Package 'pams'

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Type Package

Title Profile Analysis via Multidimensional Scaling

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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 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 partial 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. Methods are described in Kim and Kim (2024) <doi:10.20982/tqmp.20.3.p230>, de Leeuw and Mair (2009) <doi:10.18637/jss.v031.i03>, and Kruskal (1964) <doi:10.1007/BF02289565>.

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

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

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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 partial 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("ordinal", "interval", "ratio", "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). Inspect the preliminary smacofSym() coordinate plots and choose signs so that prespecified anchor variables appear on the desired side of each axis. Reversing a sign does not alter distances, stress, fit, or whether an interval excludes zero. Default is rep(1, nprofile).
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); values below 1000 issue a warning and values below 10 are rejected. 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, two CSV files are always 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 partial correlations). When `participant` is not `NULL`, `<file>WeightB.csv` and `<file>PcorrB.csv` are also written. 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 pointwise BCa CI does not include zero are statistically significant at the stated coordinate-wise level; these intervals are not adjusted for multiplicity.

`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 partial correlations with each core profile (`corDim1`, ..., `corDimK`). The raw weights are unstandardized no-intercept OLS coefficients from regressing the person's ipsatized pattern on the retained coordinate vectors. Each `corDim` value is the correlation between the residualized person pattern and residualized focal core profile after controlling for the other profiles. 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.

The returned list has class `"pams_fit"`, while retaining direct access to every component listed above.

Sign indeterminacy and alignment

MDS coordinate signs are arbitrary. For each bootstrap and jackknife sample, `BootSmacof()` aligns each dimension to its original-sample counterpart by its correlation sign and then reports the orientation selected through `direction`. This is sign alignment only: the method does not perform general rotational alignment or dimension-permutation matching. Coordinate-wise inference should therefore be interpreted cautiously when dimensions are weak or nearly interchangeable. A sign reversal changes only the reported orientation; it does not change interpoint distances, stress, model fit, or interval exclusion of zero.

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

```
# Small toy example (runs automatically)
set.seed(42)
toy_data <- as.data.frame(matrix(rnorm(8 * 4, mean = 10, sd = 2),
                                 nrow = 8, ncol = 4))
colnames(toy_data) <- paste0("S", 1:4)

result <- suppressWarnings(BootSmacof(
  testdata    = toy_data,
  participant = NULL,
  mds         = "smacof",
  type        = "ordinal",
  distance    = "euclid",
  nprofile    = 2,
```

```
  direction   = c(1, 1),
  cl          = 0.95,
  nBoot       = 10,
  testname    = colnames(toy_data)
))
result$MDS$stress
round(result$WeightmeanR2, 2)
round(result$MDSsummary[[1]], 3)
```

`plot.pams_fit` *Plot fitted PAMS core profiles*

Description

Displays selected core-profile coordinates and, optionally, their pointwise percentile or BCa confidence limits.

Usage

```
## S3 method for class 'pams_fit'
plot(
  x,
  profiles = seq_len(x$nprofile),
  interval = c("BCa", "percentile", "none"),
  layout = NULL,
  labels = TRUE,
  label.cex = 0.75,
  type = "b",
  pch = 19,
  col = "black",
  ci.col = "steelblue",
  ci.lty = 2,
  zero.line = TRUE,
  zero.col = "grey60",
  xlab = "Variable",
  ylab = "Coordinate",
  main = NULL,
  ylim = NULL,
  xaxt = if (labels) "n" else "s",
  ...
)
```

Arguments

`x`	A fitted object returned by [BootSmacof()].
`profiles`	Integer vector identifying the profiles to display.

`interval`	Confidence limits to draw: ‘"BCa"‘ (default), ‘"percentile"‘, or ‘"none"‘.
`layout`	Optional integer vector of length two giving the rows and columns of the plotting layout.
`labels`	Logical; show variable names on the horizontal axis.
`label.cex`	Character expansion used for variable labels.
`type`, `pch`, `col`	Standard graphical controls for the estimated profile.
`ci.col`, `ci.lty`	Color and line type for confidence limits.
`zero.line`	Logical; draw a horizontal reference line at zero.
`zero.col`	Color of the zero reference line.
`xlab`, `ylab`	Axis labels.
`main`	Optional plot title or character vector of titles.
`ylim`	Optional common vertical-axis limits. By default each panel includes its estimate and selected confidence limits.
`xaxt`	Axis annotation setting passed to [graphics::plot()].
`...`	Additional graphical arguments passed to [graphics::plot()].

Value

The fitted object, invisibly.

Examples

```
set.seed(42)
x <- matrix(rnorm(32), nrow = 8, ncol = 4)
fit <- suppressWarnings(BootSmacof(x, nprofile = 2, nBoot = 10))
plot(fit, profiles = 1:2)
```

`summary.pams_fit` *Summarize a fitted PAMS model*

Description

Summarize a fitted PAMS model

Usage

```
## S3 method for class 'pams_fit'
summary(object, digits = 3L, ...)

## S3 method for class 'summary.pams_fit'
print(x, ...)

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

Arguments

object	A fitted object returned by [BootSmacof()].
digits	Number of digits retained when the summary is printed.
...	Additional arguments passed to or from methods.
x	An object returned by ‘summary.pams_fit()‘ or [BootSmacof()].

Value

‘summary.pams_fit()‘ returns an object of class ‘summary.pams_fit‘ containing the analysis settings, stress, fit indices, and the number of coordinates whose pointwise BCa interval excludes zero.

Examples

```
set.seed(42)
x <- matrix(rnorm(32), nrow = 8, ncol = 4)
fit <- suppressWarnings(BootSmacof(x, nprofile = 2, nBoot = 10))
summary(fit)
```

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