIgl(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`pctpred_JRS` *Convert spirometric values to % predicted using JRS (2014) equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, VC or FEV1FVC) in lt plus demographic data (age, height, gender) and converts them to percent (%) predicted based on the JRS (Japanese Respiratory Society 2014) equations.

Usage

```
pctpred_JRS(
  age,
  height,
  gender = 1,
  FEV1 = NULL,
  FVC = NULL,
  VC = NULL,
  FEV1FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`VC`	Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC ratio

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
pctpred_JRS(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`pctpred_NHANES3` *Convert spirometric values to % predicted using NHANES III equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, etc) in lt plus demographic data (age, height, gender and ethnicity) and converts them to percent (%) predicted based on the NHANES III equations.

Usage

```
pctpred_NHANES3(
  age,
  height,
  gender = 1,
  ethnicity = 1,
  FEV1 = NULL,
  FVC = NULL,
  FEV1FVC = NULL,
  PEF = NULL,
  FEF2575 = NULL,
  FEV6 = NULL,
  FEV1FEV6 = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = Mexican-American). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC ratio
`PEF`	Peak Expiratory Flow (lt)
`FEF2575`	Forced Expiratory Flow between 25% and 75% of FVC (lt/s)
`FEV6`	Forced Expiratory Volume in 6 seconds (lt)
`FEV1FEV6`	FEV1 / FEV6 ratio

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, `gender` and `ethnicity` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
pctpred_NHANES3(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`pred_GLI` *Calculate predicted values of spirometry parameters using GLI-2012 equations*

Description

This function calculates the mean normal (predicted) values for the various spirometry parameters, using the GLI-2012 equations. It accepts as input age, height, gender and ethnicity.

Usage

```
pred_GLI(age, height, gender = 1, ethnicity = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = NE Asian, 4 = SE Asian, 5 = Other/mixed). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC", "FEF2575", "FEF75", "FEV075", "FEV075FVC"

Details

Arguments `age`, `height`, `gender` and `ethnicity` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find predicted FEV1 and FVC for Caucasian women aged 20 to 70 and with a height of 1.70 meters.
pred_GLI(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`pred_GLIdiff` *Calculate predicted values of diffusing capacity using GLI (2017) equations*

Description

This function calculates the mean normal (predicted) values for TLCO (transfer factor of the lung for carbon monoxide), KCO (transfer coefficient of the lung for carbon monoxide) and VA (alveolar volume) using the GLI (2017) equations. It accepts as input age, height and gender.

Usage

```
pred_GLIdiff(age, height, gender = 1, param = "TLCO", SI = TRUE)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "TLCO", "KCO" or "VA"
`SI`	(default TRUE) Use SI (mmol/min/kPa) or traditional (ml/min/mmHg) units?

Details

Arguments `age`, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find predicted TLCO and VA for women aged 20 to 70 and with a height of 1.70 meters.
pred_GLIdiff(20:70, 1.7, 2, param=c("TLCO","VA"))
```

`pred_GLIgl` *Calculate predicted values of spirometry parameters using GLI global (2022) equations*

Description

This function calculates the mean normal (predicted) values for the various spirometry parameters, using the GLI global (2022) equations. It accepts as input age, height and gender.

Usage

```
pred_GLIgl(age, height, gender = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC"

Details

Arguments `age`, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find predicted FEV1 and FVC for women aged 20 to 70 and with a height of 1.70 meters.
pred_GLIgl(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`pred_JRS` *Calculate predicted values of spirometry parameters using JRS (2014) equations*

Description

This function calculates the mean normal (predicted) values for the various spirometry parameters, using the JRS (Japanese Respiratory Society 2014) equations. It accepts as input age, height and gender.

Usage

```
pred_JRS(age, height, gender = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "VC", "FEV1FVC"

Details

Arguments `age`, `height` and `gender` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find predicted FEV1 and FVC for women aged 20 to 70 and with a height of 1.70 meters.
pred_JRS(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`pred_NHANES3` *Calculate predicted values of spirometry parameters using NHANES III equations*

Description

This function calculates the mean normal (predicted) values for the various spirometry parameters, using the NHANES III equations. It accepts as input age, height, gender and ethnicity.

Usage

```
pred_NHANES3(age, height, gender = 1, ethnicity = 1, param = "FEV1")
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = Mexican-American). Default is 1.
`param`	A character vector, containing one of more of the following parameters (case insensitive): "FEV1", "FVC", "FEV1FVC", "PEF", "FEF2575", "FEV6", "FEV1FEV6"

Details

Arguments `age`, `height`, `gender` and `ethnicity` are vectors of equal length, or of length one, in which case the value is recycled; if the four vectors are not of equal length, the function stops with an error.

Value

If `param` has length one, the function returns a numeric vector. If `param` has length >1, it returns a data.frame with `length(param)` columns.

Examples

```
# Find predicted FEV1 and FVC for Caucasian women aged 20 to 70 and with a height of 1.70 meters.
pred_NHANES3(20:70, 1.7, 2, param=c("FEV1","FVC"))
```

`raw_GLI` *Convert z-scores back to raw spirometric values using GLI-2012 equations*

Description

This function takes z-scores based on the GLI-2012 equations, plus demographic data (age, height, gender and ethnicity), and converts them back into absolute spirometry measurements (FEV1, FVC, etc) in lt.

Usage

```
raw_GLI(
  age,
  height,
  gender = 1,
  ethnicity = 1,
  FEV1 = NULL,
  FVC = NULL,
  FEV1FVC = NULL,
  FEF2575 = NULL,
  FEF75 = NULL,
  FEV075 = NULL,
  FEV075FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = NE Asian, 4 = SE Asian, 5 = Other/mixed). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (z-score)
`FVC`	Forced Vital Capacity (z-score)
`FEV1FVC`	FEV1 / FVC (as z-score)
`FEF2575`	Forced Expiratory Flow between 25% and 75% of FVC (z-score)
`FEF75`	Forced Expiratory Flow at 75% of FVC (z-score)
`FEV075`	Forced Expiratory Volume in 0.75 sec (z-score)
`FEV075FVC`	FEV0.75 / FVC (as z-score)

Details

At least one of the spirometric z-score arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, `gender` and `ethnicity` must be vectors of length equal to the length of the z-score vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry z-score argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one z-score parameter supplied (FEV1)
raw_GLI(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(-1.2, -1.9, 0, 0.5))
```

`raw_GLIdiff` *Convert z-scores back to raw diffusing capacity values using GLI (2017) equations*

Description

This function takes z-scores based on the GLI (2017) equations, plus demographic data (age, height and gender), and converts them back into absolute diffusing capacity measurements (TLCO, KCO and VA).

Usage

```
raw_GLIdiff(
  age,
  height,
  gender = 1,
  TLCO = NULL,
  KCO = NULL,
  VA = NULL,
  SI = TRUE
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.

`TLCO`	Transfer factor of the lung for carbon monoxide (z-score)
`KCO`	Transfer coefficient of the lung for carbon monoxide (z-score)
`VA`	Alveolar volume (z-score)
`SI`	(default TRUE) Use SI (mmol/min/kPa) or traditional (ml/min/mmHg) units?

Details

At least one of the diffusing capacity z-score arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the z-score vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one diffusing capacity z-score argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one z-score parameter supplied (TLCO)
raw_GLIdiff(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
     gender=c(2,1,2,1), TLCO=c(-1.2, -1.9, 0, 0.5))
```

`raw_GLIgl` *Convert z-scores back to raw spirometric values using GLI global (2022) equations*

Description

This function takes z-scores based on the GLI global (2022) equations, plus demographic data (age, height and gender), and converts them back into absolute spirometry measurements (FEV1, FVC, or FEV1FVC) in lt.

Usage

```
raw_GLIgl(age, height, gender = 1, FEV1 = NULL, FVC = NULL, FEV1FVC = NULL)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (z-score)
`FVC`	Forced Vital Capacity (z-score)
`FEV1FVC`	FEV1 / FVC (as z-score)

Details

At least one of the spirometric z-score arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the z-score vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry z-score argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one z-score parameter supplied (FEV1)
raw_GLIgl(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(-1.2, -1.9, 0, 0.5))
```

`raw_JRS` *Convert z-scores back to raw spirometric values using JRS (2014) equations*

Description

This function takes z-scores based on the JRS (Japanese Respiratory Society 2014) equations, plus demographic data (age, height and gender), and converts them back into absolute spirometry measurements (FEV1, FVC, VC, or FEV1FVC) in lt.

Usage

```
raw_JRS(
  age,
  height,
  gender = 1,
  FEV1 = NULL,
  FVC = NULL,
  VC = NULL,
  FEV1FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.

`FEV1`	Forced Expiratory Volume in 1 second (z-score)
`FVC`	Forced Vital Capacity (z-score)
`VC`	Vital Capacity (z-score)
`FEV1FVC`	FEV1 / FVC (as z-score)

Details

At least one of the spirometric z-score arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the z-score vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry z-score argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one z-score parameter supplied (FEV1)
raw_JRS(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(-1.2, -1.9, 0, 0.5))
```

`zscore_GLI` *Convert spirometric values to z-scores using GLI-2012 equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, etc) in lt plus demographic data (age, height, gender and ethnicity) and converts them to z-scores based on the GLI-2012 equations.

Usage

```
zscore_GLI(
  age,
  height,
  gender = 1,
  ethnicity = 1,
  FEV1 = NULL,
  FVC = NULL,
  FEV1FVC = NULL,
  FEF2575 = NULL,
  FEF75 = NULL,
  FEV075 = NULL,
  FEV075FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = NE Asian, 4 = SE Asian, 5 = Other/mixed). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC
`FEF2575`	Forced Expiratory Flow between 25% and 75% of FVC (lt/s)
`FEF75`	Forced Expiratory Flow at 75% of FVC (lt/s)
`FEV075`	Forced Expiratory Volume in 0.75 sec (lt)
`FEV075FVC`	FEV0.75 / FVC

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, `gender` and `ethnicity` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
zscore_GLI(age=seq(25,40,4), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), ethnicity=rep(1,4), FEV1=c(3.5, 4, 3.6, 3.9))
```

`zscore_GLIdiff` *Convert diffusing capacity values to z-scores using GLI (2017) equations*

Description

This function takes absolute diffusing capacity measurements (TLCO, KCO and VA) plus demographic data (age, height and gender) and converts them to z-scores based on the GLI (2017) equations.

Usage

```
zscore_GLIdiff(
  age,
  height,
  gender = 1,
  TLCO = NULL,
  KCO = NULL,
  VA = NULL,
  SI = TRUE
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`TLCO`	Transfer factor of the lung for carbon monoxide (in mmol/min/kPa if `SI=TRUE` or ml/min/mmHg if `SI=FALSE`)
`KCO`	Transfer coefficient of the lung for carbon monoxide (in mmol/min/kPa/lt if `SI=TRUE` or ml/min/mmHg/lt if `SI=FALSE`)
`VA`	Alveolar volume (in lt)
`SI`	(default TRUE) Use SI (mmol/min/kPa) or traditional (ml/min/mmHg) units?

Details

At least one of the diffusing capacity measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the diffusing capacity measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one diffusing capacity argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (TLCO)
zscore_GLIdiff(age=seq(25,40,5), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), TLCO=c(7.8, 8.8, 7.5, 8.5))
```

`zscore_GLIgl` *Convert spirometric values to z-scores using GLI global (2022) equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, FEV1/FVC) in lt plus demographic data (age, height and gender) and converts them to z-scores based on the GLI global (2022) equations.

Usage

```
zscore_GLIgl(age, height, gender = 1, FEV1 = NULL, FVC = NULL, FEV1FVC = NULL)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height` and `gender` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
zscore_GLI(age=seq(25,40,4), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`zscore_JRS` *Convert spirometric values to z-scores using JRS (2014) equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, VC, FEV1/FVC) in lt plus demographic data (age, height and gender) and converts them to z-scores based on the JRS (Japanese Respiratory Society 2014) equations.

Usage

```
zscore_JRS(
  age,
  height,
  gender = 1,
  FEV1 = NULL,
  FVC = NULL,
  VC = NULL,
  FEV1FVC = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`VC`	Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, and `gender` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
zscore_JRS(age=seq(25,40,4), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), FEV1=c(3.5, 4, 3.6, 3.9))
```

`zscore_NHANES3` *Convert spirometric values to z-scores using NHANES III equations*

Description

This function takes absolute spirometry measurements (FEV1, FVC, etc) in lt plus demographic data (age, height, gender and ethnicity) and converts them to z-scores based on the NHANES III equations.

Usage

```
zscore_NHANES3(
  age,
  height,
  gender = 1,
  ethnicity = 1,
  FEV1 = NULL,
  FVC = NULL,
  FEV1FVC = NULL,
  PEF = NULL,
  FEF2575 = NULL,
  FEV6 = NULL,
  FEV1FEV6 = NULL
)
```

Arguments

`age`	Age in years
`height`	Height in meters
`gender`	Gender (1 = male, 2 = female) or a factor with two levels (first = male). Default is 1.
`ethnicity`	Ethnicity (1 = Caucasian, 2 = African-American, 3 = Mexican-American). Default is 1.
`FEV1`	Forced Expiratory Volume in 1 second (lt)
`FVC`	Forced Vital Capacity (lt)
`FEV1FVC`	FEV1 / FVC ratio
`PEF`	Peak Expiratory Flow (lt)
`FEF2575`	Forced Expiratory Flow between 25% and 75% of FVC (lt/s)
`FEV6`	Forced Expiratory Volume in 6 seconds (lt)
`FEV1FEV6`	FEV1 / FEV6 ratio

Details

At least one of the spirometric measurement arguments must be set (i.e. be non-`NULL`). Arguments `age`, `height`, `gender` and `ethnicity` must be vectors of length equal to the length of the spirometric measurement vector(s), or of length one, in which case their value is recycled. If any input vector is not of equal length, the function stops with an error.

Normal distributions are assumed for all parameters, even though per the NHANES III equations paper (Hankinson et al) this was observed only for FEV1, FVC, PEF and FEV6.

Value

If only one spirometry argument is supplied, the function returns a numeric vector. If more are supplied, the function returns a data.frame with the same number of columns.

Examples

```
# Random data, 4 patients, one parameter supplied (FEV1)
zscore_NHANES3(age=seq(25,40,4), height=c(1.8, 1.9, 1.75, 1.85),
      gender=c(2,1,2,1), ethnicity=rep(1,4), FEV1=c(3.5, 4, 3.6, 3.9))
```

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