Package ‘AGD’

May 29, 2018

Type Package
Version 0.39
Title Analysis of Growth Data
Date 2018-05-30
Author Stef van Buuren <stef.vanbuuren@tno.nl>
Maintainer Stef van Buuren <stef.vanbuuren@tno.nl>
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://github.com/stefvanbuuren/AGD
BugReports https://github.com/stefvanbuuren/AGD/issues
RoxygenNote 6.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2018-05-29 17:18:28 UTC

R topics documented:

ageGrid ......................................................... 2
boys7482 ...................................................... 3
extractLMS ..................................................... 4
References CDC ............................................... 5
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 default 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
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


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

```r
## 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
f0166r <- 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 = f0166r, 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 = f0166r, data=data.t, flatAge=20)
nl4.hgt.boys.flat

# use log age transformation
data.t <- data.frame(data, t.age = log(data$age))
f0166rlog <- 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 = f0166rlog, 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


See Also

nl4.wgt, nl4.hgt, nl4.bmi, who.wgt
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 \( S \times M \).

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

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


See Also

cdc.wgt, who.wgt

description

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


See Also


---

**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**

```r
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=objc1$mu.x[,xvar.column]` respectively `xvar=objc2$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"`
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.iter=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


See Also

wp
Examples

library(gamlss)
data(abdom)
a <- gamlss(y~cs(x,df=1),sigma.fo=-cs(x,0),family=LO,df=LO,df=LO)
b <- gamlss(y~cs(x,df=3),sigma.fo=-cs(x,1),family=LO,df=LO,df=LO)
coeff1 <- wp.twin(a,b,line=TRUE)
coeff1
rm(a,b,coeff1)

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 \text{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
\text{length}(y).

sex
A character vector indicating whether the male ("M") of female ("F") reference
should be used. Values are replicated to match \text{length}(y).

sub
A character vector indicating the level of the sub field of the reference standard
defined in \text{ref}

ref
A data frame containing a factor \text{sex}, a numerical variable \text{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.\text{fallback}=\text{NA}
specifies that unmatched entries should receive a \text{NA} value.

sub.fallback
The level of the sub field used when no match is found. The default sub.\text{fallback}=\text{NA}
specifies that unmatched entries should receive a \text{NA} value.

tail.adjust
Logical. If \text{TRUE} then the WHO method for tail adjustment is applied. The default is \text{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(""BCTV""")` `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`

Examples

```r
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=n14.bmi))
```
# apply inverse transformation to check calculations
round(z2y(z, age, ref=n14.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=n14.wgt)),2)

# # percentage of children lighter than 15kg at ages 2-5
1 - y2z(y=rep(15,nrow(1)), x=e$age, sex=e$sex, ref=n14.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=n14.hgt)
wgt.z <- y2z(y=boys$wgt, x=boys$age, sex="M", ref=n14.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=n14.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=n14.wgt)

# 95th percentile (P95), age 10 years, wfa, Dutch boys
z2y(z=qnorm(0.95), x=10, ref=n14.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=n14.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)
z2y <- 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(0.33, 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 ex-
ternal 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") or 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=n14.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=n14.wgt)

# 95th percentile (P95), age 10 years, wfa, Dutch boys
z2y(z=qnorm(0.95), x=10, ref=n14.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=n14.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 <- n14.wgt$x
z <- rep(sds, times=length(age))
x <- rep(age, each=length(sds))
sex <- rep(c("M","F"), each=length(z)/2)
w <- z2y(z=z, x=x, sex=sex, ref=n14.wgt)
w <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(age, sds)
data.frame(sub=n14.wgt$sub, sex=n14.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=n14.bmi)
w <- matrix(w, nrow=2, byrow=TRUE)
dimnames(w) <- list(c("boys","girls"),5:8)

# data transformation of height z-scores to cm-scale
z <- c(-1.83, 0.09, 2.33, 0.81, -1.20)
x <- c(0.33, 0.23, 19.2, 24.3, 10)
sex <- c("M", "M", "F", "M", "F")
round(z2y(z=z, x=x, sex=sex, ref=n14.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="M", ref=n14.hgt)
w <- matrix(w, ncol=length(sds), byrow=TRUE)
dimnames(w) <- list(days, sds)
w
Index

*Topic **datasets**
  boys7482, 3
  References CDC, 5
  References NL3, 7
  References NL4, 8
  References WHO, 9

*Topic **distribution**
  ageGrid, 2
  extractLMS, 4
  y2z, 12
  z2y, 15

*Topic **smooth**
  wp.twin, 10

ageGrid, 2
boys7482, 3

cdc.bmi (References CDC), 5
cdc.hgt (References CDC), 5
cdc.wgt, 8–10
cdc.wgt (References CDC), 5

extractLMS, 4

n13.bmi (References NL3), 7
n14.bmi, 6
n14.bmi (References NL4), 8
n14.hdc (References NL4), 8
n14.hgt, 6
n14.hgt (References NL4), 8
n14.hip (References NL4), 8
n14.lgl (References NL4), 8
n14.shf (References NL4), 8
n14.sit (References NL4), 8
n14.wfh (References NL4), 8
n14.wgt, 6, 10
n14.wgt (References NL4), 8
n14.whr (References NL4), 8
n14.wst (References NL4), 8

References CDC, 5
References NL3, 7
References NL4, 8
References WHO, 9

who.bmi (References WHO), 9
who.hdc (References WHO), 9
who.hgt (References WHO), 9
who.wfh (References WHO), 9
who.wfl (References WHO), 9
who.wgt, 6, 8, 9
who.wgt (References WHO), 9
wp, 11
wp.twin, 10

y2z, 12, 17

z2y, 13, 15