Package: FAPA (via r-universe)

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Type Package

Title Factor Analytic Profile Analysis of Ipsatized Data

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Description Implements Factor Analytic Profile Analysis of Ipsatized Data ('FAPA'), a metric inferential framework for pattern detection and person-level reconstruction in multivariate profile data. After row-centering (ipsatization) to remove profile elevation, 'FAPA' applies singular value decomposition ('SVD') to recover shared core profiles and individual pattern weights. Dimensionality is determined by a variance-matched Horn's parallel analysis. A three-stage bootstrap verification framework assesses (1) dimensionality via parallel analysis, (2) subspace stability via Procrustes principal angles, and (3) profile replicability via Tucker's congruence coefficients. BCa bootstrap confidence intervals for core-profile coordinates are computed via the canonical 'boot' package implementation of Davison and Hinkley (1997) <doi:10.1017/CBO9780511802843>.

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VignetteBuilder knitr

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Contents

`FAPA-package` *FAPA: Factor Analytic Profile Analysis of Ipsatized Data*

Description

Implements Factor Analytic Profile Analysis of Ipsatized Data (FAPA), a metric inferential framework for pattern detection and person-level reconstruction in multivariate profile data.

After row-centering (ipsatization) to remove profile elevation, FAPA applies singular value decomposition (SVD) to recover shared *core profiles* and individual pattern weights, supporting the following workflow:

1. **Ipsatization** — `load_and_ipsatize` removes person-level elevation, isolating within-person pattern structure.
2. **Core estimation** — `fapa_core` performs SVD and returns the core-profile matrix, person weights, and variance decomposition.

3. **Stage 1: Dimensionality** — `fapa_pa` applies variance-matched Horn's parallel analysis to determine how many components to retain.
4. **Stage 2: Subspace stability** — `fapa_procrustes` assesses dimensional stability via bootstrap principal angles.
5. **Stage 3: Profile replicability** — `fapa_tucker` computes Tucker's congruence coefficients across bootstrap resamples.
6. **Inference** — `fapa_bca` provides BCa bootstrap confidence intervals for core-profile coordinates using the canonical **boot** implementation.
7. **Reconstruction** — `fapa_person` projects each person onto the retained core profiles and reports reconstruction R^2 and optional bootstrap CIs for selected participants.

Key references

- Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika, 30*(2), 179–185.
- Davison, A. C., & Hinkley, D. V. (1997). *Bootstrap Methods and Their Application*. Cambridge University Press.
- Lorenzo-Seva, U., & ten Berge, J. M. F. (2006). Tucker's congruence coefficient as a meaningful index of factor similarity. *Methodology, 2*(2), 57–64.
- Kim, S.-K. (2024). Factorization of person response profiles to identify summative profiles carrying central response patterns. *Psychological Methods, 29*(4), 723–730. doi:10.1037/met0000568

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See Also

Useful links:

- `https://github.com/sekangakim/FAPA`
- Report bugs at `https://github.com/sekangakim/FAPA/issues`

`fapa_bca` *BCa bootstrap confidence intervals for FAPA core profiles*

Description

Computes BCa (bias-corrected and accelerated) bootstrap confidence intervals for every coordinate of every retained core profile, using the canonical implementation in `boot` and `boot.ci`.

Usage

```
fapa_bca(Xtilde, K, B = 2000, alpha = 0.05, seed = NULL)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`K`	Integer. Number of core profiles (must equal the retained dimensionality from `fapa_pa`).
`B`	Integer. Number of bootstrap replicates. Default `2000`.
`alpha`	Numeric. Two-tailed significance level. Default `0.05`.
`seed`	Integer or `NULL`. Random seed.

Details

Sign ambiguity across bootstrap resamples is handled inside the statistic function via an inner-product alignment rule (see `.align_signs`), ensuring that each bootstrap distribution is unimodal before BCa adjustment.

Value

A named list:

ci List of K data frames (one per core profile), each with columns `Ori`, `Mean`, `SE`, `Lower`, `Upper`, `BCaLower`, `BCaUpper`.

X0 Original core-profile matrix ($I \times K$).

boot_out The full `boot` object for downstream diagnostics.

boot_X 3-D array ($B \times I \times K$) of bootstrap profiles.

K, B, alpha, varnames Inputs echoed for plotting and output.

References

Davison, A. C., & Hinkley, D. V. (1997). *Bootstrap Methods and Their Application*. Cambridge University Press. doi:10.1017/CBO9780511802843

See Also

`plot_fapa_core`, `write_fapa_results`

`fapa_core` *Core FAPA estimation via SVD*

Description

Computes the thin singular value decomposition (SVD) of an ipsatized person-by-variable matrix, returning the K core profiles, person weights, singular values, and variance-accounting summaries.

Usage

```
fapa_core(Xtilde, K, direction = NULL)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`K`	Integer. Number of components to extract.
`direction`	Integer vector of length K with values ± 1, overriding the automatic sign convention. `NULL` (default) triggers automatic normalisation.

Details

The core-profile (scale) matrix is defined as $\mathbf{X} = \mathbf{V}\mathbf{\Sigma}$, so that each individual's ipsatized profile satisfies $\tilde{\mathbf{m}}_p = \mathbf{X}\mathbf{u}_p$ exactly (rank-K reconstruction).

Signs of the singular vectors are normalised so that the element with the largest absolute value in each core-profile column is positive.

Value

A named list:

U Person-weight matrix ($P \times K$).

S Singular values (length K).

V Right singular vectors ($I \times K$).

X Core-profile matrix $\mathbf{V}\mathbf{\Sigma}$ ($I \times K$).

total_var Total ipsatized variance (Frobenius norm^2).

var_k Variance per component (σ_k^2).

prop_var Proportion of variance per component.

cum_var Cumulative proportion of variance.

person_cor Normalised person-core correlations ($P \times K$).

direction Sign vector applied (for reproducibility).

K Number of components extracted.

References

Kim, S.-K. (2024). Factorization of person response profiles to identify summative profiles carrying central response patterns. *Psychological Methods, 29*(4), 723–730. doi:10.1037/met0000568

`fapa_pa` *Stage 1: Horn's Parallel Analysis (variance-matched bootstrap)*

Description

Determines the number of components to retain from the SVD of an ipsatized data matrix using a variance-matched bootstrap version of Horn's (1965) parallel analysis.

Usage

```
fapa_pa(Xtilde, B = 2000, alpha = 0.05, seed = NULL)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`B`	Integer. Number of bootstrap replicates. Default `2000`.
`alpha`	Numeric. Significance level. Default `0.05`.
`seed`	Integer or `NULL`. Random seed for reproducibility.

Details

For each of `B` bootstrap replicates, a random matrix of identical dimensions is row-centred (ipsatized) and then rescaled to the same Frobenius norm as `Xtilde`. This variance-matching step is essential: without it, raw-score data trivially dominates N(0,1) random matrices and PA retains all components. Components whose observed σ_k^2 exceeds the $(1 - \alpha)$ quantile of the matched null distribution are retained.

Value

A named list:

n_retain Number of components retained.

obs_sv2 Observed squared singular values (length = $K_{\max}$).

thresh Bootstrap $(1 - \alpha)$ quantile per component.

prop_obs Proportion of variance per observed component.

prop_rand Mean proportion of variance per random component.

rand_sv2 Full $B \times K_{\max}$ matrix of random σ^2.

total_var Total ipsatized variance.

alpha, B Inputs echoed for reporting.

References

Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika, 30*(2), 179–185.

See Also

`print_pa`, `plot_pa_scree`

`fapa_person` *Person-level reconstruction and pattern weights*

Description

Projects each person onto the retained core profiles, returning reconstruction R^2, pattern weights $\mathbf{u}_p$, and normalised person-core correlations. Optionally computes percentile bootstrap confidence intervals for pattern weights of selected participants.

Usage

```
fapa_person(
  Xtilde,
  fit,
  participants = NULL,
  B_boot = 2000,
  alpha = 0.05,
  seed = NULL
)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`fit`	A list returned by `fapa_core`.
`participants`	Integer vector of row indices for which bootstrap CIs are desired, or `NULL` to skip individual inference.
`B_boot`	Integer. Bootstrap replicates for participant CIs. Default `2000`.
`alpha`	Numeric. Two-tailed significance level. Default `0.05`.
`seed`	Integer or `NULL`. Random seed.

Value

A named list:

weights Data frame (P rows) with columns `Person`, `Level`, `R2`, `w1` ... `wK`, `rDim1` ... `rDimK`.

weights_B Matrix of bootstrap summary statistics for `participants` (or `NULL`).

R2_k Partial R^2 per dimension.

R2_mean Mean person reconstruction R^2 across all persons.

`fapa_procrustes` *Stage 2: Procrustes stability via principal angles*

Description

For each of `B` bootstrap resamples of the ipsatized data matrix, computes the K right singular vectors and measures the principal angles (in degrees) between the bootstrap subspace and the original K-dimensional right singular vector subspace.

Usage

```
fapa_procrustes(Xtilde, K, B = 2000, angle_thresh = 30, seed = NULL)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`K`	Integer. Number of dimensions to assess.
`B`	Integer. Number of bootstrap replicates. Default `2000`.
`angle_thresh`	Numeric. Upper stability bound in degrees. Default `30`.
`seed`	Integer or `NULL`. Random seed.

Details

A bootstrap replicate is declared *stable* when **all** K principal angles are strictly less than `angle_thresh`. This criterion confirms that the bootstrap subspace is nearly parallel to the original, providing geometric evidence of dimensional stability.

Value

A named list:

angles_mat $B \times K$ matrix of principal angles (degrees).

angle_mean, angle_sd Per-dimension mean and SD of angles.

angle_q025, angle_q975 Per-dimension 2.5th and 97.5th percentiles.

n_stable Number of replicates satisfying the stability criterion.

prop_stable Proportion of stable replicates.

angle_thresh, K, B Inputs echoed for reporting.

References

Bjorck, A., & Golub, G. H. (1973). Numerical methods for computing angles between linear subspaces. *Mathematics of Computation, 27*(123), 579–594.

See Also

`print_procrustes`, `plot_principal_angles`

`fapa_simdata` *Synthetic EDI-2 profile data for FAPA examples*

Description

A simulated dataset approximating the structure of the calibration sample used in Kim (in preparation). It contains no real clinical records. The data comprise 500 synthetic cases on 22 variables: 11 pre-treatment and 11 post-treatment administrations of the Eating Disorder Inventory-2 (EDI-2) subscales.

Usage

```
fapa_simdata
```

Format

A data frame with 500 rows and 22 columns. The first 11 columns contain pre-treatment EDI-2 subscale scores (Drive for Thinness through Social Insecurity) and the remaining 11 columns contain the corresponding post-treatment scores. Column names follow the convention `Before_<n>_<abbr>` and `After_<n>_<abbr>`, where `n` is the subscale index and `abbr` is a two-letter abbreviation. Scores are integers in the range 0–40.

Details

The 11 EDI-2 subscales are:

- **Dt** Drive for Thinness
- **Bu** Bulimia
- **Bd** Body Dissatisfaction
- **In** Ineffectiveness
- **Pf** Perfectionism
- **Id** Interpersonal Distrust
- **Ia** Interoceptive Awareness
- **Mf** Maturity Fears
- **As** Asceticism
- **Ir** Impulse Regulation
- **Si** Social Insecurity

The latent structure was constructed to approximate two components: a normative symptom gradient (CP1) and a pre-/post-treatment change contrast (CP2).

Source

Simulated. See `data-raw/simulate_fapa_data.R`.

References

Garner, D. M. (1991). *Eating Disorder Inventory-2 Manual*. Psychological Assessment Resources.

Examples

```
data(fapa_simdata)
dim(fapa_simdata)

## Quick ipsatization check
Xtilde <- as.matrix(fapa_simdata) - rowMeans(as.matrix(fapa_simdata))
range(rowSums(Xtilde))   # should be ~0
```

`fapa_tucker` *Stage 3: Profile replicability via Tucker's congruence coefficients*

Description

For each of `B` bootstrap resamples, computes Tucker's congruence coefficient (CC) between each original core profile and its bootstrap counterpart. Sign ambiguity is resolved by choosing the sign that maximises the absolute CC before storing.

Usage

```
fapa_tucker(Xtilde, K, B = 2000, cc_thresh = 0.85, seed = NULL)
```

Arguments

`Xtilde`	Numeric matrix (persons × variables), already ipsatized.
`K`	Integer. Number of core profiles to assess.
`B`	Integer. Number of bootstrap replicates. Default `2000`.
`cc_thresh`	Numeric. Acceptability lower bound. Default `0.85`.
`seed`	Integer or `NULL`. Random seed.

Details

Conventional thresholds (Lorenzo-Seva & ten Berge, 2006):

- CC $\geq$ 0.95: high similarity ("factor replication").
- CC $\geq$ 0.85: fair similarity.
- CC $<$ 0.85: poor similarity.

Value

A named list:

cc_mat $B \times K$ matrix of Tucker CCs.

cc_mean, cc_sd Per-profile mean and SD of CCs.

cc_q025, cc_q975 Per-profile 2.5th and 97.5th percentiles.

cc_thresh, K, B Inputs echoed for reporting.

References

Lorenzo-Seva, U., & ten Berge, J. M. F. (2006). Tucker's congruence coefficient as a meaningful index of factor similarity. *Methodology, 2*(2), 57–64. doi:10.1027/16142241.2.2.57

Tucker, L. R. (1951). *A method for synthesis of factor analysis studies* (Personnel Research Section Report No. 984). Department of the Army.

See Also

`print_tucker`, `plot_tucker_cc`

`load_and_ipsatize` *Load a CSV and ipsatize (row-centre) it*

Description

Reads a person-by-variable CSV file, assigns column labels, and removes each person's mean across variables (ipsatization), isolating within-person pattern structure from overall profile elevation.

Usage

```
load_and_ipsatize(path, col_labels)
```

Arguments

`path`	Character. Path to a CSV file with a header row.
`col_labels`	Character vector of length equal to the number of columns. Column names are replaced with these labels after loading.

Value

A named list with elements:

raw Original data as a `data.frame`.

ipsatized Row-centred matrix ($\tilde{M}$).

row_means Numeric vector of per-person means (profile levels).

varnames The supplied `col_labels`.

Examples

```
## Create a small temporary CSV and ipsatize it
tmp <- tempfile(fileext = ".csv")
write.csv(matrix(sample(1:5, 30, replace = TRUE), nrow = 6),
          tmp, row.names = FALSE)
dat <- load_and_ipsatize(tmp, col_labels = paste0("V", 1:5))
round(rowSums(dat$ipsatized), 10)  # should all be 0
unlink(tmp)
```

`plot_fapa_core` *Plot a core profile with BCa confidence intervals*

Description

Displays the ith core profile from a `fapa_bca` result, split at a variable boundary (e.g., pre vs post) with BCa CI bands. Variables before `split_at` are drawn in red (dashed), variables from `split_at + 1` onward in blue (solid).

Usage

```
plot_fapa_core(
  bca,
  i = 1,
  split_at = 11,
  main = NULL,
  ylab = "Core-Profile Coordinate"
)
```

Arguments

`bca`	A list returned by `fapa_bca`.
`i`	Integer. Which core profile to plot. Default `1`.
`split_at`	Integer. Index at which to switch colour/line-type. Default `11` (11 pre + 11 post EDI-2 subscales).
`main`	Character. Plot title. Default auto-generated.
`ylab`	Character. Y-axis label.

Value

Invisibly returns `NULL`. Called for its side-effect.

`plot_pa_scree` *Scree plot for Horn's parallel analysis*

Description

Plots observed σ_k^2 versus the random 95th-percentile reference line, with a vertical cut at the retention boundary.

Usage

```
plot_pa_scree(pa, main = "Horn's Parallel Analysis — Scree")
```

Arguments

`pa`	A list returned by `fapa_pa`.
`main`	Character. Plot title.

Value

Invisibly returns `NULL`.

`plot_person_match` *Overlay a person's ipsatized profile against FAPA core profiles*

Description

Plots the standardized ipsatized profile of person `p` alongside each of the first `K` core profiles (also standardized), one panel per dimension.

Usage

```
plot_person_match(bca, Xtilde, p = 1, K = 2)
```

Arguments

`bca`	A list returned by `fapa_bca`.
`Xtilde`	Numeric matrix (persons × variables), ipsatized.
`p`	Integer. Row index of the focal person. Default `1`.
`K`	Integer. Number of core profiles to overlay. Default `2`.

Value

Invisibly returns `NULL`.

`plot_principal_angles` *Distribution plots for Stage 2 principal angles*

Description

Draws one histogram per dimension showing the bootstrap distribution of principal angles, with the stability threshold marked as a vertical line.

Usage

```
plot_principal_angles(pr)
```

Arguments

`pr`	A list returned by `fapa_procrustes`.

Value

Invisibly returns `NULL`.

`plot_tucker_cc` *Distribution plots for Stage 3 Tucker congruence coefficients*

Description

Draws one histogram per core profile showing the bootstrap distribution of Tucker CCs, with reference lines at the fair (default 0.85) and high (0.95) thresholds.

Usage

```
plot_tucker_cc(tc, cc_thresh = 0.85)
```

Arguments

`tc`	A list returned by `fapa_tucker`.
`cc_thresh`	Numeric. Fair-similarity reference line. Default `0.85`.

Value

Invisibly returns `NULL`.

`print_pa` *Print a summary of Stage 1 parallel analysis results*

Description

Print a summary of Stage 1 parallel analysis results

Usage

```
print_pa(pa)
```

Arguments

`pa`	A list returned by `fapa_pa`.

Value

Invisibly returns `NULL`. Called for its side-effect of printing a formatted table to the console.

`print_procrustes` *Print a summary of Stage 2 principal-angle results*

Description

Print a summary of Stage 2 principal-angle results

Usage

```
print_procrustes(pr, K_pa = NULL)
```

Arguments

`pr`	A list returned by `fapa_procrustes`.
`K_pa`	Integer or `NULL`. If supplied, a `PA_Retained` column is appended showing which dimensions were retained by PA.

Value

Invisibly returns `NULL`.

`print_tucker` *Print a summary of Stage 3 Tucker CC results*

Description

Print a summary of Stage 3 Tucker CC results

Usage

```
print_tucker(tc, cc_thresh, K_pa = NULL)
```

Arguments

`tc`	A list returned by `fapa_tucker`.
`cc_thresh`	Numeric. Acceptability cutoff to display (should match the value used in `fapa_tucker`).
`K_pa`	Integer or `NULL`. If supplied, a `PA_Retained` column is appended.

Value

Invisibly returns `NULL`.

`write_fapa_results` *Write core-profile BCa CI tables to CSV*

Description

Writes one CSV file per retained core profile, containing the original coordinates together with bootstrap mean, SE, percentile, and BCa confidence bounds.

Usage

```
write_fapa_results(bca, prefix)
```

Arguments

`bca`	A list returned by `fapa_bca`.
`prefix`	Character. Base name for output files (e.g., `"fapa"`). Files are named `<prefix>_CoreProfile1.csv`, etc.

Value

Invisibly returns a character vector of file paths written.

`write_verification` *Write three-stage verification results to CSV*

Description

Writes one CSV file for each of the three verification stages.

Usage

```
write_verification(pa, pr, tc, prefix, K_pa = NULL)
```

Arguments

`pa`	A list returned by `fapa_pa`.
`pr`	A list returned by `fapa_procrustes`.
`tc`	A list returned by `fapa_tucker`.
`prefix`	Character. Base name for output files.
`K_pa`	Integer or `NULL`. If supplied, a `PA_Retained` column is appended to the Stage 2 and Stage 3 CSVs.

Value

Invisibly returns a named character vector of the three file paths.

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