Package ‘childdsds’

February 10, 2022

Title Data and Methods Around Reference Values in Pediatrics

Version 0.8.0

Description Calculation of standard deviation scores and percentiles adduced from different standards (WHO, UK, Germany, Italy, China, etc). Also, references for laboratory values in children and adults are available, e.g., serum lipids, iron-related blood parameters, IGF, liver enzymes. See package documentation for full list.

Depends R (>= 3.5.0)

Imports gamlss, gamlss.dist, dplyr, magrittr, methods, tidyr, boot, class, tibble, reshape2, purrr, purrrlyr, utils, VGAM

Suggests ggplot2

BugReports https://git.sc.uni-leipzig.de/my221hepi/childdsds/-/issues

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

NeedsCompilation no

Author Mandy Vogel [aut, cre]

Maintainer Mandy Vogel <mandy.vogel@googlemail.com>

Repository CRAN

Date/Publication 2022-02-10 16:40:02 UTC

R topics documented:

aga_15.ref ............................................................... 3
aggregate_lms .......................................................... 3
belgium.ref .............................................................. 4
bone.ref ................................................................. 4
bp_wuehl_age.ref ......................................................... 5
bp_wuehl_height.ref .................................................... 5
calc_confints .......................................................... 6
R topics documented:

cdc.ref ................................................................. 7
 cn.ref ................................................................. 7
colombia_sf.ref ..................................................... 8
doyon_age.ref ....................................................... 8
doyon_height.ref .................................................... 9
do_iterations ......................................................... 9
duran_bf.ref .......................................................... 11
ethiop.ref ............................................................ 11
fit_gamlss .............................................................. 12
fit_gamlss1 ............................................................. 13
fit_vgam ................................................................. 14
fredriks05.ref ......................................................... 15
international_lab.ref ............................................... 16
iron.ref ................................................................. 16
italian.ref ............................................................. 17
japanese.ref ........................................................... 17
japan_lab.ref .......................................................... 18
kawel_boehm.ref ..................................................... 18
kiggs.ref ............................................................... 19
kiggs_bp.ref ........................................................... 19
kro.ref ................................................................. 20
life_circ.ref ............................................................ 20
life_cysc.ref ........................................................... 21
life_fibroscan.ref .................................................... 21
life_heart.ref .......................................................... 22
life_igf.ref ............................................................. 22
life_liver.ref ........................................................... 23
life_skinfold.ref ..................................................... 23
life_thyr.ref ........................................................... 24
lipids.ref ............................................................... 24
make_percentile_tab .................................................. 25
metabolom.ref ........................................................ 26
mock_df ................................................................. 26
mock_value ............................................................. 27
mock_values ............................................................ 28
momo.ref ............................................................... 28
motor.ref ............................................................... 29
nl3.ref ................................................................. 29
nl4.ref ................................................................. 30
one_iteration .......................................................... 30
ParTab-class .......................................................... 32
portug.ref ............................................................. 32
prepare_data ........................................................... 33
preterm.ref ............................................................. 34
RefGroup-class ......................................................... 34
saudi.ref ............................................................... 35
sds ...................................................................... 35
sdsold ................................................................. 36
aga_15.ref

Parameters from recommendations of the German Adiposity Association (2015, AGA)

Usage

aga_15.ref

Source


aggregate_lms

aggregate lms parameters

Description

aggregate lms parameters

Usage

aggregate_lms(lms.list)
**Arguments**

lms.list  list of parameter tables as returned by do_iterations()

**Details**

function takes the lms part of the result from the do_iterations() function and returns the mean parameters

**Value**

list of dataframes containing the aggregated parameters, each for every level of sex

**Author(s)**

Mandy Vogel

---

**belgium.ref**  
*Parameters derived from Flandern population*

---

**Description**

Parameters derived from Flandern population

**Usage**

belgium.ref

**Source**


---

**bone.ref**  
*Parameters for different bone parameters*

---

**Description**

Parameters for different bone parameters

**Usage**

bone.ref
Source

bp_wuehl_age.ref

Parameters from Wuehl et al. blood pressure reference values Germany according to age, from version 0.7.3 unplausible values are replaced by interpolated ones. For the original values check out earlier versions

Description
Parameters from Wuehl et al. blood pressure reference values Germany according to age, from version 0.7.3 unplausible values are replaced by interpolated ones. For the original values check out earlier versions

Usage
bp_wuehl_age.ref

Source
"Wuehl E, Witte K, Soergel M, Mehls O, Schaefer F. Hypertension for the GWG on P. Distribution of 24-h ambulatory blood pressure in children: normalized reference values and role of body dimensions. Journal of Hypertension. 2002 Oct;20(10):1995.”, implausible values were replaced by interpolated ones from package version 0.7.4

bp_wuehl_height.ref

Parameters from Wuehl et al. blood pressure reference values Germany according to height from version 0.7.3 unplausible values are replaced by interpolated ones. For the original values check out earlier versions

Description
Parameters from Wuehl et al. blood pressure reference values Germany according to height from version 0.7.3 unplausible values are replaced by interpolated ones. For the original values check out earlier versions

Usage
bp_wuehl_height.ref
Source

"Wuehl E, Witte K, Soergel M, Mehls O, Schaefer F. Hypertension for the GWG on P. Distribution of 24-h ambulatory blood pressure in children: normalized reference values and role of body dimensions. Journal of Hypertension. 2002 Oct;20(10):1995.", implausible values were replaced by interpolated ones from package version 0.7.4

---

calc_confints

**Calculate confidence intervals**

**Description**

Calculate confidence intervals

**Usage**

```r
calc_confints(
  lms.list,
  perc = c(2.5, 5, 50, 95, 97.5),
  level = 0.95,
  type = c("point")
)
```

**Arguments**

- `lms.list` : lms part of the returned list of `do_iterations`
- `perc` : percentiles for which the confidence bands are calculated
- `level` : confidence level
- `type` : for now only point is a valid value

**Details**

The function takes a lms list as returned by `do_iterations` and calculates the confidence bands for a given set of percentiles using `envelope` from the boot package

**Value**

list containing the respective confidence envelopes

**Author(s)**

mandy
LMS Parameters for the Centers for Disease Control and Prevention 2000 Growth Charts, contains bmi, height, head circumference, weight, weight for length.

Description

LMS Parameters for the Centers for Disease Control and Prevention 2000 Growth Charts, contains bmi, height, head circumference, weight, weight for length.

Usage
cdc.ref

Source

National health statistics reports 63.

Parameters for height of normal weight and obese children from the CrescNet database dependent on height

Description

Parameters for height of normal weight and obese children from the CrescNet database dependent on height.

Usage
cn.ref

Source

"Kempf et al. In progress"
**Description**

Parameters of skinfold measures derived from Colombian population

**Usage**

colombia_sf.ref

**Source**


---

**Description**

Parameters for different carotid artery intima-media thickness and distensibility dependent on age

**Usage**

doyon_age.ref

**Source**

doyon_height.ref

Parameters for different carotid artery intima-media thickness and distensibility dependent on height

Description

Parameters for different carotid artery intima-media thickness and distensibility dependent on height

Usage
doyon_height.ref

Source


do_iterations
do lms iterations

Description

Do lms iterations

Usage
do_iterations(
  data.list,
  n = 10,
  max.it = 1000,
  method = "gamlss",
  prop.fam = 0.75,
  prop.subject = 1,
  age.min = 0,
  age.max = 18,
  age.int = 1/12,
  keep.models = F,
  dist = "BCCGo",
  mu.df = 4,
  sigma.df = 3,
  nu.df = 2,
  tau.df = 2,
  verbose = F,
  formula = NULL,
do_iterations

sigma.formula = ~1,
nu.formula = ~1,
tau.formula = ~1,
method.pb = "ML",
trans.x = F,
lim.trans = c(0, 1.5)
)

Arguments

data.list list of dataframes as returned by prepare_data
n number of desired fits
max.it maximum number of iterations that will be run
method use vgam or gamlss
prop.fam proportion of families to be sampled
prop.subject proportion of subject to be sampled
age.min lower bound of age
age.max upper bound of age
age.int stepwidth of the age variable
keep.models indicator whether or not models in each iteration should be kept
dist distribution used for the fitting process, has to be one of BCCGo, BCPEo, BCTo as they are accepted by lms()
mu.df degree of freedom location parameter
sigma.df degree of freedom spread parameter
nu.df degree of freedom skewness parameter
tau.df degree of freedom kurtosis parameter
verbose whether or not information about sampling will be printed during while iterate
formula formula for the location parameter
sigma.formula formula for the sigma parameter
nu.formula formula for the nu parameter
tau.formula formula for the tau parameter
method.pb GAIC or ML
trans.x indicator wether age should be transformed or not
lim.trans limits for the exponent of transformation of age

Details

function samples families, samples measurements (and subjects), fits the model for a given number of iterations

Value

list of lists for models and fitted parameters
Author(s)
Mandy Vogel

Description
Parameters for bodyfat (for Whites, Blacks, and Mexican-Americans)

Usage
duran_bf.ref

Source

Description
Parameters derived Ethiopian children

Usage
ethiop.ref

Source
Description

fit gamlss

Usage

```r
fit_gamlss(
  data,
  age.min = 0.25,
  age.max = 18,
  age.int = 1/12,
  keep.models = F,
  dist = "BCCGo",
  mu.df = 4,
  sigma.df = 3,
  nu.df = 2,
  tau.df = 2,
  trans.x = F,
  lim.trans = c(0, 1.5),
  value,
  tmpdata
)
```

Arguments

data: dataframe as return by select_meas()
age.min: lower bound of age
age.max: upper bound of age
age.int: stepwidth of the age variable
keep.models: indicator whether or not models in each iteration should be kept
dist: distribution used for the fitting process, has to be one of BCCGo, BCPEo, BCTo as they are accepted by lms()
mu.df: degree of freedom location parameter
sigma.df: degree of freedom spread parameter
nu.df: degree of freedom skewness parameter
tau.df: degree of freedom kurtosis parameter
trans.x: indicator whether age should be transformed or not
lim.trans: limits for the exponent of transformation of age
value: names of the value variable (character) if different from value, ignored
tmpdata: ignored
**Details**

wrapper around the `lms` function in the gamlss package returns the fitted lms-parameter at given age points the function is called inside `do_iterations` and may not called directly

**Value**

list containing a dataframe of the fitted lms parameter at the given age points and the fitted model

**Author(s)**

Mandy Vogel

```r
fit_gamlss1(data, age.min = 0, age.max = 80, age.int = 1/12, keep.models = F, dist = "BCCGo", formula = NULL, sigma.formula = ~1, nu.formula = ~1, tau.formula = ~1, method.pb = "ML")
```

**Arguments**

data data frame as return by `select_meas()`
age.min lower bound of age
age.max upper bound of age
age.int stepwidth of the age variable
keep.models indicator whether or not models in each iteration should be kept
dist distribution used for the fitting process, has to be one of BCCGo, BCPEo, BCTo as they are accepted by lms()
formula formula for the location parameter
**fit_vgam**

sigma.formula: formula for the sigma parameter
nu.formula: formula for the nu parameter
tau.formula: formula for the tau parameter
method.pb: GAIC or ML

**Details**

wrapper around the `gamlss` function from the gamlss package returns the fitted lms-parameter at given age points the function is called inside `do_iterations` and may not be called directly.

**Value**

list containing a dataframe of the fitted lms parameter at the given age points and the fitted model

**Author(s)**

Mandy Vogel

---

**Description**

fit gamlss

**Usage**

```r
fit_vgam(
  data,
  age.min = 0.25,
  age.max = 18,
  age.int = 1/12,
  keep.models = F,
  dist = "BCN",
  mu.df = 4,
  sigma.df = 3,
  nu.df = 2,
  value
)
```

**Arguments**

data: dataframe as return by `select_meas()`
age.min: lower bound of age
age.max: upper bound of age
age.int: stepwidth of the age variable
keep.models  indicator whether or not models in each iteration should be kept
dist  distribution used for the fitting process, has to be one of BCCGo, BCPEo, BCTo as they are accepted by lms()
mu.df  degree of freedom location parameter
sigma.df  degree of freedom spread parameter
nu.df  degree of freedom skewness parameter
value  names of the value variable (character) if different from value, ignored

Details

wrapper around the vgam function in the VGAM package returns the fitted lms-parameter at given age points the function is called inside do_iterations and may not called directly

Value

list containing a dataframe of the fitted lms parameter at the given age points and the fitted model

Author(s)

mandy

Parameters derived from Dutch children (additional to nl4.ref)

Description

Parameters derived from Dutch children (additional to nl4.ref)

Usage

fredriks05.ref

Source

**international_lab.ref  International Laboratory Parameters Tables**

**Description**

International Laboratory Parameters Tables

**Usage**

`international_lab.ref`

**Source**


**iron.ref  Parameters for iron-related blood parameters in children**

**Description**

Parameters for iron-related blood parameters in children

**Usage**

`iron.ref`

**Source**

**Parameters derived from Italian children**

**Description**
Parameters derived from Italian children

**Usage**

**Source**

---

**Parameters derived from Japanese children**

**Description**
Parameters derived from Japanese children

**Usage**

**Source**
**japan_lab.ref**  
*Parameters of serum insulin-like growth factor-I (IGF-I)*

**Description**

Parameters of serum insulin-like growth factor-I (IGF-I)

**Usage**

`japan_lab.ref`

**Source**


**kawel_boehm.ref**  
*Parameters for Cardiovascular Magnetic Resonance*

**Description**

Parameters for Cardiovascular Magnetic Resonance

**Usage**

`kawel_boehm.ref`

**Source**

kiggs.ref

**Description**

LMS Parameters for German reference data (KiGGS, 2003-2006) for height, weight, bmi, hip, whr, whtr, bodyfat, skinfold sum, triceps skinfold, subscapular skinfold, and waist circumference

**Usage**

kiggs.ref

**Source**

Referenzperzentile fuer anthropometrische Masszahlen und Blutdruck aus KiGGS 2003-2006, Robert Koch Institut, Germany

kiggs_bp.ref

**Description**

Parameters derived from the German KiGGS cohort

**Usage**

kiggs_bp.ref

**Details**

contains 2-dimensional reference grid. Do not use with sds but sds_2d

**Source**

**kro.ref**

*LMS Parameters for German reference data (Kromeyer Hauschild, 2001) for height, weight, bmi, and waist circumference, including preterm correction (Voigt)*

**Description**

LMS Parameters for German reference data (Kromeyer Hauschild, 2001) for height, weight, bmi, and waist circumference, including preterm correction (Voigt)

**Usage**

kro.ref

**Source**

Perzentile fuer den Body-mass-Index fuer das Kindes- und Jugendalter unter Heranziehung verschiedener deutscher Stichproben, Monatsschrift Kinderheilkunde August 2001, Volume 149, Issue 8, pp 807-818; Fruehgeborenenkorrektur nach Voigt

---

**life_circ.ref**

*Parameters for different circumferences and whr and whtr*

**Description**

Parameters for different circumferences and whr and whtr

**Usage**

life_circ.ref

**Source**

**life_cysc.ref**

*Parameters for different metabolon parameters from the LIFE Child cohort*

**Description**

Parameters for different metabolon parameters from the LIFE Child cohort

**Usage**

`life_cysc.ref`

**Source**


---

**life_fibroscan.ref**

*Parameters for fibroscan from the LIFE Child cohort*

**Description**

Parameters for fibroscan from the LIFE Child cohort

**Usage**

`life_fibroscan.ref`

**Source**

"preliminary reference values cap med and e med from fibroscan in the life child study. Publication (Puasa et al) in preparation."

Description
hs-Troponin T and NT-proBNP from the LIFE Child cohort

Usage
life_heart.ref

Source

Description
IGF-I and IGF-BP3 from the LIFE Child cohort

Usage
life_igf.ref

Source
"Hoerenz C, Vogel M, Wirkner K. BMI and contraceptives affect new age-, sex-, and puberty-adjusted IGF-I and IGFBP-3 reference ranges across life span. JCEM 2022 (in (minor) revision)."
**life_liver.ref**

*Parameters for serum liver enzymes*

**Description**

Parameters for serum liver enzymes

**Usage**

life_liver.ref

**Source**

Bussler et al, New pediatric percentiles of liver enzyme serum levels (ALT, AST, GGT): effects of age, sex, BMI and pubertal stage, Hepatology 2017

**life_skinfold.ref**

*Parameters for different skinfolds*

**Description**

Parameters for different skinfolds

**Usage**

life_skinfold.ref

**Source**

Parameters for TSH, FT3, FT4 from the LIFE Child cohort

Description
Parameters for TSH, FT3, FT4 from the LIFE Child cohort

Usage
life_thyr.ref

Source
"Surup H., Vogel M., Koerner A., Hiemisch A., Oelkers L., Willenberg A., Kiess W., Kratzsch J. (2021). BMI and puberty have to be included into the interpretation of TSH, FT3 and FT4 measurements by new pediatric reference intervals. THYROID."

Parameters for serum lipids in children

Description
Parameters for serum lipids in children

Usage
lipids.ref

Source
Description

Calculate raw values for percentile curve

Usage

make_percentile_tab(
  ref,
  item,
  perc = c(2.5, 5, 50, 95, 97.5),
  stack = F,
  age = NULL,
  include.pars = T,
  digits = 4,
  sex
)

Arguments

ref            Refgroup object
item           name of the measurement item
perc           vector of percentiles to be calculated
stack          whether or not the data should be stacked, stacked data would most possibly be
                used in ggplot2
age            desired values of age
include.pars   indicator whether or not parameters should be included
digits         specification of number of decimal places
sex            name of the sex variable (character) if different from sex, not functional in this
                version and therefore ignored

Details

calculates quantile values for given RefGroup and given percentiles

Value

data frame either with the different percentiles as columns or, if stacked, as data frame with four
columns: age, sex, variable, value

Author(s)

Mandy Vogel
mock_df

Examples

```r
ptab <- make_percentile_tab(ref = kro.ref,
   item = "height",
   perc = c(2.5,10,50,90,97.5),
   stack = TRUE)

ggplot2::ggplot(ptab, ggplot2::aes(x = age, y = value, colour = variable)) +
   ggplot2::geom_line() +
   ggplot2::facet_wrap(~ sex, nrow = 2)
```

metabolom.ref

Parameters for different metabolom parameters from the LIFE Child cohort

Description

Parameters for different metabolom parameters from the LIFE Child cohort

Usage

```r
metabolom.ref
```

Source


mock_df

Mock a data frame

Description

mock values for a given reference

Usage

```r
mock_df(ref, item, n = 1000)
```

Arguments

```r
ref a valid RefGroup object
item a valid item present in ref
n how many values should be created
```
**mock_value**

Details

mock values for a given reference

Value

data frame containing a age, sex, and value column

Author(s)

mandy

<table>
<thead>
<tr>
<th>mock_value</th>
<th>Mock Value</th>
</tr>
</thead>
</table>

Description

mock a value for a given reference

Usage

mock_value(ref, item, sex = c("male", "female"), age)

Arguments

| ref | a valid RefGroup object |
| item | a valid item present in ref |
| sex | character male or female |
| age | numeric age value |

Details

the function creates a random value for a given age and sex value and a given reference

Value

a random value from the conditional distribution (conditionally on age and sex)

Author(s)

mandy
mock_values  

Mock Values

Description

mock values for a given reference, given age and given sex

Usage

mock_values(df, sex, age, ref, item)

Arguments

df          data frame containing the age and sex
sex         name of the sex variable
age         name of the age variable
ref         a valid ReRefGroup object
item        a valid item present in ref

Details

the function creates random values for given age and sex values and a given reference

Value

data frame containing the additional column with random numbers

Author(s)

mandy

momo.ref  

Parameters for the German MoMo study (sports test)

Description

Parameters for the German MoMo study (sports test)

Usage

momo.ref

Source

motor.ref

Parameters for 5 subtests of the KiGGS Motorik Module

Description
Parameters for 5 subtests of the KiGGS Motorik Module

Usage
motor.ref

Source
"Sobek et al. In progress"

nl3.ref

Parameters of skinfold measures derived from Colombian population

Description
Parameters of skinfold measures derived from Colombian population

Usage
nl3.ref

Source


https://cran.r-project.org/package=AGD
**nl4.ref**  
*Parameters derived from the 4th Dutch growth study*

**Description**

Parameters derived from the 4th Dutch growth study

**Usage**

nl4.ref

**Source**


---

**one_iteration**  
*one iteration*

**Description**

one iteration

**Usage**

one_iteration(
    data.list,  
    method,  
    prop.fam = 0.75,  
    prop.subject = 1,  
    age.min = 0,  
    age.max = 18,  
    age.int = 1/12,  
    keep.models = F,  
    dist = "BCCGo",  
    formula = NULL,  
    sigma.df = 3,
nu.df = 2,
mu.df = 4,
tau.df = 2,
sigma.formula = ~1,
nu.formula = ~1,
tau.formula = ~1,
verbose = F,
trans.x = F,
limit = c(0, 1.5),
method.pb = "ML"
)

Arguments

data.list list of dataframes as returned by prepare_data
method use vgam or gamlss
prop.fam proportion of families to be sampled
prop.subject proportion of subject to be sampled
age.min lower bound of age
age.max upper bound of age
age.int stepwidth of the age variable
keep.models indicator whether or not models in each iteration should be kept
dist distribution used for the fitting process, has to be one of BCCGo, BCPEo, BCTo
as they are accepted by lms()
formula formula for the location parameter
sigma.df degree of freedom spread parameter
nu.df degree of freedom skewness parameter
mu.df degree of freedom location parameter
tau.df degree of freedom kurtosis parameter
sigma.formula formula for the sigma parameter
nu.formula formula for the nu parameter
tau.formula formula for the tau parameter
verbose whether or not information about sampling will be printed during while iterate
trans.x indicator whether age should be transformed or not
limit limits for the exponent of transformation of age
method.pb GAIC or ML

Details

function samples families then measurements and fits the model the function is called inside do_iterations
and may not called directly
Value

list of lists each containing a dataframe of the fitted lms parameter at the given age points and the fitted model

Author(s)

Mandy Vogel

ParTab-class  Table of references

Description

Reference tables

Slots

item  identifier of the item
dist  named list which contains the distribution which was used in fitting the references. One entry for male and one for female

portug.ref  Parameters derived from Portuguese children

Description

Parameters derived from Portuguese children

Usage

portug.ref

Source

**prepare_data**

**prepare data for iteration process**

**Description**

prepare data for repeated iteration process

**Usage**

```r
prepare_data(
  data,
  group = NULL,
  subject = "SIC",
  sex = NULL,
  value = "value",
  age = "age",
  lb = -Inf,
  ub = Inf
)
```

**Arguments**

- **data**: dataframe containing measurement values, age, sex, and subject identifier
- **group**: optional variable indicating groups of subjects within the data frame in most cases (families)
- **subject**: subject identifier
- **sex**: column containing the sex (or any other stratum), ideally of type character, iteration process will run on each of the levels separately
- **value**: numeric column containing the measurement values
- **age**: numeric column containing the age
- **lb**: optional - lower bound for age
- **ub**: optional - upper bound for age

**Details**

given a dataframe, the column name of the subject identifier, sex, age, value and group columns, the function creates a dataframe containing only these five columns with the standard column names group, subject, sex, age, value. lines containing missing values are removed.

**Value**

list of dataframes containing the columns group, subject, sex, age, value; one dataframe for every level of sex

**Author(s)**

Mandy Vogel
RefGroup-class

---

**preterm.ref**  
*Parameters Preterm and Intrauterine*

**Description**

Parameters Preterm and Intrauterine

**Usage**

`preterm.ref`

**Source**


---

RefGroup-class  
*Class of references*

**Description**

Container for reference tables

**Slots**

- `name`  
  name of the reference group

- `refs`  
  List of references, each reference refers to one item and contains independent variable age, and the parameter values for both genders

- `citations`  
  Information about the sources of the references

- `info`  
  Additional infos regarding the references

**Author(s)**

Mandy Vogel

**Examples**

```
data(kiggs.ref)
print(kiggs.ref)
data(ukwho.ref)
print(ukwho.ref)
data(who.ref)
print(who.ref)
```
saudi.ref

Parameters derived from Saudi children

Description

Parameters derived from Saudi children

Usage

saudi.ref

Source


dsds

Calculate SDS Values

Description

Calculate SDS values

Usage

sds(value, age, sex, item, ref, type = "SDS", male = "male", female = "female")

Arguments

- value: vector of measurement values
- age: vector of age values
- sex: vector of sex
- item: name of the item e.g. "height"
- ref: RefGroup object
- type: "SDS" or "perc"
- male: coding of sex for male
- female: coding of sex for female
The function takes a vector of measurement values, and of age and of sex and a RefGroup object as arguments. It calculates the sd or percentile values.

Value

vector containing SDS or percentile values

Author(s)

Mandy Vogel

Examples

```r
anthro <- data.frame(age = c(11.61,12.49,9.5,10.42,8.42,10.75,9.57,10.48),
height = c(148.2,154.4,141.6,145.3,146,140.9,145.5,150),
sex = sample(c("male","female"), size = 8, replace = TRUE),
weight = c(69.5,72.65,47.3,51.6,45.6,48.9,53.5,58.5))

anthro$height_sds <- sds(anthro$height, age = anthro$age,
sex = anthro$sex, ref = kro.ref,
item = "height", type = "SDS")

anthro$bmi <- anthro$weight/(anthro$height**2) * 10000
anthro$bmi_perc <- sds(anthro$bmi, age = anthro$age,
sex = anthro$sex, ref = kro.ref,
item = "bmi", type = "perc")

data(who.ref)
x <- data.frame(height=c(50,100,60,54),
sex=c("m","f","f","m"),
age=c(0.2,9,6,0.2))
sds(value = x$height, age = x$age, sex = x$sex, ref = who.ref, item = "height")
```

---

sdold

Calculate SDS Values

Description

Calculate SDS values - old version for comparison
Usage

\[
\text{sdsold}(\text{value}, \text{age}, \text{sex}, \text{item}, \text{ref}, \\
\text{type = "SDS"}, \text{male = "male"}, \text{female = "female"})
\]

Arguments

- **value**: vector of measurement values
- **age**: vector of age values
- **sex**: vector of sex
- **item**: name of the item e.g. "height"
- **ref**: RefGroup object
- **type**: "SDS" or "perc"
- **male**: coding of sex for male
- **female**: coding of sex for female

Details

The function takes a vector of measurement values, and of age and of sex and a RefGroup object as arguments. It calculates the sds or percentile values.

Value

vector containing SDS or percentile values

Author(s)

Mandy Vogel

Examples

```r
anthro <- data.frame(age = c(11.61,12.49,9.5,10.42,8.42,10.75,9.57,10.48), 
height = c(148.2,154.4,141.6,145.3,146,140.9,145.5,150), 
sex = sample(c("male","female"), size = 8, replace = TRUE), 
weight = c(69.5,72.65,47.3,51.6,45.6,48.9,53.5,58.5))

anthro$height_sds <- sds(anthro$height, 
    age = anthro$age, 
    sex = anthro$sex, male = "male", female = "female", 
    ref = kro.ref, 
    item = "height", 
    type = "SDS")
```
anthro$bmi <- anthro$weight/(anthro$height**2) * 10000
anthro$bmi_perc <- sds(anthro$bmi,
    age = anthro$age,
    sex = anthro$sex, male = "male", female = "female",
    ref = kro.ref,
    item = "bmi",
    type = "perc")
data(who.ref)
x <- data.frame(height=c(50,100,60,54),
    sex=c("m","f","f","m"),
    age=c(0,2.9,0.6,0.2))
sds(value = x$height, age = x$age, sex = x$sex, male = "m", female = "f",
    ref = who.ref, item = "height")

---

**sds_2d**

*Calculate SDS Values for 2-dimensional matrix of covariates*

**Description**

Calculate SDS values for 2-dimensional matrix of covariates

**Usage**

```r
sds_2d(
    value, age, x2, sex, item, ref,
    type = "SDS", male = "male", female = "female"
)
```

**Arguments**

- `value` : vector of measurement values
- `age` : vector of age values
- `x2` : second vector of covariates
- `sex` : vector of sex
- `item` : name of the item e.g. "height"
- `ref` : RefGroup object
- `type` : "SDS" or "perc"
- `male` : coding of sex for male
- `female` : coding of sex for male
select_fams

Details

The function takes a vector of measurement values, and of age and a second covariate (like age and height for blood pressure) of sex and a RefGroup object as arguments. It calculates the sds or percentile values. This function is beta.

the function searches for the nearest given point in the reference grid. From there, the SDS/percentile value will be calculated. Different from sds, no interpolation will be applied. The procedure is according to Neuhauser et al. Blood Pressure Percentiles by Age and Height from Nonoverweight Children and Adolescents in Germany. 2011.

Value

vector containing SDS or percentile values

Author(s)

Mandy Vogel

select_fams

select families

Description

Select groups (families)

Usage

select_fams(data, prop = 0.75, group, verbose = F)

Arguments

data    dataframe as returned by prepare data
prop    proportion of families to be sampled
group    name of the group variable (character) if not "group", ignored
verbose    if TRUE information about sample size is printed out

Details

function selects a given proportion of groups/families from the data if no grouping variable is given the original data set is returned function is called inside do_iterations and may not called directly

Value

dataframe containing only prop.fam percent the families in data

Author(s)

Mandy Vogel
select_meas

choose one measurement per subject

Description

Choose one measurement per subject

Usage

select_meas(data, subject = "subject", prop = 1, verbose = F)

Arguments

data dataframe as returned by prepare data
subject name of the column containing the subject identifier
prop optional - proportion of measurements to sample
verbose if TRUE information about sample size is printed out

Details

function samples one measurement per subject, if prop < 1 additional a prop*100 percent will be sampled from the measurements the function is called inside do_iterations and may not called directly

Value

dataframe containing the sampled rows

Author(s)

Mandy Vogel

show,ParTab-method

class ParTab

Description

show method for ParTab

Usage

## S4 method for signature 'ParTab'
show(object)
Arguments
  object object of class ParTab

Details
  show method for ParTab

Value
  print information about the respective reference table

Author(s)
  Mandy Vogel

---

Description
  show method for RefGroup

Usage
  ## S4 method for signature 'RefGroup'
  show(object)

Arguments
  object object of class RefGroup

Details
  show method for RefGroup

Value
  prints information about age range, citations, etc.

Author(s)
  Mandy Vogel
turkish.ref  Parameters derived from Turkish children

Description
Parameters derived from Turkish children

Usage
turkish.ref

Source

uk1990.ref  Parameters from the 1990 UK growth study

Description
Parameters from the 1990 UK growth study

Usage
uk1990.ref

Source
**ukwho.ref**

**LMS Parameters for UK-WHO growth charts for height, weight, bmi, head circumference**

**Description**

LMS Parameters for UK-WHO growth charts for height, weight, bmi, head circumference

**Usage**

ukwho.ref

**Source**


---

**us.ref**

**Parameters derived from US children (additional to the cdc.ref)**

**Description**

Parameters derived from US children (additional to the cdc.ref)

**Usage**

us.ref

**Source**

**who.ref**

*LMS Parameters for UK-WHO growth charts for height, weight, bmi, head circumference, arm mid upper arm circumference, subscapular and triceps skinfold, weight for height*

**Description**

LMS Parameters for UK-WHO growth charts for height, weight, bmi, head circumference, arm mid upper arm circumference, subscapular and triceps skinfold, weight for height

**Usage**

who.ref

**Source**


---

**who2007.ref**

*Parameters of skinfold measures derived from Colombian population*

**Description**

Parameters of skinfold measures derived from Colombian population

**Usage**

who2007.ref

**Source**

Description
Worm plot ggplot version

Usage
wormplot_gg(
  m = NULL,
  residuals = NULL,
  age = NA,
  n.inter = 1,
  y.limits = c(-1, 1)
)

Arguments
  m          a gamlss model
  residuals  normalized quantile residuals
  age        numeric vector of ages
  n.inter    number of age intervals or cut points
  y.limits   limits of the y-axis

Details
creates a wormplot for a gamlss model or a given vector of normalized quantile residuals, either for all residuals or grouped by age intervals

Value
ggplot object

---

zong13.ref  Parameters derived from Chinese children (additional to nl4.ref)

Description
Parameters derived from Chinese children (additional to nl4.ref)

Usage
zong13.ref
Source

Index

aga_15.ref, 3
aggregate_lms, 3

belgium.ref, 4
bone.ref, 4
bp_wuehl_age.ref, 5
bp_wuehl_height.ref, 5

calc_confints, 6
cdc.ref, 7
cn.ref, 7
colombia_sf.ref, 8
do_iterations, 6, 9, 13–15, 31, 39, 40
doyon_age.ref, 8
doyon_height.ref, 9
duran_bf.ref, 11

everse, 6
ethiop.ref, 11

fit_gamlss, 12
fit_gamlss1, 13
fit_vgaml, 14
fredriks05.ref, 15

gamlss, 14

international_lab.ref, 16
iron.ref, 16
italian.ref, 17

japannese.ref, 18
japanese.ref, 17

kawel_boehm.ref, 18
kigs.ref, 19
kiggs_bp.ref, 19
kro.ref, 20

life_circ.ref, 20

life_cysc.ref, 21
life_fibroscan.ref, 21
life_heart.ref, 22
life_igf.ref, 22
life_liver.ref, 23
life_skinfold.ref, 23
life_thyr.ref, 24
lipsds.ref, 24
lms, 13

make_percentile_tab, 25
metabolom.ref, 26
mock_df, 26
mock_value, 27
mock_values, 28
momo.ref, 28
motor.ref, 29

nl3.ref, 29
nl4.ref, 30

one_iteration, 30

ParTab-class, 32
portug.ref, 32
prepare_data, 33
preterm.ref, 34

RefGroup-class, 34

saudi.ref, 35
sds, 19, 35, 39
sds_2d, 19, 38
sdsold, 36
select_fams, 39
select_meas, 40
show, ParTab-method, 40
show, RefGroup-method, 41

turkish.ref, 42
uk1990.ref, 42
ukwho.ref, 43
us.ref, 43

vgam, 15

who.ref, 44
who2007.ref, 44
wormplot_gg, 45

zong13.ref, 45