Package ‘childdsds’

March 26, 2019

Title Data and Methods Around Reference Values in Pediatrics

Version 0.7.4

Description Calculation of standard deviation scores and percentiles adduced from different growth standards (WHO, UK, Germany, Italy, China, etc). Therefore, the calculation of SDS-values for different measures like BMI, weight, height, head circumference, different ratios, etc. are easy to carry out. Also, references for laboratory values in children and adults are available, e.g., serum lipids, iron-related blood parameters, IGF, liver enzymes. In the new version, there are also functions combining the lms() function from package 'gamlss' with resampling methods for using with repeated measurements and family dependencies. A searchable list of items can be found here: <https://github.com/mvogel78/childsds/wiki>.

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://github.com/mvogel78/childsds/issues

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

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aga_15.ref

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

Description
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**


---

**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

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

calc_confints

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

cdc.ref  

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.

colombia_sf.ref  

Parameters of skinfold measures derived from Colombian population

Description

Parameters of skinfold measures derived from Colombian population

Usage

colombia_sf.ref

Source

<table>
<thead>
<tr>
<th>doyon_age.ref</th>
<th>Parameters for different carotid artery intima-media thickness and distensibility dependent on age</th>
</tr>
</thead>
</table>

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

**Usage**
doyon_age.ref

**Source**

<table>
<thead>
<tr>
<th>doyon_height.ref</th>
<th>Parameters for different carotid artery intima-media thickness and distensibility dependent on height</th>
</tr>
</thead>
</table>

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

**Usage**
doyon_height.ref

**Source**
**do_iterations**

**Description**

Do lms iterations

**Usage**

```r
do_iterations(dataNlistL n = 1PL maxNit = 1PPPL method = BgamlssBL
propNfam = PN7UL propNsubject = 1L ageNmin = PL ageNmax = 18L
ageNint = 1/1RL keepNmodels = fL dist = BbccgoBL muNdf = TL
sigmaNdf = SL nuNdf = RL tauNdf = RL verbose = fL
formula = nullL sigmaNformula = ~1L nuNformula = ~1L
tauNformula = ~1L methodNpb = BmlBL transNx = fL limNtrans = c(PL
1NUII
```

**Arguments**

- `dataNlist`: 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
- `propNfam`: proportion of families to be sampled
- `propNsubject`: proportion of subject to be sampled
- `ageNmin`: lower bound of age
- `ageNmax`: upper bound of age
- `ageNint`: stepwidth of the age variable
- `keepNmodels`: 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()
- `muNdf`: degree of freedem location parameter
- `sigmaNdf`: degree of freedem spread parameter
- `nuNdf`: degree of freedem skewness parameter
- `tauNdf`: degree of freedem kurtosis parameter
- `verbose`: whether or not information about sampling will be printed during while iterate
- `formula`: formula for the location parameter
- `sigmaNformula`: formula for the sigma parameter
- `nuNformula`: formula for the nu parameter
- `tauNformula`: formula for the tau parameter
- `methodNpb`: GAIC or ML
- `transNx`: indicator wether age should be transformed or not
- `limNtrans`: 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

duran_bf.ref

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

ehtiop.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,
u.nu.df = 2, tau.nu.df = 2, trans.x = F, lim.trans = c(0, 1.5), 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.nu.df degree of freedom location parameter
sigma.nu.df degree of freedom spread parameter
nu.nu.df degree of freedom skewness parameter
tau.nu.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

Details

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

Value

list containing a dataframe of the fitted \texttt{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
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
**fredriks05.ref**  
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**


---

### italian.ref

**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**


---

**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**

<table>
<thead>
<tr>
<th>kiggs.ref</th>
<th>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</th>
</tr>
</thead>
</table>

**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

<table>
<thead>
<tr>
<th>kiggs_bp.ref</th>
<th>Parameters derived from the German KiGGS cohort</th>
</tr>
</thead>
</table>

**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_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 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 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)
```

mock_df

Mock a data frame

Description
mock values for a given reference

Usage
`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

Details
mock values for a given reference

Value
data frame containing a age, sex, and value column

Author(s)
mandy
mock_value

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

---

**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
**Parameters derived from the 4th Dutch growth study**

**Description**

Parameters derived from the 4th Dutch growth study

**Usage**

one_iteration

**Source**


**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 wether 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
**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**

`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, iter-
ation 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

---

preterm.ref Parameters Preterm and Intrauterine

Description

Parameters Preterm and Intrauterine

Usage

preterm.ref

Source

Olsen, I.E., Lawson, M.L., Ferguson, A.N., Cantrell, R., Grabich, S.C., Zemel, B.S., Clark, R.H.,
2015. BMI Curves for Preterm Infants. PEDIATRICS 135, e572–e581. doi:10.1542/peds.2014-
2777

RefGroup-class

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

```r
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

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,
                          type = "SDS")
```
Calculate SDS Values

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, 0.9, 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

**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
select_meas

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

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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

Description

show method for ParTab

Usage

```r
## 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

show,RefGroup-method

Description

show method for RefGroup

Usage

```r
## 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**


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**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**

**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**


---

**Description**

Parameters of skinfold measures derived from Colombian population

**Usage**

who2007.ref

**Source**

wormplot_gg

**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**

`zong13.ref`

**Source**
