Package: pams (via r-universe)

May 31, 2026

Type Package

Title Profile Analysis via Multidimensional Scaling

Version 0.1.0

Date 2026-03-22

Description Implements Profile Analysis via Multidimensional Scaling (PAMS) for the identification of population-level core response profiles from cross-sectional and longitudinal person-score data. Each person profile is decomposed into a level component (the person mean) and a pattern component (ipsatized subscores). PAMS uses nonmetric multidimensional scaling via the SMACOF algorithm (de Leeuw & Mair, 2009) to identify a small number of core profiles that represent the central response patterns in a sample of any size. Bootstrap standard errors and bias-corrected and accelerated (BCa) confidence intervals for individual core profile coordinates are estimated, enabling significance testing of coordinates that is not available in other profile analysis methods such as cluster profile analysis or latent profile analysis. Person-level weights, R-squared values, and correlations with core profiles are also estimated, allowing individual profiles to be interpreted in terms of the core profile structure. PAMS can be applied to both cross-sectional data and longitudinal data, where core trajectory profiles describe how response patterns change over time.

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URL `https://github.com/sekangakim/pams`

BugReports `https://github.com/sekangakim/pams/issues`

Depends R (>= 4.0.0)

Imports smacof (>= 2.1.0)

Suggests lmtest (>= 0.9.40), testthat (>= 3.0.0)

Encoding UTF-8

RoxygenNote 7.3.3

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libx11-dev zlib1g-dev

Repository https://sekangakim.r-universe.dev

Date/Publication 2026-03-27 03:47:08 UTC

RemoteUrl https://github.com/sekangakim/pams

RemoteRef HEAD

RemoteSha e82f5e86dff21630238e7b68c78b5a29466047a2

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`BootSmacof` *Profile Analysis via Multidimensional Scaling*

Description

Identifies population-level core response profiles from cross-sectional or longitudinal person-score data using nonmetric multidimensional scaling (SMACOF algorithm). Each person profile is decomposed into a level component (person mean) and a pattern component (ipsatized subscores). `BootSmacof` fits a nonmetric MDS solution to the $J \times J$ inter-variable distance matrix, bootstraps the solution to generate empirical sampling distributions of core profile coordinates, and computes bias-corrected and accelerated (BCa) confidence intervals for each coordinate. Person-level weights, R-squared values, and correlations with core profiles are estimated for all participants, with optional bootstrap confidence intervals for a selected subset.

Usage

```
BootSmacof(
  testdata,
  participant = NULL,
  mds = c("smacof", "classical"),
  type = c("ratio", "interval", "ordinal", "mspline"),
  distance = c("euclid", "sqeuclid"),
  scale = FALSE,
  nprofile = 3,
  direction = rep(1, nprofile),
  cl = 0.95,
  nBoot = 2000,
  testname = NULL,
  file = NULL
)
```

Arguments

`testdata`	A data frame or matrix of persons (rows) by subscales (columns). Subscores are assumed to be related and continuous. For longitudinal data, columns should be ordered as all subscales at Time 1 followed by all subscales at Time 2, and so on.
`participant`	An integer vector of row indices identifying persons for whom individual bootstrap confidence intervals on weights and partial correlations are computed. If `NULL` (the default), individual bootstrapping is skipped and only population-level results are returned.
`mds`	Character string specifying the MDS algorithm. Either `"smacof"` (default, recommended; uses the majorization algorithm of de Leeuw & Mair, 2009) or `"classical"` (Torgerson's classical metric MDS via `cmdscale`).
`type`	Character string specifying the optimal scaling transformation passed to `smacofSym`. One of `"ordinal"` (default, nonmetric; recommended for most social-science data), `"interval"`, `"ratio"`, or `"mspline"`. Ignored when `mds = "classical"`.
`distance`	Character string specifying the distance measure used to compute the $J \times J$ inter-variable proximity matrix. Either `"euclid"` (default, Euclidean distance) or `"sqeuclid"` (squared Euclidean distance). Note that squaring amplifies large distances and compresses small ones; `"euclid"` is recommended unless faster convergence is specifically required.
`scale`	Logical. If `TRUE`, columns of `testdata` are standardised (zero mean, unit variance) before analysis. Set to `TRUE` when subscales have different measurement units. Default is `FALSE`.
`nprofile`	A positive integer specifying the number of core profiles (MDS dimensions) to extract. Choose by inspecting stress values across 2-, 3-, and 4-dimensional solutions; Kruskal's (1964) criterion of stress ≤ 0.05 is recommended. Must be less than the number of subscales (columns) in `testdata`.
`direction`	An integer vector of length `nprofile`, with each element either `1` or `-1`. Multiplying a dimension by `-1` flips its sign to aid substantive interpretation (e.g., so that the first core profile aligns with the subscale mean profile). Default is `rep(1, nprofile)` (no flipping).
`cl`	Numeric confidence level for BCa intervals. Default is `0.95`. Common alternatives are `0.99` and `0.90`.
`nBoot`	A positive integer specifying the number of bootstrap samples. A minimum of `1000` is recommended for stable confidence interval estimation (Efron & Tibshirani, 1993); `2000` is the default.
`testname`	An optional character vector of length equal to the number of columns in `testdata`, giving subscale names used as row labels in summary output and plots. If `NULL`, labels `"T1"`, `"T2"`, ... are generated automatically.
`file`	An optional character string giving a file path stem. If supplied, three CSV files are written: `<file>MDS.csv` (stress summary and core profile coordinates with BCa CIs), `<file>Weight.csv` (person weights, levels, R-squared values, and core-profile correlations), and `<file>WeightB.csv` (bootstrap summaries for selected participants). If `NULL` (the default), no files are written.

Value

A named list with the following components:

`MDS` The MDS fit object for the original data. When `mds = "smacof"` this is the full object returned by `smacofSym`, including `$conf` (core profile coordinate matrix, $J \times K$) and `$stress`. When `mds = "classical"` this is a minimal list with `$conf` only.

`MDSsummary` A list of `nprofile` data frames, one per core profile. Each data frame has rows corresponding to subscales and columns: `Ori` (original coordinate), `Mean` (bootstrap mean), `SE` (bootstrap standard error), `Lower` and `Upper` (percentile CI bounds), `BCaLower` and `BCaUpper` (BCa CI bounds). Coordinates whose BCa CI does not include zero are statistically significant.

`MDSprofile` A list of `nprofile` matrices, each of dimension `nBoot` $\times J$, containing the full bootstrap distribution of core profile coordinates.

`stresssummary` A one-row data frame with bootstrap summary statistics for the smacof stress value: `Ori`, `Mean`, `SE`, `Lower`, `Upper`, `BCaLower`, `BCaUpper`. `NULL` when `mds = "classical"`.

`stressprofile` A numeric vector of length `nBoot` containing bootstrap stress values. `NULL` when `mds = "classical"`.

`MDSR2` A numeric vector of length `nprofile` containing the R-squared values from regressing each core profile dimension on the remaining dimensions. Low values confirm that the core profiles are not collinear.

`Weight` A matrix of dimension $I \times (2K + 2)$ containing, for every person: raw weights (`w1`, ..., `wK`), level estimate, R-squared value, and correlations with each core profile (`corDim1`, ..., `corDimK`). Row names are `"#1"`, `"#2"`, ...

`WeightmeanR2` The mean R-squared value across all I persons, summarising how well the `nprofile` core profiles account for pattern variance in the sample.

`WeightB` A matrix of bootstrap summary statistics (original estimate, mean, SE, lower and upper CI bounds) for the weights of each person in `participant`. `NULL` if `participant` is `NULL`.

`PcorrB` A matrix of bootstrap summary statistics for the partial correlations of each person in `participant`. `NULL` if `participant` is `NULL`.

`nprofile` The number of core profiles extracted.

`nBoot` The number of bootstrap samples used.

`scale` Logical; whether columns were standardised.

`testname` Character vector of subscale names used.

References

Davison, M. L. (1996). *Multidimensional scaling interest and aptitude profiles: Idiographic dimensions, nomothetic factors*. Presidential address to Division 5, American Psychological Association, Toronto.

de Leeuw, J., & Mair, P. (2009). Multidimensional scaling using majorization: SMACOF in R. *Journal of Statistical Software*, *31*(3), 1–30. doi:10.18637/jss.v031.i03

Efron, B., & Tibshirani, R. J. (1993). *An introduction to the bootstrap*. Chapman & Hall.

Kim, S.-K., & Kim, D. (2024). Utility of profile analysis via multidimensional scaling in R for the study of person response profiles in cross-sectional and longitudinal data. *The Quantitative Methods for Psychology*, *20*(3), 230–247. doi:10.20982/tqmp.20.3.p230

Kruskal, J. B. (1964). Multidimensional scaling by optimizing goodness of fit to a nonmetric hypothesis. *Psychometrika*, *29*, 1–27. doi:10.1007/BF02289565

See Also

`smacofSym` for the underlying MDS algorithm.

Examples

```
## Not run:
# Cross-sectional example using bundled WJ-IV cognitive ability data.
library(pams)
library(smacof)

cross_data <- read.csv(
  system.file("extdata", "Cross-sectional.csv", package = "pams"),
  header = FALSE
)
colnames(cross_data) <- c(
  "OV1","NS2","VA3","LP4","PP5","SR6","VS7","GI8",
  "CF9","NR10","NP11","NW12","VA13","PR14","AS15",
  "ON16","PC17","MW18"
)

# Inspect stress across dimensionalities to choose nprofile
smacofSym(dist(t(cross_data)), ndim = 2, type = "ordinal")$stress
smacofSym(dist(t(cross_data)), ndim = 3, type = "ordinal")$stress
smacofSym(dist(t(cross_data)), ndim = 4, type = "ordinal")$stress

# Run PAMS with 3 core profiles and 2,000 bootstrap samples
set.seed(1)
result <- BootSmacof(
  testdata    = cross_data,
  participant = 1:10,
  mds         = "smacof",
  type        = "ordinal",
  distance    = "euclid",
  nprofile    = 3,
  direction   = c(-1, 1, 1),
  cl          = 0.95,
  nBoot       = 2000,
  testname    = colnames(cross_data)
)

result$MDS$stress       # should be <= 0.05
result$WeightmeanR2     # mean R^2 across all persons

# Core profile coordinates with BCa CIs
round(result$MDSsummary[[1]], 3)
```

```
round(result$MDSsummary[[2]], 3)
round(result$MDSsummary[[3]], 3)

# Weights and correlations for first 10 persons
round(result$Weight[1:10, ], 2)

## End(Not run)
```

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