

Package ‘cNORM’

October 3, 2026

Title Continuous Norming

Version 3.7.0

Description Generates continuous test norms in psychometrics and biometrics, and analyzes model fit. The package offers distribution-free modeling using Taylor polynomials, as well as parametric modeling using the beta-binomial distribution (for bounded accuracy tests), the Conway-Maxwell-Poisson distribution (for speeded tests and count data with over-, equi-, or under-dispersion), and the 'Sinh-Arcsinh' (SHASH) distribution. Originally developed for psychological and educational assessment, it is applicable to a wide range of mental, physical, or other test scores dependent on continuous or discrete explanatory variables. The package minimizes deviations from representativeness in subsamples, interpolates between discrete levels of explanatory variables, and significantly reduces the required sample size compared to conventional norming per age group. cNORM enables graphical and analytical evaluation of model fit, accommodates a wide range of scales including those with negative and descending values, and supports conventional norming. It generates norm tables including confidence intervals and provides methods for addressing representativeness issues through Iterative Proportional Fitting. Based on Lenhard et al. (2016) <[doi:10.1177/1073191116656437](https://doi.org/10.1177/1073191116656437)>, Lenhard et al. (2019) <[doi:10.1371/journal.pone.0222279](https://doi.org/10.1371/journal.pone.0222279)>, Lenhard and Lenhard (2021) <[doi:10.1177/0013164420928457](https://doi.org/10.1177/0013164420928457)>, and Gary et al. (2023) <[doi:10.1007/s00181-023-02456-0](https://doi.org/10.1007/s00181-023-02456-0)>.

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URL https://www.psychometrica.de/cNorm_en.html,
<https://github.com/WLenhard/cNORM>

BugReports <https://github.com/WLenhard/cNORM/issues>

Depends R (>= 4.0.0)

Imports ggplot2 (>= 3.5.0), leaps (>= 3.1), grDevices, parallel,
stats, utils

Suggests DT, haven, foreign, knitr, markdown, numDeriv, readxl,
rmarkdown, shiny, shinycssloaders, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

Language en-US

LazyData true

LazyDataCompression xz

Config/roxygen2/version 8.0.0

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-10-03 12:20:02 UTC

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autoselect.betabinomial

Automatic model selection for beta-binomial continuous norming via BIC

Description

Selects polynomial degrees for the two components of a beta-binomial model (α/β when mode = 2 or μ/σ when mode = 1) by minimizing BIC over the full grid of degree combinations.

Usage

```
autoselect.betabinomial(
  age,
  score,
  n = NULL,
  weights = NULL,
  mode = 2,
  max_alpha = 4,
  max_beta = 4,
  min_alpha = 1,
  min_beta = 1,
  control = NULL,
  scale = "T",
  parallel = TRUE,
  n_cores = NULL,
  plot = TRUE,
  verbose = TRUE
)
```

Arguments

age, score	Numeric vectors of predictor and response values.
n	Maximum score. Defaults to <code>max(score)</code> .
weights	Optional numeric vector of weights.
mode	1 for μ/σ , 2 for direct α/β (default).
max_alpha, max_beta	Maximum polynomial degrees. Default 4.
min_alpha, min_beta	Minimum polynomial degrees. Default 1.
control	Optional control list passed to <code>optim</code> .
scale	Norm scale (default "T").
parallel	Logical; attempt parallel execution. Default TRUE.
n_cores	Number of cores. Defaults to all logical cores.
plot	Logical; plot the selected model. Default TRUE.
verbose	Logical; print progress. Default TRUE.

Details

Parallel execution is attempted by default. If the workers cannot access the **cNORM** namespace (e.g. during `devtools::load_all()`), the function transparently falls back to sequential execution.

Value

The selected fitted model, with an additional element selection containing the evaluation table and selection details.

autoselect.cmp	<i>Automatic model selection for CMP continuous norming via BIC</i>
----------------	---

Description

Selects the polynomial degrees for the two components of a `cnorm.cmp` model (μ, ν) by minimizing BIC over a full grid.

Usage

```
autoselect.cmp(
  age,
  score,
  weights = NULL,
  max_mu = 4,
  max_nu = 2,
  min_mu = 1,
  min_nu = 0,
```

```

nu = 1,
control = NULL,
scale = "T",
max_terms = NULL,
tol = 1e-12,
parallel = TRUE,
n_cores = NULL,
plot = TRUE,
verbose = TRUE,
max_score = NULL,
warm_start = TRUE
)

```

Arguments

age, score	Numeric vectors of predictor and response values (counts).
weights	Optional numeric vector of observation weights.
max_mu, max_nu	Maximum polynomial degrees for log(mu) and log(nu). Defaults: 4, 2.
min_mu	Minimum polynomial degree for log(mu) (default 1).
min_nu	Minimum degree for log(nu). -1: fixed nu is included in the search; 0 (default): constant estimated nu is the simplest candidate.
nu	Value of the dispersion used whenever a candidate has a fixed nu (degree -1). Default 1.
control	Optional control list passed to optim .
scale	Norm scale (default "T").
max_terms, tol	Passed to cnorm.cmp .
parallel	Logical; attempt parallel execution. Default TRUE.
n_cores	Number of cores. Defaults to the number of logical cores minus one.
plot	Logical; plot the selected model. Default TRUE.
verbose	Logical; print progress. Default TRUE.
max_score	Optional ceiling for a right-truncated model, see cnorm.cmp .
warm_start	Logical; start each fit from the solution of the next lower degree of mu. Default TRUE.

Details

The degree for ν has three kinds of values: -1 fixes the dispersion at the value given in nu (nu_degree = NULL in [cnorm.cmp](#); nu = 1 is the Poisson model), 0 estimates a constant dispersion, and values ≥ 1 let the dispersion vary with age.

Selection rule. Candidates that converged and whose log(nu) predictor stays inside its admissible range at all observed ages ("clean" candidates) are preferred: the clean candidate with the lowest BIC is selected. Only if no clean candidate exists, the best of the remaining candidates (non-converged or at the nu boundary) is selected and a warning is issued. Warnings of the individual fits are collected in `$selection$evaluated` instead of being discarded.

Warm starts. With `warm_start = TRUE` (default), each fit starts from the solution of the next lower degree of μ (same degree of ν), which is faster and more reliable. Parallelization is then done across the degrees of ν (one chain per degree). With `warm_start = FALSE`, all candidates are fitted independently and in parallel.

Parallel execution is attempted by default. If the workers cannot access the **cnORM** namespace, the function transparently falls back to sequential execution.

Value

The selected fitted `cnormCMP` model with an additional element `$selection` containing:

- `evaluated`: data frame of every combination tried, sorted by BIC, with the columns `status`, `at_bound`, `n_warnings` and `message`.
- `warnings`: named list with the warnings of each candidate.
- `selected`: list with the chosen degrees and BIC.

See Also

[cnorm.cmp](#), [autoselect.shash](#)

Examples

```
## Not run:
m <- autoselect.cmp(speeeded$age, speeeded$raw)
m$selection$evaluated
summary(m, age = speeeded$age, score = speeeded$raw)

# Include the Poisson model (nu fixed at 1) as a candidate
m <- autoselect.cmp(speeeded$age, speeeded$raw, min_nu = -1)

## End(Not run)
```

autoselect.shash	<i>Automatic model selection for SinH-ArcSinH continuous norming via BIC</i>
------------------	--

Description

Selects the polynomial degrees for the four components of a [cnorm.shash](#) model (μ , σ , ϵ , δ) by minimizing BIC over a full grid.

Usage

```

autoselect.shash(
  age,
  score,
  weights = NULL,
  max_mu = 4,
  max_sigma = 3,
  max_epsilon = 3,
  max_delta = 1,
  min_mu = 1,
  min_sigma = 1,
  min_epsilon = 1,
  min_delta = 0,
  delta = 1,
  control = NULL,
  scale = "T",
  parallel = TRUE,
  n_cores = NULL,
  plot = TRUE,
  verbose = TRUE
)

```

Arguments

age, score	Numeric vectors of predictor and response values.
weights	Optional numeric vector of observation weights.
max_mu, max_sigma, max_epsilon, max_delta	Maximum polynomial degrees for the four shash parameters. Defaults: 4, 3, 3, 1.
min_mu, min_sigma, min_epsilon	Minimum polynomial degrees (default 1).
min_delta	Minimum degree for δ . 0 (default) means the fixed-delta variant is included in the search.
delta	Value of δ used whenever the candidate uses <code>delta_degree = 0</code> (i.e. fixed delta). Default 1.
control	Optional control list passed to optim .
scale	Norm scale (default "T").
parallel	Logical; attempt parallel execution. Default TRUE.
n_cores	Number of cores. Defaults to all logical cores.
plot	Logical; plot the selected model. Default TRUE.
verbose	Logical; print progress. Default TRUE.

Details

A degree of 0 for δ is interpreted as a **fixed** δ (passed to [cnorm.shash](#) as `delta_degree = NULL`) with value taken from the `delta` argument. This allows the grid search to choose between a fixed and a varying tail-weight model.

Parallel execution is attempted by default. If the workers cannot access the **cNORM** namespace, the function transparently falls back to sequential execution.

Value

The selected fitted cnormShash model with an additional element \$selection containing:

- evaluated: data frame of every combination tried, sorted by BIC.
- selected: list with the chosen degrees and BIC.

See Also

[cnorm.shash](#), [autoselect.betabinomial](#)

Examples

```
## Not run:
m <- autoselect.shash(elfe$group, elfe$raw)
m$selection$evaluated
summary(m, age = elfe$group, score = elfe$raw)

## End(Not run)
```

bestModel

Determine Regression Model

Description

Computes Taylor polynomial regression models by evaluating a series of models with increasing number of predictors. It aims to find a consistent model that effectively captures the variance in the data. It draws on the regsubsets function from the leaps package, builds up to 10 models per number of predictors, screens them for model consistency (monotonicity of the mapping between norm score and raw score over the complete age range) and selects the consistent model with the highest R^2 . This automatic model selection should usually be accompanied by visual inspection of the percentile plots and assessment of fit statistics. Set R^2 or the number of terms manually to retrieve a more parsimonious model, if desired.

Usage

```
bestModel(
  data,
  raw = NULL,
  R2 = NULL,
  k = NULL,
  t = NULL,
  predictors = NULL,
  terms = 0,
```

```

weights = NULL,
force.in = NULL,
plot = TRUE,
extensive = TRUE,
averaging = FALSE,
minDip = 0.01
)

```

Arguments

data	Preprocessed dataset with 'raw' scores, powers, interactions, and usually an explanatory variable (like age).
raw	Name of the raw score variable (default: 'raw').
R2	Adjusted R ² stopping criterion for model building.
k	Power constant influencing model complexity (default: taken from the data preparation, max: 6).
t	Age power parameter. If unset, taken from the data preparation (default 3).
predictors	List of predictors or regression formula for model selection. Overrides 'k' and can include additional variables.
terms	Desired number of terms in the model.
weights	Optional case weights. If set to FALSE, default weights (if any) are ignored.
force.in	Variables forcibly included in the regression.
plot	If TRUE (default), displays a percentile plot of the model and information about the regression object. FALSE turns off plotting and report.
extensive	If TRUE (default), screen models for consistency and - if possible - exclude inconsistent ones.
averaging	If TRUE (default FALSE), apply BIC-weighted model averaging across the consistency-screened candidate models instead of selecting a single model. Requires extensive = TRUE and age-based norming.
minDip	Tolerance for monotonicity check. Allow small violations (default: .01 or 1 for strict checking).

Details

The functions `rankBySlidingWindow`, `rankByGroup`, `bestModel`, `computePowers` and `prepareData` are usually not called directly, but accessed through other functions like `cnorm`.

Additional functions like `plotSubset(model)` and `cnorm.cv` can aid in model evaluation.

If `averaging = TRUE`, the final coefficients are not taken from a single selected model, but computed as a BIC-weighted average across all consistency-screened candidate models (weights $w_j \propto \exp(-\Delta BIC_j/2)$). Since a convex combination of functions that are all monotone in the same direction is itself monotone, the averaged model is guaranteed to remain consistent, while reducing model selection variance. This replaces the deprecated subsampling approach.

Value

The model. Further exploration can be done using `plotSubset(model)` and `plotPercentiles(data, model)`.

See Also

`plotSubset`, `plotPercentiles`, `plotPercentileSeries`, `checkConsistency`

Other model: `checkConsistency()`, `cnorm.cv()`, `derive()`, `modelSummary()`, `print.cnorm()`, `printSubset()`, `rangeCheck()`, `regressionFunction()`, `summary.cnorm()`, `weightedAverageModel()`

Examples

```
## Not run:
# It is not recommended to directly use this function. Rather use 'cnorm' instead.
normData <- prepareData(elfe)
model <- bestModel(normData)
plotSubset(model)
plotPercentiles(buildCnormObject(normData, model))

# Specifying variables explicitly
preselectedModel <- bestModel(normData, predictors = c("L1", "L3", "L1A3", "A2", "A3"))
print(regressionFunction(preselectedModel))

## End(Not run)
```

betaCoefficients

Compute Parameters of a Beta Binomial Distribution

Description

This function calculates the α (a) and β (b) parameters of a beta binomial distribution, along with the mean (m) and standard deviation (sd) based on the input vector x and the maximum number n, using the method of moments.

Usage

```
betaCoefficients(x, n = NULL)
```

Arguments

x	A numeric vector of non-negative integers representing observed counts.
n	The maximum number or the maximum possible value of x. If not specified, uses <code>max(x)</code> instead.

Details

The beta-binomial distribution is a discrete probability distribution that models the number of successes in a fixed number of trials, where the probability of success varies from trial to trial. This variability in success probability is modeled by a beta distribution. Such a calculation is particularly relevant in scenarios where there is heterogeneity in success probabilities across trials, which is common in real-world situations, as for example the number of correct solutions in a psychometric test, where the test has a fixed number of items.

Value

A numeric vector containing the calculated parameters in the following order: alpha (a), beta (b), mean (m), standard deviation (sd), and the maximum number (n). If the method of moments is degenerate (mean at the boundary of the support or a non-positive moment denominator), alpha and beta are returned as NA with a warning. Non-positive estimates (indicating dispersion incompatible with a beta-binomial distribution) are returned as-is with a warning.

buildCnormObject	<i>Build cnorm object from data and bestModel model object</i>
------------------	--

Description

Helper function to build a cnorm object from a data object and a model object from the bestModel function for compatibility reasons.

Usage

```
buildCnormObject(data, model)
```

Arguments

data	A data object from 'prepareData', or from 'rankByGroup' and 'computePower'
model	Object obtained from the bestModel function

Value

A cnorm object

Examples

```
## Not run:
data <- prepareData(elfe)
model <- bestModel(data, k = 4)
model.cnorm <- buildCnormObject(data, model)

## End(Not run)
```

calcPolyInL	<i>Internal function for retrieving regression function coefficients at specific age</i>
-------------	--

Description

The function is an inline for searching zeros in the inverse regression function. It collapses the regression function at a specific age and simplifies the coefficients.

Usage

```
calcPolyInL(raw, age, model)
```

Arguments

raw	The raw value (subtracted from the intercept)
age	The age
model	The cNORM regression model

Value

The coefficients

calcPolyInLBase2	<i>Internal function for retrieving regression function coefficients at specific age</i>
------------------	--

Description

The function is an inline for searching zeros in the inverse regression function. It collapses the regression function at a specific age and simplifies the coefficients. Optimized version of the prior 'calcPolyInLBase'

Usage

```
calcPolyInLBase2(raw, age, coeff, k)
```

Arguments

raw	The raw value (subtracted from the intercept)
age	The age
coeff	The cNORM regression model coefficients
k	The cNORM regression model power parameter

Value

The coefficients

 CDC

BMI growth curves from age 2 to 25

Description

By the courtesy of the Center of Disease Control (CDC), cNORM includes human growth data for children and adolescents age 2 to 25 that can be used to model trajectories of the body mass index and to estimate percentiles for clinical definitions of under- and overweight. The data stems from the NHANES surveys in the US and was published in 2012 as public domain. The data was cleaned by removing missing values and it includes the following variables from or based on the original dataset.

Usage

CDC

Format

A data frame with 45053 rows and 7 variables:

age continuous age in years, based on the month variable

group age group; chronological age in years at the time of examination

month chronological age in month at the time of examination

sex sex of the participant, 1 = male, 2 = female

height height of the participants in cm

weight weight of the participants in kg

bmi the body mass index, computed by $(\text{weight in kg})/(\text{height in m})^2$

A data frame with 45035 rows and 7 columns

References

Center for Disease Control and Prevention (2012). National Health and Nutrition Examination Survey: Questionnaires, datasets and related documentation. U.S. Department of Health and Human Services (original source not available anymore).

checkConsistency	<i>Check the consistency of the norm data model</i>
------------------	---

Description

While abilities increase and decline over age, within one age group, the norm scores always have to show a monotonic increase or decrease with increasing raw scores. Violations of this assumption are an indication for problems in modeling the relationship between raw and norm scores. There are several reasons, why this might occur:

1. Vertical extrapolation: Choosing extreme norm scores, e. g. values $-3 \leq x$ and $x \geq 3$. In order to model these extreme values, a large sample dataset is necessary.
2. Horizontal extrapolation: Taylor polynomials converge in a certain radius. Using the model values outside the original dataset may lead to inconsistent results.
3. The data cannot be modeled with Taylor polynomials, or you need another power parameter (k) or R2 for the model.

Usage

```
checkConsistency(  
  model,  
  minAge = NULL,  
  maxAge = NULL,  
  minNorm = NULL,  
  maxNorm = NULL,  
  minRaw = NULL,  
  maxRaw = NULL,  
  stepAge = NULL,  
  stepNorm = 1,  
  method = c("analytic", "grid"),  
  warn = FALSE,  
  silent = FALSE,  
  minDip = 0.01  
)
```

Arguments

model	The model from the bestModel function or a cnorm object
minAge	Age to start with checking
maxAge	Upper end of the age check
minNorm	Lower end of the norm value range
maxNorm	Upper end of the norm value range
minRaw	clipping parameter for the lower bound of raw scores
maxRaw	clipping parameter for the upper bound of raw scores

stepAge	Stepping parameter for the age check. If NULL, 8 equidistant age points are used. Lower values indicate higher precision.
stepNorm	Stepping parameter for the norm table check within age (only used with method = "grid")
method	Monotonicity ccheck. Either "analytic" (default; exact within age via polynomial derivative roots) or "grid" (numerical check on a norm score grid)
warn	Retained for backwards compatibility (violations below numerical tolerance are always suppressed)
silent	turn off messages
minDip	Tolerance for monotonicity check. Allow small violations (default: .01 or 1 for strict checking).

Details

In general, extrapolation (point 1 and 2) can carefully be done to a certain degree outside the original sample, but it should in general be handled with caution. Please note that at extreme values, the models most likely become independent and it is thus recommended to restrict the norm score range to the relevant range of abilities, e.g. ± 2.5 SD via the minNorm and maxNorm parameter.

With method = "analytic" (default), monotonicity within each age is verified exactly: since the model is polynomial in the norm score L, the real roots of its derivative are computed via polyroot and the sign of the derivative is checked between consecutive roots. This detects even narrow violations that a coarse norm score grid can miss. Age remains discretized; violations that are entirely clipped by the raw score bounds are ignored. method = "grid" reproduces the classical numerical check and is used automatically as a fallback for models with non-Taylor predictors.

Value

Boolean, indicating model violations (TRUE) or no problems (FALSE)

See Also

Other model: [bestModel\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

Examples

```
## Not run:
model <- cnorm(raw = elfe$raw, group = elfe$group, plot = FALSE)
modelViolations <- checkConsistency(model, minNorm = 25, maxNorm = 75)
plotDerivative(model, minNorm = 25, maxNorm = 75)

## End(Not run)
```

cmp

*Conway-Maxwell-Poisson (CMP) Distribution***Description**

Probability mass function, distribution function, quantile function and random generation for the Conway-Maxwell-Poisson distribution in the (mu, nu) parameterization used by [cnorm.cmp](#):

$$P(Y = y) \propto (\mu^y / y!)^\nu.$$

The classical rate parameter is $\lambda = \mu^\nu$. For nu = 1, the distribution is the Poisson distribution with mean mu.

Usage

```
dcmp(x, mu = 1, nu = 1, log = FALSE, max_score = Inf)
```

```
pcmp(q, mu = 1, nu = 1, lower.tail = TRUE, log.p = FALSE, max_score = Inf)
```

```
qcmp(p, mu = 1, nu = 1, lower.tail = TRUE, log.p = FALSE, max_score = Inf)
```

```
rcmp(n, mu = 1, nu = 1, max_score = Inf)
```

Arguments

x, q	vector of quantiles (non-negative integers for dcmp).
mu	location parameter (> 0, default 1); approximately the mean, $E(Y) \approx \mu - (\nu - 1)/(2\nu)$ (untruncated case).
nu	dispersion parameter (> 0, default 1). nu < 1: over-dispersion (variance > mean); nu > 1: under-dispersion (variance < mean).
log, log.p	logical; if TRUE, probabilities are given as log(p).
max_score	optional ceiling M . If finite, the distribution is right-truncated to $\{0, 1, \dots, M\}$ (default Inf: no truncation).
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise $P[X > x]$.
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required.

Details

The normalizing constant is evaluated by a vectorized, adaptively truncated series with a rigorous geometric tail bound (relative error < 1e-12). The quantile function is computed by inversion of the cumulative sums (the cumulative distribution is computed only once per distinct pair (mu, nu)), and random numbers are generated by inversion.

Value

dcmp gives the mass, pcmp the distribution function, qcmp the quantile function, and rcmp generates random deviates.

Name collision

COMpoissonReg exports functions with the same names but the arguments (λ , ν). If both packages are attached, the one attached last masks the other, and the same call is silently interpreted with a different parameterization. Use `cnorm::dcmp()` etc. explicitly, or convert with $\lambda = \mu^\nu$.

References

Shmueli, G., Minka, T. P., Kadane, J. B., Borle, S., & Boatwright, P. (2005). A useful distribution for fitting discrete data: revival of the Conway-Maxwell-Poisson distribution. *Journal of the Royal Statistical Society C*, 54(1), 127-142.

Examples

```
# Equals the Poisson distribution for nu = 1
all.equal(dcmp(0:20, mu = 8, nu = 1), dpois(0:20, 8))

# Under-dispersed (nu = 3) and over-dispersed (nu = 0.5) counts with similar mean
x <- rcmp(1000, mu = 20, nu = 3)
c(mean(x), var(x))
y <- rcmp(1000, mu = 20, nu = 0.5)
c(mean(y), var(y))

qcmp(c(0.025, 0.5, 0.975), mu = 20, nu = 3)
pcmp(20, mu = 20, nu = 3)

# Right-truncated at 25
sum(dcmp(0:25, mu = 20, nu = 1, max_score = 25))
```

cnorm

Continuous Norming

Description

Conducts continuous norming in one step and returns an object including ranked raw data and the continuous norming model. Please consult the function description of 'rankByGroup', 'rankBySlidingWindow' and 'bestModel' for specifics of the steps in the data preparation and modeling process. In addition to the raw scores, either provide

- a numeric vector for the grouping information (group)
- a numeric age vector and the width of the sliding window (age, width)

for the ranking of the raw scores. You can adjust the grade of smoothing of the regression model by setting the `k` and `terms` parameter. In general, increasing `k` to more than 4 and the number of terms lead to a higher fit, while lower values lead to more smoothing. The power parameter for the age trajectory can be specified independently by `t`. If both parameters are missing, `cnorm` uses `k = 5` and `t = 3` by default.

Usage

```
cnorm(
  raw = NULL,
  group = NULL,
  age = NULL,
  width = NA,
  weights = NULL,
  scale = "T",
  method = 4,
  descend = FALSE,
  k = NULL,
  t = NULL,
  terms = 0,
  R2 = NULL,
  plot = TRUE,
  extensive = TRUE,
  averaging = FALSE,
  minDip = 0.01
)
```

Arguments

<code>raw</code>	Numeric vector of raw scores
<code>group</code>	Numeric vector of grouping variable, e.g. grade. If no group or age variable is provided, conventional norming is applied.
<code>age</code>	Numeric vector with chronological age. If used without <code>'group'</code> , please additionally specify <code>'width'</code> .
<code>width</code>	Size of the sliding window in case an age vector is used.
<code>weights</code>	Optional numeric vector of case weights for post-stratification.
<code>scale</code>	Type of norm scale, either "T" (default), "IQ", "z" or "percentile" (= no transformation); a numeric vector with mean and SD can also be provided, e.g. <code>'c(10, 3)'</code> for Wechsler scale index points.
<code>method</code>	Ranking method in case of ties; an integer index from 1 (Blom 1958) through 7 (Yu & Huang 2001). Default is 4 (Rankit).
<code>descend</code>	If TRUE, inverts the ranking order so that higher raw scores receive lower norm scores (e.g. for error scores).
<code>k</code>	Power degree for the location dimension (max 6).
<code>t</code>	Power degree for the age dimension (max 6).
<code>terms</code>	If > 0, fix the model to this number of terms.

R2	Stopping criterion (adjusted R-squared) for model selection.
plot	If TRUE (default), display percentile plot and report. Setting it to FALSE as well deactivates potential user interactions.
extensive	If TRUE (default), screen models for monotonic consistency.
averaging	If TRUE (default FALSE), apply BIC-weighted model averaging across the consistency-screened candidate models instead of selecting a single model. Requires extensive = TRUE and age-based norming.
minDip	Tolerance for monotonicity check. Allow small violations (default: .01 or 1 for strict checking).

Value

cnorm object including the ranked raw data and the regression model.

References

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6. Lenhard, A., Lenhard, W., Gary, S. (2018). Continuous Norming (cNORM). The Comprehensive R Network, Package cNORM, available: <https://CRAN.R-project.org/package=cNORM>
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See Also

rankByGroup, rankBySlidingWindow, computePowers, bestModel

Examples

```
## Not run:
# Conventional norming
cnorm(raw = elfe$raw)
```

```

# Continuous norming via group
m1 <- cnorm(raw = elfe$raw, group = elfe$group)

# Continuous norming via continuous age + sliding window
m2 <- cnorm(raw = ppvt$raw, age = ppvt$age, width = 1)

# Norm tables with confidence intervals
normTable(c(2.125, 2.375, 2.625), m1, CI = .9, reliability = .95)
rawTable (c(2.125, 2.375, 2.625), m1, CI = .9, reliability = .95)

## End(Not run)

```

cnorm.betabinomial	<i>Fit a beta-binomial regression model for continuous norming</i>
--------------------	--

Description

This function fits a beta-binomial regression model where both the α and β parameters of the beta-binomial distribution are modeled as polynomial functions of the predictor variable (typically age). Setting mode to 1 fits a beta-binomial model on the basis of μ and σ , setting it to 2 (default and recommended) fits a beta-binomial model directly on the basis of α and β .

Usage

```

cnorm.betabinomial(
  age,
  score,
  n = NULL,
  weights = NULL,
  mode = 2,
  alpha = 3,
  beta = 3,
  control = NULL,
  scale = "T",
  plot = TRUE
)

```

Arguments

age	A numeric vector of predictor values (e.g., age).
score	A numeric vector of response values.
n	The maximum score (number of trials in the beta-binomial distribution). If NULL, max(score) is used.
weights	A numeric vector of weights for each observation. Default is NULL (equal weights).

mode	Integer specifying the mode of the model, either 1 or 2. Default is 2 (direct modelling of α and β ; recommended). If set to 1, the model is fitted on the basis of μ and σ , the predicted mean and standard deviation over age (kept for backwards compatibility).
alpha	Integer specifying the degree of the polynomial for the alpha model. Default is 3. If mode is set to 1, this parameter is used to specify the degree of the polynomial for the μ model.
beta	Integer specifying the degree of the polynomial for the beta model. Default is 3. If mode is set to 1, this parameter is used to specify the degree of the polynomial for the σ model.
control	A list of control parameters to be passed to the optim function. Parameters not specified are filled with defaults, namely <code>list(reltol = 1e-8, maxit = 1000)</code> for mode 1 and adaptive L-BFGS-B settings (factr between 1e4 and 1e6, maxit proportional to the number of parameters) for mode 2.
scale	Type of norm scale, either "T" (default), "IQ", "z" or a double vector with the mean and standard deviation.
plot	Logical indicating whether to plot the model. Default is TRUE.

Details

The function standardizes the input variables, fits polynomial models for both distribution parameters, and uses maximum likelihood estimation with analytic gradients to find the optimal parameters. In mode 2, the optimization is performed using the L-BFGS-B method.

Please note that the model fit indices (log-likelihood, AIC, BIC) of mode 1 and mode 2 models are not directly comparable, since mode 1 maximizes a normal likelihood on standardized scores, whereas mode 2 maximizes the discrete beta-binomial likelihood on the raw scores.

Value

A list of class "cnormBetaBinomial" or "cnormBetaBinomial2". In case of mode 2 containing:

alpha_est	Estimated coefficients for the alpha model
beta_est	Estimated coefficients for the beta model
se	Standard errors of the estimated coefficients
alpha_degree	Degree of the polynomial for the alpha model
beta_degree	Degree of the polynomial for the beta model
result	Full result from the optimization procedure

Examples

```
## Not run:
# Fit a beta-binomial regression model to the PPVT data
model <- cnorm.betabinomial(ppvt$age, ppvt$raw, n = 228)
summary(model)

# Use weights for post-stratification
marginals <- data.frame(var = c("sex", "sex", "migration", "migration"),
```

```

        level = c(1,2,0,1),
        prop = c(0.51, 0.49, 0.65, 0.35))
weights <- computeWeights(ppvt, marginals)
model <- cnorm.betabinomial(ppvt$age, ppvt$raw, n = 228, weights = weights)

## End(Not run)

```

cnorm.cmp

Fit a Conway-Maxwell-Poisson (CMP) Regression Model for Continuous Norming

Description

This function fits a Conway-Maxwell-Poisson regression model (Conway & Maxwell, 1962; Shmueli et al., 2005) for continuous norming of count data, e.g., speeded tests where the raw score is the number of correctly processed items within a time limit. Both the location parameter $\mu(\text{age})$ and the dispersion parameter $\nu(\text{age})$ vary smoothly as polynomial functions of age (or any other continuous predictor). In contrast to the Poisson model, the CMP distribution does not force variance = mean: it can model over-dispersion ($\nu < 1$), equi-dispersion ($\nu = 1$, Poisson) and under-dispersion ($\nu > 1$).

Usage

```

cnorm.cmp(
  age,
  score,
  weights = NULL,
  mu_degree = 3,
  nu_degree = 2,
  nu = 1,
  control = NULL,
  scale = "T",
  max_terms = NULL,
  tol = 1e-12,
  plot = TRUE,
  max_score = NULL,
  start = NULL
)

```

Arguments

age	A numeric vector of predictor values (typically age, but can be any continuous predictor).
score	A numeric vector of raw scores. Must be the same length as age and must consist of non-negative integers (counts).

weights	An optional numeric vector of non-negative weights for each observation. If NULL (default), all observations are weighted equally. Weights enter the likelihood as multipliers (e.g., post-stratification weights). AIC, BIC and the Hessian-based standard errors are strictly valid only for frequency weights; the sample size used in BIC is the number of rows.
mu_degree	Integer (≥ 1) specifying the degree of the polynomial for $\log(\mu(\text{age}))$. Default is 3. Note that the polynomial acts on the log scale, so lower degrees than in the Taylor or shash approaches are often sufficient.
nu_degree	Integer specifying the degree of the polynomial for $\log(\nu(\text{age}))$. Default is 2. Use 0 for a constant but estimated dispersion, and NULL to fix the dispersion at the value given in nu (nu = 1 yields a Poisson regression). Recommendation: keep nu_degree low to avoid overfitting.
nu	Fixed dispersion parameter (must be > 0), used only if nu_degree is NULL. Default is 1. Values < 1 : over-dispersion; > 1 : under-dispersion.
control	An optional list of control parameters passed to optim. Any parameters not specified are filled with defaults: • factr: Controls precision of optimization (default: 1e3). A less extreme value than in the shash module is used because the normalizing constant is evaluated with a finite truncation tolerance, which limits attainable function precision. • maxit: Maximum number of iterations (default: $n_parameters * 200$) • lmm: Memory limit for L-BFGS-B (default: $\min(n_parameters, 20)$)
scale	Character string or numeric vector specifying the type of norm scale for output. This affects the scaling of derived norm scores but does not influence model fitting: • "T": T-scores (mean = 50, SD = 10) - default • "IQ": IQ-like scores (mean = 100, SD = 15) • "z": z-scores (mean = 0, SD = 1) • c(M, SD): Custom scale with specified mean M and standard deviation SD
max_terms	Maximum number of terms used to evaluate the normalizing constant $Z(\mu, \nu)$. Default (NULL) is $\max(2000, 20 * \max(\text{score}))$. Increase only if a warning indicates that the series did not converge. The value is stored in the model and also applied in predict, normTable and plot.
tol	Relative truncation tolerance for the normalizing constant (default 1e-12). Also stored and re-used in all downstream functions.
plot	Logical indicating whether to automatically display a diagnostic plot of the fitted model. Default is TRUE.
max_score	Optional positive integer: the maximum attainable raw score (e.g., the number of items on the sheet). If given, the distribution is right-truncated at this value (see section "Right-truncated model"). Default NULL: no ceiling.
start	Optional list with numeric vectors mu and (optionally) nu containing starting values for the polynomial coefficients (on the scale of μ_est / ν_est , i.e., of a previously fitted model). Shorter vectors are padded with zeros, which allows warm starts from lower polynomial degrees. If the optimization fails from these values, the default starting values are used.

Details

Parameters are estimated by maximum likelihood with L-BFGS-B and analytic gradients. The CMP distribution belongs to the exponential family in $(\log \lambda, -\nu)$, so the score equations are simple moment conditions: the gradient with respect to the linear predictors only requires $E(Y)$ and $E(\log Y!)$ under the current CMP distribution, which are obtained from the same truncated series as the normalizing constant. Series evaluation is vectorized, truncation is adaptive with a rigorous geometric tail bound, and observations sharing the same (μ, ν) (e.g., age groups) are evaluated only once.

Differences to the beta-binomial and shash models: The (untruncated) CMP distribution has an unbounded support. It is appropriate for speeded tests and other open-ended counts. For tests with a fixed number of items and a hard ceiling (accuracy tests), the beta-binomial model respects this bound, whereas the untruncated CMP model assigns (small) probability mass to scores above the ceiling. Use `max_score` for speeded tests with a finite number of items.

Value

An object of class "cnormCMP" containing the fitted model results. This is a list with:

<code>mu_est</code>	Coefficients of the polynomial for $\log(\mu(\text{age}))$. The first coefficient is the intercept.
<code>nu_est</code>	Coefficients of the polynomial for $\log(\nu(\text{age}))$; NULL if <code>nu</code> is fixed.
<code>nu</code>	The fixed dispersion value (relevant if <code>nu_degree</code> is NULL).
<code>se</code>	Standard errors of all estimated coefficients (NA where they could not be computed).
<code>mu_degree, nu_degree</code>	The polynomial degrees used.
<code>max_score</code>	The ceiling used for right-truncation (NULL if none).
<code>at_bound</code>	Logical; TRUE if the predictor of $\log(\nu)$ reached the admissible range at an observed age (standard errors and Wald tests are then not valid).
<code>vcov</code>	Covariance matrix of the coefficients (mu coefficients first); NULL if unavailable.
<code>result</code>	Output from <code>optim</code> and the data attributes needed for prediction. <i>Note:</i> the optimizer works in an orthogonalized (QR) parameterization of the polynomials for numerical stability; <code>result\$par</code> and <code>result\$hessian</code> refer to this parameterization. Use <code>mu_est</code> , <code>nu_est</code> , <code>se</code> and <code>vcov</code> for coefficients on the usual polynomial scale.

Parameterization

The probability mass function is

$$P(Y = y) = \frac{1}{Z(\mu, \nu)} \left(\frac{\mu^y}{y!} \right)^\nu, \quad Z(\mu, \nu) = \sum_{j=0}^{\infty} \left(\frac{\mu^j}{j!} \right)^\nu$$

i.e., the Poisson kernel raised to the power ν . This is the classical CMP distribution with rate $\lambda = \mu^\nu$. **Note:** the coefficients are therefore *not* those of **COMPoissonReg**, which models λ

(or the mean in its mean-parametrized variants) directly. Modelling μ instead of λ (i) makes μ interpretable as an approximate mean, $E(Y) \approx \mu - (\nu - 1)/(2\nu)$, with $Var(Y) \approx \mu/\nu$ (the exact moments are available via [predictMoments](#)), (ii) decouples the location and dispersion parameters, which stabilizes the optimization and the standard errors, and (iii) yields trivial starting values (a Poisson regression). The model is

$$\log \mu(a) = \sum_{k=0}^{K_\mu} \beta_k a^k, \quad \log \nu(a) = \sum_{k=0}^{K_\nu} \gamma_k a^k$$

with standardized age $a = (\text{age} - \text{mean}(\text{age})) / \text{sd}(\text{age})$. The coefficients refer to the log scale; only the intercepts refer to the mean age.

Right-truncated model

Many speeded tests have a finite number of items on the test sheet. If `max_score` is given, the CMP distribution is truncated to $\{0, 1, \dots, M\}$ with $M = \text{max_score}$ (the normalizing constant is summed up to M only), so that no probability mass is assigned to impossible scores and percentile ranks are properly normalized at the ceiling. In this case, μ and ν are the parameters of the *truncated* distribution and the approximations of mean and variance above no longer hold near the ceiling; use [predictMoments](#) for exact moments.

Shape flexibility

For large μ , the skewness of the CMP distribution is approximately $1/\sqrt{\mu\nu}$, i.e., the shape is nearly determined by mean and variance. If skewness or kurtosis vary independently across age, the SHASH model ([cnorm.shash](#)) or the distribution-free approach are more flexible.

Name collision

COMpoissonReg also exports functions named `dcmp`, `pcmp`, `qcmp` and `rcmp`, but with the arguments `(lambda, nu)`. If both packages are attached, the one attached last masks the other and calls such as `dcmp(x, 8, 1)` are silently interpreted with a different parameterization. Use the explicit `cnorm::dcmp()` or `COMpoissonReg::dcmp()` in this case.

Note

- Raw scores must be non-negative integers.
- The dispersion is restricted to ν in $[0.05, 20]$ by clamping the predictor of $\log(\nu)$.
- Polynomial models can exhibit edge effects; predict outside the observed age range with caution.
- Because the distribution is discrete, norm tables are step-like in the raw score.
- AIC/BIC are not comparable between the discrete CMP model and continuous ([shash](#)) or distribution-free models.

Author(s)

Wolfgang Lenhard

References

- Conway, R. W., & Maxwell, W. L. (1962). A queuing model with state dependent service rates. *Journal of Industrial Engineering*, 12, 132-136.
- Shmueli, G., Minka, T. P., Kadane, J. B., Borle, S., & Boatwright, P. (2005). A useful distribution for fitting discrete data: revival of the Conway-Maxwell-Poisson distribution. *Journal of the Royal Statistical Society C*, 54(1), 127-142.
- Sellers, K. F., & Shmueli, G. (2010). A flexible regression model for count data. *The Annals of Applied Statistics*, 4(2), 943-961.
- Huang, A. (2017). Mean-parametrized Conway-Maxwell-Poisson regression models for dispersed counts. *Statistical Modelling*, 17(6), 359-380.

See Also

[cnorm.shash](#), [autoselect.cmp](#), [normTable.cmp](#), [dcmp](#), [predictMoments](#)

Examples

```
## Not run:
# Basic usage
model <- cnorm.cmp(age = speeded$age, score = speeded$raw)

# Constant but estimated dispersion
model0 <- cnorm.cmp(speeded$age, speeded$raw, mu_degree = 3, nu_degree = 0)

# Poisson regression (dispersion fixed to 1)
model_pois <- cnorm.cmp(speeded$age, speeded$raw, nu_degree = NULL, nu = 1)

# Right-truncated at the number of items on the sheet
model_t <- cnorm.cmp(speeded$age, speeded$raw, max_score = 80)

summary(model, age = speeded$age, score = speeded$raw)
AIC(model); BIC(model)
normTable.cmp(model, ages = c(8, 9), start = 0, end = 80)

## End(Not run)
```

Description

Assists in determining the optimal number of terms for the regression model using repeated Monte Carlo cross-validation. It leverages an 80-20 split between training and validation data, with stratification by norm group or random sample in case of using sliding window ranking.

Usage

```
cnorm.cv(
  data,
  formula = NULL,
  repetitions = 5,
  norms = TRUE,
  min = 4,
  max = 20,
  cv = "full",
  pCutoff = NULL,
  width = NA,
  raw = NULL,
  group = NULL,
  age = NULL,
  weights = NULL
)
```

Arguments

data	Data frame of norm sample or a cnorm object. Should have ranking, powers, and interaction of L and A.
formula	Formula from an existing regression model; min/max functions ignored. If using a cnorm object, this is automatically fetched.
repetitions	Number of repetitions for cross-validation.
norms	If TRUE, computes norm score crossfit and R^2 . Note: Computationally intensive.
min	Start with a minimum number of terms (default = 4).
max	Maximum terms in model, up to $(k + 1) * (t + 1) - 1$ (default = 20).
cv	"full" (default) splits data into training/validation, then ranks. Otherwise, expects a pre-ranked dataset.
pCutoff	Checks stratification for unbalanced data. Performs a t-test per group. Default set to 0.2 to minimize beta error.
width	If provided, ranking done via 'rankBySlidingWindow'. Otherwise, by group.
raw	Name of the raw score variable.
group	Name of the grouping variable.
age	Name of the age variable.
weights	Name of the weighting parameter.

Details

Successive models, with an increasing number of terms, are evaluated, and the RMSE for raw scores plotted. This encompasses the training, validation, and entire dataset. If 'norms' is set to TRUE (default), the function will also calculate the mean norm score reliability and crossfit measures. Note that due to the computational requirements of norm score calculations, execution can be slow, especially with numerous repetitions or terms.

When 'cv' is set to "full" (default), both test and validation datasets are ranked separately, providing comprehensive cross-validation. For a more streamlined validation process focused only on modeling, a pre-ranked dataset can be used. The output comprises RMSE for raw score models, norm score R^2 , delta R^2 , crossfit, and the norm score SE according to Oosterhuis, van der Ark, & Sijtsma (2016).

This function is not yet prepared for the 'extensive' search strategy, introduced in version 3.3, but instead relies on the first model per number of terms, without consistency check.

For assessing overfitting:

$$CROSSFIT = R(Training; Model)^2 / R(Validation; Model)^2$$

A CROSSFIT > 1 suggests overfitting, < 1 suggests potential underfitting, and values around 1 are optimal, given a low raw score RMSE and high norm score validation R^2 .

Suggestions for ideal model selection:

- Visual inspection of percentiles with 'plotPercentiles' or 'plotPercentileSeries'.
- Pair visual inspection with repeated cross-validation (e.g., 10 repetitions).
- Aim for low raw score RMSE and high norm score R^2 , avoiding terms with significant overfit (e.g., crossfit > 1.1).

Value

Table with results per term number: RMSE for raw scores, R^2 for norm scores, and crossfit measure.

References

Oosterhuis, H. E. M., van der Ark, L. A., & Sijtsma, K. (2016). Sample Size Requirements for Traditional and Regression-Based Norms. *Assessment*, 23(2), 191-202. <https://doi.org/10.1177/1073191115580638>

See Also

Other model: `bestModel()`, `checkConsistency()`, `derive()`, `modelSummary()`, `print.cnorm()`, `printSubset()`, `rangeCheck()`, `regressionFunction()`, `summary.cnorm()`, `weightedAverageModel()`

Examples

```
## Not run:
# Example: Plot cross-validation RMSE by number of terms (up to 9) with three repetitions.
result <- cnorm(raw = elfe$raw, group = elfe$group)
cnorm.cv(result$data, min = 2, max = 9, repetitions = 3)

# Using a cnorm object examines the predefined formula.
cnorm.cv(result, repetitions = 1)

## End(Not run)
```

cNORM.GUI	<i>Launcher for the graphical user interface of cNORM for distribution free continuous norming</i>
-----------	--

Description

Launcher for the graphical user interface of cNORM for distribution free continuous norming

Usage

```
cNORM.GUI(launch.browser = TRUE)
```

Arguments

launch.browser Default TRUE; automatically open browser for GUI

Examples

```
## Not run:
# Launch graphical user interface
cNORM.GUI()

## End(Not run)
```

cNORM.GUI2	<i>Launch the cNORM Parametric Modeling Shiny Application</i>
------------	---

Description

Launch the cNORM Parametric Modeling Shiny Application

Usage

```
cNORM.GUI2(launch.browser = TRUE)
```

Arguments

launch.browser Logical, whether to launch browser automatically (default: TRUE)

Examples

```
## Not run:
# Launch graphical user interface
cNORM.GUI2()

## End(Not run)
```

cnorm.shash

*Fit a Sinh-Arcsinh (shash) Regression Model for Continuous Norming***Description**

This function fits a Sinh-Arcsinh (shash; Jones & Pewsey, 2009) regression model for continuous norm score modeling, where the distribution parameters vary smoothly as polynomial functions of age or other predictors. The shash distribution is well-suited for psychometric data as it can flexibly model skewness and tail weight independently, making it ideal for handling floor effects, ceiling effects, and varying degrees of individual differences across age groups. In a simulation study (Lenhard et al, 2019), the shash model demonstrated superior performance compared to other parametric approaches from the Box Cox family of functions. In contrast to Box Cox, Sinh-Arcsinh can model distributions including zero and negative values.

Usage

```
cnorm.shash(
  age,
  score,
  weights = NULL,
  mu_degree = 3,
  sigma_degree = 2,
  epsilon_degree = 2,
  delta_degree = 1,
  delta = 1,
  control = NULL,
  scale = "T",
  plot = TRUE
)
```

Arguments

- | | |
|-----------|--|
| age | A numeric vector of predictor values (typically age, but can be any continuous predictor). |
| score | A numeric vector of response values (raw test scores). Must be the same length as age. The value range is unrestricted and it can include zeros and negative values. |
| weights | An optional numeric vector of weights for each observation. Useful for incorporating sampling weights. If NULL (default), all observations are weighted equally. |
| mu_degree | Integer specifying the degree of the polynomial for modeling the location parameter $\mu(\text{age})$. Default is 3. Higher degrees allow more flexible modeling of how the central tendency changes with age, but may lead to overfitting with small samples. Common choices: <ul style="list-style-type: none"> • 1: Linear change with age • 2: Quadratic change (allows one inflection point) |

	• 3: Cubic change (allows two inflection points, suitable for most developmental curves) • 4+: Higher-order changes (use cautiously, mainly for large samples)
sigma_degree	Integer specifying the degree of the polynomial for modeling the scale parameter $\sigma(\text{age})$. Default is 2. This controls how the variability (spread) of scores changes with age. Lower degrees are often sufficient as variability typically changes more smoothly than location.
epsilon_degree	Integer specifying the degree of the polynomial for modeling the skewness parameter $\epsilon(\text{age})$. Default is 2. This controls how the asymmetry of the distribution changes with age.
delta_degree	Integer specifying the degree of the polynomial for modeling the tail weight parameter $\delta(\text{age})$. Default is 1. The tail weight can be fixed as well in case of numerical instability. In that case, set <code>delta_degree</code> to NULL and specify a value for <code>delta</code> instead. Recommendation: Keep <code>delta_degree</code> low to avoid overfitting.
delta	Fixed tail weight parameter (must be > 0). Default is 1. This parameter controls the heaviness of the distribution tails and is kept constant across all ages when <code>delta_degree</code> is set to NULL. Common values: • $\delta = 1$: Normal-like tail behavior (baseline) • $\delta < 1$: Heavier tails, higher kurtosis (more extreme scores than normal distribution) • $\delta > 1$: Lighter tails, lower kurtosis (fewer extreme scores than normal distribution)
control	An optional list of control parameters passed to the <code>optim</code> function for maximum likelihood estimation. Any parameters not specified are filled with sensible defaults based on the model complexity. Common parameters to adjust: • <code>factr</code>: Controls precision of optimization (default: $1e-8$) • <code>maxit</code>: Maximum number of iterations (default: $n_parameters * 200$) • <code>lmm</code>: Memory limit for L-BFGS-B (default: $\min(n_parameters, 20)$) Increase <code>maxit</code> or decrease <code>factr</code> if optimization fails to converge.
scale	Character string or numeric vector specifying the type of norm scale for output. This affects the scaling of derived norm scores but does not influence model fitting: • "T": T-scores (mean = 50, SD = 10) - default • "IQ": IQ-like scores (mean = 100, SD = 15) • "z": z-scores (mean = 0, SD = 1) • <code>c(M, SD)</code>: Custom scale with specified mean M and standard deviation SD
plot	Logical indicating whether to automatically display a diagnostic plot of the fitted model. Default is TRUE.

Details

This implementation uses the Jones & Pewsey (2009) parameterization of the Sinh-Arcsinh distribution. Parameters are estimated using maximum likelihood via the L-BFGS-B algorithm with analytic gradients. In case optimization fails, try reducing model complexity by reducing polynomial degrees or fixing the `delta` parameter.

The Sinh-Arcsinh Distribution: The shash distribution is defined by the transformation:

$$X = \mu + \sigma \cdot \sinh \left(\frac{\operatorname{arcsinh}(Y) - \epsilon}{\delta} \right)$$

where Y is a standard normal variable, $Y \sim N(0,1)$.

This transformation provides:

- μ : Location parameter (similar to mean)
- σ : Scale parameter (similar to standard deviation)
- ϵ : Skewness parameter ($\epsilon = 0$ for symmetry)
- δ : Tail weight parameter ($\delta = 1$ for normal-like tails)

Model Selection: Choose polynomial degrees based on:

- Sample size (higher degrees need more data)
- Theoretical expectations about developmental trajectories
- Model comparison criteria (AIC, BIC)
- Visual inspection of fitted curves

For most applications, $\mu_degree = 3$, $\sigma_degree = 2$, $\epsilon_degree = 2$, $\delta_degree = 1$ provides a good balance of flexibility and parsimony.

Value

An object of class "cnormShash" containing the fitted model results. This is a list with components:

<code>mu_est</code>	Numeric vector of estimated coefficients for the location parameter $\mu(\text{age})$. The first coefficient is the intercept, subsequent coefficients correspond to polynomial terms.
<code>sigma_est</code>	Numeric vector of estimated coefficients for the scale parameter $\log(\sigma(\text{age}))$. Note: These are coefficients for $\log(\sigma)$ to ensure $\sigma > 0$.
<code>epsilon_est</code>	Numeric vector of estimated coefficients for the skewness parameter $\epsilon(\text{age})$.
<code>delta</code>	The fixed tail weight parameter value used in fitting (relevant if <code>delta_degree</code> is NULL).
<code>delta_est</code>	Numeric vector of estimated coefficients for $\log(\delta(\text{age}))$ - in case a degree has been set, otherwise NULL.
<code>se</code>	Numeric vector of standard errors for all estimated coefficients (if Hessian computation succeeds).
<code>mu_degree, sigma_degree, epsilon_degree</code>	The polynomial degrees used for each parameter.
<code>delta_degree</code>	The polynomial degree used for delta, or NULL if delta was fixed.
<code>result</code>	Complete output from the <code>optim</code> function, including convergence information, log-likelihood value, and other optimization details.

Note

- The function requires the input data to have sufficient variability. Very small datasets or datasets with little age spread may cause convergence problems.
- Polynomial models can exhibit edge effects at the boundaries of the age range. Predictions outside the observed age range should be made cautiously.
- If convergence fails, try: (1) reducing polynomial degrees, (2) adjusting the delta parameter, (3) providing custom control parameters, or (4) checking for data quality issues.
- If parameters end up at their box constraints, the reported standard errors and Wald tests for these parameters are not valid; a warning is issued in this case.

Author(s)

Wolfgang Lenhard

References

Jones, M. C., & Pewsey, A. (2009). Sinh-arcsinh distributions. **Biometrika**, 96(4), 761-780.

Lenhard, A., Lenhard, W., Gary, S. (2019). Continuous norming of psychometric tests: A simulation study of parametric and semi-parametric approaches. **PLOS ONE**, 14(9), e0222279. <https://doi.org/10.1371/journal.pone.0222279>

See Also

[plot](#) for plotting fitted models, [predict](#) for generating predictions, [cnorm.betabinomial2](#) for discrete beta-binomial alternative

Examples

```
## Not run:
# Basic usage with default settings
model <- cnorm.shash(age = children$age, score = children$raw_score)

# Custom polynomial degrees for complex developmental pattern
model_complex <- cnorm.shash(
  age = adolescents$age,
  score = adolescents$vocabulary_score,
  mu_degree = 4,          # Complex mean trajectory
  sigma_degree = 3,       # Changing variability pattern
  epsilon_degree = 2,     # Skewness shifts
  delta_degree = NULL,    # set to NULL to activate fixed delta
  delta = 0.8             # Slightly heavy tails
)

# With sampling weights
model_weighted <- cnorm.shash(
  age = survey$age,
  score = survey$score,
  weights = survey$sample_weight
)
```

```
# Custom optimization control for difficult convergence
model_robust <- cnorm.shash(
  age = mixed$age,
  score = mixed$score,
  control = list(factr = 1e-6, maxit = 2000),
  delta = 1.5
)

# Compare model fit
compare(model, model_complex)

## End(Not run)
```

compare

*Compare Two Norm Models Visually***Description**

This function creates a visualization comparing two norm models by displaying their percentile curves. The first model is shown with solid lines, the second with dashed lines. If age and score vectors are provided, manifest percentiles are displayed as dots. The function works with regular cnorm models (Taylor polynomials), beta-binomial models, Conway-Maxwell-Poisson (CMP) models, and shash models, allowing comparison between different model types.

Usage

```
compare(
  model1,
  model2,
  percentiles = c(0.025, 0.1, 0.25, 0.5, 0.75, 0.9, 0.975),
  age = NULL,
  score = NULL,
  weights = NULL,
  title = NULL,
  subtitle = NULL,
  discrete = FALSE
)
```

Arguments

model1	First model object (distribution-free, beta-binomial, CMP, or shash)
model2	Second model object (distribution-free, beta-binomial, CMP, or shash)
percentiles	Vector with percentile scores, ranging from 0 to 1 (exclusive)
age	Optional vector with manifest age or group values
score	Optional vector with manifest raw score values

weights	Optional vector with manifest weights
title	Custom title for plot (optional)
subtitle	Custom subtitle for plot (optional)
discrete	Logical indicating whether discrete models (beta-binomial and CMP) are displayed with their exact discrete quantiles as step functions (TRUE) or with smooth continuous curves (FALSE, default). Ignored for Taylor and shash models.

Details

For discrete count and accuracy models (beta-binomial and CMP), smooth continuous curves are displayed by default (discrete = FALSE). For CMP models, these are the continuity-corrected (mid-p) quantiles consistent with `plot.cnormCMP` and the derived norm scores. For beta-binomial models, smooth lines are based on the underlying beta (mixing) distribution. Setting discrete = TRUE displays the exact discrete quantiles as step functions. The parameter has no effect on continuous models (Taylor polynomials or shash).

Observation weights (e.g. post-stratification or frequency weights) are fully respected in the computation of manifest percentiles, age group centers, and all fit indices (R-squared, Bias, RMSE, and MAD).

Value

A ggplot object showing the comparison of both models

See Also

Other plot: `plot.cnorm()`, `plot.cnormBetaBinomial()`, `plot.cnormBetaBinomial2()`, `plotDensity()`, `plotDerivative()`, `plotNorm()`, `plotNormCurves()`, `plotPercentileSeries()`, `plotPercentiles()`, `plotRaw()`, `plotSubset()`

computePowers	<i>Compute powers of the explanatory variable a as well as of the person location l (data preparation)</i>
---------------	--

Description

The function computes powers of the norm variable e. g. T scores (location, L), an explanatory variable, e. g. age or grade of a data frame (age, A) and the interactions of both (L X A). The k variable indicates the degree up to which powers and interactions are build. These predictors can be used later on in the `bestModel` function to model the norm sample. Higher values of k allow for modeling the norm sample closer, but might lead to over-fit. In general k = 3 or k = 4 (default) is sufficient to model human performance data. For example, k = 2 results in the variables L1, L2, A1, A2, and their interactions L1A1, L2A1, L1A2 and L2A2 (but k = 2 is usually not sufficient for the modeling). Please note, that you do not need to use a normal rank transformed scale like T or IQ; you can use the percentiles for the 'normValue' as well.

Usage

```
computePowers(data, k = 5, norm = NULL, age = NULL, t = 3, silent = FALSE)
```

Arguments

data	data.frame with the norm data
k	degree of the location polynomial (1..6)
norm	name of the norm variable in the data.frame (T scores, IQ, percentiles, ...). If 'NULL', the "normValue" attribute of 'data' is used.
age	explanatory variable (e.g. age or grade). May be a column name, a numeric vector of 'nrow(data)', 'FALSE' to disable age handling, or 'NULL' to fall back to the "age" attribute of 'data'.
t	age power parameter (1..6). If 'NULL', falls back to 'k'.
silent	set to TRUE to suppress messages

Details

The functions `rankBySlidingWindow`, `rankByGroup`, `bestModel`, `computePowers` and `prepareData` are usually not called directly, but accessed through other functions like `cnorm`.

Value

data.frame with the powers and interactions of location and explanatory variable / age

See Also

`bestModel`

Other prepare: [prepareData\(\)](#), [rankByGroup\(\)](#), [rankBySlidingWindow\(\)](#)

Examples

```
## Not run:
# Dataset with grade levels as grouping
data.elfe <- rankByGroup(elfe)
data.elfe <- computePowers(data.elfe)

# Dataset with continuous age variable and k = 5
data.ppv <- rankByGroup(ppvt)
data.ppv <- computePowers(data.ppv, age = "age", k = 5)

## End(Not run)
```

computeWeights

Weighting of cases through iterative proportional fitting (Raking)

Description

Computes and standardizes weights via raking to compensate for non-stratified samples. It is based on the implementation in the survey R package. It reduces data collection biases in the norm data by the means of post stratification, thus reducing the effect of unbalanced data in percentile estimation and norm data modeling.

Usage

```
computeWeights(data, population.margins, standardized = TRUE)
```

Arguments

data	data.frame with norm sample data.
population.margins	A data.frame including three columns, specifying the variable name in the original dataset used for data stratification, the factor level of the variable and the according population share. Please ensure the original data does not include factor levels not present in the population.margins. Additionally, summing up the shares of the different levels of a variable should result in a value near 1.0. The first column must specify the name of the stratification variable, the second the level and the third the proportion.
standardized	If TRUE (default), the raking weights are scaled to weights/min(weights)

Details

This function computes standardized raking weights to overcome biases in norm samples. It generates weights by drawing on the information of population shares (e. g. for sex, ethnic group, region ...) and subsequently reduces the influence of over-represented groups or increases under-represented cases. The returned weights are either raw or standardized and scaled to be larger than 0.

Raking in general has a number of advantages over post stratification and it additionally allows cNORM to draw on larger datasets, since less cases have to be removed during stratification. To use this function, additionally to the data, a data frame with stratification variables has to be specified. The data frame should include a row with (a) the variable name, (b) the level of the variable and (c) the according population proportion.

Value

a vector with the standardized weights

Examples

```
## Not run:
# cNORM features a dataset on vocabulary development (ppvt)
# that includes variables like sex or migration. In order
# to weight the data, we have to specify the population shares.
# According to census, the population includes 52% boys
# (factor level 1 in the ppvt dataset) and 70% / 30% of persons
# without / with a history of migration (= 0 / 1 in the dataset).
# First we set up the population margins with all shares of the
# different levels:

margins <- data.frame(variables = c("sex", "sex",
                                   "migration", "migration"),
                      levels = c(1, 2, 0, 1),
                      share = c(.52, .48, .7, .3))

head(margins)

# Now we use the population margins to generate weights
# through raking

weights <- computeWeights(ppvt, margins)

# There are as many different weights as combinations of
# factor levels, thus only four in this specific case

unique(weights)

# To include the weights in the cNORM modelling, we have
# to pass them as weights. They are then used to set up
# weighted quantiles and as weights in the regression.

model <- cnorm(raw = ppvt$raw,
               group = ppvt$group,
               weights = weights)

## End(Not run)
```

derivationTable	<i>Create a table based on first order derivative of the regression model for specific age</i>
-----------------	--

Description

In order to check model assumptions, a table of the first order derivative of the model coefficients is created.

Usage

```
derivationTable(A, model, minNorm = NULL, maxNorm = NULL, step = 0.1)
```

Arguments

A	the age
model	The regression model or a cnorm object
minNorm	The lower bound of the norm value range
maxNorm	The upper bound of the norm value range
step	Stepping parameter with lower values indicating higher precision

Value

data.frame with norm scores and the predicted scores based on the derived regression function

See Also

plotDerivative, derive
Other predict: [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:  
# Generate cnorm object from example data  
cnorm.elfe <- cnorm(raw = elfe$raw, group = elfe$group)  
  
# retrieve function for time point 6  
d <- derivationTable(6, cnorm.elfe, step = 0.5)  
  
## End(Not run)
```

derive	<i>Derivative of regression model</i>
--------	---------------------------------------

Description

Calculates the derivative of the location / norm value from the regression model with the first derivative as the default. This is useful for finding violations of model assumptions and problematic distribution features as f. e. bottom and ceiling effects, non-progressive norm scores within an age group or in general intersecting percentile curves.

Usage

```
derive(model, order = 1)
```

Arguments

model	The regression model or a cnorm object
order	The degree of the derivative, default: 1

Value

The derived coefficients

See Also

Other model: `bestModel()`, `checkConsistency()`, `cnorm.cv()`, `modelSummary()`, `print.cnorm()`, `printSubset()`, `rangeCheck()`, `regressionFunction()`, `summary.cnorm()`, `weightedAverageModel()`

Examples

```
## Not run:
m <- cnorm(raw = elfe$raw, group = elfe$group)
derivedCoefficients <- derive(m, order = 1)

## End(Not run)
```

diagnostics.betabinomial

Diagnostic Information for Beta-Binomial Model

Description

This function provides diagnostic information for a fitted beta-binomial model from the `cnorm.betabinomial` function. It returns various metrics related to model convergence, fit, and complexity. In case age and raw scores are provided, the function as well computes R2, RMSE and bias for the norm scores based on the manifest and predicted norm scores.

Usage

```
diagnostics.betabinomial(model, age = NULL, score = NULL, weights = NULL)
```

Arguments

<code>model</code>	An object of class "cnormBetaBinomial" or "cnormBetaBinomial2", typically the result of a call to <code>cnorm.betabinomial()</code> .
<code>age</code>	An optional vector with age values.
<code>score</code>	An optional vector with raw values.
<code>weights</code>	An optional vector with weights.

Details

The AIC and BIC are calculated as: $AIC = 2k - 2\ln(L)$ $BIC = \ln(n)k - 2\ln(L)$ where k is the number of parameters, L is the maximum likelihood, and n is the number of observations.

Please note that fit indices of mode 1 and mode 2 models are not directly comparable, since the two modes maximize different likelihoods (normal on standardized scores vs. discrete beta-binomial).

Value

A list containing diagnostic information, including convergence, number of evaluations, log-likelihood, AIC, BIC, the maximum absolute analytic gradient at the solution (first-order optimality), parameter estimates with standard errors, z and p values, and - if age and score are provided - R2, RMSE and bias of the norm scores.

Examples

```
## Not run:
model <- cnorm.betabinomial(ppvt$age, ppvt$raw)
diag_info <- diagnostics.betabinomial(model)
print(diag_info)
summary(diag_info)

if(diag_info$converged) {
  cat("Model converged successfully.\n")
} else {
  cat("Warning: Model did not converge.\n")
}

cat("AIC:", diag_info$AIC, "\n")
cat("BIC:", diag_info$BIC, "\n")

## End(Not run)
```

elfe

Sentence completion test from ELFE 1-6

Description

A dataset containing the raw data of 1400 students from grade 2 to 5 in the sentence comprehension test from ELFE 1-6 (Lenhard & Schneider, 2006). In this test, students are presented lists of sentences with one gap. The student has to fill in the correct solution by selecting from a list of 5 alternatives per sentence. The alternatives include verbs, adjectives, nouns, pronouns and conjunctives. Each item stems from the same word type. The text is speeded, with a time cutoff of 180 seconds. The variables are as follows:

Usage

```
elfe
```

Format

A data frame with 1400 rows and 3 variables:

personID ID of the student

group grade level, with x.5 indicating the end of the school year and x.0 indicating the middle of the school year

raw the raw score of the student, spanning values from 0 to 28

A data frame with 1400 rows and 3 columns

Source

<https://www.psychometrica.de/elfe2.html>

References

Lenhard, W. & Schneider, W.(2006). Ein Leseverstaendnistest fuer Erst- bis Sechstklaesser. Goettingen/Germany: Hogrefe.

Examples

```
## Not run:
# prepare data, retrieve model and plot percentiles
model <- cnorm(group = elfe$group, raw = elfe$raw)

## End(Not run)
```

getGroups	<i>Determine groups and group means</i>
-----------	---

Description

Splits a continuous variable into n groups (either equidistant or with equal number of observations) and returns the group mean for every observation.

Usage

```
getGroups(x, n = NULL, equidistant = FALSE)
```

Arguments

x	Numeric vector to be split.
n	Desired number of groups. If NULL, the function chooses roughly one group per 100 observations, constrained to $3 \leq n \leq 20$.
equidistant	If TRUE, intervals have equal width; otherwise (default) each interval contains roughly the same number of observations.

Value

Numeric vector of the same length as x with the group mean assigned to each observation.

Examples

```
## Not run:
x <- rnorm(1000, mean = 50, sd = 10)
m <- getGroups(x, n = 10)

## End(Not run)
```

getNormCurve

*Computes the curve for a specific T value***Description**

As with this continuous norming regression approach, raw scores are modeled as a function of age and norm score (location), getNormCurve is a straightforward approach to show the raw score development over age, while keeping the norm value constant. This way, e. g. academic performance or intelligence development of a specific ability is shown.

Usage

```
getNormCurve(
  norm,
  model,
  minAge = NULL,
  maxAge = NULL,
  step = 0.1,
  minRaw = NULL,
  maxRaw = NULL
)
```

Arguments

norm	The specific norm score, e. g. T value
model	The model from the regression modeling obtained with the cnorm function
minAge	Age to start from
maxAge	Age to stop at
step	Stepping parameter for the precision when retrieving of the values, lower values indicate higher precision (default 0.1).
minRaw	lower bound of the range of raw scores (default = 0)
maxRaw	upper bound of raw scores

Value

data.frame of the variables raw, age and norm

See Also

Other predict: `derivationTable()`, `normTable()`, `predict.cnormBetaBinomial()`, `predict.cnormBetaBinomial2()`, `predict.cnormCMP()`, `predict.cnormShash()`, `predictNorm()`, `predictRaw()`, `rawTable()`

Examples

```
## Not run:
# Generate cnorm object from example data
cnorm.elfe <- cnorm(raw = elfe$raw, group = elfe$group)
getNormCurve(35, cnorm.elfe)

## End(Not run)
```

getNormScoreSE	<i>Calculates the standard error (SE) or root mean square error (RMSE) of the norm scores. In case of large datasets, both results should be almost identical.</i>
----------------	--

Description

Calculates the standard error (SE) or root mean square error (RMSE) of the norm scores. In case of large datasets, both results should be almost identical.

Usage

```
getNormScoreSE(model, type = 2)
```

Arguments

model	a cnorm object
type	either '1' for the standard error sensu Oosterhuis et al. (2016) or '2' for the RMSE (default)

Value

The standard error (SE) of the norm scores sensu Oosterhuis et al. (2016) or the RMSE

References

Oosterhuis, H. E. M., van der Ark, L. A., & Sijtsma, K. (2016). Sample Size Requirements for Traditional and Regression-Based Norms. *Assessment*, 23(2), 191-202. <https://doi.org/10.1177/1073191115580638>

logLik.cnormCMP	<i>Log-likelihood of a CMP model (enables AIC() and BIC())</i>
-----------------	--

Description

Log-likelihood of a CMP model (enables AIC() and BIC())

Usage

```
## S3 method for class 'cnormCMP'
logLik(object, ...)
```

Arguments

object	A fitted model of class "cnormCMP".
...	Not used.

Value

An object of class "logLik".

modelSummary	<i>Prints the results and regression function of a cnorm model</i>
--------------	--

Description

Prints the results and regression function of a cnorm model

Usage

```
modelSummary(object, ...)
```

Arguments

object	A regression model or cnorm object
...	additional parameters

Value

A report on the regression function, weights, R2 and RMSE

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

nobs.cnormCMP	<i>Number of observations used to fit a CMP model</i>
---------------	---

Description

Number of observations used to fit a CMP model

Usage

```
## S3 method for class 'cnormCMP'
nobs(object, ...)
```

Arguments

object	A fitted model of class "cnormCMP".
...	Not used.

Value

Integer.

normTable	<i>Create a norm table based on model for specific age</i>
-----------	--

Description

This function generates a norm table for a specific age based on the regression model by assigning raw scores to norm scores. Please specify the range of norm scores you want to cover. For Taylor polynomial models, specifying a range of $T = 25$ to $T = 75$ covers 98.4%. For parametric models (beta-binomial, CMP, shash), norm tables are computed directly from the distribution functions. In case a confidence coefficient (CI, default .9) and reliability is specified, confidence intervals are computed for the true score estimates, including a correction for regression to the mean (Eid & Schmidt, 2012, p. 272).

Usage

```
normTable(
  A,
  model,
  minNorm = NULL,
  maxNorm = NULL,
  minRaw = NULL,
  maxRaw = NULL,
  start = NULL,
  end = NULL,
```

```

    step = NULL,
    monotonuous = TRUE,
    CI = 0.9,
    reliability = NULL,
    pretty = TRUE,
    ...
)

```

Arguments

A	the age as single value or a vector of age values
model	The regression model from cnorm, cnorm.betabinomial, cnorm.cmp, or cnorm.shash
minNorm	The lower bound of the norm score range (Taylor models)
maxNorm	The upper bound of the norm score range (Taylor models)
minRaw	clipping parameter for the lower bound of raw scores (or start score for CMP/shash)
maxRaw	clipping parameter for the upper bound of raw scores (or end score for CMP/shash)
start	Minimum raw score value for the norm table (default: observed minimum)
end	Maximum raw score value for the norm table (default: observed maximum)
step	Stepping parameter with lower values indicating higher precision (for CMP: integer step size)
monotonuous	corrects for decreasing norm scores in case of model inconsistencies (default)
CI	confidence coefficient, ranging from 0 to 1, default .9
reliability	coefficient, ranging between 0 to 1
pretty	Format table by collapsing intervals and rounding to meaningful precision
...	Additional arguments passed to model-specific norm table methods (e.g., mid_p for CMP)

Value

either data.frame with norm scores, predicted raw scores and percentiles in case of simple A value or a list of norm tables if vector of A values was provided

References

Eid, M. & Schmidt, K. (2012). Testtheorie und Testkonstruktion. Hogrefe.

See Also

rawTable

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

normTable.betabinomial

Calculate Cumulative Probabilities, Density, Percentiles, and Z-Scores for Beta-Binomial Distribution

Description

This function generates a norm table for specific ages based on the beta binomial regression model. In case a confidence coefficient (CI, default .9) and the reliability is specified, confidence intervals are computed for the true score estimates, including a correction for regression to the mean (Eid & Schmidt, 2012, p. 272).

Usage

```
normTable.betabinomial(
  model,
  ages,
  n = NULL,
  m = NULL,
  range = 3,
  CI = 0.9,
  reliability = NULL
)
```

Arguments

model	The model, fitted with cnorm.betabinomial .
ages	A numeric vector of age points at which to compute the tables.
n	The number of items resp. the maximum score.
m	An optional stop criterion in table generation. Positive integer lower than n. Please note: The probabilities are always computed on the full support 0 to n; m only truncates the output table.
range	The range of the norm scores in standard deviations. Default is 3. Thus, scores in the range of +/- 3 standard deviations are considered.
CI	Confidence coefficient, ranging from 0 to 1, default .9.
reliability	Reliability coefficient, ranging between 0 to 1.

Value

A list of data frames with columns: x, Px, Pcum, Percentile, z, norm score and possibly confidence intervals.

normTable.cmp

*Calculate Norm Tables for the Conway-Maxwell-Poisson Distribution***Description**

Generates norm tables for specific ages based on a fitted CMP continuous norming model. Computes point probabilities, cumulative probabilities, mid-p percentile ranks, z-scores, norm scores, and optional true-score confidence intervals (Kelley's formula) for count raw scores.

Usage

```
normTable.cmp(
  model,
  ages,
  start = NULL,
  end = NULL,
  step = 1,
  CI = 0.9,
  reliability = NULL,
  mid_p = TRUE,
  minRaw = NULL,
  maxRaw = NULL,
  range = 3,
  ...
)
```

Arguments

model	Fitted CMP model object of class "cnormCMP". Can also be passed as the second argument if ages is given first (matching the normTable generic).
ages	Numeric vector of age points for norm table generation.
start	Minimum raw score value for the norm table. Default is 0 (the natural floor for count data).
end	Maximum raw score value for the norm table. Default is max_score for a right-truncated model, or the maximum observed score if untruncated.
step	Step size between consecutive raw scores (integer >= 1, default: 1).
CI	Confidence coefficient (0-1, default: 0.90) for confidence intervals.
reliability	Reliability coefficient (0-1) for Kelley's true score confidence intervals.
mid_p	Logical; if TRUE (default), uses mid-p adjusted percentiles for discrete scores: $P(Y < x) + 0.5P(Y = x)$.
minRaw, maxRaw	Optional aliases for start and end.
range	Range of the norm scores in standard deviations (default 3), identical to predict.cnormCMP : z-scores and norm scores are limited to +/- range. Use Inf to switch off truncation. The column Percentile is never limited.
...	Additional arguments.

Value

A list of data frames (one per age) containing:

x	Raw score count
Px	Point probability $P(Y = x)$
Pcum	Cumulative probability $P(Y \leq x)$
Percentile	Mid-p percentile rank (0 to 100)
z	Standardized z-score (bounded by +/- range)
norm	Norm score on the model's scale (e.g. T-score)
lowerCI, upperCI	True-score confidence interval limits (if reliability is given)
lowerCI_PR, upperCI_PR	Percentile rank confidence limits (if reliability is given)

normTable.shash	<i>Calculate Norm Tables for Sinh-Arcsinh Distribution</i>
-----------------	--

Description

Generates norm tables for specific ages based on a fitted Sinh-Arcsinh (shash) regression model. Computes interval probabilities, percentiles, z-scores, and norm scores for a specified range of raw scores. Optionally includes confidence intervals when reliability is provided.

Usage

```
normTable.shash(
  model,
  ages,
  start = NULL,
  end = NULL,
  step = 1,
  CI = 0.9,
  reliability = NULL
)
```

Arguments

model	Fitted shash model object of class "cnormShash"
ages	Numeric vector of age points for norm table generation
start	Minimum raw score value for the norm table
end	Maximum raw score value for the norm table
step	Step size between consecutive raw scores (default: 1)
CI	Confidence coefficient (0-1, default: 0.9) for confidence intervals
reliability	Reliability coefficient (0-1) for true score confidence intervals

Details

For continuous shash distributions, densities are converted to interval probabilities (density times step width) and cumulative probabilities. When reliability is specified, confidence intervals include correction for regression to the mean.

Value

List of data frames (one per age) containing:

x	Raw scores
Px	Approximate interval probabilities (density times step width). These are consistent with Pcum but do not necessarily sum to 1 over the tabulated score range.
Pcum	Cumulative probabilities
Percentile	Percentile ranks (0-100)
z	Standardized z-scores
norm	Norm scores in specified scale
lowerCI, upperCI	Confidence intervals (if reliability provided)
lowerCI_PR, upperCI_PR	CI as percentile ranks (if reliability provided)

Examples

```
## Not run:
# Basic norm table
model <- cnorm.shash(age, score)
tables <- normTable.shash(model, ages = c(7, 8, 9), start = 0, end = 50)

# With confidence intervals and finer granularity
tables_ci <- normTable.shash(model, ages = c(8, 9), start = 10, end = 40,
                             step = 0.5, CI = 0.95, reliability = 0.85)

## End(Not run)
```

plot.cnorm

S3 function for plotting cnorm objects

Description

S3 function for plotting cnorm objects

Usage

```
## S3 method for class 'cnorm'
plot(x, y, ...)
```

Arguments

x	the cnorm object
y	the type of plot as a string, can be one of 'raw' (1), 'norm' (2), 'curves' (3), 'percentiles' (4), 'series' (5), 'subset' (6), or 'derivative' (7), either as a string or the according index
...	additional parameters for the specific plotting function

See Also

Other plot: [compare\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDensity\(\)](#), [plotDerivative\(\)](#), [plotNorm\(\)](#), [plotNormCurves\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

plot.cnormBetaBinomial

Plot cnormBetaBinomial Model with Data and Percentile Lines

Description

This function creates a visualization of a fitted cnormBetaBinomial model, including the original data points, the manifest percentiles (diamond-shaped dots per age group) and the model-implied percentile lines.

Usage

```
## S3 method for class 'cnormBetaBinomial'
plot(x, ...)
```

Arguments

x	A fitted model object of class "cnormBetaBinomial" or "cnormBetaBinomial2".
...	Additional arguments passed to the plot method. • age A vector of the age data. • score A vector of the score data. • weights An optional numeric vector of weights for each observation. • percentiles An optional vector with the percentiles to plot. • points Logical indicating whether to plot the data points. Default is TRUE. • discrete Logical indicating whether to plot the exact discrete beta-binomial quantiles (TRUE, default) or a smooth continuous approximation via the underlying beta distribution (FALSE).

Details

By default (`discrete = TRUE`), the percentile lines represent the exact quantiles of the fitted discrete beta-binomial distribution and are therefore step functions. Setting `discrete = FALSE` draws smooth lines based on the quantiles of the underlying beta (mixing) distribution. Note that this continuous approximation omits the binomial stage of the variance and therefore displays less spread than the fitted model actually implies, particularly in the outer percentiles. Use it only for visual comparability with continuous modelling approaches.

Cases with non-finite values (NA, NaN, Inf) in age, score or weights are removed prior to plotting, mirroring the behavior of the fitting functions.

Value

A ggplot object.

See Also

Other plot: `compare()`, `plot.cnorm()`, `plot.cnormBetaBinomial2()`, `plotDensity()`, `plotDerivative()`, `plotNorm()`, `plotNormCurves()`, `plotPercentileSeries()`, `plotPercentiles()`, `plotRaw()`, `plotSubset()`

```
plot.cnormBetaBinomial2
```

Plot cnormBetaBinomial2 Model with Data and Percentile Lines

Description

This function creates a visualization of a fitted `cnormBetaBinomial2` model, including the original data points, manifest percentiles and specified percentile lines. See `plot.cnormBetaBinomial`.

Usage

```
## S3 method for class 'cnormBetaBinomial2'
plot(x, ...)
```

Arguments

- | | |
|-----|---|
| x | A fitted model object of class "cnormBetaBinomial" or "cnormBetaBinomial2". |
| ... | Additional arguments passed to the plot method. <ul style="list-style-type: none"> • age A vector of the age data. • score A vector of the score data. • weights An optional numeric vector of weights for each observation. • percentiles An optional vector with the percentiles to plot. • points Logical indicating whether to plot the data points. Default is TRUE. • discrete Logical indicating whether to plot the exact discrete beta-binomial quantiles (TRUE, default) or a smooth continuous approximation via the underlying beta distribution (FALSE). |

Value

A ggplot object.

See Also

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plotDensity\(\)](#), [plotDerivative\(\)](#), [plotNorm\(\)](#), [plotNormCurves\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

plot.cnormCMP

Plot CMP Model with Data and Percentile Lines

Description

The model-implied percentile curves are continuity-corrected quantiles, i.e., the inverse of the mid-p percentile rank used for the norm scores, so that they are directly comparable to the (interpolated) manifest percentiles.

Usage

```
## S3 method for class 'cnormCMP'
plot(x, ...)
```

Arguments

x	A fitted model object of class "cnormCMP"
...	Additional arguments including age, score, weights, percentiles, points

Value

A ggplot object

plot.cnormShash

Plot Sinh-Arcsinh Model with Data and Percentile Lines

Description

Plot Sinh-Arcsinh Model with Data and Percentile Lines

Usage

```
## S3 method for class 'cnormShash'
plot(x, ...)
```

Arguments

`x` A fitted model object of class "cnormShash"
`...` Additional arguments including age, score, weights, percentiles, points

Value

A ggplot object

plotCnorm	<i>General convenience plotting function</i>
-----------	--

Description

General convenience plotting function

Usage

```
plotCnorm(x, y, ...)
```

Arguments

`x` a cnorm object
`y` the type of plot as a string or index
`...` additional parameters for the specific plotting function

plotDensity	<i>Plot the density function per group by raw score</i>
-------------	---

Description

This function plots density curves based on the regression model against the raw scores. It supports traditional continuous norming models, beta-binomial models, Conway-Maxwell-Poisson (CMP) models, and SHASH models.

Usage

```
plotDensity(  
  model,  
  minRaw = NULL,  
  maxRaw = NULL,  
  minNorm = NULL,  
  maxNorm = NULL,  
  group = NULL  
)
```

Arguments

model	The model from the bestModel function, a cnorm object, a cnormBetaBinomial, a cnormBetaBinomial2, a cnormCMP, or a cnormShash object.
minRaw	Lower bound of the raw score. If NULL, it's automatically determined based on the model type.
maxRaw	Upper bound of the raw score. If NULL, it's automatically determined based on the model type.
minNorm	Lower bound of the norm score. If NULL, it's automatically determined based on the model type.
maxNorm	Upper bound of the norm score. If NULL, it's automatically determined based on the model type.
group	Numeric vector specifying the age groups to plot. If NULL, groups are automatically selected.

Details

The function generates density curves (or PMFs for discrete models) for specified age groups, allowing for easy comparison of score distributions across different ages.

For beta-binomial and CMP models, the display reflects the probability mass function, while for continuous models (Taylor and SHASH), it displays the probability density function.

Value

A ggplot object representing the density functions.

See Also

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDerivative\(\)](#), [plotNorm\(\)](#), [plotNormCurves\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

plotDerivative

Plot first order derivative of regression model

Description

This function plots the scores obtained via the first order derivative of the regression model. Applicable only for Taylor polynomial models.

Usage

```
plotDerivative(  
  model,  
  minAge = NULL,  
  maxAge = NULL,  
  minNorm = NULL,  
  maxNorm = NULL,  
  stepAge = NULL,  
  stepNorm = NULL,  
  order = 1  
)
```

Arguments

model	The model from the bestModel function, a cnorm object.
minAge	Minimum age to start checking.
maxAge	Maximum age for checking.
minNorm	Lower end of the norm score range.
maxNorm	Upper end of the norm score range.
stepAge	Stepping parameter for age.
stepNorm	Stepping parameter for norm scores.
order	Degree of the derivative (default = 1).

See Also

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDensity\(\)](#), [plotNorm\(\)](#), [plotNormCurves\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

plotNorm	<i>Plot manifest and fitted norm scores</i>
----------	---

Description

This function plots the manifest norm score against the fitted norm score from the inverse regression model per group. This helps to inspect the precision of the modeling process. The scores should not deviate too far from the regression line. Applicable for Taylor polynomial, beta-binomial, CMP, and shash models.

Usage

```
plotNorm(
  model,
  age = NULL,
  score = NULL,
  width = NULL,
  weights = NULL,
  group = FALSE,
  minNorm = NULL,
  maxNorm = NULL,
  type = 0
)
```

Arguments

model	The regression model, usually from the 'cnorm', 'cnorm.betabinomial', 'cnorm.cmp', or 'cnorm.shash' function
age	In case of parametric models, please provide the age vector
score	In case of parametric models, please provide the score vector
width	In case of parametric models, please provide the width for the sliding window. If null, the function tries to determine a sensible setting.
weights	Vector or variable name in the dataset with weights for each individual case. If NULL, no weights are used.
group	An optional grouping variable, use empty string for no group, the variable name for Taylor polynomial models or a vector with the groups for parametric models
minNorm	lower bound of fitted norm scores
maxNorm	upper bound of fitted norm scores
type	Type of display: 0 = plot manifest against fitted values, 1 = plot manifest against difference values

Value

A ggplot object representing the norm scores plot.

See Also

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDensity\(\)](#), [plotDerivative\(\)](#), [plotNormCurves\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

Examples

```
## Not run:
# Taylor polynomial model
model <- cnorm(raw = elfe$raw, group = elfe$group)
plot(model, "norm")
```

```
# Beta-binomial model
model.bb <- cnorm.betabinomial(elfe$group, elfe$raw, n = 28)
plotNorm(model.bb, age = elfe$group, score = elfe$raw)

# Conway-Maxwell-Poisson model
model.cmp <- cnorm.cmp(speeded$age, speeded$raw)
plotNorm(model.cmp, age = speeded$age, score = speeded$raw)

## End(Not run)
```

plotNormCurves	<i>Plot norm curves</i>
----------------	-------------------------

Description

This function plots the norm curves based on the regression model. It supports Taylor polynomial models, beta-binomial models, Conway-Maxwell-Poisson (CMP) models, and shash models.

Usage

```
plotNormCurves(
  model,
  normList = NULL,
  minAge = NULL,
  maxAge = NULL,
  step = 0.1,
  minRaw = NULL,
  maxRaw = NULL
)
```

Arguments

model	The model from the bestModel function, a cnorm object, or a cnormBetaBinomial / cnormBetaBinomial2 / cnormCMP / cnormShash object.
normList	Vector with norm scores to display. If NULL, default values are used.
minAge	Age to start with checking. If NULL, it's automatically determined from the model.
maxAge	Upper end of the age check. If NULL, it's automatically determined from the model.
step	Stepping parameter for the age check, usually 1 or 0.1; lower scores indicate higher precision.
minRaw	Lower end of the raw score range, used for clipping implausible results. If NULL, it's automatically determined from the model.
maxRaw	Upper end of the raw score range, used for clipping implausible results. If NULL, it's automatically determined from the model.

Details

Please check the function for inconsistent curves: The different curves should not intersect. Violations of this assumption are a strong indication of violations of model assumptions in modeling the relationship between raw and norm scores.

Common reasons for inconsistencies include: 1. Vertical extrapolation: Choosing extreme norm scores (e.g., scores ≤ -3 or ≥ 3). 2. Horizontal extrapolation: Using the model scores outside the original dataset. 3. The data cannot be modeled with the current approach, or you need another power parameter (k) or R2 for the model.

Value

A ggplot object representing the norm curves.

See Also

[checkConsistency](#), [plotDerivative](#), [plotPercentiles](#)

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDensity\(\)](#), [plotDerivative\(\)](#), [plotNorm\(\)](#), [plotPercentileSeries\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

Examples

```
## Not run:
# For Taylor continuous norming model
m <- cnorm(raw = ppvt$raw, group = ppvt$group)
plotNormCurves(m, minAge=2, maxAge=5)

# For beta-binomial model
bb_model <- cnorm.betabinomial(age = ppvt$age, score = ppvt$raw, n = 228)
plotNormCurves(bb_model)

# For CMP model
cmp_model <- cnorm.cmp(age = speeded$age, score = speeded$raw)
plotNormCurves(cmp_model)

## End(Not run)
```

plotPercentiles

Plot norm curves against actual percentiles

Description

The function plots the norm curves based on the regression model against the actual percentiles from the raw data. Applicable only for Taylor polynomial models. For parametric models (Beta-Binomial, CMP, or SHASH), please use `plot(model, age, score)` instead.

Usage

```
plotPercentiles(
  model,
  minRaw = NULL,
  maxRaw = NULL,
  minAge = NULL,
  maxAge = NULL,
  raw = NULL,
  group = NULL,
  percentiles = c(0.025, 0.1, 0.25, 0.5, 0.75, 0.9, 0.975),
  scale = NULL,
  title = NULL,
  subtitle = NULL,
  points = FALSE
)
```

Arguments

<code>model</code>	The Taylor polynomial regression model object from the <code>cNORM</code>
<code>minRaw</code>	Lower bound of the raw score (default = 0)
<code>maxRaw</code>	Upper bound of the raw score
<code>minAge</code>	Variable to restrict the lower bound of the plot to a specific age
<code>maxAge</code>	Variable to restrict the upper bound of the plot to a specific age
<code>raw</code>	The name of the raw variable
<code>group</code>	The name of the grouping variable; the distinct groups are automatically determined
<code>percentiles</code>	Vector with percentile scores, ranging from 0 to 1 (exclusive)
<code>scale</code>	The norm scale, either 'T', 'IQ', 'z', 'percentile' or self defined with a double vector with the mean and standard deviation
<code>title</code>	custom title for plot
<code>subtitle</code>	custom title for plot
<code>points</code>	Logical indicating whether to plot the data points. Default is TRUE.

See Also

`plotNormCurves`, `plotPercentileSeries`

Other plot: `compare()`, `plot.cnorm()`, `plot.cnormBetaBinomial()`, `plot.cnormBetaBinomial2()`, `plotDensity()`, `plotDerivative()`, `plotNorm()`, `plotNormCurves()`, `plotPercentileSeries()`, `plotRaw()`, `plotSubset()`

plotPercentileSeries *Generates a series of plots with percentile curves for different models*

Description

This function makes use of 'plotPercentiles' to generate a series of plots for models with an increasing number of terms.

Usage

```
plotPercentileSeries(
  model,
  start = 1,
  end = NULL,
  group = NULL,
  percentiles = c(0.025, 0.1, 0.25, 0.5, 0.75, 0.9, 0.975),
  filename = NULL
)
```

Arguments

model	The Taylor polynomial regression model object or a cnorm object
start	Number of terms to start with (default 1)
end	Number of terms to end with
group	The name of the grouping variable
percentiles	Vector with percentile scores
filename	Prefix of the filename if saving to png

See Also

plotPercentiles

Other plot: [compare\(\)](#), [plot.cnorm\(\)](#), [plot.cnormBetaBinomial\(\)](#), [plot.cnormBetaBinomial2\(\)](#), [plotDensity\(\)](#), [plotDerivative\(\)](#), [plotNorm\(\)](#), [plotNormCurves\(\)](#), [plotPercentiles\(\)](#), [plotRaw\(\)](#), [plotSubset\(\)](#)

plotRaw *Plot manifest and fitted raw scores*

Description

The function plots the raw data against the fitted scores from the regression model per group. This helps to inspect the precision of the modeling process. The scores should not deviate too far from regression line.

Usage

```
plotRaw(model, group = FALSE, type = 0)
```

Arguments

model	The regression model from the 'cnorm' function
group	Should the fit be displayed by group?
type	Type of display: 0 = plot manifest against fitted values, 1 = plot manifest against difference values

See Also

Other plot: `compare()`, `plot.cnorm()`, `plot.cnormBetaBinomial()`, `plot.cnormBetaBinomial2()`, `plotDensity()`, `plotDerivative()`, `plotNorm()`, `plotNormCurves()`, `plotPercentileSeries()`, `plotPercentiles()`, `plotSubset()`

Examples

```
## Not run:
# Compute model with example dataset and plot results
result <- cnorm(raw = elfe$raw, group = elfe$group)
plotRaw(result)

## End(Not run)
```

plotSubset

Evaluate information criteria for regression model

Description

This function plots various information criteria and model fit statistics for Taylor polynomial models.

Usage

```
plotSubset(model, type = 0)
```

Arguments

model	The regression model from the bestModel function or a cnorm object.
type	Integer specifying the type of plot to generate (0 to 6).

Value

A ggplot object representing the selected information criterion plot.

See Also

Other plot: `compare()`, `plot.cnorm()`, `plot.cnormBetaBinomial()`, `plot.cnormBetaBinomial2()`, `plotDensity()`, `plotDerivative()`, `plotNorm()`, `plotNormCurves()`, `plotPercentileSeries()`, `plotPercentiles()`, `plotRaw()`

ppvt

*Vocabulary development from 2.5 to 17***Description**

A dataset based on an unstratified sample of PPVT4 data (German adaption). The PPVT4 consists of blocks of items with 12 items each. Each item consists of 4 pictures. The test taker is given a word orally and he or she has to point out the picture matching the oral word. Bottom and ceiling blocks of items are determined according to age and performance. For instance, when a student knows less than 4 word from a block of 12 items, the testing stops. The sample is not identical with the norm sample and includes doublets of cases in order to align the sample size per age group. It is primarily intended for running the cNORM analyses with regard to modeling and stratification.

Usage

ppvt

Format

A data frame with 4542 rows and 6 variables:

age the chronological age of the child

sex the sex of the test taker, 1=male, 2=female

migration migration status of the family, 0=no, 1=yes

region factor specifying the region, the data were collected; grouped into south, north, east and west

raw the raw score of the student, spanning values from 0 to 228

group age group of the child, determined by the `getGroups()`-function with 12 equidistant age groups

A data frame with 5600 rows and 9 columns

Source

<https://www.psychometrica.de/ppvt4.html>

References

Lenhard, A., Lenhard, W., Segerer, R. & Suggate, S. (2015). Peabody Picture Vocabulary Test - Revision IV (Deutsche Adaption). Frankfurt a. M./Germany: Pearson Assessment.

Examples

```
## Not run:
# Example with continuous age variable, ranked with sliding window
model.ppvt.sliding <- cnorm(age=ppvt$age, raw=ppvt$raw, width=1)

# Example with age groups; you might first want to experiment with
# the granularity of the groups via the 'getGroups()' function
model.ppvt.group <- cnorm(group=ppvt$group, raw=ppvt$raw) # with predefined groups
model.ppvt.group <- cnorm(group=getGroups(ppvt$age, n=15, equidistant = T),
                          raw=ppvt$raw) # groups built 'on the fly'

# plot information function
plot(model.ppvt.group, "subset")

# check model consistency
checkConsistency(model.ppvt.group)

# plot percentiles
plot(model.ppvt.group, "percentiles")

## End(Not run)
```

predict.cnormBetaBinomial

Predict Norm Scores from Raw Scores

Description

This function calculates norm scores based on raw scores, age, and a fitted cnormBetaBinomial model.

Usage

```
## S3 method for class 'cnormBetaBinomial'
predict(object, ...)
```

Arguments

object	A fitted model object of class 'cnormBetaBinomial' or 'cnormBetaBinomial2'.
...	Additional arguments passed to the prediction method: • age A numeric vector of ages, same length as score. • score A numeric vector of raw scores. • range The range of the norm scores in standard deviations. Default is 3. Thus, scores in the range of +/- 3 standard deviations are considered.

Details

The function first predicts the alpha and beta parameters of the beta-binomial distribution for each unique age using the provided model. It then calculates the mid-p cumulative probability for each raw score given these parameters and converts these probabilities to the norm scale specified in the model. The distribution is computed only once per unique age value, which considerably speeds up predictions for grouped data.

Value

A numeric vector of norm scores (or percentiles, if no norm scale was specified in the model). Missing, non-integer or out-of-range raw scores yield NA.

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:
# Assuming you have a fitted model named 'bb_model':
model <- cnorm.betabinomial(ppvt$age, ppvt$raw)
raw <- c(100, 121, 97, 180)
ages <- c(7, 8, 9, 10)
norm_scores <- predict(model, ages, raw)

## End(Not run)
```

predict.cnormBetaBinomial2

Predict Norm Scores from Raw Scores

Description

This function calculates norm scores based on raw scores, age, and a fitted cnormBetaBinomial2 model. See [predict.cnormBetaBinomial](#) for details.

Usage

```
## S3 method for class 'cnormBetaBinomial2'
predict(object, ...)
```

Arguments

- object A fitted model object of class 'cnormBetaBinomial' or 'cnormBetaBinomial2'.
- ... Additional arguments passed to the prediction method:
- age A numeric vector of ages, same length as score.
 - score A numeric vector of raw scores.
 - range The range of the norm scores in standard deviations. Default is 3.

Value

A numeric vector of norm scores.

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

predict.cnormCMP	<i>Predict Norm Scores from Raw Scores (CMP model)</i>
------------------	--

Description

This function calculates norm scores based on raw scores, age, and a fitted cnormCMP model.

Usage

```
## S3 method for class 'cnormCMP'
predict(object, ...)
```

Arguments

- object A fitted model object of class 'cnormCMP'.
- ... Additional arguments passed to the prediction method:
- age A numeric vector of ages, same length as score.
 - score A numeric vector of raw scores (integers).
 - range The range of the norm scores in standard deviations. Default is 3. Thus, scores in the range of +/- 3 standard deviations are considered. Applies to type = "norm" and type = "z"; use Inf to switch the limit off.
 - mid_p Logical; use mid-p percentile ranks, $P(Y < x) + 0.5 * P(Y = x)$ (default TRUE), instead of $P(Y \leq x)$.
 - type What to return: "norm" (default; norm scores on the scale of the model), "z" (z-scores) or "percentile" (percentile ranks in 0 to 100, never limited by range).

Details

The function predicts the CMP parameters (μ , ν) for each age using the provided model, calculates the (mid-)percentile rank of each raw score under the corresponding discrete distribution, and converts it to the norm scale specified in the model. Extreme percentiles are mapped to the boundary of the norm score range (mean $\pm$ range standard deviations). A warning is issued for scores above `max_score` of a right-truncated model, and if the series could not be evaluated for some cases (NA is returned for them).

Value

A numeric vector of norm scores, z-scores or percentile ranks.

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:
model <- cnorm.cmp(children$age, children$score)
norm_scores <- predict(model, c(7, 8, 9, 10), c(25, 30, 18, 45))

# Mid-p percentile ranks instead of norm scores
predict(model, c(7, 8, 9, 10), c(25, 30, 18, 45), type = "percentile")

## End(Not run)
```

predict.cnormShash	<i>Predict Norm Scores from Raw Scores</i>
--------------------	--

Description

This function calculates norm scores based on raw scores, age, and a fitted `cnormShash` model.

Usage

```
## S3 method for class 'cnormShash'
predict(object, ...)
```

Arguments

<code>object</code>	A fitted model object of class <code>'cnormShash'</code> .
<code>...</code>	Additional arguments passed to the prediction method: <code>age</code> A numeric vector of ages, same length as <code>score</code>. <code>score</code> A numeric vector of raw scores. <code>range</code> The range of the norm scores in standard deviations. Default is 3. Thus, scores in the range of ± 3 standard deviations are considered.

Details

The function predicts the Sinh-Arcsinh (shash) distribution parameters (μ , σ , ϵ , δ) for each age using the provided model. It then calculates the cumulative probability for each raw score given these parameters using the continuous shash distribution. Finally, it converts these probabilities to the norm scale specified in the model. Raw scores at the extreme floor or ceiling of the distribution are mapped to the boundary of the norm score range (mean $\pm$ range standard deviations), not to the mean.

Value

A numeric vector of norm scores.

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:
# Assuming you have a fitted model named 'shash_model':
model <- cnorm.shash(children$age, children$score)
raw_scores <- c(25.5, 30.2, 18.7, 45.3)
ages <- c(7, 8, 9, 10)
norm_scores <- predict(model, ages, raw_scores)

## End(Not run)
```

predictMoments

Model-Implied Distributional Moments at Specific Ages

Description

Computes the mean, standard deviation, variance, skewness and (excess) kurtosis of the raw score distribution implied by a fitted cNORM model at one or more ages (or, more generally, values of the explanatory variable). The moments are model-implied population moments of the conditional raw score distribution, censored at the bounds of the raw score range [minRaw , maxRaw] for consistency across model families.

Usage

```
predictMoments(model, age, ...)

## Default S3 method:
predictMoments(model, age, ...)

## S3 method for class 'cnorm'
```

```

predictMoments(model, age, nNodes = 100, ...)

## S3 method for class 'cnormBetaBinomial'
predictMoments(model, age, ...)

## S3 method for class 'cnormBetaBinomial2'
predictMoments(model, age, ...)

## S3 method for class 'cnormCMP'
predictMoments(model, age, censor = TRUE, minRaw = NULL, maxRaw = NULL, ...)

## S3 method for class 'cnormShash'
predictMoments(model, age, nNodes = 100, ...)

```

Arguments

model	A model object of class <code>cnorm</code> , <code>cnormBetaBinomial</code> , <code>cnormBetaBinomial2</code> , <code>cnormCMP</code> , or <code>cnormShash</code> .
age	A numeric vector of ages (values of the explanatory variable) at which to compute the moments.
...	Additional parameters passed to the methods, e.g. <code>nNodes</code> or <code>censor</code> .
nNodes	Number of Gauss-Hermite quadrature nodes (default 100). Only relevant for the Taylor and SHASH methods; ignored for discrete models (Beta-Binomial, CMP), which are computed exactly by summation.
censor	Logical; if TRUE (default), the distribution is censored at <code>[minRaw, maxRaw]</code> to reflect the empirical score limits. If FALSE, uncensored theoretical population moments are calculated.
minRaw, maxRaw	Optional custom score bounds for censoring. If NULL (default), they are retrieved from the fitted model: the observed minimum, and the observed maximum or - for a right-truncated model fitted with <code>max_score</code> - the ceiling <code>max_score</code> , which is the upper bound of the support.

Details

The computation strategy depends on the model family:

Taylor polynomial (`cnorm`) The bivariate regression function is collapsed at the specified age into a univariate polynomial in the norm score (location) variable. Moments are then obtained by Gauss-Hermite quadrature, which is mathematically exact for polynomial quantile functions (up to the censoring at `minRaw/maxRaw`).

Beta-binomial (`cnormBetaBinomial`, `cnormBetaBinomial2`) Moments are computed exactly by summation over the discrete probability mass function on the support $0:n$, using the age-specific predicted α and β parameters. This respects the discreteness of the distribution; no continuity approximation is involved.

Conway-Maxwell-Poisson (`cnormCMP`) Moments are computed exactly by discrete summation over the probability mass function using the age-specific predicted μ and ν parameters. By default, the distribution is censored at `[minRaw, maxRaw]` to match the empirical test score range,

consistent with the other methods. Uncensored theoretical moments can be computed with `censor = FALSE`.

SHASH (`cnormShash`) Moments are obtained by Gauss-Hermite quadrature of the quantile function `qshash` evaluated at the age-specific distribution parameters, censored at `minRaw/maxRaw`.

Kurtosis is reported as *excess* kurtosis (0 for the normal distribution).

Note that the skewness and kurtosis of the *censored* distribution are reported by default. For well-fitting models whose raw score range covers the probability mass of the conditional distribution, censoring effects are negligible; for distributions with substantial floor or ceiling effects, the censored moments are the substantively meaningful ones.

Value

A data.frame with one row per age and the columns `age`, `mean`, `sd`, `variance`, `skewness` and `kurtosis` (excess). The computation method is stored in the attribute `"method"`.

References

- Conway, R. W., & Maxwell, W. L. (1962). A queuing model with state dependent service rates. *Journal of Industrial Engineering*, 12, 132-136.
- Isserlis, L. (1918). On a formula for the product-moment coefficient of any order of a normal frequency distribution in any number of variables. *Biometrika*, 12(1/2), 134-139.
- Jones, M. C. & Pewsey, A. (2009). Sinh-arcsinh distributions. *Biometrika*, 96(4), 761-780.

See Also

[normTable](#), [predictNorm](#), [predictRaw](#)

Examples

```
## Not run:
# Taylor polynomial model
model <- cnorm(raw = elfe$raw, group = elfe$group)
predictMoments(model, age = c(2.25, 2.75, 3.25, 3.75, 4.25))

# Beta-binomial model
bb <- cnorm.betabinomial(age = ppvt$age, score = ppvt$raw, n = 228)
predictMoments(bb, age = seq(4, 16, by = 2))

# Conway-Maxwell-Poisson model (speeded tests)
cmp <- cnorm.cmp(age = speeded$age, score = speeded$raw)
predictMoments(cmp, age = c(7, 8, 9, 10))

## End(Not run)
```

predictNorm	<i>Retrieve norm value for raw score at a specific age</i>
-------------	--

Description

This functions numerically determines the norm score for raw scores depending on the level of the explanatory variable A, e. g. norm scores for raw scores at given ages.

Usage

```
predictNorm(
  raw,
  A,
  model,
  minNorm = NULL,
  maxNorm = NULL,
  force = TRUE,
  silent = FALSE
)
```

Arguments

raw	The raw value, either single numeric or numeric vector
A	the explanatory variable (e. g. age), either single numeric or numeric vector
model	The regression model or a cnorm object
minNorm	The lower bound of the norm score range
maxNorm	The upper bound of the norm score range
force	Try to resolve missing norm scores in case of inconsistent models
silent	set to TRUE to suppress messages

Value

The predicted norm score for a raw score, either single value or vector

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictRaw\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:
# Generate cnorm object from example data
cnorm.elfe <- cnorm(raw = elfe$raw, group = elfe$group)

# return norm value for raw value 21 for grade 2, month 9
specificNormValue <- predictNorm(raw = 21, A = 2.75, cnorm.elfe)

## End(Not run)
```

predictRaw	<i>Predict raw values</i>
------------	---------------------------

Description

Most elementary function to predict raw score based on Location (L, T score), Age (grouping variable) and the coefficients from a regression model.

Usage

```
predictRaw(norm, age, coefficients, minRaw = -Inf, maxRaw = Inf)
```

Arguments

norm	The norm score, e. g. a specific T score or a vector of scores
age	The age value or a vector of scores
coefficients	The a cnorm object or the coefficients from the regression model
minRaw	Minimum score for the results; can be used for clipping unrealistic outcomes, usually set to the lower bound of the range of values of the test (default: 0)
maxRaw	Maximum score for the results; can be used for clipping unrealistic outcomes usually set to the upper bound of the range of values of the test

Value

the predicted raw score or a data.frame of scores in case, lists of norm scores or age is used

See Also

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [rawTable\(\)](#)

Examples

```
## Not run:
# Prediction of single scores
model <- cnorm(raw = elfe$raw, group = elfe$group)
predictRaw(35, 3.5, model)

## End(Not run)
```

prepareData

Prepare data for modeling in one step (convenience method)

Description

This is a convenience method to either load the inbuilt sample dataset, or to provide a data frame with the variables "raw" (for the raw scores) and "group". The function ranks the data within groups, computes norm values, powers of the norm scores and interactions. Afterwards, you can use these preprocessed data to determine the best fitting model.

Usage

```
prepareData(
  data = NULL,
  group = "group",
  raw = "raw",
  age = "group",
  k = 4,
  t = NULL,
  width = NA,
  weights = NULL,
  scale = "T",
  descend = FALSE,
  silent = FALSE
)
```

Arguments

data	data.frame with a grouping variable named 'group' and a raw score variable named 'raw'.
group	grouping variable in the data, e. g. age groups, grades ... Setting group = FALSE deactivates modeling in dependence of age. Use this in case you do want conventional norm tables.
raw	the raw scores
age	the continuous explanatory variable; by default set to "group"
k	The power parameter, default = 4

t	the age power parameter (default NULL). If not set, cNORM automatically uses k. The age power parameter can be used to specify the k to produce rectangular matrices and specify the course of scores per independently from k
width	if a width is provided, the function switches to rankBySlidingWindow to determine the observed raw scores, otherwise, ranking is done by group (default)
weights	Vector or variable name in the dataset with weights for each individual case. It can be used to compensate for moderate imbalances due to insufficient norm data stratification. Weights should be numerical and positive. Please use the 'computeWeights' function for this purpose.
scale	type of norm scale, either T (default), IQ, z or percentile (= no transformation); a double vector with the mean and standard deviation can as well, be provided f. e. c(10, 3) for Wechsler scale index point
descend	ranking order (default descent = FALSE): inverses the ranking order with higher raw scores getting lower norm scores; relevant for example when norming error scores, where lower scores mean higher performance
silent	set to TRUE to suppress messages

Details

The functions rankBySlidingWindow, rankByGroup, bestModel, computePowers and prepareData are usually not called directly, but accessed through other functions like cnorm.

Value

data frame including the norm scores, powers and interactions of the norm score and grouping variable

See Also

Other prepare: [computePowers\(\)](#), [rankByGroup\(\)](#), [rankBySlidingWindow\(\)](#)

Examples

```
## Not run:
# conducts ranking and computation of powers and interactions with the 'elfe' dataset
data.elfe <- prepareData(elfe)

# use vectors instead of data frame
data.elfe <- prepareData(raw=elfe$raw, group=elfe$group)

# variable names can be specified as well, here with the BMI data included in the package
data.bmi <- prepareData(CDC, group = "group", raw = "bmi", age = "age")

## End(Not run)

# modeling with only one group with the 'elfe' dataset as an example
# this results in conventional norming
data.elfe2 <- prepareData(data = elfe, group = FALSE)
m <- bestModel(data.elfe2)
```

print.cnorm	<i>S3 method for printing model selection information</i>
-------------	---

Description

After conducting the model fitting procedure on the data set, the best fitting model has to be chosen. The print function shows the R2 and other information on the different best fitting models with increasing number of predictors.

Usage

```
## S3 method for class 'cnorm'
print(x, ...)
```

Arguments

x	The model from the 'bestModel' function or a cnorm object
...	additional parameters

Value

A table with information criteria

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

print.cnormCMP	<i>Print method for CMP objects</i>
----------------	-------------------------------------

Description

Print method for CMP objects

Usage

```
## S3 method for class 'cnormCMP'
print(x, ...)
```

Arguments

x	A cnormCMP object
...	Additional arguments

print.cnormShash	<i>Print method for Sinh-Arcsinh objects</i>
------------------	--

Description

Print method for Sinh-Arcsinh objects

Usage

```
## S3 method for class 'cnormShash'
print(x, ...)
```

Arguments

x	A cnormShash object
...	Additional arguments

printSubset	<i>Print Model Selection Information</i>
-------------	--

Description

Displays R^2 and other metrics for models with varying predictors, aiding in choosing the best-fitting model after model fitting. The F-test compares each model to the preceding (smaller) one, with degrees of freedom based on the actual difference in the number of parameters.

Usage

```
printSubset(x, ...)
```

Arguments

x	Model output from 'bestModel' or a cnorm object.
...	Additional parameters.

Value

Table with model information criteria.

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

Examples

```
## Not run:
result <- cnorm(raw = elfe$raw, group = elfe$group)
printSubset(result)

## End(Not run)
```

rangeCheck

*Check for horizontal and vertical extrapolation***Description**

Regression models only work in a specific range and extrapolation horizontally (outside the original range) or vertically (extreme norm scores) might lead to inconsistent results. The function generates a message, indicating extrapolation and the range of the original data.

Usage

```
rangeCheck(
  object,
  minAge = NULL,
  maxAge = NULL,
  minNorm = NULL,
  maxNorm = NULL,
  digits = 3,
  ...
)
```

Arguments

object	The regression model or a cnorm object
minAge	The lower age bound
maxAge	The upper age bound
minNorm	The lower norm value bound
maxNorm	The upper norm value bound
digits	The precision for rounding the norm and age data
...	additional parameters

Value

the report

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

Examples

```
## Not run:
m <- cnorm(raw = elfe$raw, group = elfe$group)
rangeCheck(m)

## End(Not run)
```

rankByGroup

Determine the norm scores of the participants in each subsample

Description

This is the initial step, usually done in all kinds of test norming projects, after the scale is constructed and the norm sample is established. First, the data is grouped according to a grouping variable and afterwards, the percentile for each raw value is retrieved. The percentile can be used for the modeling procedure, but in case, the samples do not deviate too much from normality, T, IQ or z scores can be computed via a normal rank procedure based on the inverse cumulative normal distribution. In case of bindings, we use the medium rank and there are different methods for estimating the percentiles (default RankIt).

Usage

```
rankByGroup(
  data = NULL,
  group = "group",
  raw = "raw",
  weights = NULL,
  method = 4,
  scale = "T",
  descend = FALSE,
  descriptives = TRUE,
  na.rm = TRUE,
  silent = FALSE
)
```

Arguments

data	data.frame with norm sample data. If no data.frame is provided, the raw score and group vectors are directly used
group	name of the grouping variable (default 'group') or numeric vector, e. g. grade, setting group to FALSE cancels grouping (data is treated as one group)
raw	name of the raw value variable (default 'raw') or numeric vector
weights	Vector or variable name in the dataset with weights for each individual case. It can be used to compensate for moderate imbalances due to insufficient norm data stratification. Weights should be numerical and positive. Please use the 'computeWeights' function for this purpose.

method	Ranking method in case of bindings, please provide an index, choosing from the following methods: 1 = Blom (1958), 2 = Tukey (1949), 3 = Van der Warden (1952), 4 = Rankit (default), 5 = Levenbach (1953), 6 = Filliben (1975), 7 = Yu & Huang (2001)
scale	type of norm scale, either T (default), IQ, z or percentile (= no transformation); a double vector with the mean and standard deviation can as well, be provided f. e. c(10, 3) for Wechsler scale index points
descend	ranking order (default descent = FALSE): inverses the ranking order with higher raw scores getting lower norm scores; relevant for example when norming error scores, where lower scores mean higher performance
descriptives	If set to TRUE (default), information in n, mean, median and standard deviation per group is added to each observation
na.rm	remove values, where the percentiles could not be estimated, most likely happens in the context of weighting
silent	set to TRUE to suppress messages

Value

the dataset with the percentiles and norm scales per group

Remarks on using covariates

So far the inclusion of a binary covariate is experimental and far from optimized. The according variable name has to be specified in the ranking procedure and the modeling includes this in the further process. At the moment, during ranking the data are split into the according cells group x covariate, which leads to small sample sizes. Please take care to have enough cases in each combination. Additionally, covariates can lead to unstable modeling solutions. The question, if it is really reasonable to include covariates when norming a test is a decision beyond the pure data modeling. Please use with care or alternatively split the dataset into the two groups beforehand and model them separately.

The functions rankBySlidingWindow, rankByGroup, bestModel, computePowers and prepareData are usually not called directly, but accessed through other functions like cnorm.

See Also

rankBySlidingWindow, computePowers, computeWeights, weighted.rank

Other prepare: [computePowers\(\)](#), [prepareData\(\)](#), [rankBySlidingWindow\(\)](#)

Examples

```
## Not run:
# Transformation with default parameters: RankIt and converting to T scores
data.elfe <- rankByGroup(elfe, group = "group") # using a data frame with vector names
data.elfe2 <- rankByGroup(raw=elfe$raw, group=elfe$group) # use vectors for raw score and group

# Transformation into Wechsler scores with Yu & Huang (2001) ranking procedure
data.elfe <- rankByGroup(raw = elfe$raw, group = elfe$group, method = 7, scale = c(10, 3))
```

```
# cNORM can as well be used for conventional norming, in case no group is given
d <- rankByGroup(raw = elfe$raw)
d <- computePowers(d)
m <- bestModel(d)
rawTable(0, m) # please use an arbitrary value for age when generating the tables

## End(Not run)
```

rankBySlidingWindow *Determine the norm scores of the participants by sliding window*

Description

The function retrieves all individuals in the predefined age range ($x \pm \text{width}/2$) around each case and ranks that individual based on this individually drawn sample. This function can be directly used with a continuous age variable in order to avoid grouping. When collecting data on the basis of a continuous age variable, cases located far from the mean age of the group receive distorted percentiles when building discrete groups and generating percentiles with the traditional approach. The distortion increases with distance from the group mean and this effect can be avoided by the sliding window. Nonetheless, please ensure, that the optional grouping variable in fact represents the correct mean age of the respective age groups, as this variable is later on used for displaying the manifest data in the percentile plots.

Usage

```
rankBySlidingWindow(
  data = NULL,
  age = "age",
  raw = "raw",
  weights = NULL,
  width,
  method = 4,
  scale = "T",
  descend = FALSE,
  descriptives = TRUE,
  nGroup = 0,
  group = NA,
  na.rm = TRUE,
  silent = FALSE
)
```

Arguments

data	data.frame with norm sample data
age	the continuous age variable. Setting 'age' to FALSE inhibits computation of powers of age and the interactions

raw	name of the raw value variable (default 'raw')
weights	Vector or variable name in the dataset with weights for each individual case. It can be used to compensate for moderate imbalances due to insufficient norm data stratification. Weights should be numerical and positive. It can be resource intense when applied to the sliding window. Please use the 'computeWeights' function for this purpose.
width	the width of the sliding window
method	Ranking method in case of bindings, please provide an index, choosing from the following methods: 1 = Blom (1958), 2 = Tukey (1949), 3 = Van der Warden (1952), 4 = Rankit (default), 5 = Levenbach (1953), 6 = Filliben (1975), 7 = Yu & Huang (2001)
scale	type of norm scale, either T (default), IQ, z or percentile (= no transformation); a double vector with the mean and standard deviation can as well, be provided f. e. c(10, 3) for Wechsler scale index points
descend	ranking order (default descent = FALSE): inverses the ranking order with higher raw scores getting lower norm scores; relevant for example when norming error scores, where lower scores mean higher performance
descriptives	If set to TRUE (default), information in n, mean, median and standard deviation per group is added to each observation
nGroup	If set to a positive value, a grouping variable is created with the desired number of equi distant groups, named by the group mean age of each group. It creates the column 'group' in the data.frame and in case, there is already one with that name, overwrites it.
group	Optional parameter for providing the name of the grouping variable (if present; overwritten if ngroups is used)
na.rm	remove values, where the percentiles could not be estimated, most likely happens in the context of weighting
silent	set to TRUE to suppress messages

Details

In case of bindings, the function uses the medium rank and applies the algorithms already described in the [rankByGroup](#) function. At the upper and lower end of the data sample, the sliding stops and the sample is drawn from the interval $\min + \text{width}$ and $\max - \text{width}$, respectively.

Value

the dataset with the individual percentiles and norm scores

Remarks on using covariates

So far the inclusion of a binary covariate is experimental and far from optimized. The according variable name has to be specified in the ranking procedure and the modeling includes this in the further process. At the moment, during ranking the data are split into the according degrees of the covariate and the ranking is done separately. This may lead to small sample sizes. Please take care to have enough cases in each combination. Additionally, covariates can lead to unstable modeling

solutions. The question, if it is really reasonable to include covariates when norming a test is a decision beyond the pure data modeling. Please use with care or alternatively split the dataset into the two groups beforehand and model them separately.

The functions `rankBySlidingWindow`, `rankByGroup`, `bestModel`, `computePowers` and `prepareData` are usually not called directly, but accessed through other functions like `cnorm`.

See Also

`rankByGroup`, `computePowers`, `computeWeights`, `weighted.rank`, `weighted.quantile`

Other prepare: `computePowers()`, `prepareData()`, `rankByGroup()`

Examples

```
## Not run:
# Transformation using a sliding window
data.elfe2 <- rankBySlidingWindow(elfe, raw = "raw", age = "group", width = 0.5)

# Comparing this to the traditional approach should give us exactly the same
# values, since the sample dataset only has a grouping variable for age
data.elfe <- rankByGroup(elfe, group = "group")
mean(data.elfe$normValue - data.elfe2$normValue)

## End(Not run)
```

rawTable

Create a table with norm scores assigned to raw scores for a specific age based on the regression model

Description

This function is comparable to `'normTable'`, despite it reverses the assignment: A table with raw scores and the according norm scores for a specific age based on the regression model is generated. This way, the inverse function of the regression model is solved numerically with brute force. Please specify the range of raw values, you want to cover. With higher precision and smaller stepping, this function becomes computational intensive. In case a confidence coefficient (CI, default .9) and the reliability is specified, confidence intervals are computed for the true score estimates, including a correction for regression to the mean (Eid & Schmidt, 2012, p. 272).

Usage

```
rawTable(
  A,
  model,
  minRaw = NULL,
  maxRaw = NULL,
  minNorm = NULL,
  maxNorm = NULL,
  step = 1,
```

```

    monotonuous = TRUE,
    CI = 0.9,
    reliability = NULL,
    pretty = TRUE
  )

```

Arguments

A	the age, either single value or vector with age values
model	The regression model or a cnorm object
minRaw	The lower bound of the raw score range
maxRaw	The upper bound of the raw score range
minNorm	Clipping parameter for the lower bound of norm scores (default 25)
maxNorm	Clipping parameter for the upper bound of norm scores (default 25)
step	Stepping parameter for the raw scores (default 1)
monotonuous	corrects for decreasing norm scores in case of model inconsistencies (default)
CI	confidence coefficient, ranging from 0 to 1, default .9
reliability	coefficient, ranging between 0 to 1
pretty	Format table by collapsing intervals and rounding to meaningful precision

Value

either data.frame with raw scores and the predicted norm scores in case of simple A value or a list of norm tables if vector of A values was provided

References

Eid, M. & Schmidt, K. (2012). Testtheorie und Testkonstruktion. Hogrefe.

See Also

normTable

Other predict: [derivationTable\(\)](#), [getNormCurve\(\)](#), [normTable\(\)](#), [predict.cnormBetaBinomial\(\)](#), [predict.cnormBetaBinomial2\(\)](#), [predict.cnormCMP\(\)](#), [predict.cnormShash\(\)](#), [predictNorm\(\)](#), [predictRaw\(\)](#)

Examples

```

## Not run:
# Generate cnorm object from example data
cnorm.elfe <- cnorm(raw = elfe$raw, group = elfe$group)
# generate a norm table for the raw value range from 0 to 28 for the time point month 7 of grade 3
table <- rawTable(3 + 7 / 12, cnorm.elfe, minRaw = 0, maxRaw = 28)

# generate several raw tables
table <- rawTable(c(2.5, 3.5, 4.5), cnorm.elfe, minRaw = 0, maxRaw = 28)

```

```
# additionally compute confidence intervals
table <- rawTable(c(2.5, 3.5, 4.5), cnorm.elfe, minRaw = 0, maxRaw = 28, CI = .9, reliability = .94)

# conventional norming, set age to arbitrary value
model <- cnorm(raw = elfe$raw)
rawTable(0, model)

## End(Not run)
```

regressionFunction	<i>Regression function</i>
--------------------	----------------------------

Description

The method builds the regression function for the regression model, including the beta weights. It can be used to predict the raw scores based on age and location.

Usage

```
regressionFunction(model, raw = NULL, digits = NULL)
```

Arguments

model	The regression model from the bestModel function or a cnorm object
raw	The name of the raw value variable (default 'raw')
digits	Number of digits for formatting the coefficients

Value

The regression formula as a string

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [summary.cnorm\(\)](#), [weightedAverageModel\(\)](#)

Examples

```
## Not run:
result <- cnorm(raw = elfe$raw, group = elfe$group)
regressionFunction(result)

## End(Not run)
```

residuals.cnormCMP *Residuals of a CMP continuous norming model*

Description

Computes residuals on the z-scale for a diagnostic check of the fitted model. With `type = "quantile"`, randomized quantile residuals (Dunn & Smyth, 1996) are returned: if the model is correct, they are exactly standard normal, also for discrete data. With `type = "z"`, the deterministic mid-p z-scores $\Phi^{-1}(P(Y < y) + 0.5P(Y = y))$ are returned (the z-scores underlying the norm scores); they are approximately standard normal for larger counts, but their variance is slightly below 1 for small counts.

Usage

```
## S3 method for class 'cnormCMP'
residuals(object, age, score, type = c("quantile", "z"), seed = NULL, ...)
```

Arguments

<code>object</code>	A fitted model of class "cnormCMP".
<code>age</code>	Numeric vector of ages.
<code>score</code>	Numeric vector of raw scores (counts), same length as <code>age</code> .
<code>type</code>	"quantile" (randomized, default) or "z" (mid-p).
<code>seed</code>	Optional seed; if given, <code>set.seed(seed)</code> is called before the randomization (note that this changes the state of the random number generator).
<code>...</code>	Not used.

Value

A numeric vector of residuals.

References

Dunn, P. K., & Smyth, G. K. (1996). Randomized quantile residuals. *Journal of Computational and Graphical Statistics*, 5(3), 236-244.

Examples

```
## Not run:
model <- cnorm.cmp(speed$age, speed$fluency)
r <- residuals(model, speed$age, speed$fluency, seed = 1)
c(mean(r), sd(r))
qqnorm(r)

## End(Not run)
```

shash	<i>Sinh-Arcsinh (shash) Distribution</i>
-------	--

Description

Density, distribution function, quantile function and random generation for the Sinh-Arcsinh distribution with location parameter μ , scale parameter σ , skewness parameter ϵ , and tail weight parameter δ .

Usage

```
dshash(x, mu = 0, sigma = 1, epsilon = 0, delta = 1, log = FALSE)
```

```
pshash(
  q,
  mu = 0,
  sigma = 1,
  epsilon = 0,
  delta = 1,
  lower.tail = TRUE,
  log.p = FALSE
)
```

```
qshash(
  p,
  mu = 0,
  sigma = 1,
  epsilon = 0,
  delta = 1,
  lower.tail = TRUE,
  log.p = FALSE
)
```

```
rshash(n, mu = 0, sigma = 1, epsilon = 0, delta = 1)
```

Arguments

<code>x, q</code>	vector of quantiles
<code>mu</code>	location parameter (default: 0)
<code>sigma</code>	scale parameter (must be > 0 , default: 1)
<code>epsilon</code>	skewness parameter (default: 0, symmetric distribution)
<code>delta</code>	tail weight parameter (must be > 0 , default: 1 for normal-like tails; $\delta < 1$ gives heavier tails, $\delta > 1$ gives lighter tails)
<code>log, log.p</code>	logical; if TRUE, probabilities p are given as $\log(p)$
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$

p	vector of probabilities
n	number of observations. If length(n) > 1, the length is taken to be the number required.

Details

The Sinh-Arcsinh distribution (Jones & Pewsey, 2009) is defined by the transformation:

$$X = \mu + \sigma \cdot \sinh\left(\frac{\operatorname{asinh}(Z) - \epsilon}{\delta}\right)$$

where $Z \sim N(0, 1)$ is a standard normal variable.

The four parameters control:

- mu: Location (similar to mean)
- sigma: Scale (similar to standard deviation)
- epsilon: Skewness (epsilon = 0 gives symmetry)
- delta: Tail weight (delta = 1 gives normal-like tails, delta < 1 gives heavier tails, delta > 1 gives lighter tails)

Value

dshash gives the density, pshash gives the distribution function, qshash gives the quantile function, and rshash generates random deviates.

The length of the result is determined by n for rshash, and is the maximum of the lengths of the numerical arguments for the other functions.

References

Jones, M. C., & Pewsey, A. (2009). Sinh-arcsinh distributions. *Biometrika*, 96(4), 761-780.
[doi:10.1093/biomet/asp053](https://doi.org/10.1093/biomet/asp053)

See Also

[Normal](#) for the normal distribution.

Examples

```
# Generate random samples
x <- rshash(1000, mu = 0, sigma = 1, epsilon = 0.5, delta = 1.2)

# Density
plot(density(x))
curve(dshash(x, mu = 0, sigma = 1, epsilon = 0.5, delta = 1.2),
      add = TRUE, col = "red")

# Cumulative probability
pshash(0, mu = 0, sigma = 1, epsilon = 0.5, delta = 1.2)

# Quantiles
```

```

qshash(c(0.025, 0.5, 0.975), mu = 0, sigma = 1, epsilon = 0.5, delta = 1.2)

# Compare with normal distribution (epsilon = 0, delta = 1)
oldpar <- par(mfrow = c(2, 2))
x_vals <- seq(-4, 4, length.out = 200)
plot(x_vals, dshash(x_vals), type = "l", main = "Symmetric (like normal)")
plot(x_vals, dshash(x_vals, epsilon = 1), type = "l", main = "Right skewed")
plot(x_vals, dshash(x_vals, delta = 0.5), type = "l", main = "Heavy tails")
plot(x_vals, dshash(x_vals, delta = 2), type = "l", main = "Light tails")
par(oldpar)

```

simMean

Simulate mean per age

Description

Simulate mean per age

Usage

```
simMean(age)
```

Arguments

age the age variable

Value

return predicted means

Examples

```

## Not run:
x <- simMean(a)

## End(Not run)

```

simSD	<i>Simulate sd per age</i>
-------	----------------------------

Description

Simulate sd per age

Usage

```
simSD(age)
```

Arguments

age the age variable

Value

return predicted sd

Examples

```
## Not run:  
x <- simSD(a)  
  
## End(Not run)
```

simulateRasch	<i>Simulate raw test scores based on Rasch model</i>
---------------	--

Description

For testing purposes only: The function simulates raw test scores based on a virtual Rasch based test with n results per age group, an evenly distributed age variable, items.n test items with a simulated difficulty and standard deviation. The development trajectories over age group are modeled by a curve linear function of age, with at first fast progression, which slows down over age, and a slightly increasing standard deviation in order to model a scissor effects. The item difficulties can be accessed via \$theta and the raw data via \$data of the returned object.

Usage

```
simulateRasch(  
  data = NULL,  
  n = 100,  
  minAge = 1,  
  maxAge = 7,  
  items.n = 21,
```

```

    items.m = 0,
    items.sd = 1,
    Theta = "random",
    width = 1
  )

```

Arguments

<code>data</code>	data.frame from previous simulations for recomputation (overrides <code>n</code> , <code>minAge</code> , <code>maxAge</code>)
<code>n</code>	The sample size per age group
<code>minAge</code>	The minimum age (default 1)
<code>maxAge</code>	The maximum age (default 7)
<code>items.n</code>	The number of items of the test
<code>items.m</code>	The mean difficulty of the items
<code>items.sd</code>	The standard deviation of the item difficulty
<code>Theta</code>	irt scales difficulty parameters, either "random" for drawing a random sample, "even" for evenly distributed or a set of predefined values, which then overrides the <code>items.n</code> parameters
<code>width</code>	The width of the window size for the continuous age per group; +- 1/2 width around group center on <code>items.m</code> and <code>items.sd</code> ; if set to FALSE, the distribution is not drawn randomly but normally nonetheless

Value

a list containing the simulated data and thetas

data the data.frame with only age, group and raw

sim the complete simulated data with item level results

theta the difficulty of the items

Examples

```

## Not run:
# simulate data for a rather easy test (m = -1.0)
sim <- simulateRasch(n=150, minAge=1,
                    maxAge=7, items.n = 30, items.m = -1.0,
                    items.sd = 1, Theta = "random", width = 1.0)

# Show item difficulties
mean(sim$theta)
sd(sim$theta)
hist(sim$theta)

# Plot raw scores
boxplot(raw~group, data=sim$data)

# Model data

```

```

data <- prepareData(sim$data, age="age")
model <- bestModel(data, k = 4)
printSubset(model)
plotSubset(model, type=0)

## End(Not run)

```

speed

Word reading fluency test from ELFE-II

Description

A synthetic dataset containing 1438 records simulating children's performance in the word reading fluency subtest from the ELFE-II reading assessment (Lenhard, Lenhard, & Schneider, 2017). In this subtest, students are presented with individual words paired with pictures and must rapidly identify the matching item under a strict time limit (speeded decoding). The synthetic data preserves the marginal distributions, age trajectory, and variance structure of empirical test results.

Usage

```
speed
```

Format

A data frame with 1438 rows and 2 variables:

age chronological age of the student in years (decimal)

fluency the raw score achieved by the student, indicating the number of correctly processed items within the time limit

Source

<https://www.psychometrica.de/elfe2.html>

References

Lenhard, W., Lenhard, A. & Schneider, W. (2017). ELFE II: Ein Leseverstaendnistest fuer Erst- bis Siebtklaessler. Goettingen: Hogrefe.

Examples

```

## Not run:
# Model continuous norms using cnorm
model <- cnorm(age = speed$age, raw = speed$fluency)
summary(model)
plotPercentiles(model)

## End(Not run)

```

standardize	<i>Standardize a numeric vector</i>
-------------	-------------------------------------

Description

This function standardizes a numeric vector by subtracting the mean and dividing by the standard deviation. The resulting vector will have a mean of 0 and a standard deviation of 1.

Usage

```
standardize(x)
```

Arguments

x A numeric vector to be standardized.

Value

A numeric vector of the same length as x, containing the standardized values.

Examples

```
## Not run:
data <- c(1, 2, 3, 4, 5)
standardized_data <- standardize(data)
print(standardized_data)

## End(Not run)
```

summary.cnorm	<i>S3 method for printing the results and regression function of a cnorm model</i>
---------------	--

Description

S3 method for printing the results and regression function of a cnorm model

Usage

```
## S3 method for class 'cnorm'
summary(object, ...)
```

Arguments

object A regression model or cnorm object
... additional parameters

Value

A report on the regression function, weights, R2 and RMSE

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [weightedAverageModel\(\)](#)

```
summary.cnormBetaBinomial
```

Summarize a Beta-Binomial Continuous Norming Model

Description

This function provides a summary of a fitted beta-binomial continuous norming model, including model fit statistics, convergence information, and parameter estimates.

Usage

```
## S3 method for class 'cnormBetaBinomial'
summary(object, ...)
```

Arguments

- | | |
|--------|--|
| object | An object of class "cnormBetaBinomial" or "cnormBetaBinomial2", typically the result of a call to cnorm.betabinomial . |
| ... | Additional arguments passed to the summary method: <ul style="list-style-type: none"> • age An optional numeric vector of age values corresponding to the raw scores. If provided along with score, additional fit statistics (R-squared, RMSE, bias) will be calculated. • score An optional numeric vector of raw scores. Must be provided if age is given. • weights An optional numeric vector of weights for each observation. |

Details

The summary includes:

- Basic model information (type, number of observations, number of parameters)
- Model fit statistics (log-likelihood, AIC, BIC)
- R-squared, RMSE, and bias (if age and raw scores are provided) in comparison to manifest norm scores
- Convergence information, including the maximum absolute gradient at the solution (first-order optimality)
- Parameter estimates with standard errors, z-values, and p-values

Value

Invisibly returns a list containing detailed diagnostic information about the model. The function primarily produces printed output summarizing the model.

See Also

[cnorm.betabinomial](#), [diagnostics.betabinomial](#)

Examples

```
## Not run:
model <- cnorm.betabinomial(ppvt$age, ppvt$raw, n = 228)
summary(model)

# Including R-squared, RMSE, and bias in the summary:
summary(model, age = ppvt$age, score = ppvt$raw)

## End(Not run)
```

summary.cnormBetaBinomial2

Summarize a Beta-Binomial Continuous Norming Model

Description

Summary method for objects of class "cnormBetaBinomial2". See [summary.cnormBetaBinomial](#) for details.

Usage

```
## S3 method for class 'cnormBetaBinomial2'
summary(object, ...)
```

Arguments

object	An object of class "cnormBetaBinomial" or "cnormBetaBinomial2", typically the result of a call to cnorm.betabinomial .
...	Additional arguments passed to the summary method: • age An optional numeric vector of age values. • score An optional numeric vector of raw scores. • weights An optional numeric vector of weights.

Value

Invisibly returns a list containing detailed diagnostic information about the model.

See Also

[cnorm.betabinomial](#), [diagnostics.betabinomial](#)

summary.cnormCMP

Summarize a CMP Continuous Norming Model

Description

This function provides a summary of a fitted Conway-Maxwell-Poisson continuous norming model, including model fit statistics, convergence information, and parameter estimates.

Usage

```
## S3 method for class 'cnormCMP'
summary(object, ...)
```

Arguments

- | | |
|--------|---|
| object | An object of class "cnormCMP", typically the result of a call to cnorm.cmp . |
| ... | Additional arguments passed to the summary method: <ul style="list-style-type: none"> • age An optional numeric vector of age values corresponding to the raw scores. If provided along with score, additional fit statistics (R-squared, RMSE, bias) and a calibration table (mean and SD of the z-residuals per age group) are calculated. • score An optional numeric vector of raw scores. Must be provided if age is given. • weights An optional numeric vector of weights for each observation. |

Details

The summary includes basic model information, model fit statistics (log-likelihood, AIC, BIC), R-squared, RMSE and bias (if age and raw scores are provided), convergence information, and parameter estimates with standard errors, z-values and p-values. Coefficients refer to the log scale: log(μ) and log(ν); only the intercepts refer to the mean age. The calibration table should show means near 0 and SDs near 1 in every age group (the SD of mid-p z-scores is slightly below 1 for small counts; see [residuals.cnormCMP](#)).

Value

Invisibly returns a list containing detailed diagnostic information about the model. The function primarily produces printed output summarizing the model.

See Also

[cnorm.cmp](#), [diagnostics.cmp](#)

Examples

```
## Not run:
model <- cnorm.cmp(speeded$age, speeded$raw)
summary(model)
summary(model, age = speeded$age, score = speeded$raw)

## End(Not run)
```

summary.cnormShash	<i>Summarize a Sinh-Arcsinh Continuous Norming Model</i>
--------------------	--

Description

This function provides a summary of a fitted Sinh-Arcsinh (shash) continuous norming model, including model fit statistics, convergence information, and parameter estimates.

Usage

```
## S3 method for class 'cnormShash'
summary(object, ...)
```

Arguments

object	An object of class "cnormShash", typically the result of a call to cnorm.shash .
...	Additional arguments passed to the summary method: • age An optional numeric vector of age values corresponding to the raw scores. If provided along with score, additional fit statistics (R-squared, RMSE, bias) will be calculated. • score An optional numeric vector of raw scores. Must be provided if age is given. • weights An optional numeric vector of weights for each observation.

Details

The summary includes:

- Basic model information (polynomial degrees, delta parameter, number of observations)
- Model fit statistics (log-likelihood, AIC, BIC)
- R-squared, RMSE, and bias (if age and raw scores are provided)
- Convergence information
- Parameter estimates with standard errors, z-values, and p-values

Value

Invisibly returns a list containing detailed diagnostic information about the model. The function primarily produces printed output summarizing the model.

See Also

[cnorm.shash](#), [diagnostics.shash](#)

Examples

```
## Not run:
model <- cnorm.shash(children$age, children$score)
summary(model)

# Including R-squared, RMSE, and bias in the summary:
summary(model, age = children$age, score = children$score)

## End(Not run)
```

taylorSwift

Swiftly compute Taylor regression models for distribution free continuous norming

Description

Conducts distribution free continuous norming and aims to find a fitting model. Raw data are modelled as a Taylor polynomial of powers of age and location and their interactions. In addition to the raw scores, either provide a numeric vector for the grouping information (group) for the ranking of the raw scores. You can adjust the grade of smoothing of the regression model by setting the k, t and terms parameter. In general, increasing k and t leads to a higher fit, while lower values lead to more smoothing. If both parameters are missing, taylorSwift uses k = 5 and t = 3 by default.

Usage

```
taylorSwift(
  raw = NULL,
  group = NULL,
  age = NULL,
  width = NA,
  weights = NULL,
  scale = "T",
  method = 4,
  descend = FALSE,
  k = NULL,
  t = NULL,
  terms = 0,
  R2 = NULL,
  plot = TRUE,
  extensive = TRUE,
  averaging = FALSE,
  minDip = 0.01
)
```

Arguments

raw	Numeric vector of raw scores
group	Numeric vector of grouping variable, e. g. grade. If no group or age variable is provided, conventional norming is applied
age	Numeric vector with chronological age, please additionally specify width of window
width	Size of the sliding window in case an age vector is used
weights	Vector or variable name in the dataset with weights for each individual case. It can be used to compensate for moderate imbalances due to insufficient norm data stratification. Weights should be numerical and positive.
scale	type of norm scale, either T (default), IQ, z or percentile (= no transformation); a double vector with the mean and standard deviation can as well, be provided f. e. c(10, 3) for Wechsler scale index points
method	Ranking method in case of bindings, please provide an index, choosing from the following methods: 1 = Blom (1958), 2 = Tukey (1949), 3 = Van der Warden (1952), 4 = Rankit (default), 5 = Levenbach (1953), 6 = Filliben (1975), 7 = Yu & Huang (2001)
descend	ranking order (default descent = FALSE): inverses the ranking order with higher raw scores getting lower norm scores; relevant for example when norming error scores, where lower scores mean higher performance
k	The power constant. Higher values result in more detailed approximations but have the danger of over-fit (max = 6). If not set, it uses t and if both parameters are NULL, k is set to 5.
t	The age power parameter (max = 6). If not set, it uses k and if both parameters are NULL, k is set to 3, since age trajectories are most often well captured by cubic polynomials.
terms	Selection criterion for model building. The best fitting model with this number of terms is used
R2	Adjusted R square as a stopping criterion for the model building (default R2 = 0.99)
plot	Default TRUE; plots the regression model and prints reportSetting it to FALSE as well deactivates potential user interactions.
extensive	If TRUE, screen models for consistency and - if possible, exclude inconsistent ones
averaging	If TRUE (default FALSE), apply BIC-weighted model averaging across the consistency-screened candidate models instead of selecting a single model. Requires extensive = TRUE and age-based norming.
minDip	Tolerance for monotonicity check. Allow small violations (default: .01 or 1 for strict checking).

Value

cnorm object including the ranked raw data and the regression model

References

1. Gary, S. & Lenhard, W. (2021). In norming we trust. Diagnostica.
2. Gary, S., Lenhard, W. & Lenhard, A. (2021). Modelling Norm Scores with the cNORM Package in R. Psych, 3(3), 501-521. <https://doi.org/10.3390/psych3030033>
3. Lenhard, A., Lenhard, W., Suggate, S. & Segerer, R. (2016). A continuous solution to the norming problem. Assessment, Online first, 1-14. doi:10.1177/1073191116656437
4. Lenhard, A., Lenhard, W., Gary, S. (2018). Continuous Norming (cNORM). The Comprehensive R Network, Package cNORM, available: <https://CRAN.R-project.org/package=cNORM>
5. Lenhard, A., Lenhard, W., Gary, S. (2019). Continuous norming of psychometric tests: A simulation study of parametric and semi-parametric approaches. PLoS ONE, 14(9), e0222279. doi:10.1371/journal.pone.0222279
6. Lenhard, W., & Lenhard, A. (2020). Improvement of Norm Score Quality via Regression-Based Continuous Norming. Educational and Psychological Measurement(Online First), 1-33. <https://doi.org/10.1177/0013164420928457>

See Also

rankByGroup, rankBySlidingWindow, computePowers, bestModel

Examples

```
## Not run:
# Using this function with the example dataset 'ppvt'
# You can use the 'getGroups()' function to set up grouping variable in case,
# you have a continuous age variable.
model <- taylorSwift(raw = ppvt$raw, group = ppvt$group)

# return norm tables including 90% confidence intervals for a
# test with a reliability of r = .85; table are set to mean of quartal
# in grade 3 (children completed 2 years of schooling)
normTable(c(5, 15), model, CI = .90, reliability = .95)

# ... or instead of raw scores for norm scores, the other way round
rawTable(c(8, 12), model, CI = .90, reliability = .95)

## End(Not run)
```

weighted.quantile

Weighted quantile estimator

Description

Computes weighted quantiles (code from Andrey Akinshin (2023) "Weighted quantile estimators" arXiv:2304.07265 [stat.ME] Code made available via the CC BY-NC-SA 4.0 license) on the basis of either the weighted Harrell-Davis quantile estimator or an adaption of the type 7 quantile estimator of the generic quantile function in the base package. Please provide a vector with raw values, the

probabilities for the quantiles and an additional vector with the weight of each observation. In case the weight vector is NULL, a normal quantile estimation is done. The vectors may not include NAs and the weights should be positive non-zero values. Please draw on the `computeWeights()` function for retrieving weights in post stratification.

Usage

```
weighted.quantile(x, probs, weights = NULL, type = "Harrell-Davis")
```

Arguments

<code>x</code>	A numerical vector
<code>probs</code>	Numerical vector of quantiles
<code>weights</code>	A numerical vector with weights; should have the same length as <code>x</code>
<code>type</code>	Type of estimator, can either be "inflation", "Harrell-Davis" using a beta function to approximate the weighted percentiles (Harrell & Davis, 1982) or "Type7" (default; Hyndman & Fan, 1996), an adaption of the generic quantile function in R, including weighting. The inflation procedure is essentially a numerical, non-parametric solution that gives the same results as Harrel-Davis. It requires less ressources with small datasets and always finds a solution (e. g. 1000 cases with weights between 1 and 10). If it becomes too resource intense, it switches to Harrell-Davis automatically. Harrel-Davis and Type7 code is based on the work of Akinshin (2023).

Value

the weighted quantiles

References

1. Harrell, F.E. & Davis, C.E. (1982). A new distribution-free quantile estimator. *Biometrika*, 69(3), 635-640.
2. Hyndman, R. J. & Fan, Y. (1996). Sample quantiles in statistical packages, *American Statistician* 50, 361–365.
3. Akinshin, A. (2023). Weighted quantile estimators [arXiv:2304.07265](https://arxiv.org/abs/2304.07265) [stat.ME]

See Also

`weighted.quantile.inflation`, `weighted.quantile.harrell.davis`, `weighted.quantile.type7`

`weighted.quantile.harrell.davis`*Weighted Harrell-Davis quantile estimator*

Description

Computes weighted quantiles; code from Andrey Akinshin (2023) "Weighted quantile estimators" arXiv:2304.07265 [stat.ME] Code made available via the CC BY-NC-SA 4.0 license

Usage

```
weighted.quantile.harrell.davis(x, probs, weights = NULL)
```

Arguments

<code>x</code>	A numerical vector
<code>probs</code>	Numerical vector of quantiles
<code>weights</code>	A numerical vector with weights; should have the same length as <code>x</code> . If no weights are provided (NULL), it falls back to the base quantile function, type 7

Value

the quantiles

`weighted.quantile.inflation`*Weighted quantile estimator through case inflation*

Description

Applies weighted ranking numerically by inflating cases according to weight. This function will be resource intensive, if inflated cases get too high and in this cases, it switches to the parametric Harrell-Davis estimator.

Usage

```
weighted.quantile.inflation(  
  x,  
  probs,  
  weights = NULL,  
  degree = 3,  
  cutoff = 1e+07  
)
```

Arguments

x	A numerical vector
probs	Numerical vector of quantiles
weights	A numerical vector with weights; should have the same length as x.
degree	power parameter for case inflation (default = 3, equaling factor 1000) If no weights are provided (NULL), it falls back to the base quantile function, type 7
cutoff	stop criterion for the sum of standardized weights to switch to Harrell-Davis, default = 1000000

Value

the quantiles

<code>weighted.quantile.type7</code>
<i>Weighted type7 quantile estimator</i>

Description

Computes weighted quantiles; code from Andrey Akinshin (2023) "Weighted quantile estimators" [arXiv:2304.07265](https://arxiv.org/abs/2304.07265) [stat.ME] Code made available via the CC BY-NC-SA 4.0 license

Usage

```
weighted.quantile.type7(x, probs, weights = NULL)
```

Arguments

x	A numerical vector
probs	Numerical vector of quantiles
weights	A numerical vector with weights; should have the same length as x. If no weights are provided (NULL), it falls back to the base quantile function, type 7

Value

the quantiles

weighted.rank	<i>Weighted rank estimation</i>
---------------	---------------------------------

Description

Conducts weighted ranking on the basis of sums of weights per unique raw score. Please provide a vector with raw values and an additional vector with the weight of each observation. In case the weight vector is NULL, a normal ranking is done. The vectors may not include NAs and the weights should be positive non-zero values. With equal weights, the result reproduces the mid-ranks of base R's `rank()` (`ties.method = "average"`).

Usage

```
weighted.rank(x, weights = NULL)
```

Arguments

<code>x</code>	A numerical vector
<code>weights</code>	A numerical vector with weights; should have the same length as <code>x</code>

Value

the weighted absolute ranks

weightedAverageModel	<i>BIC-Weighted Model Averaging Across Consistent Candidate Models</i>
----------------------	--

Description

Computes a weighted average of the regression coefficients across the consistency-screened candidate models returned by `regsubsets` and `screenSubset`. Weights are information-theoretic model weights $w_j \propto \exp(-\Delta BIC_j/2)$, restricted to models within `deltaBIC` of the best model. Each candidate is refitted on the complete sample via (weighted) least squares; coefficients of terms not included in a candidate are treated as zero.

Usage

```
weightedAverageModel(results, data, raw, weights = NULL, deltaBIC = 10)
```

Arguments

<code>results</code>	A (screened) <code>summary.regsubsets</code> object, including a consistent flag per row.
<code>data</code>	The preprocessed norm data.
<code>raw</code>	Name of the raw score variable.
<code>weights</code>	Optional numeric vector of case weights.
<code>deltaBIC</code>	Only models within this BIC distance of the best candidate are averaged (default 10; Burnham & Anderson, 2002).

Details

Because all candidates passed the monotonicity screening (same direction), and the averaging weights are positive and sum to one, the averaged model is itself monotone and thus consistent. In contrast to averaging coefficients over subsamples (deprecated `subsample_lm`), this approach targets the actual source of variance - model selection - while each component estimate remains a full-sample least squares fit.

Value

An `lm`-type object with averaged coefficients over the union of the candidate terms; `fitted.values` and `residuals` are updated accordingly.

References

Burnham, K. P., & Anderson, D. R. (2002). *Model Selection and Multimodel Inference*. Springer.

See Also

Other model: [bestModel\(\)](#), [checkConsistency\(\)](#), [cnorm.cv\(\)](#), [derive\(\)](#), [modelSummary\(\)](#), [print.cnorm\(\)](#), [printSubset\(\)](#), [rangeCheck\(\)](#), [regressionFunction\(\)](#), [summary.cnorm\(\)](#)

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