

Package: nlcs (via r-universe)

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Type Package

Title N-LCS: Normative Latent Cognitive Structure

Version 1.0

Description Provides functions to construct a normative latent cognitive structure (N-LCS) from cognitive test data standardized to healthy controls, and to compute cognitive deviation magnitude (CDM) and cognitive deviation angle (CDA). Methods are described in Chen (2026)
<doi:10.1080/23279095.2026.2691088>.

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compute_nlcs_metrics *Compute N-LCS CDM and CDA Metrics*

Description

Computes cognitive deviation magnitude (CDM) and cognitive deviation angle (CDA) relative to a fitted healthy-control reference model.

Usage

```
compute_nlcs_metrics(nlcs_result, data_z, ids = NULL)
```

Arguments

<code>nlcs_result</code>	An object of class <code>nlcs_result</code> returned by fit_nlcs .
<code>data_z</code>	A complete, finite numeric matrix or data frame standardized using the same healthy-control reference as the model. Rows are subjects. Columns must have the model's test names and are reordered to model order.
<code>ids</code>	An optional vector of subject identifiers, with one identifier per row of <code>data_z</code> .

Value

A data frame with one row per input subject, in input row order, containing:

id Subject identifiers, included only when `ids` is supplied.

CDM A numeric cognitive deviation measure. When `CDM_type` is "axis_projection", this is the signed projection of the healthy-control-centered, whitened score vector onto the fitted unit axis. Its sign follows the orientation of the fitted loadings. When `CDM_type` is "whitened_magnitude", it is the nonnegative Euclidean length of that vector, representing distance from the healthy-control center in healthy-control covariance-standardized coordinates.

CDA_raw The numeric angle in degrees, between 0 and 180, from the whitened score vector to the fitted axis. Smaller angles indicate closer directional alignment. The angle is NA when the whitened score vector has zero length.

CDA Numeric `CDA_raw` minus the median raw healthy-control angle stored in the model. Positive values indicate angles above the healthy-control median; negative values indicate angles below it. Undefined raw angles remain NA.

CDM_type A character column containing "axis_projection" or "whitened_magnitude", as determined by the model.

Examples

```
set.seed(42)
ability <- rnorm(100)
hc <- sapply(seq_len(4), function(j) {
  ability + rnorm(100, sd = 0.4)
})
colnames(hc) <- paste0("test", seq_len(4))

new <- hc[1:3, , drop = FALSE] - 0.5
std <- standardize_normative(hc, new)

# Few iterations keep the example fast; use the default for analysis.
model <- fit_nlcs(std$hc_z, parallel_iter = 10L)

scores <- compute_nlcs_metrics(
  model,
  std$new_z,
  ids = c("A", "B", "C")
)
scores
```

fit_nlcs

Construct a Normative Latent Cognitive Structure

Description

Fits a one-factor normative latent cognitive structure (N-LCS) when both parallel analysis and the original MAP procedure recommend one factor.

Usage

```
fit_nlcs(hc_z, parallel_iter = 1000L, loading_tolerance = 1e-8)
```

Arguments

hc_z	A complete, finite numeric matrix or data frame of healthy-control scores standardized using standardize_normative . Rows are subjects and columns are named cognitive tests.
parallel_iter	Number of parallel-analysis iterations.
loading_tolerance	Absolute loading threshold below which loadings are treated as zero when selecting the cognitive deviation magnitude (CDM) definition.

Details

Parallel analysis uses random simulations. Use `set.seed()` for reproducibility. Factor-retention recommendations are reported as messages.

Value

A named list of class `nlcs_result` containing:

variables A character vector of test names in model order.

hc_z_mean A named numeric vector of healthy-control means in standardized units.

covariance The numeric healthy-control sample covariance matrix.

whitening_matrix The numeric symmetric inverse square root of the healthy-control covariance matrix. This transforms centered scores into healthy-control covariance-standardized coordinates.

fa The one-factor fit returned by `psych::fa()`, with classes `psych` and `fa`.

loadings A named numeric vector of one-factor loadings.

latent_axis_whitened A named numeric unit vector defining the fitted latent axis in whitened space. Its orientation follows the fitted loadings.

parallel_analysis The full parallel-analysis result from `psych::fa.parallel()`, with classes `psych` and `parallel`.

map The full MAP result from `EFAtools::N_FACTORS()`, with classes `efa_retain` and `N_FACTORS`.

retention A list containing integer factor counts `parallel_analysis` and `map_tr2`. Both equal one in a successfully returned model.

loading_tolerance The numeric loading threshold used to classify loading signs.

cdm_type A character string: "axis_projection" when all nonzero loadings have the same sign, or "whitened_magnitude" when they have mixed signs.

cda_reference_median The numeric median raw healthy-control cognitive deviation angle in degrees, excluding undefined angles. This is subtracted when computing adjusted CDA.

The model defines the healthy-control reference geometry used by `compute_nlcs_metrics`. An error is raised if either retention procedure does not recommend one factor.

Examples

```
set.seed(42)
ability <- rnorm(100)
hc <- sapply(seq_len(4), function(j) {
  ability + rnorm(100, sd = 0.4)
})
colnames(hc) <- paste0("test", seq_len(4))
std <- standardize_normative(hc)

# Few iterations keep the example fast; use the default for analysis.
model <- fit_nlcs(std$hc_z, parallel_iter = 10L)
model$loadings
model$retention
```

nlcs_result	<i>Print a Fitted Normative Latent Cognitive Structure</i>
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Description

Prints the number of cognitive tests, factor-retention results, and the cognitive deviation magnitude (CDM) definition.

Usage

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

Arguments

x	An object of class <code>nlcs_result</code> returned by fit_nlcs .
...	Additional arguments, currently unused.

Value

The input `x`, a named list of class `nlcs_result`, returned invisibly and unchanged. Its components describe the fitted healthy-control reference model and are documented in [fit_nlcs](#).

The function is called for the side effect of printing a concise model summary to the console.

Examples

```
set.seed(42)  
ability <- rnorm(100)  
hc <- sapply(seq_len(4), function(j) {  
  ability + rnorm(100, sd = 0.4)  
})  
colnames(hc) <- paste0("test", seq_len(4))  
std <- standardize_normative(hc)  
  
# Few iterations keep the example fast; use the default for analysis.  
model <- fit_nlcs(std$hc_z, parallel_iter = 10L)  
print(model)
```

standardize_normative *Standardize Cognitive Tests to Healthy Controls*

Description

Uses healthy-control means and sample standard deviations as the normative reference for both healthy controls and new subjects.

Usage

```
standardize_normative(hc_data, new_data = NULL)
```

Arguments

hc_data	A complete, finite numeric matrix or data frame. Rows are healthy controls and columns are cognitive tests. Column names are required. At least two healthy controls are required, and each test must have a nonzero sample standard deviation.
new_data	An optional complete, finite numeric matrix or data frame for new subjects, with the same test names as hc_data . Columns are reordered to match the healthy-control reference.

Details

Data cleaning, test selection, missing-data handling, and direction recoding must be completed before using this function.

Value

A named list of class `nlcs_standardization` containing:

hc_z A numeric matrix of standardized healthy-control scores, with the same dimensions and column names as **hc_data**.

new_z A numeric matrix of standardized new-subject scores, with columns in healthy-control order, or `NULL` if **new_data** is omitted.

means A named numeric vector of healthy-control test means.

sds A named numeric vector of healthy-control sample standard deviations.

variables A character vector of test names in healthy-control column order.

Each standardized score is the original score minus the healthy-control mean, divided by the healthy-control sample standard deviation. Positive values are above the healthy-control mean and negative values are below it. Whether higher scores indicate better performance depends on the original test coding.

Examples

```
hc <- cbind(  
  test1 = c(8, 10, 12, 14, 16),  
  test2 = c(3, 5, 4, 7, 6)  
)  
new <- cbind(test1 = c(9, 13), test2 = c(4, 6))  
  
std <- standardize_normative(hc, new)  
std$hc_z  
std$new_z  
std$means  
std$sds
```

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