

# Package ‘FAPA’

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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](https://doi.org/10.1017/CBO9780511802843)>.

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## Contents

|                                 |           |
|---------------------------------|-----------|
| FAPA-package . . . . .          | 2         |
| fapa_bca . . . . .              | 3         |
| fapa_core . . . . .             | 4         |
| fapa_pa . . . . .               | 6         |
| fapa_person . . . . .           | 7         |
| fapa_procrustes . . . . .       | 8         |
| fapa_simdata . . . . .          | 9         |
| fapa_tucker . . . . .           | 10        |
| load_and_ipsatize . . . . .     | 11        |
| plot_fapa_core . . . . .        | 12        |
| plot_pa_scree . . . . .         | 12        |
| plot_person_match . . . . .     | 13        |
| plot_principal_angles . . . . . | 13        |
| plot_tucker_cc . . . . .        | 14        |
| print_pa . . . . .              | 14        |
| print_procrustes . . . . .      | 15        |
| print_tucker . . . . .          | 15        |
| write_fapa_results . . . . .    | 16        |
| write_verification . . . . .    | 16        |
| <b>Index</b>                    | <b>17</b> |

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FAPA-package

*FAPA: 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, 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/sekangkim/FAPA>
- Report bugs at <https://github.com/sekangkim/FAPA/issues>

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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 $\times$ variables), already ipsatized.  |
| K      | Integer. Number of core profiles (must equal the retained dimensionality from <a href="#">fapa_pa</a> ). |
| 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](https://doi.org/10.1017/CBO9780511802843)

**See Also**

[plot\\_fapa\\_core](#), [write\\_fapa\\_results](#)

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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**

|                  |   |
|------------------|---|
| <b>Xtilde</b>    | Numeric matrix (persons $\times$ variables), already ipsatized.   |
| <b>K</b>         | Integer. Number of components to extract.   |
| <b>direction</b> | Integer vector of length $K$ with values $\pm 1$ , 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<sup>2</sup>).

**var\_k** Variance per component ( $\sigma_k^2$ ).

**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 $\times$ 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  $\sigma_k^2$  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  $\sigma^2$ .
- 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 | <i>Person-level reconstruction and pattern weights</i> |
|-------------|--|

---

**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 $\times$ variables), already ipsatized.  |
| fit          | A list returned by <a href="#">fapa_core</a> .   |
| 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

|                           |   |
|---------------------------|---|
| <code>Xtilde</code>       | Numeric matrix (persons $\times$ variables), already ipsatized. |
| <code>K</code>            | Integer. Number of dimensions to assess.                        |
| <code>B</code>            | Integer. Number of bootstrap replicates. Default 2000.          |
| <code>angle_thresh</code> | Numeric. Upper stability bound in degrees. Default 30.          |
| <code>seed</code>         | 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 $\times$ 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 | <i>Plot a core profile with BCa confidence intervals</i> |
|----------------|--|

---

### Description

Displays the  $i$ th 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

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

### Value

Invisibly returns NULL. Called for its side-effect.

---

|              |  |
|--------------|--|
| plot_pa_scee | <i>Scree plot for Horn's parallel analysis</i> |
|--------------|--|

---

### Description

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

### Usage

```
plot_pa_scee(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  $\times$  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 <a href="#">fapa_procrustes</a> .   |
| 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 <a href="#">fapa_tucker</a> .  |
| cc_thresh | Numeric. Acceptability cutoff to display (should match the value used in <a href="#">fapa_tucker</a> ). |
| 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 <a href="#">fapa_bca</a> .   |
| 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 <a href="#">fapa_pa</a> .  |
| pr     | A list returned by <a href="#">fapa_procrustes</a> .  |
| tc     | A list returned by <a href="#">fapa_tucker</a> .  |
| 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.

# Index

## \* datasets

fapa\_simdata, 9

boot, 3

boot.ci, 3

FAPA (FAPA-package), 2

FAPA-package, 2

fapa\_bca, 3, 3, 12, 13, 16

fapa\_core, 2, 4, 7

fapa\_pa, 2, 4, 6, 13, 14, 16

fapa\_person, 3, 7

fapa\_procrustes, 3, 8, 14–16

fapa\_simdata, 9

fapa\_tucker, 3, 10, 14–16

load\_and\_ipsatize, 2, 11

plot\_fapa\_core, 4, 12

plot\_pa\_scree, 7, 12

plot\_person\_match, 13

plot\_principal\_angles, 8, 13

plot\_tucker\_cc, 11, 14

print\_pa, 7, 14

print\_procrustes, 8, 15

print\_tucker, 11, 15

write\_fapa\_results, 4, 16

write\_verification, 16