

Package ‘tanner’

August 6, 2026

Type Package

Title Puberty Stage Line Diagrams and SDS for Tanner Pubertal Stages

Version 1.8.0

Date 2026-07-18

Description Plots Tanner pubertal stage measurements (genital, pubic hair, testicular volume, breast, menarche) against Dutch 1997 growth-study references as stage line diagrams, and converts observed stages to age-conditional standard deviation scores (SDS). Testicular volume can be entered as a raw orchidometer reading in ml. Implements the method of van Buuren and Ooms (2009) <[doi:10.1002/sim.3567](https://doi.org/10.1002/sim.3567)>.

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URL <https://github.com/growthcharts/tanner>,
<https://growthcharts.org/tanner/>

BugReports <https://github.com/growthcharts/tanner/issues>

Encoding UTF-8

Depends R (>= 3.5.0)

Imports haven

LazyData true

RoxygenNote 7.3.3

Suggests testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-08-06 13:10:02 UTC

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calculate_sds	<i>Calculate the standard deviation score (SDS) of a pubertal stage</i>
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Description

Calculates the SDS for a pubertal stage measurement, given the patient’s age and observed stage, by interpolating between the surrounding reference percentiles.

Usage

```
calculate_sds(age, stage, type, ref = tanner::nl1997)
```

Arguments

age	Vector of patient ages. The length of age determines the length of the return value (see Value below).
stage	Vector of patient stages, the same length as age (one stage per age; not recycled). For type = "tv" this is the raw testicular volume in **ml** , as read off a Prader orchidometer or otherwise measured; it need not be one of the 12 Prader bead volumes (1, 2, 3, 4, 5, 6, 8, 10, 12, 15, 20, 25) — any intermediate value (e.g. 11 or 16 ml) is bracketed between the surrounding reference percentiles. For all other types, stage is the integer Tanner stage (1-5 for "gen", "phb", "bre", "phg"; 1-2 for "men"). A stage shorter or longer than age is not supported: it is silently truncated or padded rather than recycled (e.g. a length-1 stage does <i>not</i> apply to every element of age) and can also produce NAs, a warning, or a "subscript out of bounds" error depending on type – do not rely on any of these behaviors, always pass stage the same length as age.
type	Reference type: one of "gen", "phb", "tv", "bre", "phg" or "men".
ref	Reference data, as produced by nl1997 .

Details

Implements the mid-P value method of van Buuren & Ooms (2009), equation (6): treating the observed stage c as a coarsened version of a continuous latent variable, uniformly distributed within the stage's probability interval $[P(Y < c | X), P(Y < c + 1 | X)]$. The mid-P value $\text{pi}_c = P(Y < c | X) + P(Y = c | X) / 2$ is the mean of that latent variable, and $Z = \text{qnorm}(1 - \text{pi}_c) = \text{qnorm}(1 - (P(Y = c | X) + P(Y >= c + 1 | X)) / 2)$ converts it to a Z-score/SDS. This is why the SDS averages the surrounding-stage percentiles rather than looking up a single stage's percentile directly: the averaging is the mid-P value itself, not an ad hoc smoothing step. The same formula applies to tv 's 12 Prader bead categories, treating each raw ml reading as belonging to the bead-category interval it falls into (see below).

Value

A numeric vector of SDS values, the same length as `age` (one value per element of `age`).

References

van Buuren S, Ooms JCL (2009). Stage line diagram: An age-conditional reference diagram for tracking development. *Statistics in Medicine*, 28(11), 1569-1579. doi:10.1002/sim.3567

Examples

```
# a single boy, genital stage 3 at age 12
calculate_sds(age = 12, stage = 3, type = "gen")

# a boy's genital-stage trajectory over three visits
calculate_sds(age = c(10, 12, 14), stage = c(1, 3, 4), type = "gen")

# testicular volume in ml, interpolated between Prader beads
calculate_sds(age = 13, stage = 11, type = "tv")
```

find_stage_segments	<i>Find segments of constant stage in a vector</i>
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Description

Determines the runs (segments) in `z` over which the value does not change, ignoring missing values. Used by [interpolate_trajectory](#) to split a patient's stage trajectory into per-stage segments.

Usage

```
find_stage_segments(z)
```

Arguments

`z` A vector, typically of pubertal stages.

Value

A logical matrix with one row per segment and one column per element of *z*, where TRUE marks membership of that element in the segment.

interpolate_trajectory

Interpolate a pubertal stage trajectory along reference curves

Description

Computes the x/y coordinates needed to plot a patient's pubertal stage trajectory along the reference curves, including the interpolated segments between measurement ages within the same stage.

Usage

```
interpolate_trajectory(refx, refy, patx, pats)
```

Arguments

refx	Vector of reference ages.
refy	Matrix of reference values, one column per stage.
patx	Vector of patient ages.
pats	Vector of patient stages (column indices into refy).

Value

A list with components *x*, *y*, *stage* and *patient* (a logical flag indicating whether a point is an observed patient measurement or an interpolated reference point).

Examples

```
# reference ages and genital stage percentile curves for boys
refx <- seq(8, 21, 0.25)
refy <- tanner::n11997_lines$gen[, -1]

# a boy observed at G1 at age 10, still G1 at age 11, then G3 at age 13
patx <- c(10, 11, 13)
pats <- c(1, 1, 3)

curve <- interpolate_trajectory(
  refx = refx, refy = refy, patx = patx, pats = pats
)
curve

# curve$patient flags the observed measurements; the other points
# interpolate along the reference curve between them
plot(curve$x, curve$y, type = "l")
points(curve$x[curve$patient], curve$y[curve$patient], pch = 16)
```

nl1997*Dutch 1997 pubertal stage references*

Description

Reference percentiles for pubertal stage variables by age, based on the Dutch 1997 growth study (Fredriks et al., 2000). Used by [calculate_sds](#) to convert an observed age/stage combination into a standard deviation score.

Usage

nl1997

Format

A list with six components, one per pubertal stage variable: gen, phb, tv, bre, phg and men. Each component is a data frame whose first column is age and whose remaining columns hold the age at which 50 the reference population reaches each stage.

Source

Fredriks AM, van Buuren S, Burgmeijer RJ, et al. (2000). Continuing positive secular growth change in The Netherlands 1955-1997. *Pediatric Research*, 47(3), 316-323. Percentiles were refit in R from data-raw/data/pub.ref.1997r.txt, correcting testis-volume (tv) fitting errors present in the original S-Plus-fitted pub.ref.1997.txt; the genital-stage columns match Table 5 of van Buuren S (2014). Growth charts of human development. *Statistical Methods in Medical Research*, 23(4), 346-368. doi:10.1177/0962280212473300

nl1997_lines*Dutch 1997 pubertal stage reference lines*

Description

Reference curves, expressed as standard deviation scores (SDS) by age, derived from [nl1997](#). Used by [plot_stadia](#) to draw the percentile lines on a puberty stadia plot.

Usage

nl1997_lines

Format

A list with six components, one per pubertal stage variable: gen, phb, tv, bre, phg and men. Each component is a matrix whose first column is age and whose remaining columns hold the SDS curve for each stage.

Source

Derived from [n11997](#); see `data-raw/R/create_references.R`.

<code>plotdumpdir</code>	<i>Directory where generated plot and data files are written</i>
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Description

Set on package load to a "plotfiles" subdirectory of `tempdir()`. Used by the rApache handlers `plotter` and `plotterpro` as the destination directory for generated PDF, PNG, CSV and TXT files, and by `upload_tryCatch_pro` as the destination for uploaded data files and the .RData file it hands off to `plotterpro`. The directory itself is only created lazily, on the first actual write inside these handlers – not merely by loading the package – so calling `library(tanner)` to use unrelated functions like `calculate_sds` has no disk side effects. Reassign this before calling the handlers to change where they read/write.

Usage

```
plotdumpdir
```

Format

An object of class character of length 1.

<code>plotter</code>	<i>rApache handler for the puberty plot webapp</i>
----------------------	--

Description

Reads pubertal staging data from the rApache GET request, builds a puberty plot and writes it to PDF and PNG files in `plotdumpdir`. This function is intended to be called from the rApache web frontend shipped in `inst/webapps`, not interactively from R.

Usage

```
plotter()
```

Value

Invisibly returns the generated file name stem (also written, via `cat()`, to the response – under rApache, standard output *is* the HTTP response body).

See Also

Other webapp-internals: `plotterpro()`, `upload_tryCatch_pro()`

plotterpro

rApache handler for the professional puberty plot webapp

Description

Reads a saved data file (written by [upload_tryCatch_pro](#)) from [plotdumpdir](#), as referenced in the rApache POST request, calculates SDS values for the pubertal stages, and writes the results and a puberty plot to CSV, TXT and PDF files, also in [plotdumpdir](#). This function is intended to be called from the rApache web frontend shipped in `inst/webapps`, not interactively from R.

Usage

```
plotterpro()
```

Value

Invisibly returns the JSON response string (also written, via `cat()`, to the response – under rApache, standard output *is* the HTTP response body).

See Also

Other webapp-internals: [plotter\(\)](#), [upload_tryCatch_pro\(\)](#)

plot_stadia

Plot a puberty stadia diagram

Description

Plots Tanner pubertal stage measurements for one or more persons against the Dutch 1997 reference curves, expressed as standard deviation scores (SDS) by age.

Usage

```
plot_stadia(
  data = pub.data,
  persons = unique(data$id),
  plotline = c(TRUE, FALSE, FALSE),
  type = c(TRUE, FALSE, FALSE),
  colors = c("#0060A0", "#00A000", "#A00000"),
  overlay = FALSE,
  ovsex = "M",
  ref = tanner::nl1997_lines,
  title = "Tanner pubertal stages - Patient ",
  padid = TRUE
)
```

Arguments

data	A data frame with columns id, age, sex and the pubertal stage variables (gen, phb, tv for males; bre, phg, men for females). tv (testicular volume) is the raw reading in ml — any value, not just the 12 Prader orchidometer bead volumes (1, 2, 3, 4, 5, 6, 8, 10, 12, 15, 20, 25) — the trajectory is traced along the nearest reference curve. The other stage variables are the integer Tanner stage.
persons	Vector of person identifiers (values of data\$id) to plot.
plotline	Logical vector of length 3 indicating which reference lines to draw.
type	Logical vector of length 3 indicating which pubertal stage variables to plot.
colors	Character vector of length 3 with the colors used for the three pubertal stage variables.
overlay	If TRUE, plot all persons on a single graph.
ovsex	Sex ("M" or "F") used to select the reference lines when overlay = TRUE.
ref	Reference data used to draw the reference lines, as produced by nl1997_lines .
title	Plot title.
padid	If TRUE, append the person identifier to the title.

Value

Invisibly returns NULL; the function draws on the current graphics device.

plot_stadia_data	<i>Draw a person's pubertal stage trajectory on a puberty stadia plot</i>
------------------	---

Description

Internal helper used by [plot_stadia](#) to draw a single person's pubertal stage trajectory, interpolated along the reference curves, on the current plot.

Usage

```
plot_stadia_data(ages, pubs, sex, type, colors, ref)
```

Arguments

ages	Vector of ages at measurement.
pubs	Data frame with the pubertal stage variables for this person; tv is the raw testicular volume in ml (see plot_stadia).
sex	"M" or "F".
type	Logical vector of length 3 indicating which pubertal stage variables to plot.
colors	Character vector of length 3 with the colors for the three pubertal stage variables.
ref	Reference data, as produced by nl1997_lines .

Value

Invisibly returns NULL; the function draws on the current graphics device.

plot_stadia_general	<i>Draw the frame, percentile bands and axes of a puberty stadia plot</i>
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Description

Internal helper used by `plot_stadia` to draw the plot frame, the early/late percentile bands, the TNO logo and the axes.

Usage

```
plot_stadia_general(
  i = " ",
  opt = c(TRUE, TRUE, TRUE, TRUE, TRUE),
  title = " ",
  padid = TRUE
)
```

Arguments

<code>i</code>	Person identifier appended to the title when <code>padid = TRUE</code> .
<code>opt</code>	Logical vector of length 5 selecting which elements to draw: frame and title, extreme percentile regions, TNO logo, axes, margin reference text.
<code>title</code>	Plot title.
<code>padid</code>	If TRUE, append <code>i</code> to the title.

Value

Invisibly returns NULL; the function draws on the current graphics device.

plot_stadia_lines	<i>Draw reference percentile lines on a puberty stadia plot</i>
-------------------	---

Description

Internal helper used by `plot_stadia` to add the Dutch reference lines for males (Genital, Pubic hair, Testis) or females (Breast, Pubic hair, Menarche) to the current plot.

Usage

```
plot_stadia_lines(plotlines, colors, sex, ref)
```

Arguments

plotlines	Logical vector of length 3 indicating which reference lines to draw.
colors	Character vector of length 3 with the colors for the three pubertal stage variables.
sex	"M" or "F".
ref	Reference data, as produced by nl1997_lines .

Value

Invisibly returns NULL; the function draws on the current graphics device.

tnologo

Draw the TNO logo

Description

Plots the current TNO logo (upright "TN" wordmark plus a ring-shaped "O") using the current coordinate system. Used by [plot_stadia_general](#) to brand the puberty stadia plots.

Usage

```
tnologo(col = "darkblue", bcol = "white", at = c(0, 0), size = 300, aspect = 1)
```

Arguments

col	Foreground color.
bcol	Background color.
at	(x, y) coordinate of the lower left corner of the logo.
size	Horizontal size, measured in the units of the x-axis.
aspect	Unit size of the y-axis divided by the unit size of the x-axis.

Value

Invisibly returns NULL; the function draws on the current graphics device.

upload_tryCatch_pro	<i>rApache handler for uploading puberty data files</i>
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Description

Validates an uploaded data file (referenced in the rApache FILES request), saves it as an .RData file in [plotdumpdir](#), and writes a JSON summary of the data per person to the response. This function is intended to be called from the rApache web frontend shipped in `inst/webapps`, not interactively from R.

Usage

```
upload_tryCatch_pro()
```

Value

Invisibly returns the HTML/JSON response string (also written, via `cat()`, to the response – under rApache, standard output *is* the HTTP response body).

See Also

Other webapp-internals: [plotter\(\)](#), [plotterpro\(\)](#)

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