Package ‘childds’

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)
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Suggests ggplot2
BugReports https://git.sc.uni-leipzig.de/my221hepi/childds/-/issues
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Parameters from recommendations of the German Adiposity Association (2015, AGA)

Usage

aga_15.ref

Source


aggregate_lms

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 implausible 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 implausible 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 implausible 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 implausible values are replaced by interpolated ones. For the original values check out earlier versions

Usage

bp_wuehl_height.ref
calc_confints

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

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

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,
\begin{verbatim}
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
\end{verbatim}
**duran_bf.ref**

**Author(s)**
Mandy Vogel

---

**Parameters for bodyfat (for Whites, Blacks, and Mexican-Americans**

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

**Usage**
duran_bf.ref

**Source**

---

**ethiop.ref**

**Parameters derived Ethiopian children**

**Description**
Parameters derived Ethiopian children

**Usage**
ethiop.ref

**Source**
Description

fit_gamlss

Usage

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 wether 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

Description

fit_gamlss

Usage

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 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()
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

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

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**

italian.ref

**Source**


---

**Parameters derived from Japanese children**

**Description**
Parameters derived from Japanese children

**Usage**

japanese.ref

**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**

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

**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**

Parameters derived from the German KiGGS cohort

**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**

Parameters for different metabolom parameters from the LIFE Child cohort

Description

Parameters for different metabolom parameters from the LIFE Child cohort

Usage

life_cysc.ref

Source


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."
life_heart.ref  

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

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

**Usage**
life_heart.ref

**Source**

---

life_igf.ref  

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

**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)."
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

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
**make_percentile_tab**  
*calculate raw values*

**Description**

Calculate raw values for percentile curve

**Usage**

```r
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`  
  wether 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
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

- **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

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  

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 RefGroup 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,
lim.trans = 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
lim.trans 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

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

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

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>group</td>
<td>optional variable indicating groups of subjects within the data frame in most cases (families)</td>
</tr>
<tr>
<td>subject</td>
<td>subject identifier</td>
</tr>
<tr>
<td>sex</td>
<td>column containing the sex (or any other stratum), ideally of type character, iteration process will run on each of the levels separately</td>
</tr>
<tr>
<td>value</td>
<td>numeric column containing the measurement values</td>
</tr>
<tr>
<td>age</td>
<td>numeric column containing the age</td>
</tr>
<tr>
<td>lb</td>
<td>optional - lower bound for age</td>
</tr>
<tr>
<td>ub</td>
<td>optional - upper bound for age</td>
</tr>
</tbody>
</table>

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


sds

Calculate SDS Values

Description
Calculate SDS values

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

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>value</td>
<td>vector of measurement values</td>
</tr>
<tr>
<td>age</td>
<td>vector of age values</td>
</tr>
<tr>
<td>sex</td>
<td>vector of sex</td>
</tr>
<tr>
<td>item</td>
<td>name of the item e.g. &quot;height&quot;</td>
</tr>
<tr>
<td>ref</td>
<td>RefGroup object</td>
</tr>
<tr>
<td>type</td>
<td>&quot;SDS&quot; or &quot;perc&quot;</td>
</tr>
<tr>
<td>male</td>
<td>coding of sex for male</td>
</tr>
<tr>
<td>female</td>
<td>coding of sex for female</td>
</tr>
</tbody>
</table>
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")
```

Description

Calculate SDS values - old version for comparison
Usage

sdsoln(
  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

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

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

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

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)
show,RefGroup-method

Arguments

object object of class ParTab

Details

show method for ParTab

Value

print information about the respective reference table

Author(s)

Mandy Vogel

show,RefGroup-method  class RefGroup

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**

<table>
<thead>
<tr>
<th>Description</th>
<th>Parameters derived from US children (additional to the cdc.ref)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Usage</td>
<td>ukwho.ref</td>
</tr>
</tbody>
</table>

### us.ref

<table>
<thead>
<tr>
<th>Description</th>
<th>Parameters derived from US children (additional to the cdc.ref)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Usage</td>
<td>us.ref</td>
</tr>
</tbody>
</table>
**who.ref**

*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**

*Description*

Parameters of skinfold measures derived from Colombian population

*Usage*

who2007.ref

*Source*

wormplot_gg  Worm Plot ggplot version

Description
Worm plot ggplot version

Usage

```r
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

```r
zong13.ref
```
Source

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