Package 'AGD'

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Type Package

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Title Analysis of Growth Data

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Depends R (>= 2.10.0)

Imports gamlss, gamlss.dist

Description Tools for the analysis of growth data: to extract an
LMS table from a gamlss object, to calculate the standard
deviation scores and its inverse, and to superpose two wormplots
from different models. The package contains a some varieties of
reference tables, especially for The Netherlands.

License GPL-2 | GPL-3

LazyLoad yes

LazyData yes

URL https://stefvanbuuren.name/AGD/

BugReports https://github.com/stefvanbuuren/AGD/issues

Encoding UTF-8

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NeedsCompilation no

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Repository CRAN

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Contents

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ageGrid   *Creates an age grid according to a specified format.*

Description

Creates an age grid according to a specified format.

Usage

```
ageGrid(grid = "compact")
```

Arguments

grid   A character string specifying one of the following: `"compact"`, `"classic"`,
                `"extensive"`, `"0-104w"`, `"0-24m"`, `"0-21y"`, `"0-21yd"` or `"0-21yc"`. The de-
                fault is `"compact"`, which produces an age grid between 0 and 21 years with 95
                points.

Value

A list with five components: `format`, `year`, `month`, `week` and `day` containing the age grid in different
units.

Author(s)

Stef van Buuren, 2010

Examples

```
age <- ageGrid("classic")$year
```

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boys7482	*Growth of Dutch boys*

Description

Height, weight, head circumference and puberty of 7482 Dutch boys.

Format

A data frame with 7482 rows on the following 9 variables:

age Decimal age (0-21 years)

hgt Height (cm)

wgt Weight (kg)

bmi Body mass index

hc Head circumference (cm)

gen Genital Tanner stage (G1-G5)

phb Pubic hair (Tanner P1-P6)

tv Testicular volume (ml)

reg Region (north, east, west, south, city)

Details

The complete sample of cross-sectional data from boys 0-21 years used to construct the Dutch growth references 1997. Variables gen and phb are ordered factors. reg is a factor. Note: A 10% sample from this data is available in data set boys in the mice package.

Author(s)

Stef van Buuren, 2012

Source

Fredriks, A.M,, van Buuren, S., Burgmeijer, R.J., Meulmeester JF, Beuker, R.J., Brugman, E., Roede, M.J., Verloove-Vanhorick, S.P., Wit, J.M. (2000) Continuing positive secular growth change in The Netherlands 1955-1997. *Pediatric Research*, **47**, 316-323.

Fredriks, A.M., van Buuren, S., Wit, J.M., Verloove-Vanhorick, S.P. (2000). Body index measurements in 1996-7 compared with 1980. *Archives of Disease in Childhood*, **82**, 107-112.

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extractLMS   *Extracts LMS values from a gamlss object.*

Description

Extract LMS values from a gamlss object for solutions that transform the age axis according to the M-curve.

Usage

```
extractLMS(
  fit,
  data,
  sex = "M",
  grid = "classic",
  decimals = c(4, 4, 4),
  flatAge = NULL
)
```

Arguments

fit	A gamlss object containing the final fit on transformed age, t.age.
data	A data frame containing the original data, with both age and t.age
sex	A character vector indicating whether the fit applied to males sex="M" or females sex="F". The default is sex="M".
grid	A character vector indicating the desired age grid. See ageGrid() for possible options. The default is a grid="classic", a grid of 59 age points.
decimals	A numerical vector of length 3 indicating the number of significant digits for rounding of the L, M and S curves, respectively.
flatAge	A scalar indicating the age beyond which the L, M and S values should be constant. The default (NULL) is not to flatten the curves.

Details

It is crucial that t.age in data correspond to exactly the same age transformation as used to fit the gamlss object. Age grid values beyond the range of data$age produce NA in the L, M and S values. Parameter flatAge should be one of the values of the age grid.

Value

A data frame with rows corresponding to time points, and with the following columns: sex,x,L,M,S.

Author(s)

Stef van Buuren, 2010

Examples

```
## Not run:
#
library(gamlss)
boys <- boys7482

# calculate initial M curve
data <- na.omit(boys[,1:2])
f0154  <- gamlss(hgt~cs(age,df=15,c.spar=c(-1.5,2.5)),
                 sigma.formula=~cs(age,df=4,c.spar=c(-1.5,2.5)),
                 data=data,family=NO,
                 control=gamlss.control(n.cyc=3))

# calculate transformed age
t.age <- fitted(lm(data$age~fitted(f0154)))
t.age <- t.age - min(t.age)
data.t <- data.frame(data,t.age=t.age)

# calculate final solution
f0106r <- gamlss(hgt~cs(t.age,df=10,c.spar=c(-1.5,2.5)),
                 sigma.formula=~cs(t.age,df=6,c.spar=c(-1.5,2.5)),
                 data=data.t,family=NO,
                 control=gamlss.control(n.cyc=3))

# extract the LMS reference table in the 'classic' age grid
nl4.hgt.boys <- extractLMS(fit = f0106r, data=data.t, grid="compact",
                dec = c(0,2,5))
nl4.hgt.boys


# flatten the reference beyond age 20Y (not very useful in this data)
nl4.hgt.boys.flat <- extractLMS(fit = f0106r, data=data.t, flatAge=20)
nl4.hgt.boys.flat

# use log age transformation
data.t <- data.frame(data, t.age = log(data$age))
f0106rlog <- gamlss(hgt~cs(t.age,df=10,c.spar=c(-1.5,2.5)),
                 sigma.formula=~cs(t.age,df=6,c.spar=c(-1.5,2.5)),
                 data=data.t,family=NO,
                 control=gamlss.control(n.cyc=1))

nl4.hgt.boys.log <- extractLMS(fit = f0106rlog, data=data.t)
nl4.hgt.boys.log

## End(Not run)
```

References CDC   *Reference tables from CDC 2000*

Description

Reference tables from CDC 2000

Format

A data frame with seven variables:

list("pop") Study Population

list("sub") Subpopulation

list("sex") Sex (M,F)

list("x") Decimal age (0-5 years)

list("L") Lambda (skewness) curve

list("M") Median curve

list("S") Coefficient of Variation curve

Details

The models were fitted by the LMS model. Parameters are stored as type LMS. Tabulated values are point ages.

The naming conventions are as follows:

list("cdc.hgt") Combined length/height (cm) for Age, 0-20 years. Measures <2 years apply to length (lying), while ages >= 2 years apply to height, or stature (standing).

list("cdc.wgt") Weight (kg) for Age, 0-20 years.

list("cdc.bmi") Body Mass Index (kg/m2) for Age, 2-20 years.

Source

Kuczmarski RJ, Ogden CL, Guo SS, Grummer-Strawn LM, Flegal KM, Mei Z, Wei R, Curtin LR, Roche AF, Johnson CL. 2000 CDC growth charts for the United States: methods and development. *Vital Health Stat*, 2002, **11**, 246, 1-190.

See Also

nl4.wgt, nl4.hgt, nl4.bmi, who.wgt

| References NL3 | *Reference tables from Third Dutch Growth Study 1980* |

Description

Reference table from the Third Dutch Growth Study 1980

Format

A data frame with seven variables:

list("pop") Study Population

list("sub") Subpopulation, e.g. ethnicity or age group (for nl4.wfh)

list("sex") Sex (M,F)

list("x") Decimal age (0-21 years) or Height (for nl4.wfh)

list("L") Lambda (skewness) curve

list("M") Median curve

list("S") Coefficient of Variation curve

Details

The model was fitted by the LMS model. Parameters are stored as type LMS. Tabulated values are point ages.

Height follows a normal distribution, with all lambda parameters set equal to 1. The standard deviation (in cm) is obtained as S*M.

The naming conventions are as follows:

list("nl4.hgt") Length/Height (cm) for Age

list("nl4.wgt") Weight (kg) for Age

list("nl4.wfh") Weight (kg) for Height (cm)

list("nl4.bmi") Head circumference (cm) for Age

list("nl4.lgl") Leg Length (cm) for Age

list("nl4.hip") Hip circumference (cm) for Age

list("nl4.wst") Waist circumference (cm) for Age

list("nl4.whr") Waist/Hip ratio for Age

list("nl4.sit") Sitting Height for Age

list("nl4.shh") Sitting Height/Height ratio for Age

Source

Fredriks, A.M,, van Buuren, S., Burgmeijer, R.J., Meulmeester JF, Beuker, R.J., Brugman, E., Roede, M.J., Verloove-Vanhorick, S.P., Wit, J.M. (2000) Continuing positive secular growth change in The Netherlands 1955-1997. *Pediatric Research*, **47**, 316-323.

Fredriks, A.M., van Buuren, S., Wit, J.M., Verloove-Vanhorick, S.P. (2000). Body index measurements in 1996-7 compared with 1980. *Archives of Disease in Childhood*, **82**, 107-112.

See Also

[cdc.wgt](cdc.wgt), [who.wgt](who.wgt)

References NL4   *Reference tables from Fourth Dutch Growth Study 1997*

Description

Reference table from the Fourth Dutch Growth Study 1997

Format

A data frame with seven variables:

list("pop") Study Population

list("sub") Subpopulation, e.g. ethnicity or age group (for nl4.wfh)

list("sex") Sex (M,F)

list("x") Decimal age (0-21 years) or Height (for nl4.wfh)

list("L") Lambda (skewness) curve

list("M") Median curve

list("S") Coefficient of Variation curve

Details

The model was fitted by the LMS model. Parameters are stored as type LMS. Tabulated values are point ages.

Height follows a normal distribution, with all lambda parameters set equal to 1. The standard deviation (in cm) is obtained as S*M.

The naming conventions are as follows:

list("nl4.hgt") Length/Height (cm) for Age

list("nl4.wgt") Weight (kg) for Age

list("nl4.wfh") Weight (kg) for Height (cm)

list("nl4.bmi") Head circumference (cm) for Age

list("nl4.lgl") Leg Length (cm) for Age

list("nl4.hip") Hip circumference (cm) for Age

list("nl4.wst") Waist circumference (cm) for Age

list("nl4.whr") Waist/Hip ratio for Age

list("nl4.sit") Sitting Height for Age

list("nl4.shh") Sitting Height/Height ratio for Age

Source

Fredriks, A.M,, van Buuren, S., Burgmeijer, R.J., Meulmeester JF, Beuker, R.J., Brugman, E., Roede, M.J., Verloove-Vanhorick, S.P., Wit, J.M. (2000) Continuing positive secular growth change in The Netherlands 1955-1997. *Pediatric Research*, **47**, 316-323.

Fredriks, A.M., van Buuren, S., Wit, J.M., Verloove-Vanhorick, S.P. (2000). Body index measurements in 1996-7 compared with 1980. *Archives of Disease in Childhood*, **82**, 107-112.

See Also

cdc.wgt, who.wgt

References WHO   *References WHO*

Description

Reference tables, combined from the WHO Multicentre Growth Reference Study (MGRS) (ages 0-5 years) and the WHO 2007 reference (5-19 years).

Format

A data frame with seven variables:

pop Study Population (always *"who"*)

sub Subpopulation (always *"N"*)

sex Sex (M, F)

x Decimal age, height (cm) or length(cm)

L Lambda (skewness) curve

M Median curve

S Coefficient of variation

Details

The data were fitted by the LMS model. Parameters are stored as type LMS. Tabulated values are point ages.

The naming conventions are as follows:

who.hgt Length (cm, 0-2 Yrs) or height (cm, 2-19 years)

who.wgt Weight (kg) for age (0-10 years)

who.bmi BMI (kg/m^2) for age (0-19 years)

who.hdc Head circumference (cm) for age (0-5 years)

who.wfh Weight (kg) for height (65-120 cm)

who.wfl Weight (kg) for length (45-110 cm)

Source

WHO Multicentre Growth Reference Study Group. WHO Child Growth Standards based on length/height, weight and age. *Acta Paediatr*, Suppl. 2006, 450, 76-85.

de Onis M, Onyango AW, Borghi E, Siyam A, Nishida C, Siekmann J. Development of a WHO growth reference for school-aged children and adolescents *Bulletin of the World Health Organization*, 2007;85:660-7.

See Also

[nl4.wgt](), [cdc.wgt]()

---

wp.twin	*Superposes two worm plots*

Description

Superposes two worm plots from GAMLSS fitted objects. This is a diagnostic tool for comparing two solutions.

Usage

```
wp.twin(
  obj1,
  obj2 = NULL,
  xvar = NULL,
  xvar.column = 2,
  n.inter = 16,
  show.given = FALSE,
  ylim.worm = 0.5,
  line = FALSE,
  cex = 1,
  col1 = "black",
  col2 = "orange",
  warnings = FALSE,
  ...
)
```

Arguments

obj1	a GAMLSS fitted object
obj2	an optional second GAMLSS fitted object
xvar	the explanatory variable against which the worm plots will be plotted
xvar.column	the number referring to the column of obj1$mu.x and obj2$mu.x. If xvar=NULL then the explanatory variable is set to xvar=obj1$mu.x[,xvar.column] respectively xvar=obj2$mu.x[,xvar.column]. The default is xvar.column=2, which selects the variable following the intercept (which is typically age in most applications).

n.inter	the number of intervals in which the explanatory variable xvar will be cut. The default is 16.
show.given	whether to show the x-variable intervals in the top of the graph, default is show.given=FALSE
ylim.worm	for multiple plots, this values is the y-variable limit, default value is ylim.worm=0.5
line	whether to plot the polynomial line in the worm plot, default value is line=FALSE
cex	the cex plotting parameter with default cex=1
col1	the color for the points of obj1. The default col="black"
col2	the color for the points of obj2. The default col="orange"
warnings	a logical indicating whether warnings should be produced. The default warnings=FALSE
...	for extra arguments, overlap, xlim.worm or pch

Details

This function is a customized version of the wp() function found in the gamlss package. Function wp.twin() allows overplotting of two worm plots, each in its own color. The points of obj1 are plotted first, the points of obj2 are superposed. This twin worm plot provide a visual assessment of the differences between the solutions. Extra arguments can be specified (e.g. xvar) that are passed down to the wp() function of gamlss if specified. The worm plot is a detrended normal QQ-plot that highlight departures from normality.

Argument xvar takes priority over xvar.column. The xvar variable is cut into n.iter intervals with an equal number observations and detrended normal QQ (i.e. worm) plots for each interval are plotted. This is a way of highlighting failures of the model within different ranges of the explanatory variable.

If line=TRUE and n.inter>1, the fitted coefficients from fitting cubic polynomials to the residuals (within each x-variable interval) can be obtain by e.g. coeffs<-wp.twin(model1,xvar=x,n.iner=9). van Buuren *et al.* (2001) used these residuals to identify regions (intervals) of the explanatory variable within which the model does not fit adequately the data (called "model violation")

Value

For multiple plots the xvar intervals and the coefficients of the fitted cubic polynomials to the residuals (within each xvar interval) are returned.

Author(s)

Stef van Buuren, using R code of Mikis Stasinopoulos and Bob Rigby

References

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, https://www.jstatsoft.org/v23/i07.

van Buuren and Fredriks M. (2001) Worm plot: simple diagnostic device for modelling growth reference curves. *Statistics in Medicine*, **20**, 1259–1277.

van Buuren and Fredriks M. (2007) Worm plot to diagnose fit in quantile regression. *Statistical Modelling*, **7**, 4, 363–376.

Examples

```
## Not run:
library(gamlss)
data(abdom)
a <- gamlss(y~cs(x,df=1),sigma.fo=~cs(x,0),family=LO,data=abdom)
b <- gamlss(y~cs(x,df=3),sigma.fo=~cs(x,1),family=LO,data=abdom)
coeff1 <- wp.twin(a,b,line=TRUE)

## End(Not run)
```

---

y2z   *Converts measurements to standard deviation scores (SDS)*

Description

Converts measurements into age- and sex-conditional standard deviation score (SDS) using an external reference.

Usage

```
y2z(
  y = c(75, 80, 85),
  x = 1,
  sex = "M",
  sub = "N",
  ref = get("nl4.hgt"),
  dist = "LMS",
  dec = 3,
  sex.fallback = NA,
  sub.fallback = NA,
  tail.adjust = FALSE
)
```

Arguments

y	A numerical vector containing the outcome measurements. The length `length(y)` determines the size of the output vector.
x	A vector containing the values of the numerical covariate (typically decimal age or height) at which conversion is desired. Values are replicated to match `length(y)`.
sex	A character vector indicating whether the male ("M") of female ("F")reference should be used. Values are replicated to match `length(y)`.
sub	A character vector indicating the level of the sub field of the reference standard defined in `ref`
ref	A data frame containing a factor `sex`, a numerical variable `age` containing the tabulated decimal point ages, and two or more numerical variables with reference values. See details.

dist	A string identifying the type of distribution. Values values are: ″NO″, ″BCCG″, ″LMS″, ″BCPE″ and ″BCT″. The default is ″LMS″.
dec	A scalar value indicating the number of decimals used to round the value.
sex.fallback	The level of the sex field used when no match is found. The default sex.fallback=NA specifies that unmatched entries should receive a NA value.
sub.fallback	The level of the sub field used when no match is found. The default sub.fallback=NA specifies that unmatched entries should receive a NA value.
tail.adjust	Logical. If TRUE then the WHO method for tail adjustment is applied. The default is FALSE.

Details

Functions z2y() and y2z() are the inverse of each other.

The argument dist determines the statistical distribution. The possibilities are as follows:

list("\"NO\"") ref should contain columns mean and sd, containing the mean and the standard deviation in the external reference population.

list("\"LMS\"") ref should contain columns L, S and M containing the LMS parameters.

list("\"BCCG\"") ref should contain columns mu, sigma and nu containing the Box-Cox Cole-Green parameters.

list("\"BCPE\"") ref should contain columns mu, sigma, nu and tau containing the Box-Cox Power Exponential parameters.

list("\"BCT\"") ref should contain columns mu, sigma, nu and tau containing the Box-Cox T distribution parameters.

Value

For y2z(): A vector with length(y) elements containing the standard deviation score. For z2y(): A vector with length(z) elements containing quantiles.

Author(s)

Stef van Buuren, 2010

See Also

[z2y](z2y)

Examples

```
boys <- boys7482

# SDS of height 115 cm at age 5 years,
# relative to Dutch boys reference
y2z(y=115, x=5)

# same relative to Dutch girls
```

```
y2z(y=115, x=5, sex="F")

# SDS of IOTF BMI cut-off value for overweight (boys 2-18)
# relative to Dutch boys reference
cutoff <- c(
18.41, 18.15, 17.89, 17.72, 17.55, 17.49, 17.42, 17.49, 17.55, 17.74,
17.92, 18.18, 18.44, 18.77, 19.10, 19.47, 19.84, 20.20, 20.55, 20.89,
21.22, 21.57, 21.91, 22.27, 22.62, 22.96, 23.29, 23.60, 23.90, 24.18,
24.46, 24.73, 25.00)
age <- seq(2, 18, by=0.5)
(z <- y2z(y=cutoff, x=age, sex="M", ref=nl4.bmi))

# apply inverse transformation to check calculations
round(z2y(z, age, ref=nl4.bmi), 2)
cutoff

# calculate percentiles of weight 12 kg at 2 years (boys, girls)
100*round(pnorm(y2z(y=c(12,12), x=2, sex=c("M","F"), ref=nl4.wgt)),2)

# # percentage of children lighter than 15kg at ages 2-5
e <- expand.grid(age=2:5, sex=c("M","F"))
z <- y2z(y=rep(15,nrow(e)), x=e$age, sex=e$sex, ref=nl4.wgt)
w <- matrix(100*round(pnorm(z),2), nrow=2, byrow=TRUE)
dimnames(w) <- list(c("boys","girls"),2:5)
w

# analysis in Z scale
hgt.z <- y2z(y=boys$hgt, x=boys$age, sex="M", ref=nl4.hgt)
wgt.z <- y2z(y=boys$wgt, x=boys$age, sex="M", ref=nl4.wgt)
plot(hgt.z, wgt.z, col="blue")


# z2y

# quantile at SD=0 of age 2 years,
# height Dutch boys
z2y(z=0, x=2)

# same for Dutch girls
z2y(z=0, x=2, sex="F")

# quantile at SD=c(-1,0,1) of age 2 years, BMI Dutch boys
z2y(z=c(-1,0,+1), x=2, ref=nl4.bmi)

# 0SD line (P50) in kg of weight for age in 5-10 year, Dutch boys
z2y(z=rep(0,6), x=5:10, ref=nl4.wgt)

# 95th percentile (P95), age 10 years, wfa, Dutch boys
z2y(z=qnorm(0.95), x=10, ref=nl4.wgt)

# table of P3, P10, P50, P90, P97 of weight for 5-10 year old dutch boys
# age per year
age <- 5:10
```

```
p <- c(0.03,0.1,0.5,0.9,0.97)
z <- rep(qnorm(p), length(age))
x <- rep(age, each=length(p))
w <- matrix(z2y(z, x=x, sex="M", ref=nl4.wgt), ncol=length(p),
 byrow=TRUE)
dimnames(w) <- list(age, p)
round(w,1)

# standard set of Z-scores of weight for all tabulated ages, boys & girls
# and three etnicities
sds <- c(-2.5, -2, -1, 0, 1, 2, 2.5)
age <- nl4.wgt$x
z <- rep(sds, times=length(age))
x <- rep(age, each=length(sds))
sex <- rep(c("M","F"), each=length(z)/2)
w <- z2y(z=z, x=x, sex=sex, ref=nl4.wgt)
w <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(age, sds)
data.frame(sub=nl4.wgt$sub,sex=nl4.wgt$sex,round(w,2), row.names=NULL)

# P85 of BMI in 5-8 year old Dutch boys and girls
e <- expand.grid(age=5:8, sex=c("M","F"))
w <- z2y(z=rep(qnorm(0.85),nrow(e)), x=e$age, sex=e$sex, ref=nl4.bmi)
w <- matrix(w, nrow=2, byrow=TRUE)
dimnames(w) <- list(c("boys","girls"),5:8)
w

# data transformation of height z-scores to cm-scale
z <- c(-1.83, 0.09, 2.33, 0.81, -1.20)
x <- c(8.33,  0.23, 19.2, 24.3, 10)
sex <- c("M", "M", "F", "M", "F")
round(z2y(z=z, x=x, sex=sex, ref=nl4.hgt), 1)

# interpolate published height standard
# to daily values, days 0-31, boys
# on centiles -2SD, 0SD and +2SD
days <- 0:31
sds  <- c(-2, 0, +2)
z    <- rep(sds, length(days))
x    <- rep(round(days/365.25,4), each=length(sds))
w    <- z2y(z, x, sex="M", ref=nl4.hgt)
w    <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(days, sds)
w
```

---

z2y   *Convert standard deviation scores (SDS) to measurements*

Description

Converts standard deviation score (SDS) into measurements using an age- and sex-conditional external reference.

Usage

```
z2y(
  z = c(-2, 0, 2),
  x = 1,
  sex = "M",
  sub = "N",
  ref = get("nl4.hgt"),
  dist = "LMS",
  dec = 3,
  sex.fallback = NA,
  sub.fallback = NA
)
```

Arguments

z	A numerical vector containing standard deviation scores that are to be converted. The length `length(z)` determines the size of the output vector.
x	A vector containing the values of the numerical covariate (typically decimal age or height) at which conversion is desired. Values are replicated to match `length(y)`.
sex	A character vector indicating whether the male ("M") of female ("F")reference should be used. Values are replicated to match `length(y)`.
sub	A character vector indicating the level of the sub field of the reference standard defined in `ref`
ref	A data frame containing a factor `sex`, a numerical variable `age` containing the tabulated decimal point ages, and two or more numerical variables with reference values. See details.
dist	A string identifying the type of distribution. Values values are: "NO", "BCCG", "LMS", "BCPE" and "BCT". The default is "LMS".
dec	A scalar value indicating the number of decimals used to round the value.
sex.fallback	The level of the `sex` field used when no match is found. The default `sex.fallback=NA` specifies that unmatched entries should receive a NA value.
sub.fallback	The level of the `sub` field used when no match is found. The default `sub.fallback=NA` specifies that unmatched entries should receive a NA value.

Details

Functions `z2y()` and `y2z()` are the inverse of each other.

The argument `dist` determines the statistical distribution. The possibilities are as follows:

list("\"NO\"") `ref` should contain columns `mean` and `sd`, containing the mean and the standard deviation in the external reference population.

list("\"LMS\"") ref should contain columns L, S and M containing the LMS parameters.

list("\"BCCG\"") ref should contain columns mu, sigma and nu containing the Box-Cox Cole-Green parameters.

list("\"BCPE\"") ref should contain columns mu, sigma, nu and tau containing the Box-Cox Power Exponential parameters.

list("\"BCT\"") ref should contain columns mu, sigma, nu and tau containing the Box-Cox T distribution parameters.

Value

For y2z(): A vector with length(y) elements containing the standard deviation score. For z2y(): A vector with length(z) elements containing quantiles.

Author(s)

Stef van Buuren, 2010

See Also

[y2z](#)

Examples

```
boys <- boys7482

# quantile at SD=0 of age 2 years,
# height Dutch boys
z2y(z=0, x=2)

# same for Dutch girls
z2y(z=0, x=2, sex="F")

# quantile at SD=c(-1,0,1) of age 2 years, BMI Dutch boys
z2y(z=c(-1,0,+1), x=2, ref=nl4.bmi)

# 0SD line (P50) in kg of weight for age in 5-10 year, Dutch boys
z2y(z=rep(0,6), x=5:10, ref=nl4.wgt)

# 95th percentile (P95), age 10 years, wfa, Dutch boys
z2y(z=qnorm(0.95), x=10, ref=nl4.wgt)

# table of P3, P10, P50, P90, P97 of weight for 5-10 year old dutch boys
# age per year
age <- 5:10
p <- c(0.03,0.1,0.5,0.9,0.97)
z <- rep(qnorm(p), length(age))
x <- rep(age, each=length(p))
w <- matrix(z2y(z, x=x, sex="M", ref=nl4.wgt), ncol=length(p),
 byrow=TRUE)
dimnames(w) <- list(age, p)
```

```
round(w,1)

# standard set of Z-scores of weight for all tabulated ages, boys & girls
# and three etnicities
sds <- c(-2.5, -2, -1, 0, 1, 2, 2.5)
age <- nl4.wgt$x
z <- rep(sds, times=length(age))
x <- rep(age, each=length(sds))
sex <- rep(c("M","F"), each=length(z)/2)
w <- z2y(z=z, x=x, sex=sex, ref=nl4.wgt)
w <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(age, sds)
data.frame(sub=nl4.wgt$sub,sex=nl4.wgt$sex,round(w,2), row.names=NULL)

# P85 of BMI in 5-8 year old Dutch boys and girls
e <- expand.grid(age=5:8, sex=c("M","F"))
w <- z2y(z=rep(qnorm(0.85),nrow(e)), x=e$age, sex=e$sex, ref=nl4.bmi)
w <- matrix(w, nrow=2, byrow=TRUE)
dimnames(w) <- list(c("boys","girls"),5:8)
w

# data transformation of height z-scores to cm-scale
z <- c(-1.83, 0.09, 2.33, 0.81, -1.20)
x <- c(8.33,  0.23, 19.2, 24.3, 10)
sex <- c("M", "M", "F", "M", "F")
round(z2y(z=z, x=x, sex=sex, ref=nl4.hgt), 1)

# interpolate published height standard
# to daily values, days 0-31, boys
# on centiles -2SD, 0SD and +2SD
days <- 0:31
sds  <- c(-2, 0, +2)
z    <- rep(sds, length(days))
x    <- rep(round(days/365.25,4), each=length(sds))
w    <- z2y(z, x, sex="M", ref=nl4.hgt)
w    <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(days, sds)
w
```

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