

# Package ‘EFAtools’

May 8, 2026

**Title** Fast and Flexible Implementations of Exploratory Factor Analysis Tools

**Version** 0.7.1

**Description** Provides functions to perform exploratory factor analysis (EFA) procedures and compare their solutions. The goal is to provide state-of-the-art factor retention methods and a high degree of flexibility in the EFA procedures. This way, for example, implementations from R 'psych' and 'SPSS' can be compared. Moreover, functions for Schmid-Leiman transformation and the computation of omegas are provided. To speed up the analyses, some of the iterative procedures, like principal axis factoring (PAF), are implemented in C++.

**Depends** R (>= 3.6.0)

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**URL** <https://github.com/mdsteiner/EFAtools>

**BugReports** <https://github.com/mdsteiner/EFAtools/issues>

**RoxygenNote** 7.3.3

**Imports** lavaan, psych, crayon, stringr, stats, ggplot2, tibble, magrittr, dplyr, cli, Rcpp, viridisLite, graphics, future.apply, future, GPArotation, checkmate, tidyr, progressr, progress, rlang, clue

**LinkingTo** Rcpp, RcppArmadillo

**Suggests** testthat, knitr, rmarkdown, microbenchmark

**VignetteBuilder** knitr

**NeedsCompilation** yes

**Author** Markus Steiner [aut, cre],  
Silvia Grieder [aut],  
William Revelle [ctb],  
Max Auerswald [ctb],  
Morten Moshagen [ctb],  
John Ruscio [ctb],  
Brendan Roche [ctb],

Urbano Lorenzo-Seva [ctb],  
 David Navarro-Gonzalez [ctb],  
 Johan Braeken [ctb],  
 Andreas Soteriades [ctb]

**Maintainer** Markus Steiner <markus.d.steiner@gmail.com>

**Repository** CRAN

**Date/Publication** 2026-05-08 12:20:02 UTC

## Contents

.average_matrices . . . . .	4
.calc_cis . . . . .	4
.change_class . . . . .	6
.compute_vars . . . . .	6
.consensus_loss . . . . .	7
.consensus_target_procrustes_single . . . . .	7
.extract_list_object . . . . .	9
.factor_corres . . . . .	10
.hyperplane_count . . . . .	10
.nest_sym . . . . .	11
.numformat . . . . .	11
.oblique_procrustes . . . . .	12
.orthogonal_procrustes . . . . .	13
.paf_iter . . . . .	14
.parallel_sim . . . . .	15
.stat_over_list . . . . .	15
.tucker_congruence . . . . .	16
BARTLETT . . . . .	16
CD . . . . .	18
COMPARE . . . . .	20
CONSENSUS_PROCRUSTES . . . . .	22
DOSPERT . . . . .	25
DOSPERT_raw . . . . .	25
EFA . . . . .	26
EFA_AVERAGE . . . . .	32
EFA_POOLED . . . . .	38
EKC . . . . .	40
FACTOR_SCORES . . . . .	43
GRiPS_raw . . . . .	44
HULL . . . . .	45
IDS2_R . . . . .	48
KGC . . . . .	49
KMO . . . . .	52
MAP . . . . .	53
NEST . . . . .	55
N_FACTORS . . . . .	57
OMEGA . . . . .	61

PARALLEL . . . . .	66
plot.CD . . . . .	69
plot.EFA_AVERAGE . . . . .	70
plot.EKC . . . . .	70
plot.HULL . . . . .	71
plot.KGC . . . . .	71
plot.PARALLEL . . . . .	72
plot.SCREEN . . . . .	72
population_models . . . . .	73
print.BARTLETT . . . . .	75
print.CD . . . . .	76
print.COMPARE . . . . .	76
print.EFA . . . . .	77
print.EFA_AVERAGE . . . . .	81
print.EKC . . . . .	81
print.HULL . . . . .	82
print.KGC . . . . .	83
print.KMO . . . . .	83
print.LOADINGS . . . . .	84
print.MAP . . . . .	86
print.NEST . . . . .	86
print.N_FACTORS . . . . .	87
print.OMEGA . . . . .	87
print.PARALLEL . . . . .	88
print.SCREEN . . . . .	88
print.SL . . . . .	89
print.SLLOADINGS . . . . .	90
print.SMT . . . . .	90
PROCRUSTES . . . . .	91
residuals.EFA . . . . .	93
RiskDimensions . . . . .	93
SCREEN . . . . .	94
SL . . . . .	95
SMT . . . . .	98
SPSS_23 . . . . .	100
SPSS_27 . . . . .	101
test_models . . . . .	103
UPPS_raw . . . . .	103
WJIV_ages_14_19 . . . . .	104
WJIV_ages_20_39 . . . . .	106
WJIV_ages_3_5 . . . . .	108
WJIV_ages_40_90 . . . . .	109
WJIV_ages_6_8 . . . . .	111
WJIV_ages_9_13 . . . . .	113

---

`.average_matrices`      *Average a list of matrices elementwise*

---

### Description

Average a list of matrices elementwise

### Usage

```
.average_matrices(x)
```

### Arguments

`x`                      List of conformable matrices.

### Value

A matrix with the same dimensions as the inputs.

---

`.calc_cis`                      *Confidence intervals around mean*

---

### Description

Confidence intervals around mean

### Usage

```
.calc_cis(means, sds, p = 0.05, n)
```

### Arguments

`means`                      A matrix with the pooled loadings or pooled interfactor correlations

`sds`                         A matrix with the standard deviations for the loadings or interfactor correlations

`p`                            Numeric. One minus the confidence level of the CIs. Defaults to 0.05 for 95% CIs.

`n`                            Numeric. Typically, the number of permutations  $m$ . See [EFA\\_POOLED](#).

## Details

The standard error (SE) to use in the creation of the CIs is calculated according to Rubin's (1987) formula (eq. 11 in Hayes & Enders, 2023):

$$\sqrt{\text{mean}(SE^2) + \text{var}(\hat{\theta}_m) + \text{var}(\hat{\theta}_m)/M}$$

According to Hayes & Enders (2023) p. 42:

*[T]he first term under the radical represents the average squared standard error (the within imputation sampling variance [...]), the second term depends on the variance of the M parameter estimates around their average (the between imputation variance [...]), and the final term represents the squared standard error of the pooled estimate [...]. Conceptually, the first term estimates the sampling error of a complete-data analysis, and the next two terms are essentially correction factors that inflate the standard error to compensate for uncertainty due to the imputations—that is, additional uncertainty (sampling variability) in the parameter estimates caused by missing data.*

Currently, it is not possible to calculate the first term, because EFA does not calculate SEs for the loadings. Only the second and third terms are used in the calculation of SE for the CIs.

The CI is generally calculated as:

CI = Point estimate ± Margin of error,

where

Margin of error = Critical value × SE of point estimate.

To account for situations where the sample size is small, instead of using z-values, the critical value is derived from the *t* distribution with *n* - 1 degrees of freedom (Hazra, 2017).

## Value

A list with the lower and upper CIs.

## Author(s)

Andreas Soteriades

This function is used internally by EFA\_POOLED to calculate confidence intervals (CIs) around the pooled loadings and pooled interfactor correlations.

## References

Hayes, T. & Enders, C. K. (2023). Maximum likelihood and multiple imputation missing data handling: how they work, and how to make them work in practice. In *APA Handbook of Research Methods in Psychology, Second Edition* Vol. 3. Data Analysis and Research Publication, H. Cooper (Editor-in-Chief).

Hazra, A. (2017). Using the confidence interval confidently. *Journal of Thoracic Disease* 9(10), 4125–4130.

Rubin, D. B. (1987). Multiple imputation for nonresponse in surveys. Wiley. <https://doi.org/10.1002/9780470316696>

---

<code>.change_class</code>	<i>Covert a "LOADINGS" table to matrix or a matrix to "LOADINGS"</i>
----------------------------	--

---

**Description**

Covert a "LOADINGS" table to matrix or a matrix to "LOADINGS"

**Usage**

```
.change_class(x, cl = "matrix")
```

**Arguments**

<code>x</code>	A table of class "matrix" or "LOADINGS".
<code>cl</code>	A string with the class to change the table to. Should be "LOADINGS" or "matrix".

**Value**

A table with the loadings, of class either "LOADINGS" or "matrix".

**Author(s)**

Andreas Soteriades

The loadings tables returned by [EFA](#) are of class "LOADINGS", which prevents applying functions on them. This function allows to change their class to "matrix", and to change back to "LOADINGS" when done.

---

<code>.compute_vars</code>	<i>Compute explained variances from loadings</i>
----------------------------	--

---

**Description**

From unrotated loadings compute the communalities and uniquenesses for total variance. Compute explained variances per factor from rotated loadings (and factor intercorrelations Phi if oblique rotation was used).

**Usage**

```
.compute_vars(L_unrot, L_rot, Phi = NULL)
```

**Arguments**

<code>L_unrot</code>	matrix. Unrotated factor loadings.
<code>L_rot</code>	matrix. Rotated factor loadings.
<code>Phi</code>	matrix. Factor intercorrelations. Provide only if oblique rotation is used.

**Value**

A matrix with sum of squared loadings, proportion explained variance from total variance per factor, same as previous but cumulative, Proportion of explained variance from total explained variance, and same as previous but cumulative.

---

.consensus_loss	<i>Mean squared discrepancy to a consensus target</i>
-----------------	---

---

**Description**

Mean squared discrepancy to a consensus target

**Usage**

```
.consensus_loss(aligned_loadings, target)
```

**Arguments**

- aligned\_loadings  
List of aligned loading matrices.
- target  
Consensus target matrix.

**Value**

Mean sum of squared deviations from the target across matrices.

---

.consensus_target_procrustes_single	<i>Internal single-start consensus engine</i>
-------------------------------------	---

---

**Description**

This internal helper performs a single consensus-target run from one starting target. Users should normally call [CONSENSUS\_PROCRUSTES()] instead.

**Usage**

```
.consensus_target_procrustes_single(  
  unrotated_list,  
  init_targets = NULL,  
  rotation = c("orthogonal", "oblique"),  
  start = 1,  
  tol = 0.001,  
  loss_tol = 1e-07,  
  loss_patience = 5,  
)
```

```

convergence = c("either", "target", "loss", "both"),
min_iter = 2,
max_iter = 200,
alpha = 1,
match_target = TRUE,
hyper_cutoff = 0.15,
oblique_maxit = 300,
oblique_eps = 1e-05,
oblique_max_line_search = 10,
oblique_step0 = 1,
oblique_normalize = FALSE,
oblique_random_starts = 0,
oblique_random_starts_stage = c("final", "none", "outer", "both"),
oblique_screen_keep = 2,
oblique_triage_maxit = 25,
oblique_triage_improve_tol = 0,
verbose = FALSE
)

```

### Arguments

<code>unrotated_list</code>	List of unrotated loading matrices to be aligned. All matrices must be numeric, finite, and have identical dimensions.
<code>init_targets</code>	Optional list of starting target matrices. These are typically rotated loading matrices from the corresponding analyses. If 'NULL', 'unrotated_list' is used.
<code>rotation</code>	Character string, either "orthogonal" or "oblique".
<code>start</code>	Either a single integer selecting an element of 'init_targets', or an explicit target matrix. Used when 'multi_start = FALSE'.
<code>tol</code>	Positive relative Frobenius-norm convergence tolerance for the outer target update.
<code>loss_tol</code>	Positive tolerance for the relative change in the outer consensus loss. If 'NULL', loss-based convergence is disabled. It cannot be 'NULL' when 'convergence' is "loss" or "both".
<code>loss_patience</code>	Positive integer. Number of consecutive iterations with relative loss change below 'loss_tol' required for loss-based convergence.
<code>convergence</code>	Character string controlling the stopping rule. "either" stops when either target or loss convergence is satisfied; "target" uses only target change; "loss" uses only loss change; "both" requires both.
<code>min_iter</code>	Non-negative integer. Minimum number of outer iterations before convergence can be declared.
<code>max_iter</code>	Positive integer. Maximum number of outer consensus iterations.
<code>alpha</code>	Damping factor for the target update. 'alpha = 1' uses the full centroid update. Smaller values, such as '0.5', can reduce oscillation.
<code>match_target</code>	Logical. If 'TRUE', the updated centroid is signed and column-matched to the previous target before convergence is evaluated.



---

<code>.factor_corres</code>	<i>Compute number of non-matching indicator-to-factor correspondences</i>
-----------------------------	---

---

**Description**

Compute number of non-matching indicator-to-factor correspondences

**Usage**

```
.factor_corres(x, y, thresh = 0.3)
```

**Arguments**

<code>x</code>	numeric matrix. A matrix of pattern coefficients.
<code>y</code>	numeric matrix. A second matrix of coefficients.
<code>thresh</code>	numeric. The threshold to classify a pattern coefficient as substantial.

---

<code>.hyperplane_count</code>	<i>Count near-zero loadings</i>
--------------------------------	---------------------------------

---

**Description**

Hyperplane count is the number of loadings with absolute value smaller than a user-specified cutoff.

**Usage**

```
.hyperplane_count(L, cutoff = 0.15)
```

**Arguments**

<code>L</code>	Numeric loading matrix.
<code>cutoff</code>	Numeric scalar. Loadings with $ \text{abs}(L) < \text{cutoff} $ are counted as being in the hyperplane.

**Value**

A list with the total hyperplane count and counts by factor and item.

---

.nest\_sym *Get reference values for nest.*

---

### Description

Function called from within NEST so usually no call to this is needed by the user. Provides a C++ implementation of the NEST simulation procedure

### Usage

```
.nest_sym(nf, N, M, nreps = 1000L)
```

### Arguments

nf	numeric. Current number of factors.
N	numeric. Number of cases / observations in dataset.
M	numeric matrix. A transposed matrix of <code>cbind(loadings, diag(sqrt(uniquenesses)))</code> .
nreps	numeric. Number of datasets to create.

---

.numformat *Format numbers for print method*

---

### Description

Helper function used in the print method for class `LOADINGS` and `SLLOADINGS`. Strips the 0 in front of the decimal point of a number if `number < 1`, only keeps the first `digits` number of digits, and adds an empty space in front of the number if the number is positive. This way all returned strings (except for those `> 1`, which are exceptions in `LOADINGS`) have the same number of characters.

### Usage

```
.numformat(x, digits = 2, print_zero = FALSE, pad = TRUE)
```

### Arguments

x	numeric. Number to be formatted.
digits	numeric. Number of digits after the comma to keep.
print_zero	logical. Whether, if a number is between <code>[-1, 1]</code> , the zero should be omitted or printed (default is <code>FALSE</code> , i.e. omit zeros).
pad	logical. Whether, if a number starts with a 0 and the 0 is not printed a white-space should be added.

### Value

A formatted number

---

*.oblique\_procrustes*    *Oblique Procrustes target rotation using a  $k \times k$  inner objective*

---

### Description

Compute an oblique target rotation for a loading matrix using a ‘targetQ’-compatible parameterization and a ‘ $k \times k$ ’ objective.

### Usage

```
.oblique_procrustes(
  A,
  B,
  S_r = NULL,
  T_init_r = NULL,
  eps = 1e-05,
  maxit = 1000L,
  max_line_search = 10L,
  step0 = 1,
  normalize = FALSE,
  random_starts = 0L,
  screen_keep = 2L,
  triage_maxit = 25L,
  triage_improve_tol = 0
)
```

### Arguments

A	Numeric matrix. Loading matrix to be rotated.
B	Numeric matrix. Target loading matrix with the same dimensions as ‘A’.
S_r	Optional numeric ‘ $k \times k$ ’ matrix containing ‘ <code>crossprod(A)</code> ’. Supplying this is useful when the same ‘A’ is rotated repeatedly. Ignored when ‘normalize = TRUE’ because the normalized cross-product is different.
T_init_r	Optional numeric ‘ $k \times k$ ’ starting transformation matrix. If ‘NULL’, the identity matrix is used for the primary start.
eps	Numeric scalar. Convergence tolerance for the projected-gradient norm.
maxit	Integer scalar. Maximum number of full projected-gradient updates.
max_line_search	Integer scalar. Maximum number of step-halving attempts after the initial trial step in each line-search phase.
step0	Numeric scalar. Initial step size used in the projected-gradient update.
normalize	Logical scalar. If ‘TRUE’, apply Kaiser normalization before rotation and reverse it after rotation.
random_starts	Integer scalar. Number of additional random starts.

- screen\_keep     Integer scalar. Number of screened random starts retained for triage optimization.
- trriage\_maxit    Integer scalar. Number of short optimization iterations used in the triage stage.
- trriage\_improve\_tol     Numeric scalar. Relative improvement required for a triaged start to be promoted to full optimization.

**Details**

The rotated loading matrix is defined as  $L = A \Phi = t(T)$  matrix  $T$  under the oblique normalization constraint  $diag(t(T))$

The line search is monotone: a candidate is accepted only if it satisfies the sufficient-decrease condition, or, as a numerical fallback, if it at least decreases the objective after all step halvings are exhausted. Non-invertible candidate transformations are rejected rather than evaluated through a pseudo-inverse.

Additional random starts may be requested. To reduce runtime, the solver uses a two-stage strategy for extra starts: cheap objective screening, followed by short triage optimization, followed by full optimization only for starts that improve on the current incumbent by at least `trriage_improve_tol`.

The routine is intended for repeated oblique target rotations in workflows such as bootstrap alignment or consensus alignment of exploratory factor solutions across multiply imputed datasets. It follows the same oblique transformation convention as `GPArotation::targetQ()`.

**Value**

A named list containing the rotated loadings, transformation matrix, factor correlation matrix, target criterion value, convergence diagnostics, line-search diagnostics, and multi-start summaries.

**References**

Bernaards, C. A., & Jennrich, R. I. (2005). Gradient projection algorithms and software for arbitrary rotation criteria in factor analysis. *Educational and Psychological Measurement*, 65, 676-696.

Gower, J. C. (1975). Generalized Procrustes analysis. *Psychometrika*, 40, 33-51.

---

.orthogonal\_procrustes  
*Closed-form orthogonal Procrustes rotation*

---

**Description**

Rotate  $A$  to the orthogonal target  $B$  by minimizing  $\|A - B\|_F$

**Usage**

`.orthogonal_procrustes(A, B)`

**Arguments**

A	Numeric matrix to be rotated.
B	Numeric target matrix with the same dimensions as 'A'.

**Value**

A list with the rotated loadings, orthogonal transformation matrix, target criterion value, and basic diagnostics.

**References**

Schoenemann, P. H. (1966). A generalized solution of the orthogonal Procrustes problem. *\*Psychometrika\**, 31, 1-10.

---

<i>.paf_iter</i>	<i>Perform the iterative PAF procedure</i>
------------------	--

---

**Description**

Function called from within PAF so usually no call to this is needed by the user. Provides a C++ implementation of the PAF procedure

**Usage**

```
.paf_iter(h2, criterion, R, n_fac, abs_eig, crit_type, max_iter)
```

**Arguments**

h2	numeric. The initial communalities estimates.
criterion	double. The convergence criterion to use.
R	matrix. The correlation matrix with the initial communalities estimates in the diagonal.
n_fac	numeric. The number of factors to extract.
abs_eig	logical. Whether absolute eigenvalues should be used to compute the loadings.
crit_type	numeric. Whether maximum absolute differences (crit_type = 1), or sum of differences (crit_type = 2) should be used
max_iter	numeric. The number of iterations after which to end the procedure if no convergence has been reached by then.

---

.parallel\_sim                      *Parallel analysis on simulated data.*

---

**Description**

Function called from within PARALLEL so usually no call to this is needed by the user. Provides a C++ implementation of the PARALLEL simulation procedure

**Usage**

```
.parallel_sim(n_datasets, n_vars, N, eigen_type, maxit = 10000L)
```

**Arguments**

n_datasets	numeric. Number of datasets with dimensions (N, n_vars) to simulate.
n_vars	numeric. Number of variables / indicators in dataset.
N	numeric. Number of cases / observations in dataset.
eigen_type	numeric. Whether PCA (eigen_type = 1; i.e., leaving diagonal of correlation matrix at 1) or PAF (eigen_type = 2; i.e., setting diagonal of correlation matrix to SMCs).
maxit	numeric. Maximum iterations to perform after which to abort.

---

.stat\_over\_list                      *Calculate statistics for a list of matrices*

---

**Description**

Calculate statistics for a list of matrices

**Usage**

```
.stat_over_list(alist, stat)
```

**Arguments**

alist	A list of sub-lists, typically a list of $m$ matrices from "EFA", where $m$ is the number of imputations passed to <a href="#">EFA_POOLED</a> .
stat	A function, e.g. mean or sd.

**Value**

A matrix with the aggregated results

**Author(s)**

Andreas Soteriades

Given a list of matrices, this function calculates user-supplied statistics (e.g. mean, median) over the matrices. This function is useful for averaging results from [EFA](#) (e.g. loadings) over all permutation runs in [EFA\\_POOLED](#).

---

`.tucker_congruence`      *Tucker congruence between factors*

---

**Description**

Compute the Tucker congruence matrix between the columns of two loading matrices.

**Usage**

```
.tucker_congruence(L1, L2)
```

**Arguments**

L1                      Numeric matrix.  
L2                      Numeric matrix with the same dimensions as 'L1'.

**Value**

A square matrix whose '(i, j)' entry is the Tucker congruence between column 'i' of 'L1' and column 'j' of 'L2'.

**References**

Lorenzo-Seva, U., and ten Berge, J. M. F. (2006). Tucker's congruence coefficient as a meaningful index of factor similarity. *\*Methodology\**, 2, 57-64.

---

BARTLETT                      *Bartlett's test of sphericity*

---

**Description**

This function tests whether a correlation matrix is significantly different from an identity matrix (Bartlett, 1951). If the Bartlett's test is not significant, the correlation matrix is not suitable for factor analysis because the variables show too little covariance.

**Usage**

```
BARTLETT(
  x,
  N = NA,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
          "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall")
)
```

**Arguments**

x	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations.
N	numeric. The number of observations. Needs only be specified if a correlation matrix is used.
use	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
cor_method	character. Passed to <code>stats::cor</code> . Default is "pearson".

**Details**

Bartlett (1951) proposed this statistic to determine a correlation matrix' suitability for factor analysis. The statistic is approximately chi square distributed with  $df = \frac{p(p-1)}{2}$  and is given by

$$chi^2 = -\log(\det(R))(N - 1 - (2 * p + 5)/6)$$

where  $\det(R)$  is the determinant of the correlation matrix,  $N$  is the sample size, and  $p$  is the number of variables.

This tests requires multivariate normality. If this condition is not met, the Kaiser-Meyer-Olkin criterion (**KMO**) can still be used.

This function was heavily influenced by the `psych::cortest.bartlett` function from the psych package.

The BARTLETT function can also be called together with the (**KMO**) function and with factor retention criteria in the `N_FACTORS` function.

**Value**

A list containing

chisq	The chi square statistic.
p_value	The p value of the chi square statistic.
df	The degrees of freedom for the chi square statistic.
settings	A list of the settings used.

**Source**

Bartlett, M. S. (1951). The effect of standardization on a Chi-square approximation in factor analysis. *Biometrika*, 38, 337-344.

**See Also**

[KMO](#) for another measure to determine suitability for factor analysis.

[N\\_FACTORS](#) as a wrapper function for this function, [KMO](#) and several factor retention criteria.

**Examples**

```
BARTLETT(test_models$baseline$cormat, N = 500)
```

---

 CD

---

*Comparison Data*


---

**Description**

Factor retention method introduced by Ruscio and Roche (2012). The code was adapted from the CD code by Auerswald and Moshagen (2017) available at [https://osf.io/x5cz2/?view\\_only=d03efba1fd0f4c849a87db82e6705668](https://osf.io/x5cz2/?view_only=d03efba1fd0f4c849a87db82e6705668)

**Usage**

```
CD(
  x,
  n_factors_max = NA,
  N_pop = 10000,
  N_samples = 500,
  alpha = 0.3,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
    "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  max_iter = 50
)
```

**Arguments**

<code>x</code>	data.frame or matrix. Dataframe or matrix of raw data.
<code>n_factors_max</code>	numeric. The maximum number of factors to test against. Larger numbers will increase the duration the procedure takes, but test more possible solutions. If left NA (default) the maximum number of factors for which the model is still over-identified ( $df > 0$ ) is used.
<code>N_pop</code>	numeric. Size of finite populations of comparison data. Default is 10000.
<code>N_samples</code>	numeric. Number of samples drawn from each population. Default is 500.

alpha	numeric. The alpha level used to test the significance of the improvement added by an additional factor. Default is .30.
use	character. Passed to <code>stats::cor</code> . Default is "pairwise.complete.obs". However, for the comparison data procedure, NA values will be excluded using <code>na.omit()</code> . If missing data should be handled differently (e.g., imputation), do this before passing the data to <code>CD()</code> .
cor_method	character. Passed to <code>stats::cor</code> . Default is "pearson".
max_iter	numeric. The maximum number of iterations to perform after which the iterative PAF procedure is halted. Default is 50.

### Details

"Parallel analysis (PA) is an effective stopping rule that compares the eigenvalues of randomly generated data with those for the actual data. PA takes into account sampling error, and at present it is widely considered the best available method. We introduce a variant of PA that goes even further by reproducing the observed correlation matrix rather than generating random data. Comparison data (CD) with known factorial structure are first generated using 1 factor, and then the number of factors is increased until the reproduction of the observed eigenvalues fails to improve significantly" (Ruscio & Roche, 2012, p. 282).

The CD implementation here is based on the code by Ruscio and Roche (2012), but is slightly adapted to increase speed by performing the principal axis factoring using a C++ based function.

Note that if the data contains missing values, these will be removed for the comparison data procedure using `stats::na.omit`. If missing data should be treated differently, e.g., by imputation, do this outside CD and then pass the complete data.

The CD function can also be called together with other factor retention criteria in the `N_FACTORS` function.

### Value

A list of class CD containing

n_factors	The number of factors to retain according to comparison data results.
eigenvalues	A vector containing the eigenvalues of the entered data.
RMSE_eigenvalues	A matrix containing the RMSEs between the eigenvalues of the generated data and those of the entered data.
settings	A list of the settings used.

### Source

Auerswald, M., & Moshagen, M. (2019). How to determine the number of factors to retain in exploratory factor analysis: A comparison of extraction methods under realistic conditions. *Psychological Methods*, 24(4), 468–491. <https://doi.org/10.1037/met0000200>

Ruscio, J., & Roche, B. (2012). Determining the number of factors to retain in an exploratory factor analysis using comparison data of known factorial structure. *Psychological Assessment*, 24, 282–292. doi: 10.1037/a0025697

**See Also**

Other factor retention criteria: [EKC](#), [HULL](#), [KGC](#), [PARALLEL](#), [SMT](#)  
[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

**Examples**

```
# determine n factors of the GRiPS
CD(GRiPS_raw)

# determine n factors of the DOSPERT risk subscale
CD(DOSPERT_raw)
```

---

 COMPARE

---

*Compare two vectors or matrices (communalities or loadings)*


---

**Description**

The function takes two objects of the same dimensions containing numeric information (loadings or communalities) and returns a list of class COMPARE containing summary information of the differences of the objects.

**Usage**

```
COMPARE(
  x,
  y,
  reorder = c("congruence", "names", "none"),
  corres = TRUE,
  thresh = 0.3,
  digits = 4,
  m_red = 0.001,
  range_red = 0.001,
  round_red = 3,
  print_diff = TRUE,
  na.rm = FALSE,
  x_labels = c("x", "y"),
  plot = TRUE,
  plot_red = 0.01
)
```

**Arguments**

**x** matrix, or vector. Loadings or communalities of a factor analysis output.  
**y** matrix, or vector. Loadings or communalities of another factor analysis output to compare to x.

reorder	character. Whether and how elements / columns should be reordered. If "congruence" (default), reordering is done according to Tuckers correspondence coefficient, if "names", objects according to their names, if "none", no reordering is done.
corres	logical. Whether factor correspondences should be compared if a matrix is entered.
thresh	numeric. The threshold to classify a pattern coefficient as substantial. Default is .3.
digits	numeric. Number of decimals to print in the output. Default is 4.
m_red	numeric. Number above which the mean and median should be printed in red (i.e., if .001 is used, the mean will be in red if it is larger than .001, otherwise it will be displayed in green.) Default is .001.
range_red	numeric. Number above which the min and max should be printed in red (i.e., if .001 is used, min and max will be in red if the max is larger than .001, otherwise it will be displayed in green. Default is .001). Note that the color of min also depends on max, that is min will be displayed in the same color as max.
round_red	numeric. Number above which the max decimals to round to where all corresponding elements of x and y are still equal are displayed in red (i.e., if 3 is used, the number will be in red if it is smaller than 3, otherwise it will be displayed in green). Default is 3.
print_diff	logical. Whether the difference vector or matrix should be printed or not. Default is TRUE.
na.rm	logical. Whether NAs should be removed in the mean, median, min, and max functions. Default is FALSE.
x_labels	character. A vector of length two containing identifying labels for the two objects x and y that will be compared. These will be used as labels on the x-axis of the plot. Default is "x" and "y".
plot	logical. If TRUE (default), a plot illustrating the differences will be shown.
plot_red	numeric. Threshold above which to plot the absolute differences in red. Default is .001.

### Value

A list of class COMPARE containing summary statistics on the differences of x and y.

diff	The vector or matrix containing the differences between x and y.
mean_abs_diff	The mean absolute difference between x and y.
median_abs_diff	The median absolute difference between x and y.
min_abs_diff	The minimum absolute difference between x and y.
max_abs_diff	The maximum absolute difference between x and y.
max_dec	The maximum number of decimals to which a comparison makes sense. For example, if x contains only values up to the third decimals, and y is a normal double, max_dec will be three.

are_equal	The maximal number of decimals to which all elements of x and y are equal.
diff_corres	The number of differing variable-to-factor correspondences between x and y, when only the highest loading is considered.
diff_corres_cross	The number of differing variable-to-factor correspondences between x and y when all loadings $\geq$ thresh are considered.
g	The root mean squared distance (RMSE) between x and y.
settings	List of the settings used.

### Examples

```
# A type SPSS EFA to mimick the SPSS implementation
EFA_SPSS_6 <- EFA(test_models$case_11b$cormat, n_factors = 6, type = "SPSS")

# A type psych EFA to mimick the psych::fa() implementation
EFA_psych_6 <- EFA(test_models$case_11b$cormat, n_factors = 6, type = "psych")

# compare the two
COMPARE(EFA_SPSS_6$unrot_loadings, EFA_psych_6$unrot_loadings,
        x_labels = c("SPSS", "psych"))
```

---

CONSENSUS\_PROCRUSTES *Consensus Procrustes alignment across multiple loading matrices*

---

### Description

Align several loading matrices to a common Procrustes consensus target.

### Usage

```
CONSENSUS_PROCRUSTES(
  unrotated_list,
  init_targets = NULL,
  rotation = c("orthogonal", "oblique"),
  start = 1,
  multi_start = FALSE,
  starts = NULL,
  tol = 0.001,
  loss_tol = 1e-06,
  loss_patience = 5,
  convergence = c("either", "target", "loss", "both"),
  min_iter = 2,
  max_iter = 200,
  alpha = 1,
  match_target = TRUE,
  hyper_cutoff = 0.15,
  oblique_maxit = 500,
```

```

    oblique_eps = 1e-05,
    oblique_max_line_search = 10,
    oblique_step0 = 1,
    oblique_normalize = FALSE,
    oblique_random_starts = 0,
    oblique_random_starts_stage = c("final", "none", "outer", "both"),
    oblique_screen_keep = 2,
    oblique_triage_maxit = 25,
    oblique_triage_improve_tol = 0,
    verbose = FALSE
)

```

### Arguments

<code>unrotated_list</code>	List of unrotated loading matrices to be aligned. All matrices must be numeric, finite, and have identical dimensions.
<code>init_targets</code>	Optional list of starting target matrices. These are typically rotated loading matrices from the corresponding analyses. If 'NULL', 'unrotated_list' is used.
<code>rotation</code>	Character string, either "orthogonal" or "oblique".
<code>start</code>	Either a single integer selecting an element of 'init_targets', or an explicit target matrix. Used when 'multi_start = FALSE'.
<code>multi_start</code>	Logical. If 'FALSE', perform one consensus-target run. If 'TRUE', repeat the single-start algorithm for each element of 'starts'.
<code>starts</code>	Integer vector selecting elements of 'init_targets' used as starting targets when 'multi_start = TRUE'. If 'NULL', all elements of 'init_targets' are used. Duplicate entries are removed.
<code>tol</code>	Positive relative Frobenius-norm convergence tolerance for the outer target update.
<code>loss_tol</code>	Positive tolerance for the relative change in the outer consensus loss. If 'NULL', loss-based convergence is disabled. It cannot be 'NULL' when 'convergence' is "loss" or "both".
<code>loss_patience</code>	Positive integer. Number of consecutive iterations with relative loss change below 'loss_tol' required for loss-based convergence.
<code>convergence</code>	Character string controlling the stopping rule. "either" stops when either target or loss convergence is satisfied; "target" uses only target change; "loss" uses only loss change; "both" requires both.
<code>min_iter</code>	Non-negative integer. Minimum number of outer iterations before convergence can be declared.
<code>max_iter</code>	Positive integer. Maximum number of outer consensus iterations.
<code>alpha</code>	Damping factor for the target update. 'alpha = 1' uses the full centroid update. Smaller values, such as '0.5', can reduce oscillation.
<code>match_target</code>	Logical. If 'TRUE', the updated centroid is signed and column-matched to the previous target before convergence is evaluated.
<code>hyper_cutoff</code>	Non-negative cutoff used by '.hyperplane_count()' for summary output.



---

DOSPERT
*DOSPERT***Description**

A list containing the the bivariate correlations (cormat) of the 40 items of the Domain Specific Risk Taking Scale (DOSPERT; Weber, Blais, & Betz, 2002) and the sample size (N) based on the publicly available dataset at (<https://osf.io/rce7g>) of the Basel-Berlin Risk Study (Frey et al., 2017). The items measure risk-taking propensity on six different domains: social, recreational, gambling, health/ safety, investment, and ethical.

**Usage**

DOSPERT

**Format**An object of class `list` of length 2.**Source**

Weber, E. U., Blais, A.-R., & Betz, N. E. (2002). A domain specific risk-attitude scale: Measuring risk perceptions and risk behaviors. *Journal of Behavioral Decision Making*, 15(4), 263–290. doi: 10.1002/bdm.414

Frey, R., Pedroni, A., Mata, R., Rieskamp, J., & Hertwig, R. (2017). Risk preference shares the psychometric structure of major psychological traits. *Science Advances*, 3, e1701381.

<https://osf.io/rce7g>

---

DOSPERT\_raw
*DOSPERT\_raw***Description**

A `data.frame` containing responses to the risk subscale of the Domain Specific Risk Taking Scale (DOSPERT; Weber, Blais, & Betz, 2002) based on the publicly available dataset (at <https://osf.io/pjt57/>) by Frey, Duncan, and Weber (2020). The items measure risk-taking propensity on six different domains: social, recreational, gambling, health/ safety, investment, and ethical.

**Usage**

DOSPERT\_raw

**Format**An object of class `data.frame` with 3123 rows and 30 columns.

## Source

Blais, A.-R., & Weber, E. U. (2002). A domain-specific risk-taking (DOSPERT) scale for adult populations. *Judgment and Decision Making*, 15(4), 263–290. doi: 10.1002/bdm.414

Frey, R., Duncan, S. M., & Weber, E. U. (2020). Towards a typology of risk preference: Four risk profiles describe two thirds of individuals in a large sample of the U.S. population. *PsyArXiv Preprint*. doi:10.31234/osf.io/yjwr9

---

EFA

*Exploratory factor analysis (EFA)*

---

## Description

This function does an EFA with either PAF, ML, or ULS with or without subsequent rotation. All arguments with default value NA can be left to default if type is set to one of "EFAtools", "SPSS", or "psych". The respective specifications are then handled according to the specified type (see details). For all rotations except varimax and promax, the GPArotation package is needed.

## Usage

```
EFA(
  x,
  n_factors,
  N = NA,
  method = c("PAF", "ML", "ULS"),
  rotation = c("none", "varimax", "equamax", "quartimax", "geominT", "bentlerT",
    "bifactorT", "promax", "oblimin", "quartimin", "simplimax", "bentlerQ", "geominQ",
    "bifactorQ"),
  se = c("none", "np-boot"),
  type = c("EFAtools", "psych", "SPSS", "none"),
  max_iter = NA,
  init_comm = NA,
  criterion = NA,
  criterion_type = NA,
  abs_eigen = NA,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
    "na.or.complete"),
  varimax_type = NA,
  k = NA,
  normalize = TRUE,
  P_type = NA,
  precision = 1e-05,
  order_type = NA,
  start_method = "psych",
  cor_method = c("pearson", "spearman", "kendall"),
  b_boot = 1000,
  ci = 0.95,
```

```

    randomStarts = 10,
    ...
)

```

### Arguments

<code>x</code>	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations. If raw data is entered, the correlation matrix is found from the data.
<code>n_factors</code>	numeric. Number of factors to extract.
<code>N</code>	numeric. The number of observations. Needs only be specified if a correlation matrix is used. If input is a correlation matrix and <code>N = NA</code> (default), not all fit indices can be computed.
<code>method</code>	character. One of "PAF", "ML", or "ULS" to use principal axis factoring, maximum likelihood, or unweighted least squares (also called minres), respectively, to fit the EFA.
<code>rotation</code>	character. Either perform no rotation ("none"; default), an orthogonal rotation ("varimax", "equamax", "quartimax", "geominT", "bentlerT", or "bifactorT"), or an oblique rotation ("promax", "oblimin", "quartimin", "simplimax", "bentlerQ", "geominQ", or "bifactorQ").
<code>se</code>	character. Whether and how standard errors should be computed. Currently, only "np-boot" for non-parametric bootstrap is available and needs raw data to work. Default is "none".
<code>type</code>	character. If one of "EFAtools" (default), "psych", or "SPSS" is used, and the following arguments with default NA are left with NA, these implementations are executed according to the respective program ("psych" and "SPSS") or according to the best solution found in Grieder & Steiner (2020; "EFAtools"). Individual properties can be adapted using one of the three types and specifying some of the following arguments. If set to "none" additional arguments must be specified depending on the method and rotation used (see details).
<code>max_iter</code>	numeric. The maximum number of iterations to perform after which the iterative PAF procedure is halted with a warning. If <code>type</code> is one of "EFAtools", "SPSS", or "psych", this is automatically specified if <code>max_iter</code> is left to be NA, but can be overridden by entering a number. Default is NA.
<code>init_comm</code>	character. The method to estimate the initial communalities in PAF. "smc" will use squared multiple correlations, "mac" will use maximum absolute correlations, "unity" will use 1s (see details). Default is NA.
<code>criterion</code>	numeric. The convergence criterion used for PAF. If the change in communalities from one iteration to the next is smaller than this criterion the solution is accepted and the procedure ends. Default is NA.
<code>criterion_type</code>	character. Type of convergence criterion used for PAF. "max_individual" selects the maximum change in any of the communalities from one iteration to the next and tests it against the specified criterion. This is also used by SPSS. "sum" takes the difference of the sum of all communalities in one iteration and the sum of all communalities in the next iteration and tests this against the criterion. This procedure is used by the <code>psych::fa</code> function. Default is NA.

<code>abs_eigen</code>	logical. Which algorithm to use in the PAF iterations. If FALSE, the loadings are computed from the eigenvalues. This is also used by the <code>psych::fa</code> function. If TRUE the loadings are computed with the absolute eigenvalues as done by SPSS. Default is NA.
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>varimax_type</code>	character. The type of the varimax rotation performed. If "svd", singular value decomposition is used, as <code>stats::varimax</code> does. If "kaiser", the varimax procedure performed in SPSS is used. This is the original procedure from Kaiser (1958), but with slight alterations in the varimax criterion (see details, and Grieder & Steiner, 2020). Default is NA.
<code>k</code>	numeric. Either the power used for computing the target matrix P in the promax rotation or the number of 'close to zero loadings' for the simplimax rotation (see <code>GPArotation::GPFoblq</code> ). If left to NA (default), the value for promax depends on the specified type. For simplimax, $nrow(L)$ , where L is the matrix of unrotated loadings, is used by default.
<code>normalize</code>	logical. If TRUE, a kaiser normalization is performed before the specified rotation. Default is TRUE.
<code>P_type</code>	character. This specifies how the target matrix P is computed in promax rotation. If "unnorm" it will use the unnormalized target matrix as originally done in Hendrickson and White (1964). This is also used in the psych and stats packages. If "norm" it will use the normalized target matrix as used in SPSS. Default is NA.
<code>precision</code>	numeric. The tolerance for stopping in the rotation procedure. Default is $10^{-5}$ for all rotation methods.
<code>order_type</code>	character. How to order the factors. "eigen" will reorder the factors according to the largest to lowest eigenvalues of the matrix of rotated loadings. "ss_factors" will reorder the factors according to descending sum of squared factor loadings per factor. Default is NA.
<code>start_method</code>	character. How to specify the starting values for the optimization procedure for ML. Default is "psych" which takes the starting values specified in <code>psych::fa</code> . "factanal" takes the starting values specified in the <code>stats::factanal</code> function. Solutions are very similar.
<code>cor_method</code>	character. Passed to <code>stats::cor</code> . Default is "pearson".
<code>b_boot</code>	numeric. The number of bootstrap samples to draw. Default is 1000.
<code>ci</code>	numeric. The confidence interval to create from the bootstrap samples. Must be between 0 and 1. Default is .95 for 95% CIs.
<code>randomStarts</code>	numeric. The number of random starts to use in rotations that use the <code>GPArotation</code> package. Some rotations are prone to produce local minima and sometimes many random starts are needed (see the <code>GPArotation</code> package documentation for details).
<code>...</code>	Additional arguments passed to rotation functions from the <code>GPArotation</code> package (e.g., <code>maxit</code> for maximum number of iterations).

## Details

There are two main ways to use this function. The easiest way is to use it with a specified type (see above), which sets most of the other arguments accordingly. Another way is to use it more flexibly by explicitly specifying all arguments used and set type to "none" (see examples). A mix of the two can also be done by specifying a type as well as additional arguments. However, this will throw warnings to avoid unintentional deviations from the implementations according to the specified type.

The type argument is evaluated for PAF and for all rotations (mainly important for the varimax and promax rotations). The type-specific settings for these functions are detailed below.

For PAF, the values of `init_comm`, `criterion`, `criterion_type`, and `abs_eigen` depend on the type argument.

`type = "EFAtools"` will use the following argument specification: `init_comm = "smc"`, `criterion = .001`, `criterion_type = "sum"`, `abs_eigen = TRUE`.

`type = "psych"` will use the following argument specification: `init_comm = "smc"`, `criterion = .001`, `criterion_type = "sum"`, `abs_eigen = FALSE`.

`type = "SPSS"` will use the following argument specification: `init_comm = "smc"`, `criterion = .001`, `criterion_type = "max_individual"`, `abs_eigen = TRUE`.

If SMCs fail, SPSS takes "mac". However, as SPSS takes absolute eigenvalues, this is hardly ever the case. Psych, on the other hand, takes "unity" if SMCs fail, but uses the Moore-Penrose Pseudo Inverse of a matrix, thus, taking "unity" is only necessary if negative eigenvalues occur afterwards in the iterative PAF procedure. The EFAtools type setting combination was the best in terms of accuracy and number of Heywood cases compared to all the other setting combinations tested in simulation studies in Grieder & Steiner (2020), which is why this type is used as a default here.

For varimax, the values of `varimax_type` and `order_type` depend on the type argument.

`type = "EFAtools"` will use the following argument specification: `varimax_type = "kaiser"`, `order_type = "eigen"`.

`type = "psych"` will use the following argument specification: `varimax_type = "svd"`, `order_type = "eigen"`.

`type = "SPSS"` will use the following argument specification: `varimax_type = "kaiser"`, `order_type = "ss_factors"`.

For promax, the values of `P_type`, `order_type`, and `k` depend on the type argument.

`type = "EFAtools"` will use the following argument specification: `P_type = "norm"`, `order_type = "eigen"`, `k = 4`.

`type = "psych"` will use the following argument specification: `P_type = "unnorm"`, `order_type = "eigen"`, `k = 4`.

`type = "SPSS"` will use the following argument specification: `P_type = "norm"`, `order_type = "ss_factors"`, `k = 4`.

The `P_type` argument can take two values, "unnorm" and "norm". It controls which formula is used to compute the target matrix  $P$  in the promax rotation. "unnorm" uses the formula from Hendrickson and White (1964), specifically:  $P = \text{abs}(A^{(k+1)}) / A$ , where  $A$  is the unnormalized matrix containing varimax rotated loadings. "SPSS" uses the normalized varimax rotated loadings. Specifically it used the following formula, which can be found in the SPSS 23 and SPSS 27 Algorithms manuals:  $P = \text{abs}(A / \sqrt{\text{rowSums}(A^2)})^{(k+1)} * (\sqrt{\text{rowSums}(A^2)} / A)$ . As

for PAF, the EFAtools type setting combination for promax was the best compared to the other setting combinations tested in simulation studies in Grieder & Steiner (2020).

The `varimax_type` argument can take two values, "svd", and "kaiser". "svd" uses singular value decomposition, by calling `stats::varimax`. "kaiser" performs the varimax procedure as described in the SPSS 23 Algorithms manual and as described by Kaiser (1958). However, there is a slight alteration in computing the varimax criterion, which we found to better align with the results obtain from SPSS. Specifically, the original varimax criterion as described in the SPSS 23 Algorithms manual is  $\sum(n * \text{colSums}(\lambda^4) - \text{colSums}(\lambda^2)^2) / n^2$ , where  $n$  is the number of indicators, and  $\lambda$  is the rotated loadings matrix. However, we found the following to produce results more similar to those of SPSS:  $\sum(n * \text{colSums}(\text{abs}(\lambda)) - \text{colSums}(\lambda^4)^2) / n^2$ .

For all other rotations except varimax and promax, the type argument only controls the `order_type` argument with the same values as stated above for the varimax and promax rotations. For these other rotations, the `GPARotation` package is needed. Additional arguments can also be specified and will be passed to the respective `GPARotation` function (e.g., `maxit` to change the maximum number of iterations for the rotation procedure).

The type argument has no effect on ULS and ML. For ULS, no additional arguments are needed. For ML, an additional argument `start_method` is needed to determine the starting values for the optimization procedure. Default for this argument is "factanal" which takes the starting values specified in the `stats::factanal` function.

## Value

A list of class EFA containing (a subset of) the following:

<code>orig_R</code>	Original correlation matrix.
<code>h2_init</code>	Initial communality estimates from PAF.
<code>h2</code>	Final communality estimates from the unrotated solution.
<code>orig_eigen</code>	Eigen values of the original correlation matrix.
<code>init_eigen</code>	Initial eigenvalues, obtained from the correlation matrix with the initial communality estimates as diagonal in PAF.
<code>final_eigen</code>	Eigenvalues obtained from the correlation matrix with the final communality estimates as diagonal.
<code>iter</code>	The number of iterations needed for convergence.
<code>convergence</code>	Integer code for convergence as returned by <code>stats::optim</code> (only for ML and ULS). 0 indicates successful completion.
<code>unrot_loadings</code>	Loading matrix containing the final unrotated loadings.
<code>vars_accounted</code>	Matrix of explained variances and sums of squared loadings. Based on the unrotated loadings.
<code>fit_indices</code>	For ML and ULS: Fit indices derived from the unrotated factor loadings: Chi Square, including significance level, degrees of freedom (df), Comparative Fit Index (CFI), Root Mean Square Error of Approximation (RMSEA), including its 90% confidence interval, Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and the common part accounted for (CAF) index as proposed by Lorenzo-Seva, Timmerman, & Kiers (2011). For PAF, only the CAF and dfs are returned.

<code>model_implied_R</code>	The model implied correlation matrix.
<code>residuals</code>	Residual correlations, i.e., <code>orig_R - model_implied_R</code>
<code>rot_loadings</code>	Loading matrix containing the final rotated loadings (pattern matrix).
<code>Phi</code>	The factor intercorrelations (only for oblique rotations).
<code>Structure</code>	The structure matrix (only for oblique rotations).
<code>rotmat</code>	The rotation matrix.
<code>vars_accounted_rot</code>	Matrix of explained variances and sums of squared loadings. Based on rotated loadings and, for oblique rotations, the factor intercorrelations.
<code>settings</code>	A list of the settings used.
<code>boot.SE</code>	A list bootstrap standard errors for loadings (rotated and unrotated), structure coefficients (if rotated obliquely), factor correlations (Phi, only if rotated), and fit indices. Only returned, if <code>se = "np-boot"</code> .
<code>boot.CI</code>	A list bootstrap confidence intervals of width <code>ci</code> for loadings (rotated and unrotated), structure coefficients (if rotated obliquely), factor correlations (Phi, if obliquely rotated), and fit indices. Only returned, if <code>se = "np-boot"</code> .
<code>boot.arrays</code>	A list of arrays with the bootstrapped loadings (aligned rotated and unrotated), aligned structure coefficients (if rotated obliquely), aligned factor correlations (Phi, if obliquely rotated), and fit indices. Only returned, if <code>se = "np-boot"</code> .

### Source

Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.

Hendrickson, A. E., & White, P. O. (1964). Promax: A quick method for rotation to oblique simple structure. *British Journal of Statistical Psychology*, 17, 65–70. doi: 10.1111/j.2044-8317.1964.tb00244.x

Lorenzo-Seva, U., Timmerman, M. E., & Kiers, H. A. L. (2011). The Hull Method for Selecting the Number of Common Factors, *Multivariate Behavioral Research*, 46, 340-364, doi: 10.1080/00273171.2011.564527

Kaiser, H. F. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, 23, 187–200. doi: 10.1007/BF02289233

### Examples

```
# A type EFAtools (as presented in Steiner and Grieder, 2020) EFA
EFAtools_PAF <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
  type = "EFAtools", method = "PAF", rotation = "none")

# A type SPSS EFA to mimick the SPSS implementation (this will throw a warning,
# see below)
SPSS_PAF <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
  type = "SPSS", method = "PAF", rotation = "none")

# A type psych EFA to mimick the psych::fa() implementation
```

```

psych_PAF <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
                type = "psych", method = "PAF", rotation = "none")

# Use ML instead of PAF with type EFAtools
EFAtools_ML <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
                  type = "EFAtools", method = "ML", rotation = "none")

# Use oblimin rotation instead of no rotation with type EFAtools
EFAtools_oblim <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
                     type = "EFAtools", method = "PAF", rotation = "oblimin")

# Do a PAF without rotation without specifying a type, so the arguments
# can be flexibly specified (this is only recommended if you know what you're
# doing)
PAF_none <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
                type = "none", method = "PAF", rotation = "none",
                max_iter = 500, init_comm = "mac", criterion = 1e-4,
                criterion_type = "sum", abs_eigen = FALSE)

# Add a promax rotation
PAF_pro <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
               type = "none", method = "PAF", rotation = "promax",
               max_iter = 500, init_comm = "mac", criterion = 1e-4,
               criterion_type = "sum", abs_eigen = FALSE, k = 3,
               P_type = "unnorm", precision = 1e-5, order_type = "eigen",
               varimax_type = "svd")

```

---

EFA\_AVERAGE

*Model averaging across different EFA methods and types*


---

## Description

Not all EFA procedures always arrive at the same solution. This function allows you perform a number of EFAs from different methods (e.g., Maximum Likelihood and Principal Axis Factoring), with different implementations (e.g., the SPSS and psych implementations of Principal Axis Factoring), and across different rotations of the same type (e.g., multiple oblique rotations, like promax and oblimin). EFA\_AVERAGE will then run all these EFAs (using the [EFA](#) function) and provide a summary across the different solutions.

## Usage

```

EFA_AVERAGE(
  x,
  n_factors,
  N = NA,
  method = "PAF",
  rotation = "promax",
  type = "none",

```

```

averaging = c("mean", "median"),
trim = 0,
saliency_threshold = 0.3,
max_iter = 10000,
init_comm = c("smc", "mac", "unity"),
criterion = c(0.001),
criterion_type = c("sum", "max_individual"),
abs_eigen = c(TRUE),
varimax_type = c("svd", "kaiser"),
normalize = TRUE,
k_promax = 2:4,
k_simplimax = ncol(x),
P_type = c("norm", "unnorm"),
precision = 1e-05,
start_method = c("psych", "factanal"),
use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
      "na.or.complete"),
cor_method = c("pearson", "spearman", "kendall"),
show_progress = TRUE
)

```

### Arguments

x	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations. If raw data is entered, the correlation matrix is found from the data.
n_factors	numeric. Number of factors to extract.
N	numeric. The number of observations. Needs only be specified if a correlation matrix is used. If input is a correlation matrix and N = NA (default), not all fit indices can be computed.
method	character vector. Any combination of "PAF", "ML", and "ULS", to use principal axis factoring, maximum likelihood, or unweighted least squares (also called minres), respectively, to fit the EFAs. Default is "PAF".
rotation	character vector. Either perform no rotation ("none"), any combination of orthogonal rotations ("varimax", "equamax", "quartimax", "geominT", "bentlerT", and "bifactorT"; using "orthogonal" runs all of these), or of oblique rotations ("promax", "oblimin", "quartimin", "simplimax", "bentlerQ", "geominQ", and "bifactorQ"; using "oblique" runs all of these). Rotation types (no rotation, orthogonal rotations, and oblique rotations) cannot be mixed. Default is "promax".
type	character vector. Any combination of "none" (default), "EFAtools", "psych", and "SPSS" can be entered. "none" allows the specification of various combinations of the arguments controlling both factor extraction methods and the rotations. The others ("EFAtools", "psych", and "SPSS"), control the execution of the respective factor extraction method and rotation to be in line with how it is executed in this package (i.e., the respective default procedure), in the psych package, and in SPSS. A specific psych implementation exists for PAF, ML, varimax, and promax. The SPSS implementation exists for PAF, varimax, and promax. For details, see <a href="#">EFA</a> .

averaging	character. One of "mean" (default), and "median". Controls whether the different results should be averaged using the (trimmed) mean, or the median.
trim	numeric. If averaging is set to "mean", this argument controls the trimming of extremes (for details see <code>base::mean</code> ). By default no trimming is done (i.e., <code>trim = 0</code> ).
saliency_threshold	numeric. The threshold to use to classify a pattern coefficient or loading as salient (i.e., substantial enough to assign it to a factor). Default is 0.3. Indicator-to-factor correspondences will be inferred based on this threshold. Note that this may not be meaningful if <code>rotation = "none"</code> and <code>n_factors &gt; 1</code> are used, as no simple structure is present there.
max_iter	numeric. The maximum number of iterations to perform after which the iterative PAF procedure is halted with a warning. Default is 10,000. Note that non-converged procedures are excluded from the averaging procedure.
init_comm	character vector. Any combination of "smc", "mac", and "unity". Controls the methods to estimate the initial communalities in PAF if "none" is among the specified types. "smc" will use squared multiple correlations, "mac" will use maximum absolute correlations, "unity" will use 1s (for details see <a href="#">EFA</a> ). Default is <code>c("smc", "mac", "unity")</code> .
criterion	numeric vector. The convergence criterion used for PAF if "none" is among the specified types. If the change in communalities from one iteration to the next is smaller than this criterion the solution is accepted and the procedure ends. Default is <code>0.001</code> .
criterion_type	character vector. Any combination of "max_individual" and "sum". Type of convergence criterion used for PAF if "none" is among the specified types. "max_individual" selects the maximum change in any of the communalities from one iteration to the next and tests it against the specified criterion. "sum" takes the difference of the sum of all communalities in one iteration and the sum of all communalities in the next iteration and tests this against the criterion (for details see <a href="#">EFA</a> ). Default is <code>c("sum", "max_individual")</code> .
abs_eigen	logical vector. Any combination of TRUE and FALSE. Which algorithm to use in the PAF iterations if "none" is among the specified types. If FALSE, the loadings are computed from the eigenvalues. This is also used by the <code>psych::fa</code> function. If TRUE the loadings are computed with the absolute eigenvalues as done by SPSS (for details see <a href="#">EFA</a> ). Default is TRUE.
varimax_type	character vector. Any combination of "svd" and "kaiser". The type of the varimax rotation performed if "none" is among the specified types and "varimax", "promax", "orthogonal", or "oblique" is among the specified rotations. "svd" uses singular value decomposition, as <code>stats::varimax</code> does, and "kaiser" uses the varimax procedure performed in SPSS. This is the original procedure from Kaiser (1958), but with slight alterations in the varimax criterion (for details, see <a href="#">EFA</a> and <a href="#">Grieder &amp; Steiner, 2020</a> ). Default is <code>c("svd", "kaiser")</code> .
normalize	logical vector. Any combination of TRUE and FALSE. TRUE performs a kaiser normalization before the specified rotation(s). Default is TRUE.
k_promax	numeric vector. The power used for computing the target matrix P in the promax rotation if "none" is among the specified types and "promax" or "oblique" is among the specified rotations. Default is <code>2:4</code> .

<code>k_simplimax</code>	numeric. The number of 'close to zero loadings' for the simplimax rotation (see <a href="#">GPARotation::GPFoblq</a> ) if "simplimax" or "oblique" is among the specified rotations. Default is <code>ncol(x)</code> , where <code>x</code> is the entered data.
<code>P_type</code>	character vector. Any combination of "norm" and "unnorm". This specifies how the target matrix <code>P</code> is computed in promax rotation if "none" is among the specified types and "promax" or "oblique" is among the specified rotations. "unnorm" will use the unnormalized target matrix as originally done in Hendrickson and White (1964). "norm" will use a normalized target matrix (for details see <a href="#">EFA</a> ). Default is <code>c("norm", "unnorm")</code> .
<code>precision</code>	numeric vector. The tolerance for stopping in the rotation procedure(s). Default is $10^{-5}$ .
<code>start_method</code>	character vector. Any combination of "psych" and "factanal". How to specify the starting values for the optimization procedure for ML. "psych" takes the starting values specified in <a href="#">psych::fa</a> . "factanal" takes the starting values specified in the <a href="#">stats::factanal</a> function. Default is <code>c("psych", "factanal")</code> .
<code>use</code>	character. Passed to <a href="#">stats::cor</a> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <a href="#">stats::cor</a> . Default is "pearson".
<code>show_progress</code>	logical. Whether a progress bar should be shown in the console. Default is TRUE.

## Details

As a first step in this function, a grid is produced containing the setting combinations for the to-be-performed EFAs. These settings are then entered as arguments to the [EFA](#) function and the EFAs are run in a second step. After all EFAs are run, the factor solutions are averaged and their variability determined in a third step.

The grid containing the setting combinations is produced based on the entries to the respective arguments. To this end, all possible combinations resulting in unique EFA models are considered. That is, if, for example, the type argument was set to `c("none", "SPSS")` and one combination of the specific settings entered was identical to the SPSS combination, this combination would be included in the grid and run only once. We include here a list of arguments that are only evaluated under specific conditions:

The arguments `init_comm`, `criterion`, `criterion_type`, `abs_eigen` are only evaluated if "PAF" is included in method and "none" is included in type.

The argument `varimax_type` is only evaluated if "varimax", "promax", "oblique", or "orthogonal" is included in rotation and "none" is included in type.

The argument `normalize` is only evaluated if rotation is not set to "none" and "none" is included in type.

The argument `k_simplimax` is only evaluated if "simplimax" or "oblique" is included in rotation.

The arguments `k_promax` and `P_type` are only evaluated if "promax" or "oblique" is included in rotation and "none" is included in type.

The argument `start_method` is only evaluated if "ML" is included in method.

To avoid a bias in the averaged factor solutions from problematic solutions, these are excluded prior to averaging. A solution is deemed problematic if at least one of the following is true: an

error occurred, the model did not converge, or there is at least one Heywood case (defined as a communality of  $\geq 1 + .Machine\$double.eps$ ). Information on errors, convergence, and Heywood cases are returned in the `implementations_grid` and a summary of these is given when printing the output. In addition to these, information on the admissibility of the factor solutions is also included. A solution was deemed admissible if (1) no error occurred, (2) the model converged, (3) no Heywood cases are present, and (4) there are at least two salient loadings (i.e., loadings exceeding the specified `salience_threshold`) for each factor. So, solutions failing one of the first three of these criteria of admissibility are also deemed problematic and therefore excluded from averaging. However, solutions failing only the fourth criterion of admissibility are still included for averaging. Finally, if all solutions are problematic (e.g., all solutions contain Heywood cases), no averaging is performed and the respective outputs are NA. In this case, the `implementations_grid` should be inspected to see if there are any error messages, and the separate EFA solutions that are also included in the output can be inspected as well, for example, to see where Heywood cases occurred.

A core output of this function includes the average, minimum, and maximum loadings derived from all non-problematic (see above) factor solutions. Please note that these are not entire solutions, but the matrices include the average, minimum, or maximum value for each cell (i.e., each loading separately). This means that, for example, the matrix with the minimum loadings will contain the minimum value in any of the factor solutions for each specific loading, and therefore most likely contains loadings from different factor solutions. The matrices containing the minimum and maximum factor solutions can therefore not be interpreted as whole factor solutions.

The output also includes information on the average, minimum, maximum, and variability of the fit indices across the non-problematic factor solutions. It is important to note that not all fit indices are computed for all fit methods: For ML and ULS, all fit indices can be computed, while for PAF, only the common part accounted for (CAF) index (Lorenzo-Seva, Timmerman, & Kiers, 2011) can be computed. As a consequence, if only "PAF" is included in the method argument, averaging can only be performed for the CAF, and the other fit indices are NA. If a combination of "PAF" and "ML" and/or "ULS" are included in the method argument, the CAF is averaged across all non-problematic factor solutions, while all other fit indices are only averaged across the ML and ULS solutions. The user should therefore keep in mind that the number of EFAs across which the fit indices are averaged can diverge for the CAF compared to all other fit indices.

## Value

A list of class `EFA_AVERAGE` containing

<code>orig_R</code>	Original correlation matrix.
<code>h2</code>	A list with the average, standard deviation, minimum, maximum, and range of the final communality estimates across the factor solutions.
<code>loadings</code>	A list with the average, standard deviation, minimum, maximum, and range of the final loadings across the factor solutions. If rotation was "none", the unrotated loadings, otherwise the rotated loadings (pattern coefficients).
<code>Phi</code>	A list with the average, standard deviation, minimum, maximum, and range of the factor intercorrelations across factor solutions obtained with oblique rotations.
<code>ind_fac_corres</code>	A matrix with each cell containing the proportion of the factor solutions in which the respective indicator-to-factor correspondence occurred, i.e., in which the

loading exceeded the specified salience threshold. Note: Rowsums can exceed 1 due to cross-loadings.

vars_accounted	A list with the average, standard deviation, minimum, maximum, and range of explained variances and sums of squared loadings across the factor solutions. Based on the unrotated loadings.
fit_indices	A matrix containing the average, standard deviation, minimum, maximum, and range for all applicable fit indices across the respective factor solutions, and the degrees of freedom (df). If the method argument contains ML or ULS: Fit indices derived from the unrotated factor loadings: Chi Square (chisq), including significance level, Comparative Fit Index (CFI), Root Mean Square Error of Approximation (RMSEA), Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC) and the common part accounted for (CAF) index as proposed by Lorenzo-Seva, Timmerman, & Kiers (2011). For PAF, only the CAF can be calculated (see details).
implementations_grid	A matrix containing, for each performed EFA, the setting combination, if an error occurred (logical), the error message (character), an integer code for convergence as returned by <code>stats::optim</code> (0 indicates successful completion.), if heywood cases occurred (logical, see details for definition), if the solution was admissible (logical, see details for definition), and the fit indices.
efa_list	A list containing the outputs of all performed EFAs. The names correspond to the rownames from the <code>implementations_grid</code> .
settings	A list of the settings used.

### Source

Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.

Hendrickson, A. E., & White, P. O. (1964). Promax: A quick method for rotation to oblique simple structure. *British Journal of Statistical Psychology*, 17, 65–70. doi: 10.1111/j.2044-8317.1964.tb00244.x

Lorenzo-Seva, U., Timmerman, M. E., & Kiers, H. A. L. (2011). The Hull Method for Selecting the Number of Common Factors, *Multivariate Behavioral Research*, 46, 340-364, doi: 10.1080/00273171.2011.564527

Kaiser, H. F. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, 23, 187–200. doi: 10.1007/BF02289233

### Examples

```
## Not run:
# Averaging across different implementations of PAF and promax rotation (72 EFAs)
Aver_PAF <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500)

# Use median instead of mean for averaging (72 EFAs)
Aver_PAF_md <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500,
                           averaging = "median")
```

```

# Averaging across different implementations of PAF and promax rotation,
# and across ULS and different versions of ML (108 EFAs)
Aver_meth_ext <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500,
                             method = c("PAF", "ULS", "ML"))

# Averaging across one implementation each of PAF (EFAtools type), ULS, and
# ML with one implementation of promax (EFAtools type) (3 EFAs)
Aver_meth <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500,
                          method = c("PAF", "ULS", "ML"), type = "EFAtools",
                          start_method = "psych")

# Averaging across different oblique rotation methods, using one implementation
# of ML and one implementation of promax (EFAtools type) (7 EFAs)
Aver_rot <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500,
                         method = "ML", rotation = "oblique", type = "EFAtools",
                         start_method = "psych")

## End(Not run)

```

---

EFA\_POOLED

*Exploratory factor analysis on multiple data imputations*


---

## Description

Fits [EFA](#) to each of several imputed datasets, aligns the factor solutions to a common factor space, and pools the resulting estimates and selected fit quantities across imputations.

## Usage

```

EFA_POOLED(
  data_list,
  p = 0.05,
  target_method = c("consensus", "first_target"),
  align_unrotated = c("signed_tucker_congruence", "none", "procrustes"),
  fit_pool_method = c("D2"),
  consensus_args = list(),
  procrustes_args = list(),
  rmsea_ci_level = 0.9,
  rmsr_upper = TRUE,
  ...
)

```

## Arguments

`data_list` A list of length  $m$ , where  $m$  is the number of imputations. Each list element is a data frame or matrix of raw data, or a correlation matrix. See argument `x` in [EFA](#).

<code>p</code>	Numeric in (0,1). One minus the confidence level used for pooled Wald-type bootstrap/MI confidence intervals when bootstrap arrays are available. For example, <code>p = .05</code> gives 95% intervals.
<code>target_method</code>	Character. "consensus" aligns all solutions to an iteratively updated consensus target. "first_target" aligns all solutions to the first imputation's rotated solution.
<code>align_unrotated</code>	Character. How to align unrotated loadings before pooling. "signed_tucker_congruence" preserves the unrotated axes up to factor reordering and sign changes using Tucker congruence. "procrustes" aligns the unrotated matrices to the first imputation by orthogonal Procrustes rotation. "none" averages unrotated loadings as returned by EFA.
<code>fit_pool_method</code>	Character. Currently only "D2" is implemented for chi-square-type fit. If no chi-square is available, only residual-based fit and descriptive quantities are returned.
<code>consensus_args</code>	List of additional arguments passed to CONSENSUS_PROCRUSTES.
<code>procrustes_args</code>	List of additional arguments passed to PROCRUSTES for fixed-target alignment.
<code>rmsea_ci_level</code>	Numeric. Confidence level for the RMSEA CI.
<code>rmsr_upper</code>	Logical. If TRUE, compute RMSR from the unique off-diagonal residual correlations. If FALSE, use the full off-diagonal matrix.
<code>...</code>	Additional arguments passed to <a href="#">EFA</a> .

## Details

The function first fits the same [EFA](#) model to each imputed dataset. Unrotated loading matrices can optionally be put into a common signed/permutated factor order before averaging. Rotated loading matrices are aligned with either a consensus Procrustes target or with the first imputation's rotated solution as a fixed target. For oblique solutions, factor intercorrelations are transformed/aligned together with the loading matrices so that the factor model remains internally consistent.

Point estimates are pooled by arithmetic averaging after alignment. For oblique rotations, the returned structure matrix is computed from the pooled aligned pattern matrix and the pooled factor correlation matrix,  $Structure = \Lambda\Phi$ . Communalities are always computed as the diagonal of the common-factor reproduced correlation matrix,  $diag(\Lambda\Phi\Lambda')$  for oblique rotations and  $diag(\Lambda\Lambda')$  otherwise.

Residuals are not averaged from the per-imputation residual matrices. Instead, the observed correlation matrices are averaged across imputations and residuals are calculated from the pooled observed correlation matrix minus the model-implied correlation matrix of the pooled solution. Consequently, residual-based fit indices such as RMSR/SRMR are based on pooled residuals.

Fit indices based on the model chi-square are not arithmetic means of the per-imputation fit indices. If possible, chi-square-type fit is pooled with the D2 rule. For CFI, the null-model chi-square is D2-pooled as well when complete-data null-model chi-squares are available. The asymptotic chi-square approximation to D2 is then used for RMSEA and CFI. AIC and BIC, if returned, are chi-square-derived descriptive quantities based on this D2 approximation and should not be interpreted

as likelihood-based MI information criteria. D3/D4 pooling is not implemented here because the current EFA objects do not expose the likelihood quantities needed for those methods.

If each component EFA call was run with `se = "np-boot"` and returned `boot.arrays`, pooled bootstrap SEs and Wald-type MI confidence intervals are computed for loadings, communalities, residuals, and, when applicable, factor correlations and structure coefficients. Importantly, the rotated bootstrap loading matrices stored by the component EFA calls are not reused directly, because they were aligned to imputation-specific targets. Instead, the unrotated bootstrap loading matrices are re-aligned to the final MI target before estimating within-imputation bootstrap covariance matrices. Rubin-type MI pooling is then applied with  $T = U\bar{b} + (1+1/m)B$ . Confidence intervals for loadings, Phi, communalities, residuals, and structure coefficients are Wald-type MI intervals. The confidence level of these pooled intervals is controlled by `p`; the `ci` argument passed through `...` to the component EFA calls is not used for the pooled intervals. `boot.CI$fit_indices_pooled_algorithm`, when available, is a percentile-style summary obtained by re-running the pooled-fit algorithm over matched bootstrap replicate indices.

### Value

A list of class "EFA\_POOLED" containing pooled estimates, residuals, fit indices, the individual fits, and MI diagnostics.

### Author(s)

Andreas Soteriades, Markus Steiner

### Examples

```
# create a list of three datasets, mimicking a list you would obtain from
# e.g. mice.
dat_list <- lapply(1:3, function(x) GRiPS_raw[sample(1:nrow(GRiPS_raw), replace = TRUE),])
mod <- EFA_POOLED(dat_list, n_factors = 1, method = "ML")
mod

# add computation of standard errors and CIs
mod <- EFA_POOLED(dat_list, n_factors = 1, method = "ML", se = "np-boot")
mod
```

---

EKC

*Empirical Kaiser Criterion*

---

### Description

The empirical Kaiser criterion incorporates random sampling variations of the eigenvalues from the Kaiser-Guttman criterion (KGC; see Auerswald & Moshagen, 2019; Braeken & van Assen, 2017). The code is based on Braeken & van Assen, (2017) and on Auerswald and Moshagen (2019).

**Usage**

```
EKC(
  x,
  N = NA,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
         "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  type = "BvA2017"
)
```

**Arguments**

x	data.frame or matrix. data.frame or matrix of raw data or matrix with correlations.
N	numeric. The number of observations. Only needed if x is a correlation matrix.
use	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
cor_method	character. Passed to <code>stats::cor</code> . Default is "pearson".
type	character. The calculation of EKC. type "BvA2017" is the original implementation; type "AM2019" differs from the original implementation but was used in simulation studies (Auerswald & Moshagen, 2019; Caron, 2025). See details. Use <code>type = c("BvA2017", "AM2019")</code> for both implementations. Make sure to report which version you used.

**Details**

The Kaiser-Guttman criterion was defined with the intend that a factor should only be extracted if it explains at least as much variance as a single factor (see [KGC](#)). However, this only applies to population-level correlation matrices. Due to sampling variation, the KGC strongly overestimates the number of factors to retrieve (e.g., Zwick & Velicer, 1986). To account for this and to introduce a factor retention method that performs well with small number of indicators and correlated factors (cases where the performance of parallel analysis, see [PARALLEL](#), is known to deteriorate) Braeken and van Assen (2017) introduced the empirical Kaiser criterion in which a series of reference eigenvalues is created as a function of the variables-to-sample-size ratio and the observed eigenvalues.

Braeken and van Assen (2017) showed that "(a) EKC performs about as well as parallel analysis for data arising from the null, 1-factor, or orthogonal factors model; and (b) clearly outperforms parallel analysis for the specific case of oblique factors, particularly whenever factor intercorrelation is moderate to high and the number of variables per factor is small, which is characteristic of many applications these days" (p.463-464).

In EFAtools version  $\leq 0.5.0$  only the implementation of Auerswald and Moshagen (2019) was implemented (now available with `type = "AM2019"`). However, this implementation, that was probably also used in Caron (2025), differs from the original implementation by Braeken and van Assen (2017) in that it corrects by the reference values, i.e., without using the empirical eigenvalues used in the original implementation. Thanks to Luis Eduardo Garrido for pointing this out and to Johan Braeken for sharing sample code, based on which the original version is now implemented and used by default with `type = "BvA2017"`.

While the adapted version performed relatively well in the simulation studies by Auerwald and Moshagen (2019) and Caron (2025), the theoretical derivations of the EKC as introduced by Braeken and van Assen (2017) may no longer hold. Currently we are unaware of studies comparing the two implementations, but based on our own brief comparisons across multiple datasets, the two implementations appear to often differ substantially regarding the number of factors suggested.

As both implementations exist in different packages and studies, we provide both versions here. Be sure to state clearly which version you use when reporting your results to avoid confusion and ensure reproducibility.

The EKC function can also be called together with other factor retention criteria in the [N\\_FACTORS](#) function.

### Value

A list of class EKC containing

eigenvalues	A vector containing the eigenvalues found on the correlation matrix of the entered data.
n_factors_BVA2017	The number of factors to retain according to the original empirical Kaiser criterion by Braeken and van Assen (2017).
n_factors_AM2019	The number of factors to retain according to the adapted empirical Kaiser criterion by Auerwald and Moshagen (2019).
references	The reference eigenvalues.
settings	A list with the settings used.

### Source

Auerwald, M., & Moshagen, M. (2019). How to determine the number of factors to retain in exploratory factor analysis: A comparison of extraction methods under realistic conditions. *Psychological Methods*, 24(4), 468–491. <https://doi.org/10.1037/met0000200>

Braeken, J., & van Assen, M. A. (2017). An empirical Kaiser criterion. *Psychological Methods*, 22, 450 – 466. <http://dx.doi.org/10.1037/met0000074>

Caron, P.-O. (2025). A Comparison of the Next Eigenvalue Sufficiency Test to Other Stopping Rules for the Number of Factors in Factor Analysis. *Educational and Psychological Measurement*, Online-first publication. <https://doi.org/10.1177/00131644241308528>

Zwick, W. R., & Velicer, W. F. (1986). Comparison of five rules for determining the number of components to retain. *Psychological Bulletin*, 99, 432–442. <http://dx.doi.org/10.1037/0033-2909.99.3.432>

### See Also

Other factor retention criteria: [CD](#), [HULL](#), [KGC](#), [PARALLEL](#), [SMT](#)

[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

**Examples**

```
# original implementation
EKC(test_models$baseline$cormat, N = 500)
```

---

FACTOR_SCORES	<i>Estimate factor scores for an EFA model</i>
---------------	--

---

**Description**

This is a wrapper function for `psych::factor.scores` to be used directly with an output from [EFA](#) or by manually specifying the factor loadings and intercorrelations. Calculates factor scores according to the specified methods if raw data are provided, and only factor weights if a correlation matrix is provided.

**Usage**

```
FACTOR_SCORES(
  x,
  f,
  Phi = NULL,
  rho = NULL,
  method = c("Thurstone", "tenBerge", "Anderson", "Bartlett", "Harman", "components"),
  impute = c("none", "means", "median")
)
```

**Arguments**

x	data.frame or matrix. Dataframe or matrix of raw data (needed to get factor scores) or matrix with correlations.
f	object of class <a href="#">EFA</a> or matrix.
Phi	matrix. A matrix of factor intercorrelations. Only needs to be specified if a factor loadings matrix is entered directly into f. Default is NULL, in which case all intercorrelations are assumed to be zero.
rho	matrix. Used when x is a matrix of raw data and the user wishes to get factor scores for a correlation matrix other than Pearson's (e.g. polychoric). Defaults to NULL, in which case <code>psych::factor.scores</code> uses <code>cor(x, use = "pairwise")</code> .
method	character. The method used to calculate factor scores. One of "Thurstone" (regression-based; default), "tenBerge", "Anderson", "Bartlett", "Harman", or "components". See <code>psych::factor.scores</code> for details.
impute	character. Whether and how missing values in x should be imputed. One of "none" (default, only complete cases are scored), "median", or "mean".

**Value**

A list of class `FACTOR_SCORES` containing the following:

<code>scores</code>	The factor scores (only if raw data are provided.)
<code>weights</code>	The factor weights.
<code>r.scores</code>	The correlations of the factor score estimates.
<code>missing</code>	A vector of the number of missing observations per subject (only if raw data are provided).
<code>R2</code>	Multiple R2 of the scores with the factors.
<code>settings</code>	A list of the settings used.

**Examples**

```
# Example with raw data with method "Bartlett" and no imputation
EFA_raw <- EFA(DOSPERT_raw, n_factors = 10, type = "EFAtools", method = "PAF",
              rotation = "oblimin", randomStarts = 0)
fac_scores_raw <- FACTOR_SCORES(DOSPERT_raw, f = EFA_raw, method = "Bartlett",
                               impute = "none")

# Same as above, but with raw data AND a correlation matrix
cor_pearson <- cor(DOSPERT_raw)
EFA_cor_pearson <- EFA(cor_pearson, n_factors = 10, N = nrow(DOSPERT_raw),
                      type = "EFAtools", method = "PAF",
                      rotation = "oblimin", randomStarts = 0)
fac_scores_cor_pearson <- FACTOR_SCORES(DOSPERT_raw, f = EFA_cor_pearson,
                                       rho = cor_pearson,
                                       method = "Bartlett", impute = "none")

# Scores between two alternatives above are identical
all(dplyr::near(fac_scores_raw$scores, fac_scores_cor_pearson$scores))

# Example with a correlation matrix only (does not return factor scores)
EFA_cor <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
              type = "EFAtools", method = "PAF", rotation = "oblimin")
fac_scores_cor <- FACTOR_SCORES(test_models$baseline$cormat, f = EFA_cor)
```

---

GRiPS\_raw

*GRiPS\_raw*

---

**Description**

A data.frame containing responses to the General Risk Propensity Scale (GRiPS, Zhang, Highhouse & Nye, 2018) of 810 participants of Study 1 of Steiner and Frey (2020). The original data can be accessed via <https://osf.io/kxp8t/>.

**Usage**

```
GRiPS_raw
```

**Format**

An object of class `data.frame` with 810 rows and 8 columns.

**Source**

Zhang, D. C., Highhouse, S., & Nye, C. D. (2018). Development and validation of the general risk propensity scale (GRiPS). *Journal of Behavioral Decision Making*, 32, 152–167. doi:10.1002/bdm.2102

Steiner, M., & Frey, R. (2020). Representative design in psychological assessment: A case study using the Balloon Analogue Risk Task (BART). *PsyArXiv Preprint*. doi:10.31234/osf.io/dg4ks

---

HULL

*Hull method for determining the number of factors to retain*


---

**Description**

Implementation of the Hull method suggested by Lorenzo-Seva, Timmerman, and Kiers (2011), with an extension to principal axis factoring. See details for parallelization.

**Usage**

```
HULL(
  x,
  N = NA,
  n_fac_theor = NA,
  method = c("PAF", "ULS", "ML"),
  gof = c("CAF", "CFI", "RMSEA"),
  eigen_type = c("SMC", "PCA", "EFA"),
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
    "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  n_datasets = 1000,
  percent = 95,
  decision_rule = c("means", "percentile", "crawford"),
  n_factors = 1,
  ...
)
```

**Arguments**

<code>x</code>	matrix or data.frame. Dataframe or matrix of raw data or matrix with correlations.
<code>N</code>	numeric. Number of cases in the data. This is passed to <code>PARALLEL</code> . Only has to be specified if <code>x</code> is a correlation matrix, otherwise it is determined based on the dimensions of <code>x</code> .
<code>n_fac_theor</code>	numeric. Theoretical number of factors to retain. The maximum of this number and the number of factors suggested by <code>PARALLEL</code> plus one will be used in the Hull method.
<code>method</code>	character. The estimation method to use. One of "PAF", "ULS", or "ML", for principal axis factoring, unweighted least squares, and maximum likelihood, respectively.
<code>gof</code>	character. The goodness of fit index to use. Either "CAF", "CFI", or "RMSEA", or any combination of them. If <code>method = "PAF"</code> is used, only the CAF can be used as goodness of fit index. For details on the CAF, see Lorenzo-Seva, Timmerman, and Kiers (2011).
<code>eigen_type</code>	character. On what the eigenvalues should be found in the parallel analysis. Can be one of "SMC", "PCA", or "EFA". If using "SMC" (default), the diagonal of the correlation matrices is replaced by the squared multiple correlations (SMCs) of the indicators. If using "PCA", the diagonal values of the correlation matrices are left to be 1. If using "EFA", eigenvalues are found on the correlation matrices with the final communalities of an EFA solution as diagonal. This is passed to <code>PARALLEL</code> .
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <code>stats::cor</code> . Default is "pearson".
<code>n_datasets</code>	numeric. The number of datasets to simulate. Default is 1000. This is passed to <code>PARALLEL</code> .
<code>percent</code>	numeric. A vector of percentiles to take the simulated eigenvalues from. Default is 95. This is passed to <code>PARALLEL</code> .
<code>decision_rule</code>	character. Which rule to use to determine the number of factors to retain. Default is "means", which will use the average simulated eigenvalues. "percentile", uses the percentiles specified in <code>percent</code> . "crawford" uses the 95th percentile for the first factor and the mean afterwards (based on Crawford et al, 2010). This is passed to <code>PARALLEL</code> .
<code>n_factors</code>	numeric. Number of factors to extract if "EFA" is included in <code>eigen_type</code> . Default is 1. This is passed to <code>PARALLEL</code> .
<code>...</code>	Further arguments passed to <code>EFA</code> , also in <code>PARALLEL</code> .

**Details**

The Hull method aims to find a model with an optimal balance between model fit and number of parameters. That is, it aims to retrieve only major factors (Lorenzo-Seva, Timmerman, & Kiers, 2011). To this end, it performs the following steps (Lorenzo-Seva, Timmerman, & Kiers, 2011, p.351):

1. It performs parallel analysis and adds one to the identified number of factors (this number is denoted  $J$ ).  $J$  is taken as an upper bound of the number of factors to retain in the hull method. Alternatively, a theoretical number of factors can be entered. In this case  $J$  will be set to whichever of these two numbers (from parallel analysis or based on theory) is higher.
2. For all 0 to  $J$  factors, the goodness-of-fit (one of *CAF*, *RMSEA*, or *CFI*) and the degrees of freedom (*df*) are computed.
3. The solutions are ordered according to their *df*.
4. Solutions that are not on the boundary of the convex hull are eliminated (see Lorenzo-Seva, Timmerman, & Kiers, 2011, for details).
5. All the triplets of adjacent solutions are considered consecutively. The middle solution is excluded if its point is below or on the line connecting its neighbors in a plot of the goodness-of-fit versus the degrees of freedom.
6. Step 5 is repeated until no solution can be excluded.
7. The *st* values of the “hull” solutions are determined.
8. The solution with the highest *st* value is selected.

The `PARALLEL` function and the principal axis factoring of the different number of factors can be parallelized using the future framework, by calling the `future::plan` function. The examples provide example code on how to enable parallel processing.

Note that if `gof = "RMSEA"` is used,  $1 - \text{RMSEA}$  is actually used to compare the different solutions. Thus, the threshold of `.05` is then `.95`. This is necessary due to how the heuristic to locate the elbow of the hull works.

The ML estimation method uses the `stats::factanal` starting values. See also the `EFA` documentation.

The `HULL` function can also be called together with other factor retention criteria in the `N_FACTORS` function.

## Value

A list of class `HULL` containing the following objects

<code>n_fac_CAF</code>	The number of factors to retain according to the Hull method with the CAF.
<code>n_fac_CFI</code>	The number of factors to retain according to the Hull method with the CFI.
<code>n_fac_RMSEA</code>	The number of factors to retain according to the Hull method with the RMSEA.
<code>solutions_CAF</code>	A matrix containing the CAFs, degrees of freedom, and for the factors lying on the hull, the <i>st</i> values of the hull solution (see Lorenzo-Seva, Timmerman, and Kiers 2011 for details).
<code>solutions_CFI</code>	A matrix containing the CFIs, degrees of freedom, and for the factors lying on the hull, the <i>st</i> values of the hull solution (see Lorenzo-Seva, Timmerman, and Kiers 2011 for details).
<code>solutions_RMSEA</code>	A matrix containing the RMSEAs, degrees of freedom, and for the factors lying on the hull, the <i>st</i> values of the hull solution (see Lorenzo-Seva, Timmerman, and Kiers 2011 for details).
<code>n_fac_max</code>	The upper bound $J$ of the number of factors to extract (see details).
<code>settings</code>	A list of the settings used.

**Source**

Lorenzo-Seva, U., Timmerman, M. E., & Kiers, H. A. (2011). The Hull method for selecting the number of common factors. *Multivariate Behavioral Research*, 46(2), 340-364.

**See Also**

Other factor retention criteria: [CD](#), [EKC](#), [KGC](#), [PARALLEL](#), [SMT](#)

[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

**Examples**

```
# using PAF (this will throw a warning if gof is not specified manually
# and CAF will be used automatically)
HULL(test_models$baseline$cormat, N = 500, gof = "CAF")

# using ML with all available fit indices (CAF, CFI, and RMSEA)
HULL(test_models$baseline$cormat, N = 500, method = "ML")

# using ULS with only RMSEA
HULL(test_models$baseline$cormat, N = 500, method = "ULS", gof = "RMSEA")

## Not run:
# using parallel processing (Note: plans can be adapted, see the future
# package for details)
future::plan(future::multisession)
HULL(test_models$baseline$cormat, N = 500, gof = "CAF")

## End(Not run)
```

---

 IDS2\_R

---

*Intelligence subtests from the Intelligence and Development Scales–2*


---

**Description**

A matrix containing the bivariate correlations of the 14 intelligence subtests from the Intelligence and Development Scales–2 (IDS-2; Grob & Hagmann-von Arx, 2018), an intelligence and development test battery for children and adolescents aged 5 to 20 years, for the standardization and validation sample (N = 1,991). Details can be found in Grieder & Grob (2019).

**Usage**

IDS2\_R

**Format**

A 14 x 14 matrix of bivariate correlations

**GS** (numeric) - Geometric shapes.

**PL** (numeric) - Plates.

**TC** (numeric) - Two characteristics.

**CB** (numeric) - Crossing out boxes.

**NL** (numeric) - Numbers / letters.

**NLM** (numeric) - Numbers / letter mixed.

**GF** (numeric) - Geometric figures.

**RGF** (numeric) - Rotated geometric figures.

**CM** (numeric) - Completing matrices.

**EP** (numeric) - Excluding pictures.

**CA** (numeric) - Categories.

**OP** (numeric) - Opposites.

**RS** (numeric) - Retelling a story.

**DP** (numeric) - Describing pictures.

**Source**

Grieder, S., & Grob, A. (2019). Exploratory factor analyses of the intelligence and development scales–2: Implications for theory and practice. *Assessment*. Advance online publication. doi:10.1177/10731911198450

Grob, A., & Hagemann-von Arx, P. (2018). *Intelligence and Development Scales–2 (IDS-2). Intelligenz- und Entwicklungsskalen für Kinder und Jugendliche. [Intelligence and Development Scales for Children and Adolescents.]*. Bern, Switzerland: Hogrefe.

---

KGC

*Kaiser-Guttman Criterion*

---

**Description**

Probably the most popular factor retention criterion. Kaiser and Guttman suggested to retain as many factors as there are sample eigenvalues greater than 1. This is why the criterion is also known as eigenvalues-greater-than-one rule.

**Usage**

```
KGC(
  x,
  eigen_type = c("PCA", "SMC", "EFA"),
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
         "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  n_factors = 1,
  ...
)
```

**Arguments**

<code>x</code>	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations.
<code>eigen_type</code>	character. On what the eigenvalues should be found. Can be either "PCA", "SMC", or "EFA", or some combination of them. If using "PCA", the diagonal values of the correlation matrices are left to be 1. If using "SMC", the diagonal of the correlation matrices is replaced by the squared multiple correlations (SMCs) of the indicators. If using "EFA", eigenvalues are found on the correlation matrices with the final communalities of an exploratory factor analysis solution (default is principal axis factoring extracting 1 factor) as diagonal.
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <code>stats::cor</code> . Default is "pearson".
<code>n_factors</code>	numeric. Number of factors to extract if "EFA" is included in <code>eigen_type</code> . Default is 1.
<code>...</code>	Additional arguments passed to <a href="#">EFA</a> . For example, to change the extraction method (PAF is default).

**Details**

Originally, the Kaiser-Guttman criterion was intended for the use with principal components, hence with eigenvalues derived from the original correlation matrix. This can be done here by setting `eigen_type` to "PCA". However, it is well-known that this criterion is often inaccurate and that it tends to overestimate the number of factors, especially for unidimensional or orthogonal factor structures (e.g., Zwick & Velicer, 1986).

The criterion's inaccuracy in these cases is somewhat addressed if it is applied on the correlation matrix with communalities in the diagonal, either initial communalities estimated from SMCs (done setting `eigen_type` to "SMC") or final communality estimates from an EFA (done setting `eigen_type` to "EFA"; see Auerswald & Moshagen, 2019). However, although this variant of the KGC is more accurate in some cases compared to the traditional KGC, it is at the same time less accurate than the PCA-variant in other cases, and it is still often less accurate than other factor retention methods, for example parallel analysis ([PARALLEL](#)), the Hull method [HULL](#), or sequential  $\chi^2$  model tests ([SMT](#); see Auerswald & Moshagen, 2019).

The KGC function can also be called together with other factor retention criteria in the `N_FACTORS` function.

**Value**

A list of class KGC containing

eigen_PCA	A vector containing the eigenvalues found with PCA.
eigen_SMC	A vector containing the eigenvalues found with SMCs.
eigen_EFA	A vector containing the eigenvalues found with EFA.
n_fac_PCA	The number of factors to retain according to the Kaiser- Guttman criterion with PCA eigenvalues type.
n_fac_SMC	The number of factors to retain according to the Kaiser- Guttman criterion with SMC eigenvalues type.
n_fac_EFA	The number of factors to retain according to the Kaiser- Guttman criterion with EFA eigenvalues type.
settings	A list of the settings used.

**Source**

Auerswald, M., & Moshagen, M. (2019). How to determine the number of factors to retain in exploratory factor analysis: A comparison of extraction methods under realistic conditions. *Psychological Methods*, 24(4), 468–491. <https://doi.org/10.1037/met0000200>

Guttman, L. (1954). Some necessary conditions for common-factor analysis. *Psychometrika*, 19, 149–161. <http://dx.doi.org/10.1007/BF02289162>

Kaiser, H. F. (1960). The application of electronic computers to factor analysis. *Educational and Psychological Measurement*, 20, 141–151. <http://dx.doi.org/10.1177/001316446002000116>

Zwick, W. R., & Velicer, W. F. (1986). Comparison of five rules for determining the number of components to retain. *Psychological Bulletin*, 99, 432–442. <http://dx.doi.org/10.1037/0033-2909.99.3.432>

**See Also**

Other factor retention criteria: [CD](#), [EKC](#), [HULL](#), [PARALLEL](#), [SMT](#)

[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

**Examples**

```
KGC(test_models$baseline$cormat, eigen_type = c("PCA", "SMC"))
```

KMO

*Kaiser-Meyer-Olkin criterion***Description**

This function computes the Kaiser-Meyer-Olkin (KMO) criterion overall and for each variable in a correlation matrix. The KMO represents the degree to which each observed variable is predicted by the other variables in the dataset and with this indicates the suitability for factor analysis.

**Usage**

```
KMO(
  x,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
         "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall")
)
```

**Arguments**

`x` data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations.

`use` character. Passed to `stats::cor` if raw data is given as input. Default is "pairwise.complete.obs".

`cor_method` character. Passed to `stats::cor`. Default is "pearson".

**Details**

Kaiser (1970) proposed this index, originally called measure of sampling adequacy (MSA), that indicates how near the inverted correlation matrix  $R^{-1}$  is to a diagonal matrix  $S$  to determine a given correlation matrix's ( $R$ ) suitability for factor analysis. The index is

$$KMO = \frac{\sum_{i < j} \sum r_{ij}^2}{\sum_{i < j} \sum r_{ij}^2 + \sum_{i < j} \sum q_{ij}^2}$$

with  $Q = SR^{-1}S$  and  $S = (diagR^{-1})^{-1/2}$  where  $\sum_{i < j} \sum r_{ij}^2$  is the sum of squares of the upper off-diagonal elements of  $R$  and  $\sum_{i < j} \sum q_{ij}^2$  is the sum of squares of the upper off-diagonal elements of  $Q$  (see also Cureton & D'Augustino, 1983).

So KMO varies between 0 and 1, with larger values indicating higher suitability for factor analysis. Kaiser and Rice (1974) suggest that KMO should at least exceed .50 for a correlation matrix to be suitable for factor analysis.

This function was heavily influenced by the `psych::KMO` function.

See also `BARTLETT` for another test of suitability for factor analysis.

The KMO function can also be called together with the `BARTLETT` function and with factor retention criteria in the `N_FACTORS` function.

**Value**

A list containing

KMO	Overall KMO.
KMO_i	KMO for each variable.
settings	A list of the settings used.

**Source**

Kaiser, H. F. (1970). A second generation little jiffy. *Psychometrika*, 35, 401-415.

Kaiser, H. F. & Rice, J. (1974). Little jiffy, mark IV. *Educational and Psychological Measurement*, 34, 111-117.

Cureton, E. E. & D'Augustino, R. B. (1983). *Factor analysis: An applied approach*. Hillsdale, N.J.: Lawrence Erlbaum Associates, Inc.

**See Also**

[BARTLETT](#) for another measure to determine suitability for factor analysis.

[N\\_FACTORS](#) as a wrapper function for this function, [BARTLETT](#) and several factor retention criteria.

**Examples**

```
KMO(test_models$baseline$scormat)
```

---

MAP

*Velicer's Minimum Average Partial (MAP) Criterion*


---

**Description**

Computes Velicer's Minimum Average Partial (MAP) criterion for determining the number of factors/components to retain. The function implements the original MAP criterion (Velicer, 1976), expressed via the TR2 representation, and the revised TR4 variant proposed by Velicer, Eaton, and Fava (2000).

**Usage**

```
MAP(
  x,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
    "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall")
)
```

### Arguments

<code>x</code>	A numeric matrix or data.frame. Can be either (a) a correlation matrix, or (b) raw data (rows = observations, columns = variables) from which correlations are computed.
<code>use</code>	Character string specifying the treatment of missing values when computing correlations. Passed to <code>cor</code> . Defaults to "pairwise.complete.obs".
<code>cor_method</code>	Character string specifying the correlation coefficient to be computed if raw data are supplied. Passed to <code>cor</code> . Defaults to "pearson".

### Details

#' MAP is based on the idea that systematic common variance is increasingly removed from a correlation matrix  $R$  as principal components are partialled out. After removing the first  $m$  components, a residual (partial) covariance matrix is obtained as

$$C_m = R - A_m A_m'$$

where  $A_m$  contains the first  $m$  principal component loading vectors (PCA loadings). This residual matrix is then standardized to a partial correlation matrix

$$R_m^* = D_m^{-1/2} C_m D_m^{-1/2},$$

with  $D_m = \text{diag}(C_m)$ . The MAP criteria summarize the off-diagonal association remaining in  $R_m^*$ . The recommended number of factors/components is the  $m$  that minimizes the chosen criterion.

This function returns two MAP criteria:

- **TR2 (original MAP):**

$$\text{MAP}_m = \frac{\text{Trace}(R_m^{*2}) - p}{p(p-1)}$$

which is algebraically equivalent to the mean squared off-diagonal partial correlations and corresponds to Velicer's original MAP procedure.

- **TR4 (revised MAP):**

$$\text{MAP}_4_m = \frac{\text{Trace}(R_m^{*4}) - p}{p(p-1)}$$

a higher-order variant that places more weight on dominant residual association structure.

**Input handling.** `x` can be a correlation matrix or raw data. If `x` is not a correlation matrix, correlations are computed using `cor` with the requested missing-data handling (`use`) and association measure (`cor_method`). If a correlation matrix is supplied, `N` must be provided.

**Matrix conditioning.** The function stops if the correlation matrix is singular (non-invertible), because subsequent computations rely on stable matrix operations. If the correlation matrix is not positive definite (e.g., due to sampling error), it is smoothed using `cor.smooth`.

**PCA-based partialing.** The PCA loading matrix  $A$  is obtained from the eigen-decomposition of  $R$  as  $A = V\Lambda^{1/2}$ . For each  $m = 0, \dots, p-1$ , the first  $m$  columns of  $A$  are used to compute  $C_m = R - A_m A_m'$ . The residual is re-standardized to the partial correlation matrix  $R_m^*$  using  $D_m^{-1/2}$  (i.e., dividing by the square roots of residual variances).

**Termination.** If residual variances (the diagonal of  $C_m$ ) become non-positive or numerically unstable, the loop terminates early because  $R_m^*$  cannot be formed reliably.

**Value**

An object of class "MAP" with the following elements:

- `eigenvalues`: Eigenvalues of the (possibly smoothed) correlation matrix.
- `n_factors_TR2`: Index  $m$  that minimizes the TR2 (original MAP) criterion.
- `n_factors_TR4`: Index  $m$  that minimizes the TR4 (revised MAP) criterion.
- `criteria`: A matrix with columns `m`, TR2 (orig. MAP), and TR4 (revised MAP).
- `settings`: A list containing `use`, `cor_method`, and `N`.

**References**

Velicer, W. F. (1976). Determining the number of components from the matrix of partial correlations. *Psychometrika*, *41*, 321–327.

Velicer, W. F., Eaton, C. A., & Fava, J. L. (2000). Construct explication through factor or component analysis: A review and evaluation of alternative procedures for determining the number of factors or components. In Goffin, R. D. & Helmes, E. (Eds.), *Problems and Solutions in Human Assessment: Honoring Douglas N. Jackson at Seventy* (pp. 41–71). Boston: Kluwer.

**Examples**

```
## Example with raw data
res <- MAP(GRIPS_raw)
res

## Example with a correlation matrix
res2 <- MAP(test_models$baseline$cormat)
res2
```

---

 NEST

*Next eigenvalue sufficiency test (NEST)*


---

**Description**

NEST uses many synthetic datasets to generate reference eigenvalues against which to compare the empirical eigenvalues. This is similar to parallel analysis, but other than parallel analysis, NEST does not just rely on synthetic eigenvalues based on an identity matrix as null model. It was introduced by Achim (2017), see also Brandenburg and Papenberg (2024) and Caron (2025) for further simulation studies including NEST.

**Usage**

```
NEST(
  x,
  N = NA,
  alpha = 0.05,
```

```

use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
       "na.or.complete"),
cor_method = c("pearson", "spearman", "kendall"),
n_datasets = 1000,
...
)

```

## Arguments

<code>x</code>	data.frame or matrix. data.frame or matrix of raw data or matrix with correlations.
<code>N</code>	numeric. The number of observations. Only needed if <code>x</code> is a correlation matrix.
<code>alpha</code>	numeric. The alpha level to use (i.e., 1-alpha percentile of eigenvalues is used for reference values).
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <code>stats::cor</code> . Default is "pearson".
<code>n_datasets</code>	numeric. The number of datasets to simulate. Default is 1000.
<code>...</code>	Additional arguments passed to <a href="#">EFA</a> . For example, the extraction method can be changed here (default is "PAF"). PAF is more robust, but it will take longer compared to the other estimation methods available ("ML" and "ULS").

## Details

NEST compares the first empirical eigenvalue against the first eigenvalues of `n_dataset` synthetic datasets based on a null model (i.e., with uncorrelated variables; same as in parallel analysis, see [PARALLEL](#)). The following eigenvalues are compared against synthetic datasets based on an EFA-model with one fewer factors than the position of the respective empirical eigenvalue. E.g, the second empirical eigenvalue is compared against synthetic data based on a one-factor model. The alpha-level defines against which percentile of the synthetic eigenvalue distribution to compare the empirical eigenvalues against, i.e., an alpha of .05 (the default) uses the 95th percentile as reference value.

For details on the method, including simulation studies, see [Achim \(2017\)](#), [Brandenburg and Papenberg \(2024\)](#), and [Caron \(2025\)](#).

The NEST function can also be called together with other factor retention criteria in the [N\\_FACTORS](#) function.

## Value

A list of class NEST containing the following objects

<code>eigenvalues</code>	A vector containing the empirical eigenvalues of the entered data.
<code>n_factors</code>	The number of factors to retain according to the NEST procedure.
<code>references</code>	A vector containing the reference eigenvalues.
<code>prob</code>	For the first <code>n_factors + 1</code> empirical eigenvalues, the proportion $\leq$ the set of <code>n_datasets</code> reference eigenvalues.
<code>settings</code>	A list of control settings used in the print function.

### Source

Achim, A. (2017). Testing the number of required dimensions in exploratory factor analysis. *The Quantitative Methods for Psychology*, 13(1), 64–74. <https://doi.org/10.20982/tqmp.13.1.p064>

Brandenburg, N., & Papenberg, M. (2024). Reassessment of innovative methods to determine the number of factors: A simulation-based comparison of exploratory graph analysis and Next Eigenvalue Sufficiency Test. *Psychological Methods*, 29(1), 21–47. <https://doi.org/10.1037/met0000527>

Caron, P.-O. (2025). A Comparison of the Next Eigenvalue Sufficiency Test to Other Stopping Rules for the Number of Factors in Factor Analysis. *Educational and Psychological Measurement*, Online-first publication. <https://doi.org/10.1177/00131644241308528>

### Examples

```
# with correlation matrix
NEST(test_models$baseline$cormat, N = 500)
```

```
# with raw data
NEST(GRiPS_raw)
```

---

N\_FACTORS

*Various Factor Retention Criteria*

---

### Description

Among the most important decisions for an exploratory factor analysis (EFA) is the choice of the number of factors to retain. Several factor retention criteria have been developed for this. With this function, various factor retention criteria can be performed simultaneously. Additionally, the data can be checked for their suitability for factor analysis.

### Usage

```
N_FACTORS(
  x,
  criteria = c("CD", "EKC", "HULL", "MAP", "NEST", "PARALLEL"),
  suitability = TRUE,
  N = NA,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
    "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  n_factors_max = NA,
  N_pop = 10000,
  N_samples = 500,
  alpha = 0.3,
  max_iter_CD = 50,
  n_fac_theor = NA,
  method = c("ML", "PAF", "ULS"),
  gof = c("CAF", "CFI", "RMSEA"),
```

```

eigen_type_HULL = c("SMC", "PCA", "EFA"),
eigen_type_other = c("SMC"),
n_factors = 1,
n_datasets = 1000,
percent = 95,
decision_rule = c("means", "percentile", "crawford"),
ekc_type = c("BvA2017"),
n_datasets_nest = 1000,
alpha_nest = 0.05,
show_progress = FALSE,
...
)

```

### Arguments

x	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations. If "CD" is included as a criterion, x must be raw data.
criteria	character. A vector with the factor retention methods to perform. Possible inputs are: "CD", "EKC", "HULL", "KGC", "MAP", "NEST", "PARALLEL", "SCREE", and "SMT" (see details). By default, a subset of often used, well-performing methods are performed.
suitability	logical. Whether the data should be checked for suitability for factor analysis using the Bartlett's test of sphericity and the Kaiser-Guttman criterion (see details). Default is TRUE.
N	numeric. The number of observations. Only needed if x is a correlation matrix.
use	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
cor_method	character. Passed to <code>stats::cor</code> Default is "pearson".
n_factors_max	numeric. Passed to <code>CD</code> . The maximum number of factors to test against. Larger numbers will increase the duration the procedure takes, but test more possible solutions. Maximum possible is number of variables / 2. Default is NA. If not specified, number of variables / 2 is used.
N_pop	numeric. Passed to <code>CD</code> . Size of finite populations of comparison data. Default is 10000.
N_samples	numeric. Passed to <code>CD</code> . Number of samples drawn from each population. Default is 500.
alpha	numeric. Passed to <code>CD</code> . The alpha level used to test the significance of the improvement added by an additional factor. Default is .30.
max_iter_CD	numeric. Passed to <code>CD</code> . The maximum number of iterations to perform after which the iterative PAF procedure is halted. Default is 50.
n_fac_theor	numeric. Passed to <code>HULL</code> . Theoretical number of factors to retain. The maximum of this number and the number of factors suggested by <code>PARALLEL</code> plus one will be used in the Hull method.
method	character. Passed to <code>EFA</code> in <code>HULL</code> , <code>KGC</code> , <code>SCREE</code> , <code>PARALLEL</code> , and <code>NEST</code> . The estimation method to use. One of "PAF", "ULS", or "ML", for principal axis factoring, unweighted least squares, and maximum likelihood, respectively.

<code>gof</code>	character. Passed to <a href="#">HULL</a> . The goodness of fit index to use. Either "CAF", "CFI", or "RMSEA", or any combination of them. If method = "PAF" is used, only the CAF can be used as goodness of fit index. For details on the CAF, see Lorenzo-Seva, Timmerman, and Kiers (2011).
<code>eigen_type_HULL</code>	character. Passed to <a href="#">PARALLEL</a> in <a href="#">HULL</a> . On what the eigenvalues should be found in the parallel analysis. Can be one of "SMC", "PCA", or "EFA". If using "SMC" (default), the diagonal of the correlation matrices is replaced by the squared multiple correlations (SMCs) of the indicators. If using "PCA", the diagonal values of the correlation matrices are left to be 1. If using "EFA", eigenvalues are found on the correlation matrices with the final communalities of an EFA solution as diagonal.
<code>eigen_type_other</code>	character. Passed to <a href="#">KGC</a> , <a href="#">SCREE</a> , and <a href="#">PARALLEL</a> . The same as <code>eigen_type_HULL</code> , but multiple inputs are possible here. Default is to use all inputs, that is, <code>c("PCA", "SMC", "EFA")</code>
<code>n_factors</code>	numeric. Passed to <a href="#">PARALLEL</a> (also within <a href="#">HULL</a> ), <a href="#">KGC</a> , and <a href="#">SCREE</a> . Number of factors to extract if "EFA" is included in <code>eigen_type_HULL</code> or <code>eigen_type_other</code> . Default is 1.
<code>n_datasets</code>	numeric. Passed to <a href="#">PARALLEL</a> (also within <a href="#">HULL</a> ). The number of datasets to simulate. Default is 1000.
<code>percent</code>	numeric. Passed to <a href="#">PARALLEL</a> (also within <a href="#">HULL</a> ). A vector of percentiles to take the simulated eigenvalues from. Default is 95.
<code>decision_rule</code>	character. Passed to <a href="#">PARALLEL</a> (also within <a href="#">HULL</a> ). Which rule to use to determine the number of factors to retain. Default is "means", which will use the average simulated eigenvalues. "percentile", uses the percentiles specified in percent. "crawford" uses the 95th percentile for the first factor and the mean afterwards (based on Crawford et al, 2010).
<code>ekc_type</code>	character. Passed to the type argument of <a href="#">EKC</a> . Either "BvA2017" for the original implementation by Braeken and van Assen (2017), or "AM2019" for the adapted implementation by Auerswald and Moshagen (2019).
<code>n_datasets_nest</code>	numeric. The number of datasets to simulate in <a href="#">NEST</a> . Default is 1000.
<code>alpha_nest</code>	numeric. The alpha level to use in <a href="#">NEST</a> (i.e., 1-alpha percentile of eigenvalues is used for reference values).
<code>show_progress</code>	logical. Whether a progress bar should be shown in the console. Default is FALSE.
<code>...</code>	Further arguments passed to <a href="#">EFA</a> in <a href="#">PARALLEL</a> (also within <a href="#">HULL</a> ) and <a href="#">KGC</a> .

## Details

By default, the entered data are checked for suitability for factor analysis using the following methods (see respective documentations for details):

- Bartlett's test of sphericity (see [BARTLETT](#))
- Kaiser-Meyer-Olkin criterion (see [KMO](#))

The available factor retention criteria are the following (see respective documentations for details):

- Comparison data (see [CD](#))
- Empirical Kaiser criterion (see [EKC](#))
- Hull method (see [HULL](#))
- Kaiser-Guttman criterion (see [KGC](#))
- Parallel analysis (see [PARALLEL](#))
- Next Eigenvalue Sufficiency Test, NEST (see [NEST](#))
- Scree plot (see [SCREE](#))
- Sequential chi-square model tests, RMSEA lower bound, and AIC (see [SMT](#))

### Value

A list of class N\_FACTORS containing

outputs	A list with the outputs from <a href="#">BARTLETT</a> and <a href="#">KMO</a> and the factor retention criteria.
n_factors	A named vector containing the suggested number of factors from each factor retention criterion.
settings	A list of the settings used.

### Examples

```
# Default criteria, with correlation matrix and fit method "ML" (where needed)
# This will throw a warning for CD, as no raw data were specified
nfac_all <- N_FACTORS(test_models$baseline$cormat, N = 500, method = "ML")

# The same as above, but without "CD"
nfac_wo_CD <- N_FACTORS(test_models$baseline$cormat, criteria = c("EKC",
  "HULL", "PARALLEL", "NEST"), N = 500,
  method = "ML")

# Use PAF instead of ML (this will take longer). For this, gof has
# to be set to "CAF" for the Hull method.
nfac_PAF <- N_FACTORS(test_models$baseline$cormat, criteria = c("EKC",
  "HULL", "PARALLEL", "NEST"), N = 500,
  gof = "CAF")

# Do KGC and PARALLEL with only "PCA" type of eigenvalues
nfac_PCA <- N_FACTORS(test_models$baseline$cormat, criteria = c("EKC",
  "HULL", "PARALLEL", "NEST"), N = 500,
  method = "ML", eigen_type_other = "PCA")

# Use raw data, such that CD can also be performed
nfac_raw <- N_FACTORS(GRiPS_raw, method = "ML")
```

OMEGA

*McDonald's omega***Description**

This function finds omega total, hierarchical, and subscale, as well as additional model-based indices of interpretive relevance (H index, ECV, PUC) from a Schmid-Leiman (SL) solution or lavaan single factor, second-order (see below), or bifactor solution. The SL-based omegas can either be found from a `psych::schmid, SL`, or, in a more flexible way, by leaving `model = NULL` and specifying additional arguments. By setting the `type` argument, results from `psych::omega` can be reproduced.

**Usage**

```
OMEGA(
  model = NULL,
  type = c("EFAtools", "psych"),
  g_name = "g",
  group_names = NULL,
  add_ind = TRUE,
  factor_corres = NULL,
  var_names = NULL,
  fac_names = NULL,
  g_load = NULL,
  s_load = NULL,
  u2 = NULL,
  cormat = NULL,
  pattern = NULL,
  Phi = NULL,
  variance = c("correlation", "sums_load")
)
```

**Arguments**

<code>model</code>	class <code>SL</code> , class <code>schmid</code> , or class <code>lavaan</code> object. That is, an output object from <code>SL</code> or <code>psych::schmid</code> , or a <code>lavaan</code> fit object with a single factor, second-order, or bifactor solution. If of class <code>lavaan</code> , only <code>g_name</code> needs to be specified additionally. If of class <code>SL</code> or <code>schmid</code> , only the arguments <code>factor_corres</code> and <code>cormat</code> need to be specified additionally.
<code>type</code>	character. Either "EFAtools" (default) or "psych" (see details)
<code>g_name</code>	character. The name of the general factor from the <code>lavaan</code> solution. This needs only be specified if <code>model</code> is a <code>lavaan</code> second-order or bifactor solution. Default is "g".
<code>group_names</code>	character. An optional vector of group names. The length must correspond to the number of groups for which the <code>lavaan</code> model was fitted.

<code>add_ind</code>	logical. Whether additional indices (H index, ECV, PUC) should be calculated or not (see details for these indices). If FALSE, only omegas are returned. Default is TRUE.
<code>factor_corres</code>	matrix. A logical matrix or a numeric matrix containing 0's and 1's that indicates which variable corresponds to which group factor. Must have the same dimensions as the matrix of group factor loadings from the SL solution. Cross-loadings are allowed here. See examples for use.
<code>var_names</code>	character. A vector with subtest names in the order of the rows from the SL solution. This needs only be specified if <code>model</code> is left NULL.
<code>fac_names</code>	character. An optional vector of group factor names in the order of the columns of the SL solution. If left NULL, names of the group factors from the entered solution are taken.
<code>g_load</code>	numeric. A vector of general factor loadings from an SL solution. This needs only be specified if <code>model</code> is left NULL.
<code>s_load</code>	matrix. A matrix of group factor loadings from an SL solution. This needs only be specified if <code>model</code> is left NULL.
<code>u2</code>	numeric. A vector of uniquenesses from an SL solution. This needs only be specified if <code>model</code> is left NULL.
<code>cormat</code>	matrix. A correlation matrix to be used when <code>variance = "correlation"</code> . If left NULL and an SL output is entered in <code>model</code> , the correlation matrix is taken from the output. If left NULL and a <code>psych::schmid</code> output is entered, the correlation matrix will be found based on the pattern matrix and Phi from the <code>psych::schmid</code> output using <code>psych::factor.model</code> . If left NULL and <code>model</code> is also left NULL, the correlation matrix is found based on the pattern matrix and Phi entered. However, if the correlation matrix is available, <code>cormat</code> should be specified instead of Phi and <code>pattern</code> .
<code>pattern</code>	matrix. Pattern coefficients from an oblique factor solution. This needs only be specified if <code>model</code> is left NULL, <code>variance = "correlation"</code> and <code>cormat</code> is also left NULL.
<code>Phi</code>	matrix. Factor intercorrelations from an oblique factor solution. This needs only be specified if <code>model</code> is left NULL, <code>variance = "correlation"</code> and <code>cormat</code> is also left NULL.
<code>variance</code>	character. If <code>"correlation"</code> (default), then total variances for the whole scale as well as for the subscale composites are calculated based on the correlation matrix. If <code>"sums_load"</code> , then total variances are calculated using the squared sums of general factor loadings and group factor loadings and the sum of uniquenesses (see details).

### Details

## What this function does

This function calculates McDonald's omegas (McDonald, 1978, 1985, 1999), the H index (Hancock & Mueller, 2001), the explained common variance (ECV; Sijtsma, 2009), and the percent of uncontaminated correlations (PUC; Bonifay et al., 2015; Reise et al., 2013).

All types of omegas (total, hierarchical, and subscale) are calculated for the general factor as well as for the subscales / group factors (see, e.g., Gignac, 2014; Rodriguez et al., 2016a, 2016b). Omegas

refer to the correlation between a factor and a unit-weighted composite score and thus the true score variance in a unit-weighted composite based on the respective indicators. Omega total is the total true score variance in a composite. Omega hierarchical is the true score variance in a composite that is attributable to the general factor, and omega subscale is the true score variance in a composite attributable to all subscales / group factors (for the whole scale) or to the specific subscale / group factor (for subscale composites).

The H index (also construct reliability or replicability index) is the correlation between an optimally-weighted composite score and a factor (Hancock & Mueller, 2001; Rodriguez et al., 2016a, 2016b). It, too, can be calculated for the whole scale / general factor as well as for the subscales / group factors. Low values indicate that a latent variable is not well defined by its indicators.

The ECV (Sijtsma, 2009, Rodriguez et al., 2016a, 2016b) is the ratio of the variance explained by the general factor and the variance explained by the general factor and the group factors.

The PUC (Bonifay et al., 2015; Reise et al., 2013, Rodriguez et al., 2016a, 2016b) refers to the proportion of correlations in the underlying correlation matrix that is not contaminated by variance of both the general factor and the group factors (i.e., correlations between indicators from different group factors, which reflect only general factor variance). The higher the PUC, the more similar a general factor from a multidimensional model will be to the single factor from a unidimensional model.

## How to use this function

If `model` is a lavaan second-order or bifactor solution, only the name of the general factor from the lavaan model needs to be specified additionally with the `g_name` argument. It is then determined whether this general factor is a second-order factor (second-order model with one second-order factor assumed) or a breadth factor (bifactor model assumed). Please note that this function only works for second-order models if they contain no more than one second-order factor. In case of a second-order solution, a Schmid-Leiman transformation is performed on the first- and second-order loadings and omega coefficients are obtained from the transformed (orthogonalized) solution (see [SL](#) for more information on Schmid-Leiman transformation). There is also the possibility to enter a lavaan single factor solution. In this case, `g_name` is not needed. Finally, if a solution from a lavaan multiple group analysis is entered, the indices are computed for each group. The `type` argument is not evaluated if `model` is of class `lavaan`.

If `model` is of class `SL` or `psych::schmid` only the `type` and, depending on the type (see below), the `factor_corres` arguments need to be specified additionally. If `model` is of class `psych::schmid` and `variance = "correlation"` (default), it is recommended to also provide the original correlation matrix in `cormat` to get more accurate results. Otherwise, the correlation matrix will be found based on the pattern matrix and Phi from the `psych::schmid` output using the `psych::factor.model` function.

If `model = NULL`, the arguments `type`, `factor_corres` (depending on the type, see below), `var_names`, `g_load`, `s_load`, and `u2` and either `cormat` (recommended) or `Phi` and `pattern` need to be specified. If `Phi` and `pattern` are specified instead of `cormat`, the correlation matrix is found using the `psych::factor.model` function.

The only difference between `type = "EFAtools"` and `type = "psych"` is the determination of variable-to-factor correspondences. `type = "psych"` reproduces the `psych::omega` results, where variable-to-factor correspondences are found by taking the highest group factor loading for each variable as the relevant group factor loading. To do this, `factor_corres` must be left `NULL`.

The calculation of the total variance (for the whole scale as well as the subscale composites) can also be controlled in this function using the `variance` argument. For both types—"EFAtools"

and "psych" —variance is set to "correlation" by default, which means that total variances are found using the correlation matrix. If `variance = "sums_load"` the total variance is calculated using the squared sums of general loadings and group factor loadings and the sum of the uniquenesses. This will only get comparable results to `variance = "correlation"` if no cross-loadings are present and simple structure is well-achieved in general with the SL solution (i.e., the uniquenesses should capture almost all of the variance not explained by the general factor and the variable's allocated group factor).

### Value

If found for an SL or lavaan second-order or bifactor solution without multiple groups: A matrix with omegas for the whole scale and for the subscales and (only if `add_ind = TRUE`) with the H index, ECV, and PUC.

tot	Omega total.
hier	Omega hierarchical.
sub	Omega subscale.
H	H index.
ECV	Explained common variance.
PUC	Percent of uncontaminated correlations.

If found for a lavaan single factor solution without multiple groups: A (named) vector with omega total and (if `add_ind = TRUE`) the H index for the single factor.

If found for a lavaan output from a multiple group analysis: A list containing the output described above for each group.

### Source

- McDonald, R. P. (1978). Generalizability in factorable domains: "Domain validity and generalizability". *Educational and Psychological Measurement*, 38, 75–79.
- McDonald, R. P. (1985). *Factor analysis and related methods*. Hillsdale, NJ: Erlbaum.
- McDonald, R. P. (1999). *Test theory: A unified treatment*. Mahwah, NJ: Erlbaum.
- Rodriguez, A., Reise, S. P., & Haviland, M. G. (2016a). Applying bifactor statistical indices in the evaluation of psychological measures. *Journal of Personality Assessment*, 98, 223–237.
- Rodriguez, A., Reise, S. P., & Haviland, M. G. (2016b). Evaluating bifactor models: Calculating and interpreting statistical indices. *Psychological Methods*, 21, 137–150.
- Hancock, G. R., & Mueller, R. O. (2001). Rethinking construct reliability within latent variable systems. In R. Cudeck, S. du Toit, & D. Sörbom (Eds.), *Structural equation modeling: Present and future—A Festschrift in honor of Karl Jöreskog* (pp. 195–216). Lincolnwood, IL: Scientific Software International.
- Sijtsma, K. (2009). On the use, the misuse, and the very limited usefulness of Cronbach's alpha. *Psychometrika*, 74, 107–120.
- Reise, S. P., Scheines, R., Widaman, K. F., & Haviland, M. G. (2013). Multidimensionality and structural coefficient bias in structural equation modeling: A bifactor perspective. *Educational and Psychological Measurement*, 73, 5–26.

Bonifay, W. E., Reise, S. P., Scheines, R., & Meijer, R. R. (2015). When are multidimensional data unidimensional enough for structural equation modeling?: An evaluation of the DETECT multidimensionality index. *Structural Equation Modeling*, 22, 504—516.

Gignac, G. E. (2014). On the Inappropriateness of Using Items to Calculate Total Scale Score Reliability via Coefficient Alpha for Multidimensional Scales. *European Journal of Psychological Assessment*, 30, 130-139.

## Examples

```
## Use with lavaan outputs

# Create and fit bifactor model in lavaan (assume all variables have SDs of 1)
mod <- 'F1 =~ V1 + V2 + V3 + V4 + V5 + V6
        F2 =~ V7 + V8 + V9 + V10 + V11 + V12
        F3 =~ V13 + V14 + V15 + V16 + V17 + V18
        g =~ V1 + V2 + V3 + V4 + V5 + V6 + V7 + V8 + V9 + V10 + V11 + V12 +
            V13 + V14 + V15 + V16 + V17 + V18'
fit_bi <- lavaan::cfa(mod, sample.cov = test_models$baseline$cormat,
                    sample.nobs = 500, estimator = "ml", orthogonal = TRUE)

# Compute omegas and additional indices for bifactor solution
OMEGA(fit_bi, g_name = "g")

# Compute only omegas
OMEGA(fit_bi, g_name = "g", add_ind = FALSE)

# Create and fit second-order model in lavaan (assume all variables have SDs of 1)
mod <- 'F1 =~ V1 + V2 + V3 + V4 + V5 + V6
        F2 =~ V7 + V8 + V9 + V10 + V11 + V12
        F3 =~ V13 + V14 + V15 + V16 + V17 + V18
        g =~ F1 + F2 + F3'
fit_ho <- lavaan::cfa(mod, sample.cov = test_models$baseline$cormat,
                    sample.nobs = 500, estimator = "ml")

# Compute omegas and additional indices for second-order solution
OMEGA(fit_ho, g_name = "g")

## Use with an output from the SL function, with type EFAtools
efa_mod <- EFA(test_models$baseline$cormat, N = 500, n_factors = 3,
              type = "EFAtools", method = "PAF", rotation = "promax")
sl_mod <- SL(efa_mod, type = "EFAtools", method = "PAF")

# Two examples how to specify the indicator-to-factor correspondences:

# Based on a specific salience threshold for the loadings (here: .20):
factor_corres_1 <- sl_mod$sl[, c("F1", "F2", "F3")] >= .2

# Or more flexibly (could also be TRUE and FALSE instead of 0 and 1):
factor_corres_2 <- matrix(c(rep(0, 12), rep(1, 6), rep(0, 6), rep(1, 6),
                          rep(0, 6), rep(1, 6), rep(0, 12)), ncol = 3,
                        byrow = FALSE)
```

```

OMEGA(sl_mod, type = "EFAtools", factor_corres = factor_corres_1)

## Use with an output from the psych::schmid function, with type psych for
## OMEGA
schmid_mod <- psych::schmid(test_models$baseline$cormat, nfactors = 3,
                           n.obs = 500, fm = "pa", rotate = "Promax")
# Find correlation matrix from phi and pattern matrix from psych::schmid output
OMEGA(schmid_mod, type = "psych")
# Use specified correlation matrix
OMEGA(schmid_mod, type = "psych", cormat = test_models$baseline$cormat)

## Manually specify components (useful if omegas should be computed for a SL
## or bifactor solution found with another program)
## As an example, we extract the elements from an SL output here. This gives
## the same results as in the second example above.

efa_mod <- EFA(test_models$baseline$cormat, N = 500, n_factors = 3,
              type = "EFAtools", method = "PAF", rotation = "promax")
sl_mod <- SL(efa_mod, type = "EFAtools", method = "PAF")

factor_corres <- matrix(c(rep(0, 12), rep(1, 6), rep(0, 6), rep(1, 6),
                          rep(0, 6), rep(1, 6), rep(0, 12)), ncol = 3,
                       byrow = FALSE)

OMEGA(model = NULL, type = "EFAtools", var_names = rownames(sl_mod$sl),
      g_load = sl_mod$sl[, "g"], s_load = sl_mod$sl[, c("F1", "F2", "F3")],
      u2 = sl_mod$sl[, "u2"], cormat = test_models$baseline$cormat,
      factor_corres = factor_corres)

```

---

PARALLEL

*Parallel analysis*

---

## Description

Various methods for performing parallel analysis. This function uses [future\\_lapply](#) for which a parallel processing plan can be selected. To do so, call `library(future)` and, for example, `plan(multisession)`; see examples.

## Usage

```

PARALLEL(
  x = NULL,
  N = NA,
  n_vars = NA,
  n_datasets = 1000,
  percent = 95,
  eigen_type = c("PCA", "SMC", "EFA"),

```

```

use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
       "na.or.complete"),
cor_method = c("pearson", "spearman", "kendall"),
decision_rule = c("means", "percentile", "crawford"),
n_factors = 1,
...
)

```

### Arguments

<code>x</code>	matrix or data.frame. The real data to compare the simulated eigenvalues against. Must not contain variables of classes other than numeric. Can be a correlation matrix or raw data.
<code>N</code>	numeric. The number of cases / observations to simulate. Only has to be specified if <code>x</code> is either a correlation matrix or NULL. If <code>x</code> contains raw data, <code>N</code> is found from the dimensions of <code>x</code> .
<code>n_vars</code>	numeric. The number of variables / indicators to simulate. Only has to be specified if <code>x</code> is left as NULL as otherwise the dimensions are taken from <code>x</code> .
<code>n_datasets</code>	numeric. The number of datasets to simulate. Default is 1000.
<code>percent</code>	numeric. The percentile to take from the simulated eigenvalues. Default is 95.
<code>eigen_type</code>	character. On what the eigenvalues should be found. Can be either "SMC", "PCA", or "EFA". If using "SMC", the diagonal of the correlation matrix is replaced by the squared multiple correlations (SMCs) of the indicators. If using "PCA", the diagonal values of the correlation matrices are left to be 1. If using "EFA", eigenvalues are found on the correlation matrices with the final communalities of an EFA solution as diagonal.
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <code>stats::cor</code> Default is "pearson".
<code>decision_rule</code>	character. Which rule to use to determine the number of factors to retain. Default is "means", which will use the average simulated eigenvalues. "percentile", uses the percentiles specified in <code>percent</code> . "crawford" uses the 95th percentile for the first factor and the mean afterwards (based on Crawford et al, 2010).
<code>n_factors</code>	numeric. Number of factors to extract if "EFA" is included in <code>eigen_type</code> . Default is 1.
<code>...</code>	Additional arguments passed to <code>EFA</code> . For example, the extraction method can be changed here (default is "PAF"). PAF is more robust, but it will take longer compared to the other estimation methods available ("ML" and "ULS").

### Details

Parallel analysis (Horn, 1965) compares the eigenvalues obtained from the sample correlation matrix against those of null model correlation matrices (i.e., with uncorrelated variables) of the same sample size. This way, it accounts for the variation in eigenvalues introduced by sampling error and thus eliminates the main problem inherent in the Kaiser-Guttman criterion (KGC).

Three different ways of finding the eigenvalues under the factor model are implemented, namely "SMC", "PCA", and "EFA". PCA leaves the diagonal elements of the correlation matrix as they are and is thus equivalent to what is done in PCA. SMC uses squared multiple correlations as communality estimates with which the diagonal of the correlation matrix is replaced. Finally, EFA performs an EFA with one factor (can be adapted to more factors) to estimate the communalities and based on the correlation matrix with these as diagonal elements, finds the eigenvalues.

Parallel analysis is often argued to be one of the most accurate factor retention criteria. However, for highly correlated factor structures it has been shown to underestimate the correct number of factors. The reason for this is that a null model (uncorrelated variables) is used as reference. However, when factors are highly correlated, the first eigenvalue will be much larger compared to the following ones, as later eigenvalues are conditional on the earlier ones in the sequence and thus the shared variance is already accounted in the first eigenvalue (e.g., Braeken & van Assen, 2017).

The PARALLEL function can also be called together with other factor retention criteria in the `N_FACTORS` function.

### Value

A list of class PARALLEL containing the following objects

<code>eigenvalues_PCA</code>	A matrix containing the eigenvalues of the real and the simulated data found with <code>eigen_type = "PCA"</code>
<code>eigenvalues_SMC</code>	A matrix containing the eigenvalues of the real and the simulated data found with <code>eigen_type = "SMC"</code>
<code>eigenvalues_EFA</code>	A matrix containing the eigenvalues of the real and the simulated data found with <code>eigen_type = "EFA"</code>
<code>n_fac_PCA</code>	The number of factors to retain according to the parallel procedure with <code>eigen_type = "PCA"</code> .
<code>n_fac_SMC</code>	The number of factors to retain according to the parallel procedure with <code>eigen_type = "SMC"</code> .
<code>n_fac_EFA</code>	The number of factors to retain according to the parallel procedure with <code>eigen_type = "EFA"</code> .
<code>settings</code>	A list of control settings used in the print function.

### Source

Braeken, J., & van Assen, M. A. (2017). An empirical Kaiser criterion. *Psychological Methods*, 22, 450 – 466. <http://dx.doi.org/10.1037/met0000074>

Crawford, A. V., Green, S. B., Levy, R., Lo, W. J., Scott, L., Svetina, D., & Thompson, M. S. (2010). Evaluation of parallel analysis methods for determining the number of factors. *Educational and Psychological Measurement*, 70(6), 885-901.

Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika*, 30(2), 179–185. doi: 10.1007/BF02289447

**See Also**

Other factor retention criteria: [CD](#), [EKC](#), [HULL](#), [KGC](#), [SMT](#)

[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

**Examples**

```
# example without real data
pa_unreal <- PARALLEL(N = 500, n_vars = 10)

# example with correlation matrix with all eigen_types and PAF estimation
pa_paf <- PARALLEL(test_models$case_11b$cormat, N = 500)

# example with correlation matrix with all eigen_types and ML estimation
# this will be faster than the above with PAF)
pa_ml <- PARALLEL(test_models$case_11b$cormat, N = 500, method = "ML")

## Not run:
# for parallel computation
future::plan(future::multisession)
pa_faster <- PARALLEL(test_models$case_11b$cormat, N = 500)

## End(Not run)
```

---

plot.CD

*Plot CD object*

---

**Description**

Plot method showing a summarized output of the [CD](#) function

**Usage**

```
## S3 method for class 'CD'
plot(x, ...)
```

**Arguments**

x                    a list of class CD. An output from the [CD](#) function.  
 ...                    not used.

---

plot.EFA\_AVERAGE      *Plot EFA\_AVERAGE object*

---

**Description**

Plot method showing a summarized output of the [EFA\\_AVERAGE](#) function

**Usage**

```
## S3 method for class 'EFA_AVERAGE'  
plot(x, ...)
```

**Arguments**

x                    list. An output from the [EFA\\_AVERAGE](#) function.  
...                    not used.

**Examples**

```
## Not run:  
EFA_aver <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500)  
EFA_aver  
  
## End(Not run)
```

---

plot.EKC                    *Plot EKC object*

---

**Description**

Plot method showing a summarized output of the [EKC](#) function

**Usage**

```
## S3 method for class 'EKC'  
plot(x, ...)
```

**Arguments**

x                    a list of class EKC. An output from the [EKC](#) function.  
...                    not used.

**Examples**

```
EKC_base <- EKC(test_models$baseline$cormat, N = 500)  
plot(EKC_base)
```

---

plot.HULL	<i>Plot HULL object</i>
-----------	-------------------------

---

**Description**

Plot method showing a summarized output of the [HULL](#) function

**Usage**

```
## S3 method for class 'HULL'  
plot(x, ...)
```

**Arguments**

x	list of class HULL. An output from the <a href="#">HULL</a> function.
...	not used.

**Examples**

```
x <- HULL(test_models$baseline$cormat, N = 500, method = "ML")  
plot(x)
```

---

plot.KGC	<i>Plot KGC object</i>
----------	------------------------

---

**Description**

Plot method showing a summarized output of the [KGC](#) function

**Usage**

```
## S3 method for class 'KGC'  
plot(x, ...)
```

**Arguments**

x	a list of class KGC. An output from the <a href="#">KGC</a> function.
...	not used.

**Examples**

```
KGC_base <- KGC(test_models$baseline$cormat)  
plot(KGC_base)
```

---

plot.PARALLEL            *Plot PARALLEL object*

---

**Description**

Plot method showing a summarized output of the [PARALLEL](#) function

**Usage**

```
## S3 method for class 'PARALLEL'  
plot(x, ...)
```

**Arguments**

x                    list of class PARALLEL. An output from the [PARALLEL](#) function.  
...                  not used.

**Examples**

```
# example with correlation matrix and "ML" estimation  
x <- PARALLEL(test_models$case_11b$cormat, N = 500, method = "ML")  
plot(x)
```

---

plot.SCREEN            *Plot SCREEN object*

---

**Description**

Plot method showing a summarized output of the [SCREEN](#) function

**Usage**

```
## S3 method for class 'SCREEN'  
plot(x, ...)
```

**Arguments**

x                    a list of class SCREEN An output from the [SCREEN](#) function.  
...                  not used.

**Examples**

```
SCREEN_base <- SCREEN(test_models$baseline$cormat)  
plot(SCREEN_base)
```

---

population\_models      *population\_models*

---

### Description

Population factor models, some of which (baseline to case\_11e) used for the simulation analyses reported in Grieder and Steiner (2019). All combinations of the pattern matrices and the factor intercorrelations were used in the simulations. Many models are based on cases used in de Winter and Dodou (2012).

### Usage

population\_models

### Format

A list of 3 lists "loadings", "phis\_3", and "phis\_6".

loadings contains the following matrices of pattern coefficients:

**baseline** (matrix) - The pattern coefficients of the baseline model. Three factors with six indicators each, all with pattern coefficients of .6. Same baseline model as used in de Winter and Dodou (2012).

**case\_1a** (matrix) - Three factors with 2 indicators per factor.

**case\_1b** (matrix) - Three factors with 3 indicators per factor. Case 5 in de Winter and Dodou (2012).

**case\_1c** (matrix) - Three factors with 4 indicators per factor.

**case\_1d** (matrix) - Three factors with 5 indicators per factor.

**case\_2** (matrix) - Same as baseline model but with low pattern coefficients of .3.

**case\_3** (matrix) - Same as baseline model but with high pattern coefficients of .9.

**case\_4** (matrix) - Three factors with different pattern coefficients *between* factors (one factor with .9, one with .6, and one with .3, respectively). Case 7 in de Winter and Dodou (2012).

**case\_5** (matrix) - Three factors with different pattern coefficients *within* factors (each factor has two pattern coefficients of each .9, .6, and .3). Similar to cases 8/ 9 in de Winter and Dodou (2012).

**case\_6a** (matrix) - Same as baseline model but with one cross loading of .4. Similar to case 10 in de Winter and Dodou (2012).

**case\_6b** (matrix) - Same as baseline model but with three cross loading of .4 (One factor with 2 and one with 1 crossloading). Similar to case 10 in de Winter and Dodou (2012).

**case\_7** (matrix) - Three factors with different number of indicators per factor (2, 4, and 6 respectively). Similar to cases 11/ 12 in de Winter and Dodou (2012).

**case\_8** (matrix) - Three factors with random variation in pattern coefficients added, drawn from a uniform distribution between [-.2, .2]. Case 13 in de Winter and Dodou (2012).

**case\_9a** (matrix) - Three factors with 2 indicators per factor, with different pattern coefficients within one of the factors.

- case\_9b** (matrix) - Three factors with 3 indicators per factor, with different pattern coefficients.
- case\_9c** (matrix) - Three factors with 4 indicators per factor, with different pattern coefficients.
- case\_9d** (matrix) - Three factors with 5 indicators per factor, with different pattern coefficients.
- case\_10a** (matrix) - Six factors with 2 indicators per factor, all with pattern coefficients of .6.
- case\_10b** (matrix) - Six factors with 3 indicators per factor, all with pattern coefficients of .6.
- case\_10c** (matrix) - Six factors with 4 indicators per factor, all with pattern coefficients of .6.
- case\_10d** (matrix) - Six factors with 5 indicators per factor, all with pattern coefficients of .6.
- case\_10e** (matrix) - Six factors with 6 indicators per factor, all with pattern coefficients of .6.
- case\_11a** (matrix) - Six factors with 2 indicators per factor, with different pattern coefficients within and between factors (.3, .6, and .9).
- case\_11b** (matrix) - Six factors with 3 indicators per factor, with different pattern coefficients within and between factors (.3, .6, and .9).
- case\_11c** (matrix) - Six factors with 4 indicators per factor, with different pattern coefficients within and between factors (.3, .6, and .9).
- case\_11d** (matrix) - Six factors with 5 indicators per factor, with different pattern coefficients within and between factors (.3, .6, and .9).
- case\_11e** (matrix) - Six factors with 6 indicators per factor, with different pattern coefficients within and between factors (.3, .6, and .9).
- case\_12a** (matrix) - One factor, with 2 equal pattern coefficients (.6).
- case\_12b** (matrix) - One factor, with 3 equal pattern coefficients (.6).
- case\_12c** (matrix) - One factor, with 6 equal pattern coefficients (.6).
- case\_12d** (matrix) - One factor, with 10 equal pattern coefficients (.6).
- case\_12e** (matrix) - One factor, with 15 equal pattern coefficients (.6).
- case\_13a** (matrix) - One factor, with 2 different pattern coefficients (.3, and .6).
- case\_13b** (matrix) - One factor, with 3 different pattern coefficients (.3, .6, and .9).
- case\_13c** (matrix) - One factor, with 6 different pattern coefficients (.3, .6, and .9).
- case\_13d** (matrix) - One factor, with 10 different pattern coefficients (.3, .6, and .9).
- case\_13e** (matrix) - One factor, with 15 different pattern coefficients (.3, .6, and .9).
- case\_14a** (matrix) - No factor, 2 variables (0).
- case\_14b** (matrix) - No factor, 3 variables (0).
- case\_14c** (matrix) - No factor, 6 variables (0).
- case\_14d** (matrix) - No factor, 10 variables (0).
- case\_14e** (matrix) - No factor, 15 variables (0). `phis_3` contains the following 3x3 matrices:
- zero** (matrix) - Matrix of factor intercorrelations of 0. Same intercorrelations as used in de Winter and Dodou (2012).
- moderate** (matrix) - Matrix of moderate factor intercorrelations of .3.
- mixed** (matrix) - Matrix of mixed (.3, .5, and .7) factor intercorrelations.
- strong** (matrix) - Matrix of strong factor intercorrelations of .7. Same intercorrelations as used in de Winter and Dodou (2012). `phis_6` contains the following 6x6 matrices:

**zero** (matrix) - Matrix of factor intercorrelations of 0. Same intercorrelations as used in de Winter and Dodou (2012).

**moderate** (matrix) - Matrix of moderate factor intercorrelations of .3.

**mixed** (matrix) - Matrix of mixed (around .3, .5, and .7; smoothing was necessary for the matrix to be positive definite) factor intercorrelations.

**strong** (matrix) - Matrix of strong factor intercorrelations of .7. Same intercorrelations as used in de Winter and Dodou (2012).

## Source

Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.

de Winter, J.C.F., & Dodou, D. (2012). Factor recovery by principal axis factoring and maximum likelihood factor analysis as a function of factor pattern and sample size. *Journal of Applied Statistics*. 39.

---

print.BARTLETT      *Print BARTLETT object*

---

## Description

Print BARTLETT object

## Usage

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

## Arguments

x                    list of class BARTLETT (output from the [BARTLETT](#) function)  
...                   additional arguments passed to print

## Examples

```
BARTLETT(test_models$baseline$scormat, N = 500)
```

print.CD *Print function for CD objects*

---

**Description**

Print function for CD objects

**Usage**

```
## S3 method for class 'CD'  
print(x, plot = TRUE, ...)
```

**Arguments**

x a list of class CD. Output from [CD](#) function.  
plot logical. Whether to plot the results.  
... Further arguments for print.

**Examples**

```
# determine n factors of the GRiPS  
CD(GRiPS_raw)
```

---

print.COMPARE *Print COMPARE object*

---

**Description**

Print Method showing a summarized output of the [COMPARE](#) function.

**Usage**

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

**Arguments**

x list. An object of class COMPARE to be printed  
... Further arguments for print.

**Examples**

```
# A type SPSS EFA to mimick the SPSS implementation
EFA_SPSS_5 <- EFA(IDS2_R, n_factors = 5, type = "SPSS")

# A type psych EFA to mimick the psych::fa() implementation
EFA_psych_5 <- EFA(IDS2_R, n_factors = 5, type = "psych")

# compare the two
COMPARE(EFA_SPSS_5$unrot_loadings, EFA_psych_5$unrot_loadings,
        x_labels = c("SPSS", "psych"))
```

---

```
print.EFA          Print EFA object
```

---

**Description**

Print Method showing a summarized output of the [EFA](#) function.

**Usage**

```
## S3 method for class 'EFA'
print(
  x,
  cutoff = 0.3,
  digits = 3,
  max_name_length = 10,
  ci = c("auto", "none", "separate"),
  ci_filter = c("salient", "all", "nonzero"),
  details = c("standard", "compact", "full"),
  diagnostics = TRUE,
  diagnostics_top_n = 10,
  residual_cutoff = 0.1,
  residual_top_n = 10,
  show_structure = FALSE,
  sort_loadings = c("none", "primary", "clustered"),
  show_loading_legend = TRUE,
  cross_loading_cutoff = cutoff,
  min_primary_gap = 0.2,
  min_salient_per_factor = 3,
  max_factors_per_block = NULL,
  show_mi_diagnostics = NULL,
  ...
)

## S3 method for class 'EFA_POOLED'
print(
  x,
```

```

    cutoff = 0.3,
    digits = 3,
    max_name_length = 10,
    ci = c("auto", "none", "separate"),
    ci_filter = c("salient", "all", "nonzero"),
    details = c("standard", "compact", "full"),
    diagnostics = TRUE,
    diagnostics_top_n = 10,
    residual_cutoff = 0.1,
    residual_top_n = 10,
    show_structure = FALSE,
    sort_loadings = c("none", "primary", "clustered"),
    show_loading_legend = TRUE,
    cross_loading_cutoff = cutoff,
    min_primary_gap = 0.2,
    min_salient_per_factor = 3,
    max_factors_per_block = NULL,
    show_mi_diagnostics = NULL,
    ...
)

```

```

## S3 method for class 'EFA'
format(
  x,
  cutoff = 0.3,
  digits = 3,
  max_name_length = 10,
  ci = c("auto", "none", "separate"),
  ci_filter = c("salient", "all", "nonzero"),
  details = c("standard", "compact", "full"),
  diagnostics = TRUE,
  diagnostics_top_n = 10,
  residual_cutoff = 0.1,
  residual_top_n = 10,
  show_structure = FALSE,
  sort_loadings = c("none", "primary", "clustered"),
  show_loading_legend = TRUE,
  cross_loading_cutoff = cutoff,
  min_primary_gap = 0.2,
  min_salient_per_factor = 3,
  max_factors_per_block = NULL,
  show_mi_diagnostics = NULL,
  ...
)

```

```

## S3 method for class 'EFA_POOLED'
format(
  x,

```

```

    cutoff = 0.3,
    digits = 3,
    max_name_length = 10,
    ci = c("auto", "none", "separate"),
    ci_filter = c("salient", "all", "nonzero"),
    details = c("standard", "compact", "full"),
    diagnostics = TRUE,
    diagnostics_top_n = 10,
    residual_cutoff = 0.1,
    residual_top_n = 10,
    show_structure = FALSE,
    sort_loadings = c("none", "primary", "clustered"),
    show_loading_legend = TRUE,
    cross_loading_cutoff = cutoff,
    min_primary_gap = 0.2,
    min_salient_per_factor = 3,
    max_factors_per_block = NULL,
    show_mi_diagnostics = NULL,
    ...
)

```

### Arguments

x	list. An object of class EFA to be printed
cutoff	numeric. Passed to <code>print.LOADINGS</code> . The number above which to print loadings in bold. Default is .3.
digits	numeric. Passed to <code>print.LOADINGS</code> Number of digits to round the loadings to (default is 3).
max_name_length	numeric. Passed to <code>print.LOADINGS</code> . The maximum length of the variable names to display. Everything beyond this will be cut from the right.
ci	character. Whether to print confidence intervals for loadings and factor intercorrelations, if available. "auto" and "separate" print separate CI sections when CIs were computed; "none" suppresses these sections. Default is "auto".
ci_filter	character. Which loading CIs to print. "salient" prints CIs for loadings with absolute values greater than or equal to cutoff; "all" prints all loading CIs; "nonzero" prints loading CIs that exclude zero. Default is "salient".
details	character. Amount of information to print. "standard" prints the regular output, "compact" suppresses longer diagnostic sections, and "full" additionally prints available optional sections.
diagnostics	logical. Whether to print model and simple-structure diagnostics. Default is TRUE.
diagnostics_top_n	numeric. Maximum number of item-level diagnostic entries to print per diagnostic type.
residual_cutoff	numeric. Absolute residual cutoff used in the residual diagnostics section. Default is .1.

`residual_top_n` numeric. Maximum number of residuals to print. Use `Inf` to print all residuals above `residual_cutoff`.

`show_structure` logical. Whether to print the structure matrix for oblique solutions when available. Default is `FALSE`.

`sort_loadings` character. Optional row sorting for loading tables. See `print.LOADINGS`.

`show_loading_legend` logical. Whether to print a compact legend for loading-table styling. Default is `TRUE`.

`cross_loading_cutoff` numeric. Cutoff for counting cross-loadings in the diagnostics. Defaults to `cutoff`.

`min_primary_gap` numeric. Minimum desired absolute difference between the largest and second-largest absolute loading of an item. Used only for descriptive diagnostics.

`min_salient_per_factor` numeric. Minimum number of salient indicators per factor used in the diagnostics. Default is 3.

`max_factors_per_block` numeric or `NULL`. Maximum number of factor columns per loading-table block. If `NULL`, this is chosen from the console width.

`show_mi_diagnostics` logical or `NULL`. Whether to print a compact MI uncertainty summary for pooled EFAs when available. `NULL` prints it only for `details = "full"`.

`...` Further arguments passed to `print.LOADINGS`.

## Details

The method is shared by single-imputation ‘EFA’ objects and pooled ‘EFA\_POOLED’ objects. It prints, in order, a compact model header, optional diagnostics, the loading table, optional confidence-interval tables, variance accounted for, model fit, bootstrap notes, optional multiple-imputation uncertainty diagnostics, and residual diagnostics.

For ‘EFA\_POOLED’ objects, the header and diagnostics report the number of imputations and the alignment/pooling settings stored in the object. Loading and factor-correlation confidence intervals are printed only when ‘boot.CI’ is present. Pooled intervals created by ‘EFA\_POOLED()’ are labelled as bootstrap/MI intervals.

‘ci\_filter’ controls which loading intervals are shown. ‘salient’ reports intervals for loadings whose absolute point estimate is at least ‘cutoff’; ‘nonzero’ reports intervals excluding zero; and ‘all’ reports every finite interval.

## Examples

```

mod <- EFA(test_models$baseline$cormat, n_factors = 3, N = 500,
           method = "PAF", rotation = "promax")
mod

# With SEs and CIs, needs raw-data
mod <- EFA(GRIPS_raw, n_factors = 1, method = "ML", se = "np-boot")

```

```

mod
# with additional infos
print(mod, details = "full")
# omit some diagnostic parts
print(mod, details = "compact")

```

---

```

print.EFA_AVERAGE      Print EFA_AVERAGE object

```

---

### Description

Print Method showing a summarized output of the [EFA\\_AVERAGE](#) function

### Usage

```

## S3 method for class 'EFA_AVERAGE'
print(x, stat = c("average", "range"), plot = TRUE, ...)

```

### Arguments

x	list. An object of class EFA_AVERAGE to be printed
stat	character. A vector with the statistics to print. Possible inputs are "average", "sd", "range", "min", and "max". Default is "average" and "range".
plot	logical. Whether a plot of the average and min- max loadings should be created. Default is TRUE. If more than 10 factors are extracted, no plot is created.
...	Further arguments for print.

### Examples

```

## Not run:
EFA_aver <- EFA_AVERAGE(test_models$baseline$cormat, n_factors = 3, N = 500)
EFA_aver

## End(Not run)

```

---

```

print.EKC              Print function for EKC objects

```

---

### Description

Print function for EKC objects

### Usage

```

## S3 method for class 'EKC'
print(x, plot = TRUE, ...)

```

**Arguments**

x a list of class EKC. Output from [EKC](#) function.  
plot logical. Whether to plot the results.  
... Further arguments for print.

**Examples**

```
EKC_base <- EKC(test_models$baseline$cormat, N = 500)
EKC_base
```

---

print.HULL *Print function for HULL objects*

---

**Description**

Print function for HULL objects

**Usage**

```
## S3 method for class 'HULL'
print(x, plot = TRUE, ...)
```

**Arguments**

x a list of class HULL. Output from the [HULL](#) function.  
plot logical. Whether to plot the results.  
... Further arguments for print.

**Examples**

```
HULL(test_models$baseline$cormat, N = 500, method = "ML")
```

---

print.KGC                      *Print function for KGC objects*

---

**Description**

Print function for KGC objects

**Usage**

```
## S3 method for class 'KGC'  
print(x, plot = TRUE, ...)
```

**Arguments**

x                      a list of class KGC. Output from [KGC](#) function.  
plot                    logical. Whether to plot the results.  
...                     Further arguments for print.

**Examples**

```
KGC_base <- KGC(test_models$baseline$cormat)  
KGC_base
```

---

print.KMO                      *Print KMO object*

---

**Description**

Print KMO object

**Usage**

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

**Arguments**

x                      list of class KMO (output from the [KMO](#) function)  
...                     additional arguments passed to print

**Examples**

```
KMO_base <- KMO(test_models$baseline$cormat)  
KMO_base
```

---

```
print.LOADINGS          Print LOADINGS object
```

---

### Description

Print LOADINGS object

### Usage

```
## S3 method for class 'LOADINGS'
print(
  x,
  cutoff = 0.3,
  digits = 3,
  max_name_length = 10,
  h2 = NULL,
  color = TRUE,
  name_style = c("truncate", "abbreviate", "full"),
  max_factor_name_length = NULL,
  max_factors_per_block = NULL,
  sort_loadings = c("none", "primary", "clustered"),
  legend = FALSE,
  ...
)
```

```
## S3 method for class 'LOADINGS'
format(
  x,
  cutoff = 0.3,
  digits = 3,
  max_name_length = 10,
  h2 = NULL,
  color = TRUE,
  name_style = c("truncate", "abbreviate", "full"),
  max_factor_name_length = NULL,
  max_factors_per_block = NULL,
  sort_loadings = c("none", "primary", "clustered"),
  legend = FALSE,
  ...
)
```

### Arguments

<code>x</code>	class <code>LOADINGS</code> matrix.
<code>cutoff</code>	numeric. The number above which to print loadings in bold default is <code>.3</code> .
<code>digits</code>	numeric. Passed to <code>round</code> . Number of digits to round the loadings to (default is <code>3</code> ).

max_name_length	numeric. The maximum length of the variable names to display. Everything beyond this will be cut from the right unless name_style = "abbreviate" or name_style = "full" is used.
h2	numeric. Vector of communalities to print. If named and x has row names, names are used to align communalities to rows.
color	logical. Whether to apply console styling using <b>crayon</b> . Default is TRUE.
name_style	character. How to shorten variable names longer than max_name_length. "truncate" cuts names from the right, "abbreviate" uses <a href="#">abbreviate</a> , and "full" prints full names.
max_factor_name_length	numeric or NULL. Optional maximum length of factor names. If NULL, factor names are not shortened.
max_factors_per_block	numeric or NULL. Maximum number of factor columns to print per block. If NULL, the number is chosen from the console width.
sort_loadings	character. Optional row sorting. "none" preserves the input order, "primary" groups rows by the factor with the largest absolute loading, and "clustered" additionally sorts within each factor by the size of the primary loading.
legend	logical. Whether to append a short explanation of the styling. Default is FALSE for standalone loading matrices.
...	additional arguments passed to print or format

## Details

The method prints a loading matrix in a compact, console-oriented table. Loadings with absolute value greater than or equal to 'cutoff' are emphasized, smaller loadings are de-emphasized, and Heywood-relevant communality/ uniqueness values are marked when 'h2' is supplied. Long variable names can be truncated, abbreviated, or printed in full. If the matrix has many factor columns, the table is split into column blocks so that the output remains readable in narrower consoles.

If 'h2' is named and 'x' has row names, 'h2' is matched to the row names of 'x' before any optional row sorting is applied. If 'x' has no row names, a named 'h2' vector is used in the supplied order.

## Examples

```
EFAtools_PAF <- EFA(test_models$baseline$format, n_factors = 3, N = 500,
                  type = "EFAtools", method = "PAF", rotation = "promax")
EFAtools_PAF
```

---

print.MAP                    *Print function for MAP objects*

---

**Description**

Print function for MAP objects

**Usage**

```
## S3 method for class 'MAP'  
print(x, plot = TRUE, ...)
```

**Arguments**

x                    a list of class MAP. Output from [MAP](#) function.  
plot                logical. Whether to plot the results.  
...                 Further arguments for print.

**Examples**

```
MAP_base <- MAP(test_models$baseline$cormat)  
MAP_base
```

---

print.NEST                    *Print function for NEST objects*

---

**Description**

Print function for NEST objects

**Usage**

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

**Arguments**

x                    a list of class NEST Output from [NEST](#) function.  
...                 Further arguments for print.

**Examples**

```
NEST(test_models$baseline$cormat, N = 500)
```

---

print.N\_FACTORS      *Print function for N\_FACTORS objects*

---

**Description**

Print function for N\_FACTORS objects

**Usage**

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

**Arguments**

x                    a list of class N\_FACTORS. Output from [N\\_FACTORS](#) function.  
...                  Further arguments for print.

**Examples**

```
# All criteria except "CD", with correlation matrix and fit method "ML"  
# (where needed)  
N_FACTORS(test_models$baseline$cormat, criteria = c("EKC", "HULL", "KGC",  
          "PARALLEL", "SCREE", "SMT"), N = 500, method = "ML")
```

---

print.OMEGA            *Print OMEGA object*

---

**Description**

Print OMEGA object

**Usage**

```
## S3 method for class 'OMEGA'  
print(x, digits = 3, ...)
```

**Arguments**

x                    output of class OMEGA (output from the [OMEGA](#) function)  
digits                numeric. Passed to [round](#). Number of digits to round to (default is 3).  
...                    additional arguments passed to print

**Examples**

```
efa_mod <- EFA(test_models$baseline$cormat, N = 500, n_factors = 3,
              type = "EFAtools", method = "PAF", rotation = "promax")
sl_mod <- SL(efa_mod, type = "EFAtools", method = "PAF")

OMEGA(sl_mod, type = "EFAtools",
      factor_corres = sl_mod$sl[, c("F1", "F2", "F3")] >= .2)
```

---

print.PARALLEL            *Print function for PARALLEL objects*

---

**Description**

Print function for PARALLEL objects

**Usage**

```
## S3 method for class 'PARALLEL'
print(x, plot = TRUE, ...)
```

**Arguments**

x                    a list of class PARALLEL. Output from [PARALLEL](#) function.  
plot                 logical. Whether to plot the results.  
...                   Further arguments for print.

**Examples**

```
# example without real data
PARALLEL(N = 500, n_vars = 10)

# example with correlation matrix and "ML" estimation
PARALLEL(test_models$case_11b$cormat, N = 500, method = "ML")
```

---

print.SCREEN            *Print function for SCREE objects*

---

**Description**

Print function for SCREE objects

**Usage**

```
## S3 method for class 'SCREE'
print(x, plot = TRUE, ...)
```

**Arguments**

x                    a list of class SCREE Output from [SCREE](#) function.  
plot                logical. Whether to plot the results.  
...                 Further arguments for print.

**Examples**

```
SCREE_base <- SCREE(test_models$baseline$cormat)
SCREE_base
```

---

print.SL                    *Print SL object*

---

**Description**

Print Method showing a summarized output of the [SL](#) function.

**Usage**

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

**Arguments**

x                    list. An object of class SL to be printed  
...                 Further arguments for print.

**Examples**

```
EFA_mod <- EFA(test_models$baseline$cormat, N = 500, n_factors = 3,
               type = "EFAtools", method = "PAF", rotation = "promax")
SL(EFA_mod, type = "EFAtools", method = "PAF")
```

---

```
print.SLLOADINGS      Print SLLOADINGS object
```

---

### Description

Print SLLOADINGS object

### Usage

```
## S3 method for class 'SLLOADINGS'
print(x, cutoff = 0.2, digits = 3, ...)
```

### Arguments

x	class SLLOADINGS matrix.
cutoff	numeric. The number above which to print loadings in bold (default is .2).
digits	numeric. Passed to <a href="#">round</a> . Number of digits to round the loadings to (default is 3).
...	additional arguments passed to print

### Examples

```
EFA_mod <- EFA(test_models$baseline$cormat, N = 500, n_factors = 3,
               type = "EFAtools", method = "PAF", rotation = "promax")
SL(EFA_mod, type = "EFAtools", method = "PAF")
```

---

```
print.SMT              Print SMT object
```

---

### Description

Print SMT object

### Usage

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

### Arguments

x	list of class SMT (output from the <a href="#">SMT</a> function)
...	additional arguments passed to print

**Examples**

```
SMT_base <- SMT(test_models$baseline$cormat, N = 500)
SMT_base
```

---

PROCRUSTES

*Rotate a loading matrix to a target using Procrustes alignment*


---

**Description**

‘PROCRUSTES()’ aligns one loading matrix to a target loading matrix with the same dimensions. It is used internally by ‘EFA\_POOLED()’, but can also be used directly when factor columns must be brought into a common orientation before averaging or comparing solutions.

**Usage**

```
PROCRUSTES(
  A,
  Target,
  rotation = c("orthogonal", "oblique"),
  S = NULL,
  T_init = NULL,
  oblique_eps = 1e-05,
  oblique_maxit = 1000,
  oblique_max_line_search = 10,
  oblique_step0 = 1,
  oblique_normalize = FALSE,
  oblique_random_starts = 0,
  oblique_screen_keep = 2,
  oblique_triage_maxit = 25,
  oblique_triage_improve_tol = 0
)
```

**Arguments**

A	Numeric loading matrix to be aligned.
Target	Numeric target matrix with the same dimensions as ‘A’.
rotation	Character string, either “orthogonal” or “oblique”.
S	Optional ‘k x k’ cross-product matrix ‘crossprod(A)’. Supplying this is useful when the same ‘A’ is rotated repeatedly. ‘S’ is used only when ‘oblique_normalize = FALSE’; if Kaiser normalization is requested, the cross-product must be re-computed on the normalized matrix.
T_init	Optional ‘k x k’ nonsingular starting transformation matrix for the oblique solver. Its columns are normalized internally.
oblique_eps	Positive convergence tolerance for the projected-gradient norm in the oblique solver.

<code>oblique_maxit</code>	Non-negative integer. Maximum number of projected-gradient updates in the full oblique solver.
<code>oblique_max_line_search</code>	Non-negative integer. Maximum number of step-halving attempts after the initial line-search step.
<code>oblique_step0</code>	Positive initial step size for the oblique solver.
<code>oblique_normalize</code>	Logical; if 'TRUE', apply Kaiser row normalization in the oblique solver and back-transform the aligned loadings afterwards.
<code>oblique_random_starts</code>	Non-negative integer. Number of additional random starts used by the oblique solver.
<code>oblique_screen_keep</code>	Non-negative integer. Number of random starts retained after cheap objective screening and sent to triage optimization.
<code>oblique_triage_maxit</code>	Non-negative integer. Number of short optimization iterations used in the triage stage.
<code>oblique_triage_improve_tol</code>	Non-negative scalar. Relative improvement required for a triaged start to be promoted to full optimization.

### Details

For 'rotation = "orthogonal"', the function solves the closed-form orthogonal Procrustes problem

$$\min_T \frac{1}{2} \|AT - B\|_F^2 \quad \text{subject to} \quad T'T = I,$$

where 'A' is the loading matrix and 'B' is 'Target'.

For 'rotation = "oblique"', the function calls the compiled '`.oblique_procrustes()`' optimizer. The oblique convention is the same as in '`GPArotation::targetQ()`':

$$L = AT^{-T}, \quad \Phi = T'T, \quad \text{diag}(\Phi) = 1.$$

Random starts are only used for oblique alignment. For one-factor models, oblique and orthogonal alignment are equivalent, so the function uses the stable one-factor orthogonal solution instead of calling the oblique optimizer.

### Value

A list containing aligned 'loadings', transformation matrix 'T', factor intercorrelation matrix 'Phi', target criterion 'value', convergence diagnostics, line-search diagnostics, and multi-start summaries. Row and column names are preserved where possible.

---

residuals.EFA	<i>Residuals function for EFA objects</i>
---------------	---

---

**Description**

Residuals function for EFA objects

**Usage**

```
## S3 method for class 'EFA'
residuals(object, print = TRUE, digits = 3, ...)
```

**Arguments**

object	a list of class EFA. Output from <a href="#">EFA</a> or <a href="#">EFA_POOLED</a> .
print	logical. Whether to print residuals. If FALSE, they are just returned.
digits	numeric. The number of digits to round printed residuals.
...	Further arguments.

---

RiskDimensions	<i>RiskDimensions</i>
----------------	-----------------------

---

**Description**

A list containing the bivariate correlations (cormat) of the 9 dimensions on which participants in Fischhoff et al. (1978) rated different activities and technologies as well as the sample size (N). This was then analyzed together with ratings of the risks and benefits of these activities and technologies.

**Usage**

```
RiskDimensions
```

**Format**

An object of class list of length 2.

**Source**

Fischhoff, B, Slovic, P, Lichtenstein, S, Read, S, and Combs, B. (1978). How safe is safe enough? A psychometric study of attitudes towards technological risks and benefits. *Policy Sciences*, 9, 127-152. doi: 10.1007/BF00143739

SCREE

*Scree Plot***Description**

The scree plot was originally introduced by Cattell (1966) to perform the scree test. In a scree plot, the eigenvalues of the factors / components are plotted against the index of the factors / components, ordered from 1 to N factors components, hence from largest to smallest eigenvalue. According to the scree test, the number of factors / components to retain is the number of factors / components to the left of the "elbow" (where the curve starts to level off) in the scree plot.

**Usage**

```
SCREE(
  x,
  eigen_type = c("PCA", "SMC", "EFA"),
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
         "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall"),
  n_factors = 1,
  ...
)
```

**Arguments**

<code>x</code>	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations.
<code>eigen_type</code>	character. On what the eigenvalues should be found. Can be either "PCA", "SMC", or "EFA", or some combination of them. If using "PCA", the diagonal values of the correlation matrices are left to be 1. If using "SMC", the diagonal of the correlation matrices is replaced by the squared multiple correlations (SMCs) of the indicators. If using "EFA", eigenvalues are found on the correlation matrices with the final communalities of an exploratory factor analysis solution (default is principal axis factoring extracting 1 factor) as diagonal.
<code>use</code>	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
<code>cor_method</code>	character. Passed to <code>stats::cor</code> . Default is "pearson".
<code>n_factors</code>	numeric. Number of factors to extract if "EFA" is included in <code>eigen_type</code> . Default is 1.
<code>...</code>	Additional arguments passed to <code>EFA</code> . For example, to change the extraction method (PAF is default).

**Details**

As the scree test requires visual examination, the test has been especially criticized for its subjectivity and with this low inter-rater reliability. Moreover, a scree plot can be ambiguous if there are

either no clear "elbow" or multiple "elbows", making it difficult to judge just where the eigenvalues do level off. Finally, the scree test has also been found to be less accurate than other factor retention criteria. For all these reasons, the scree test has been recommended against, at least for exclusive use as a factor retention criterion (Zwick & Velicer, 1986)

The SCREE function can also be called together with other factor retention criteria in the [N\\_FACTORS](#) function.

## Value

A list of class SCREE containing

<code>eigen_PCA</code>	A vector containing the eigenvalues found with PCA.
<code>eigen_SMC</code>	A vector containing the eigenvalues found with SMCs.
<code>eigen_EFA</code>	A vector containing the eigenvalues found with EFA.
<code>settings</code>	A list of the settings used.

## Source

Cattell, R. B. (1966). The scree test for the number of factors. *Multivariate Behavioral Research*, 1(2), 245–276. [https://doi.org/10.1207/s15327906mbr0102\\_10](https://doi.org/10.1207/s15327906mbr0102_10)

Zwick, W. R., & Velicer, W. F. (1986). Comparison of five rules for determining the number of components to retain. *Psychological Bulletin*, 99, 432–442. <http://dx.doi.org/10.1037/0033-2909.99.3.432>

## See Also

Other factor retention criteria: [CD](#), [EKC](#), [HULL](#), [PARALLEL](#), [SMT](#)

[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

## Examples

```
SCREE(test_models$baseline$cormat, eigen_type = c("PCA", "SMC"))
```

---

 SL

---

*Schmid-Leiman Transformation*


---

## Description

This function implements the Schmid-Leiman (SL) transformation (Schmid & Leiman, 1957). It takes the pattern coefficients and factor intercorrelations from an oblique factor solution as input and can reproduce the results from `psych::schmid` and from the SPSS implementation from Wolff & Preising (2005). Other arguments from `EFA` can be used to control the procedure to find the second-order loadings more flexibly. The function can also be used on a second-order confirmatory factor analysis (CFA) solution from `lavaan`.

**Usage**

```
SL(
  x,
  Phi = NULL,
  type = c("EFAtools", "psych", "SPSS", "none"),
  method = c("PAF", "ML", "ULS"),
  g_name = "g",
  ...
)
```

**Arguments**

x	object of class <a href="#">EFA</a> , class <code>psych::fa</code> , class <code>lavaan</code> or matrix. If class <a href="#">EFA</a> or class <code>psych::fa</code> , pattern coefficients and factor intercorrelations are taken from this object. If class <code>lavaan</code> , it must be a second-order CFA solution. In this case first-order and second-order factor loadings are taken from this object and the <code>g_name</code> argument has to be specified. <code>x</code> can also be a pattern matrix from an oblique factor solution (see <code>Phi</code> ) or a matrix of first-order factor loadings from a higher-order confirmatory factor analysis (see <a href="#">L2</a> ).
Phi	matrix. A matrix of factor intercorrelations from an oblique factor solution. Only needs to be specified if a pattern matrix is entered directly into <code>x</code> .
type	character. One of "EFAtools" (default), "psych", "SPSS", or "none". This is used to control the procedure of the second-order factor analysis. See <a href="#">EFA</a> for details.
method	character. One of "PAF", "ML", or "ULS" to use principal axis factoring, maximum likelihood, or unweighted least squares (also called minres), respectively, used in <a href="#">EFA</a> to find the second-order loadings.
g_name	character. The name of the general factor. This needs only be specified if <code>x</code> is a <code>lavaan</code> second-order solution. Default is "g".
...	Arguments to be passed to <a href="#">EFA</a> .

**Details**

The SL transformation (also called SL orthogonalization) is a procedure with which an oblique factor solution is transformed into a hierarchical, orthogonalized solution. As a first step, the factor intercorrelations are again factor analyzed to find second-order factor loadings. If there is only one higher-order factor, this step of the procedure stops there, resulting in a second-order factor structure. The first-order factor and the second-order factor are then orthogonalized, resulting in an orthogonalized factor solution with proportionality constraints. The procedure thus makes a suggested hierarchical data structure based on factor intercorrelations explicit. One major advantage of SL transformation is that it enables variance partitioning between higher-order and first-order factors, including the calculation of McDonald's omegas (see [OMEGA](#)).

**Value**

A list of class SL containing the following

<code>orig_R</code>	Original correlation matrix.
---------------------	------------------------------



```
SL_lav <- SL(fit, g_name = "g")
```

---

SMT

*Sequential Chi Square Model Tests, RMSEA lower bound, and AIC*


---

### Description

Sequential Chi Square Model Tests (SMT) are a factor retention method where multiple EFAs with increasing numbers of factors are fitted and the number of factors for which the Chi Square value first becomes non-significant is taken as the suggested number of factors. Preacher, Zhang, Kim, & Mels (2013) suggested a similar approach with the lower bound of the 90% confidence interval of the Root Mean Square Error of Approximation (RMSEA; Browne & Cudeck, 1992; Steiger & Lind, 1980), and with the Akaike Information Criterion (AIC). For the RMSEA, the number of factors for which this lower bound first falls below .05 is the suggested number of factors to retain. For the AIC, it is the number of factors where the AIC is lowest.

### Usage

```
SMT(
  x,
  N = NA,
  use = c("pairwise.complete.obs", "all.obs", "complete.obs", "everything",
         "na.or.complete"),
  cor_method = c("pearson", "spearman", "kendall")
)
```

### Arguments

x	data.frame or matrix. Dataframe or matrix of raw data or matrix with correlations.
N	numeric. The number of observations. Needs only be specified if a correlation matrix is used.
use	character. Passed to <code>stats::cor</code> if raw data is given as input. Default is "pairwise.complete.obs".
cor_method	character. Passed to <code>stats::cor</code> . Default is "pearson".

### Details

As a first step in the procedure, a maximum number of factors to extract is determined for which the model is still over-identified ( $df > 0$ ).

Then, EFAs with increasing numbers of factors from 1 to the maximum number are fitted with maximum likelihood estimation.

For the SMT, first the significance of the chi square value for a model with 0 factors is determined. If this value is not significant, 0 factors are suggested to retain. If it is significant, a model with 1 factor is estimated and the significance of its chi square value is determined, and so on, until a non-significant result is obtained. The suggested number of factors is the number of factors for the model where the chi square value first becomes non-significant.

Regarding the RMSEA, the suggested number of factors is the number of factors for the model where the lower bound of the 90% confidence interval of the RMSEA first falls below the .05 threshold.

Regarding the AIC, the suggested number of factors is the number of factors for the model with the lowest AIC.

In comparison with other prominent factor retention criteria, SMT performed well at determining the number of factors to extract in EFA (Auerswald & Moshagen, 2019). The RMSEA lower bound also performed well at determining the true number of factors, while the AIC performed well at determining the most generalizable model (Preacher, Zhang, Kim, & Mels, 2013).

The SMT function can also be called together with other factor retention criteria in the `N_FACTORS` function.

### Value

A list of class SMT containing

<code>nfac_chi</code>	The number of factors to retain according to the significance of the chi square value.
<code>nfac_RMSEA</code>	The number of factors to retain according to the RMSEA lower bound
<code>nfac_AIC</code>	The number of factors to retain according to the AIC
<code>p_null</code>	The p-value for the null model (zero factors)
<code>ps_chi</code>	The p-values for EFA models with increasing numbers of factors, starting with 1 factor
<code>RMSEA_LB_null</code>	The lower bounds of the 90% confidence interval for the RMSEA for the null model (zero factors).
<code>RMSEA_LBs</code>	The lower bounds of the 90% confidence interval for the RMSEA for EFA models with increasing numbers of factors, starting with 1 factor
<code>AIC_null</code>	The AICs for the null model (zero factors)
<code>AICs</code>	The AICs for EFA models with increasing numbers of factors, starting with 1 factor

### Source

Auerswald, M., & Moshagen, M. (2019). How to determine the number of factors to retain in exploratory factor analysis: A comparison of extraction methods under realistic conditions. *Psychological Methods*, 24(4), 468–491. <https://doi.org/10.1037/met0000200>

Browne, M.W., & Cudeck, R. (1992). Alternative ways of assessing model fit. *Sociological Methods and Research*, 21, 230–258.

Preacher, K. J., Zhang G., Kim, C., & Mels, G. (2013). Choosing the Optimal Number of Factors in Exploratory Factor Analysis: A Model Selection Perspective, *Multivariate Behavioral Research*, 48(1), 28-56, doi:10.108/00273171.2012.710386

Steiger, J. H., & Lind, J. C. (1980, May). Statistically based tests for the number of common factors. Paper presented at the annual meeting of the Psychometric Society, Iowa City, IA.

### See Also

Other factor retention criteria: [CD](#), [EKC](#), [HULL](#), [KGC](#), [PARALLEL](#)  
[N\\_FACTORS](#) as a wrapper function for this and all the above-mentioned factor retention criteria.

### Examples

```
SMT_base <- SMT(test_models$baseline$cormat, N = 500)
SMT_base
```

---

 SPSS\_23

*Various outputs from SPSS (version 23) FACTOR*


---

### Description

Various outputs from SPSS (version 23) FACTOR for the IDS-2 (Grob & Hagemann-von Arx, 2018), the WJIV (3 to 5 and 20 to 39 years; McGrew, LaForte, & Schrank, 2014), the DOSPERT (Frey et al., 2017; Weber, Blais, & Betz, 2002), the NEO-PI-R (Costa, & McCrae, 1992), and four simulated datasets (baseline, case\_1a, case\_6b, and case\_11b, see [test\\_models](#) and [population\\_models](#)) used in Grieder and Steiner (2020).

### Usage

SPSS\_23

### Format

A list of 9 containing EFA results for each of the data sets mentioned above. Each of these nine entries is a list of 4 or 8 (see details), of the following structure:

**paf\_comm** (vector) - The final communalities obtained with the FACTOR algorithm with PAF and no rotation. For details, see Grieder and Grob (2019).

**paf\_load** (matrix) - F1 to FN = unrotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**paf\_iter** (numeric) - Number of iterations needed for the principal axis factoring to converge.

**var\_load** (matrix) - F1 to FN = varimax rotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**pro\_load** (matrix) - F1 to FN = promax rotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**pro\_phi** (matrix) - F1 to FN = intercorrelations of the promax rotated loadings.

- sl** (matrix) - g = General / second order factor of the Schmid-Leiman solution. F1 to FN = First order factors of the Schmid-Leiman solution. h2 = Communalities of the Schmid-Leiman solution. This Schmid-Leiman solution was found using the SPSS Syntax provided by Wolff and Preising (2005).
- L2** (matrix) - Second order loadings used for the Schmid-Leiman transformation. This Schmid-Leiman solution was found using the SPSS Syntax provided by Wolff and Preising (2005).

### Details

The IDS-2, the two WJIV, the DOSPERT, and the NEO-PI-R contain all the above entries, while the four simulated datasets contain only paf\_load, var\_load, pro\_load, and pro\_phi.

### Source

- Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.
- Wolff, H.G., & Preising, K. (2005). Exploring item and higher order factor structure with the Schmid-Leiman solution: Syntax codes for SPSS and SAS. *Behavior Research Methods*, 37, 48–58. doi: 10.3758/BF03206397
- Grieder, S., & Grob, A. (2019). Exploratory factor analyses of the intelligence and development scales–2: Implications for theory and practice. *Assessment*. Advance online publication. doi:10.1177/10731911198450
- Grob, A., & Hagemann-von Arx, P. (2018). *Intelligence and Development Scales–2 (IDS-2). Intelligenz- und Entwicklungsskalen für Kinder und Jugendliche. [Intelligence and Development Scales for Children and Adolescents.]*. Bern, Switzerland: Hogrefe.
- Frey, R., Pedroni, A., Mata, R., Rieskamp, J., & Hertwig, R. (2017). Risk preference shares the psychometric structure of major psychological traits. *Science Advances*, 3, e1701381.
- McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). *Technical Manual*. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.
- Schrank, F. A., McGrew, K. S., & Mather, N. (2014). *Woodcock-Johnson IV*. Rolling Meadows, IL: Riverside.
- Costa, P. T., & McCrae, R. R. (1992). *NEO PI-R professional manual*. Odessa, FL: Psychological Assessment Resources, Inc.

### Description

Various outputs from SPSS (version 27) FACTOR for the IDS-2 (Grob & Hagemann-von Arx, 2018), the WJIV (3 to 5 and 20 to 39 years; McGrew, LaForte, & Schrank, 2014), the DOSPERT (Frey et al., 2017; Weber, Blais, & Betz, 2002), the NEO-PI-R (Costa, & McCrae, 1992), and four simulated datasets (baseline, case\_1a, case\_6b, and case\_11b, see [test\\_models](#) and [population\\_models](#)) used in Grieder and Steiner (2020).

**Usage**

SPSS\_27

**Format**

A list of 9 containing EFA results for each of the data sets mentioned above. Each of these nine entries is a list of 4 or 8 (see details), of the following structure:

**paf\_comm** (vector) - The final communalities obtained with the FACTOR algorithm with PAF and no rotation. For details, see Grieder and Grob (2019).

**paf\_load** (matrix) - F1 to FN = unrotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**paf\_iter** (numeric) - Number of iterations needed for the principal axis factoring to converge.

**var\_load** (matrix) - F1 to FN = varimax rotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**pro\_load** (matrix) - F1 to FN = promax rotated factor loadings obtained with the FACTOR algorithm with PAF. Rownames are the abbreviated subtest names.

**pro\_phi** (matrix) - F1 to FN = intercorrelations of the promax rotated loadings.

**sl** (matrix) - g = General / second order factor of the Schmid-Leiman solution. F1 to FN = First order factors of the Schmid-Leiman solution. h2 = Communalities of the Schmid-Leiman solution. This Schmid-Leiman solution was found using the SPSS Syntax provided by Wolff and Preising (2005).

**L2** (matrix) - Second order loadings used for the Schmid-Leiman transformation. This Schmid-Leiman solution was found using the SPSS Syntax provided by Wolff and Preising (2005).

**Details**

The IDS-2, the two WJIV, the DOSPERT, and the NEO-PI-R contain all the above entries, while the four simulated datasets contain only paf\_load, var\_load, pro\_load, and pro\_phi.

**Source**

Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.

Wolff, H.G., & Preising, K. (2005). Exploring item and higher order factor structure with the Schmid-Leiman solution: Syntax codes for SPSS and SAS. *Behavior Research Methods*, 37, 48–58. doi: 10.3758/BF03206397

Grieder, S., & Grob, A. (2019). Exploratory factor analyses of the intelligence and development scales–2: Implications for theory and practice. *Assessment*. Advance online publication. doi:10.1177/10731911198450

Grob, A., & Hagemann-von Arx, P. (2018). *Intelligence and Development Scales–2 (IDS-2). Intelligenz- und Entwicklungsskalen für Kinder und Jugendliche. [Intelligence and Development Scales for Children and Adolescents.]*. Bern, Switzerland: Hogrefe.

Frey, R., Pedroni, A., Mata, R., Rieskamp, J., & Hertwig, R. (2017). Risk preference shares the psychometric structure of major psychological traits. *Science Advances*, 3, e1701381.

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Costa, P. T., & McCrae, R. R. (1992). NEO PI-R professional manual. Odessa, FL: Psychological Assessment Resources, Inc.

---

test\_models

*Four test models used in Grieder and Steiner (2020)*


---

### Description

Correlation matrices created from simulated data from four of the [population\\_models](#) cases, each with strong factor intercorrelations. These are used in Grieder & Steiner (2020) to compare the psych and SPSS implementations in this package with the actual implementations of the programs. For details on the cases, see [population\\_models](#).

### Usage

```
test_models
```

### Format

A list of 4 lists "baseline", "case\_1a", "case\_6b", and "case\_11b", each with the following elements.

**cormat** (matrix) - The correlation matrix of the simulated data.

**n\_factors** (numeric) - The true number of factors.

**N** (numeric) - The sample size of the generated data.

### Source

Grieder, S., & Steiner, M.D. (2020). Algorithmic Jingle Jungle: A Comparison of Implementations of Principal Axis Factoring and Promax Rotation in R and SPSS. Manuscript in Preparation.

---

UPPS\_raw

*UPPS\_raw*


---

### Description

A dataframe containing responses to the UPPS personality scale (Whiteside & Lynam, 2005) of 645 participants of Study 2 of Steiner and Frey (2020). Each column are the ratings to one of 45 items to assess urgency, premeditation, perseverance, and sensation seeking. The original data can be accessed via <https://osf.io/kxp8t/>.

**Usage**

UPPS\_raw

**Format**

An object of class `data.frame` with 645 rows and 45 columns.

**Source**

Whiteside, S. P., Lynam, D. R., Miller, J. D., & Reynolds, S. K. (2005). Validation of the UPPS impulsive behaviour scale: A four-factor model of impulsivity. *European Journal of Personality*, 19 (7), 559–574.

Steiner, M., & Frey, R. (2020). Representative design in psychological assessment: A case study using the Balloon Analogue Risk Task (BART). *PsyArXiv Preprint*. doi:10.31234/osf.io/dg4ks

---

WJIV\_ages\_14\_19

*Woodcock Johnson IV: ages 14 to 19*

---

**Description**

A list containing the bivariate correlations ( $N = 1,685$ ) of the 47 cognitive and achievement subtests from the WJ IV for 14- to 19-year-olds from the standardization sample obtained from the WJ-IV technical manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

**Usage**

WJIV\_ages\_14\_19

**Format**

A list of 2 with elements "cormat" (47 x 47 matrix of bivariate correlations) and "N" (scalar). The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.

**NUMSER** (numeric) - Number Series.

**VRBATN** (numeric) - Verbal Attention.

**LETPAT** (numeric) - Letter-Pattern Matching.

**PHNPRO** (numeric) - Phonological Processing.

**STYREC** (numeric) - Story Recall.

**VISUAL** (numeric) - Visualization.

**GENINF** (numeric) - General Information.

**CONFRM** (numeric) - Concept Formation.

**NUMREV** (numeric) - Numbers Reversed.

**NUMPAT** (numeric) - Number-Pattern Matching.  
**NWDREP** (numeric) - Nonword Repetition.  
**VAL** (numeric) - Visual-Auditory Learning.  
**PICREC** (numeric) - Picture Recognition.  
**ANLSYN** (numeric) - Analysis-Synthesis.  
**OBJNUM** (numeric) - Object-Number Sequencing.  
**PAIRCN** (numeric) - Pair Cancellation.  
**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.  
**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.  
**LWIDNT** (numeric) - Letter-Word Identification.  
**APPROB** (numeric) - Applied Problems.  
**SPELL** (numeric) - Spelling.  
**PSGCMP** (numeric) - Passage Comprehension.  
**CALC** (numeric) - Calculation.  
**WRTSMP** (numeric) - Writing Samples.  
**WRDATK** (numeric) - Word Attack.  
**ORLRDG** (numeric) - Oral Reading.  
**SNRDFL** (numeric) - Sentence Reading Fluency.  
**MTHFLU** (numeric) - Math Facts Fluency.  
**SNWRFL** (numeric) - Sentence Writing Fluency.  
**RDGREC** (numeric) - Reading Recall.  
**NUMMAT** (numeric) - Number Matrices.  
**EDIT** (numeric) - Editing.  
**WRDFLU** (numeric) - Word Reading Fluency.  
**SPLSND** (numeric) - Spelling of Sounds.  
**RDGVOC** (numeric) - Reading Vocabulary.  
**SCI** (numeric) - Science.  
**SOC** (numeric) - Social Studies.  
**HUM** (numeric) - Humanities.

**Source**

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

---

WJIV\_ages\_20\_39

*Woodcock Johnson IV: ages 20 to 39*

---

**Description**

A list containing the bivariate correlations ( $N = 1,251$ ) of the 47 cognitive and achievement subtests from the WJ IV for the 20- to 39-year-olds from the standardization sample obtained from the WJ-IV technical manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

**Usage**

WJIV\_ages\_20\_39

**Format**

A list of 2 with elements "cormat" (47 x 47 matrix of bivariate correlations) and "N" (scalar). The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.

**NUMSER** (numeric) - Number Series.

**VRBATN** (numeric) - Verbal Attention.

**LETPAT** (numeric) - Letter-Pattern Matching.

**PHNPRO** (numeric) - Phonological Processing.

**STYREC** (numeric) - Story Recall.

**VISUAL** (numeric) - Visualization.

**GENINF** (numeric) - General Information.

**CONFRM** (numeric) - Concept Formation.

**NUMREV** (numeric) - Numbers Reversed.

**NUMPAT** (numeric) - Number-Pattern Matching.

**NWDREP** (numeric) - Nonword Repetition.

**VAL** (numeric) - Visual-Auditory Learning.

**PICREC** (numeric) - Picture Recognition.

**ANLSYN** (numeric) - Analysis-Synthesis.

**OBJNUM** (numeric) - Object-Number Sequencing.

**PAIRCN** (numeric) - Pair Cancellation.

**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.  
**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.  
**LWIDNT** (numeric) - Letter-Word Identification.  
**APPROB** (numeric) - Applied Problems.  
**SPELL** (numeric) - Spelling.  
**PSGCMP** (numeric) - Passage Comprehension.  
**CALC** (numeric) - Calculation.  
**WRTSMP** (numeric) - Writing Samples.  
**WRDATK** (numeric) - Word Attack.  
**ORLRDG** (numeric) - Oral Reading.  
**SNRDFL** (numeric) - Sentence Reading Fluency.  
**MTHFLU** (numeric) - Math Facts Fluency.  
**SNWRFL** (numeric) - Sentence Writing Fluency.  
**RDGREC** (numeric) - Reading Recall.  
**NUMMAT** (numeric) - Number Matrices.  
**EDIT** (numeric) - Editing.  
**WRDFLU** (numeric) - Word Reading Fluency.  
**SPLSND** (numeric) - Spelling of Sounds.  
**RDGVOC** (numeric) - Reading Vocabulary.  
**SCI** (numeric) - Science.  
**SOC** (numeric) - Social Studies.  
**HUM** (numeric) - Humanities.

**Source**

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

---

 WJIV\_ages\_3\_5

 Woodcock Johnson IV: ages 3 to 5
 

---

### Description

A list containing the bivariate correlations ( $N = 435$ ) of the 29 cognitive and achievement subtests from the WJ IV for 3- to 5-year-olds from the standardization sample obtained from the WJ IV technical Manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

### Usage

WJIV\_ages\_3\_5

### Format

A list of 2 with elements "cormat" (29 x 29 matrix of bivariate correlations) and "N" (scalar). The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.  
**VRBATN** (numeric) - Verbal Attention.  
**LETPAT** (numeric) - Phonological Processing.  
**STYREC** (numeric) - Story Recall.  
**VISUAL** (numeric) - Visualization.  
**GENINF** (numeric) - General Information.  
**CONFRM** (numeric) - Concept Formation.  
**NUMREV** (numeric) - Numbers Reversed.  
**NUMPAT** (numeric) - Number-Pattern Matching.  
**NWDREP** (numeric) - Nonword Repetition.  
**VAL** (numeric) - Visual-Auditory Learning.  
**PICREC** (numeric) - Picture Recognition.  
**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.  
**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.

**LWIDNT** (numeric) - Letter-Word Identification.

**APPROB** (numeric) - Applied Problems.

**SPELL** (numeric) - Spelling.

**PSGCMP** (numeric) - Passage Comprehension.

**SCI** (numeric) - Science.

**SOC** (numeric) - Social Studies.

**HUM** (numeric) - Humanities.

### Source

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

---

WJIV\_ages\_40\_90

*Woodcock Johnson IV: ages 40 to 90 plus*

---

### Description

A list containing the bivariate correlations ( $N = 1,146$ ) of the 47 cognitive and achievement subtests from the WJ IV for 40- to 90+-year-olds from the standardization sample obtained from the WJ-IV technical manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

### Usage

WJIV\_ages\_40\_90

### Format

A list of 2 with elements "cormat" (47 x 47 matrix of bivariate correlations) and "N". The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.

**NUMSER** (numeric) - Number Series.

**VRBATN** (numeric) - Verbal Attention.

**LETPAT** (numeric) - Letter-Pattern Matching.

**PHNPRO** (numeric) - Phonological Processing.

**STYREC** (numeric) - Story Recall.

**VISUAL** (numeric) - Visualization.

**GENINF** (numeric) - General Information.

**CONFRM** (numeric) - Concept Formation.

**NUMREV** (numeric) - Numbers Reversed.  
**NUMPAT** (numeric) - Number-Pattern Matching.  
**NWDREP** (numeric) - Nonword Repetition.  
**VAL** (numeric) - Visual-Auditory Learning.  
**PICREC** (numeric) - Picture Recognition.  
**ANLSYN** (numeric) - Analysis-Synthesis.  
**OBJNUM** (numeric) - Object-Number Sequencing.  
**PAIRCN** (numeric) - Pair Cancellation.  
**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.  
**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.  
**LWIDNT** (numeric) - Letter-Word Identification.  
**APPROB** (numeric) - Applied Problems.  
**SPELL** (numeric) - Spelling.  
**PSGCMP** (numeric) - Passage Comprehension.  
**CALC** (numeric) - Calculation.  
**WRTSMP** (numeric) - Writing Samples.  
**WRDATK** (numeric) - Word Attack.  
**ORLRDG** (numeric) - Oral Reading.  
**SNRDFL** (numeric) - Sentence Reading Fluency.  
**MTHFLU** (numeric) - Math Facts Fluency.  
**SNWRFL** (numeric) - Sentence Writing Fluency.  
**RDGREC** (numeric) - Reading Recall.  
**NUMMAT** (numeric) - Number Matrices.  
**EDIT** (numeric) - Editing.  
**WRDFLU** (numeric) - Word Reading Fluency.  
**SPLSND** (numeric) - Spelling of Sounds.  
**RDGVOC** (numeric) - Reading Vocabulary.  
**SCI** (numeric) - Science.  
**SOC** (numeric) - Social Studies.  
**HUM** (numeric) - Humanities.

**Source**

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

---

WJIV\_ages\_6\_8

*Woodcock Johnson IV: ages 6 to 8*


---

**Description**

A list containing the bivariate correlations ( $N = 825$ ) of the 47 cognitive and achievement subtests from the WJ IV for 6- to 8-year-olds from the standardization sample obtained from the WJ-IV technical manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

**Usage**

WJIV\_ages\_6\_8

**Format**

A list of 2 with elements "cormat" (47 x 47 matrix of bivariate correlations) and "N". The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.

**NUMSER** (numeric) - Number Series.

**VRBATN** (numeric) - Verbal Attention.

**LETPAT** (numeric) - Letter-Pattern Matching.

**PHNPRO** (numeric) - Phonological Processing.

**STYREC** (numeric) - Story Recall.

**VISUAL** (numeric) - Visualization.

**GENINF** (numeric) - General Information.

**CONFRM** (numeric) - Concept Formation.

**NUMREV** (numeric) - Numbers Reversed.

**NUMPAT** (numeric) - Number-Pattern Matching.

**NWDREP** (numeric) - Nonword Repetition.

**VAL** (numeric) - Visual-Auditory Learning.

**PICREC** (numeric) - Picture Recognition.

**ANLSYN** (numeric) - Analysis-Synthesis.

**OBJNUM** (numeric) - Object-Number Sequencing.

**PAIRCN** (numeric) - Pair Cancellation.

**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.  
**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.  
**LWIDNT** (numeric) - Letter-Word Identification.  
**APPROB** (numeric) - Applied Problems.  
**SPELL** (numeric) - Spelling.  
**PSGCMP** (numeric) - Passage Comprehension.  
**CALC** (numeric) - Calculation.  
**WRTSMP** (numeric) - Writing Samples.  
**WRDATK** (numeric) - Word Attack.  
**ORLRDG** (numeric) - Oral Reading.  
**SNRDFL** (numeric) - Sentence Reading Fluency.  
**MTHFLU** (numeric) - Math Facts Fluency.  
**SNWRFL** (numeric) - Sentence Writing Fluency.  
**RDGREC** (numeric) - Reading Recall.  
**NUMMAT** (numeric) - Number Matrices.  
**EDIT** (numeric) - Editing.  
**WRDFLU** (numeric) - Word Reading Fluency.  
**SPLSND** (numeric) - Spelling of Sounds.  
**RDGVOC** (numeric) - Reading Vocabulary.  
**SCI** (numeric) - Science.  
**SOC** (numeric) - Social Studies.  
**HUM** (numeric) - Humanities.

**Source**

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

---

WJIV\_ages\_9\_13

*Woodcock Johnson IV: ages 9 to 13*


---

### Description

A list containing the bivariate correlations ( $N = 1,572$ ) of the 47 cognitive and achievement subtests from the WJ IV for 9- to 13-year-olds from the standardization sample obtained from the WJ-IV technical manual (McGrew, LaForte, & Schrank, 2014). Tables are reproduced with permission from the publisher.

### Usage

WJIV\_ages\_9\_13

### Format

A list of 2 with elements "cormat" (47 x 47 matrix of bivariate correlations) and "N". The correlation matrix contains the following variables:

**ORLVOC** (numeric) - Oral Vocabulary.  
**NUMSER** (numeric) - Number Series.  
**VRBATN** (numeric) - Verbal Attention.  
**LETPAT** (numeric) - Letter-Pattern Matching.  
**PHNPRO** (numeric) - Phonological Processing.  
**STYREC** (numeric) - Story Recall.  
**VISUAL** (numeric) - Visualization.  
**GENINF** (numeric) - General Information.  
**CONFRM** (numeric) - Concept Formation.  
**NUMREV** (numeric) - Numbers Reversed.  
**NUMPAT** (numeric) - Number-Pattern Matching.  
**NWDREP** (numeric) - Nonword Repetition.  
**VAL** (numeric) - Visual-Auditory Learning.  
**PICREC** (numeric) - Picture Recognition.  
**ANLSYN** (numeric) - Analysis-Synthesis.  
**OBJNUM** (numeric) - Object-Number Sequencing.  
**PAIRCN** (numeric) - Pair Cancellation.  
**MEMWRD** (numeric) - Memory for Words.  
**PICVOC** (numeric) - Picture Vocabulary.  
**ORLCMP** (numeric) - Oral Comprehension.  
**SEGMNT** (numeric) - Segmentation.  
**RPCNAM** (numeric) - Rapid Picture Naming.

**SENREP** (numeric) - Sentence Repetition.  
**UNDDIR** (numeric) - Understanding Directions.  
**SNDBLN** (numeric) - Sound Blending.  
**RETFLU** (numeric) - Retrieval Fluency.  
**SNDAWR** (numeric) - Sound Awareness.  
**LWIDNT** (numeric) - Letter-Word Identification.  
**APPROB** (numeric) - Applied Problems.  
**SPELL** (numeric) - Spelling.  
**PSGCMP** (numeric) - Passage Comprehension.  
**CALC** (numeric) - Calculation.  
**WRTSMP** (numeric) - Writing Samples.  
**WRDATK** (numeric) - Word Attack.  
**ORLRDG** (numeric) - Oral Reading.  
**SNRDFL** (numeric) - Sentence Reading Fluency.  
**MTHFLU** (numeric) - Math Facts Fluency.  
**SNWRFL** (numeric) - Sentence Writing Fluency.  
**RDGREC** (numeric) - Reading Recall.  
**NUMMAT** (numeric) - Number Matrices.  
**EDIT** (numeric) - Editing.  
**WRDFLU** (numeric) - Word Reading Fluency.  
**SPLSND** (numeric) - Spelling of Sounds.  
**RDGVOC** (numeric) - Reading Vocabulary.  
**SCI** (numeric) - Science.  
**SOC** (numeric) - Social Studies.  
**HUM** (numeric) - Humanities.

**Source**

McGrew, K. S., LaForte, E. M., & Schrank, F. A. (2014). Technical Manual. Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

Schrank, F. A., McGrew, K. S., & Mather, N. (2014). Woodcock-Johnson IV. Rolling Meadows, IL: Riverside.

# Index

## \* datasets

- DOSPERT, [25](#)
- DOSPERT\_raw, [25](#)
- GRiPS\_raw, [44](#)
- IDS2\_R, [48](#)
- population\_models, [73](#)
- RiskDimensions, [93](#)
- SPSS\_23, [100](#)
- SPSS\_27, [101](#)
- test\_models, [103](#)
- UPPS\_raw, [103](#)
- WJIV\_ages\_14\_19, [104](#)
- WJIV\_ages\_20\_39, [106](#)
- WJIV\_ages\_3\_5, [108](#)
- WJIV\_ages\_40\_90, [109](#)
- WJIV\_ages\_6\_8, [111](#)
- WJIV\_ages\_9\_13, [113](#)
- .average\_matrices, [4](#)
- .calc\_cis, [4](#)
- .change\_class, [6](#)
- .compute\_vars, [6](#)
- .consensus\_loss, [7](#)
- .consensus\_target\_procrustes\_single, [7](#)
- .extract\_list\_object, [9](#)
- .factor\_corres, [10](#)
- .hyperplane\_count, [10](#)
- .nest\_sym, [11](#)
- .numformat, [11](#)
- .oblique\_procrustes, [12](#)
- .orthogonal\_procrustes, [13](#)
- .paf\_iter, [14](#)
- .parallel\_sim, [15](#)
- .stat\_over\_list, [15](#)
- .tucker\_congruence, [16](#)
  
- abbreviate, [85](#)
  
- BARTLETT, [16](#), [52](#), [53](#), [59](#), [60](#), [75](#)
- base::mean, [34](#)
  
- CD, [18](#), [42](#), [48](#), [51](#), [58](#), [60](#), [69](#), [76](#), [95](#), [100](#)
- COMPARE, [20](#), [76](#)
- CONSENSUS\_PROCRUSTES, [22](#)
- cor, [54](#)
- cor.smooth, [54](#)
  
- DOSPERT, [25](#)
- DOSPERT\_raw, [25](#)
  
- EFA, [5](#), [6](#), [9](#), [16](#), [26](#), [32–35](#), [38](#), [39](#), [43](#), [46](#), [47](#),  
[50](#), [56](#), [58](#), [59](#), [67](#), [68](#), [77](#), [93–96](#)
- EFA\_AVERAGE, [32](#), [70](#), [81](#)
- EFA\_POOLED, [4](#), [5](#), [9](#), [15](#), [16](#), [38](#), [93](#)
- EKC, [20](#), [40](#), [48](#), [51](#), [59](#), [60](#), [69](#), [70](#), [82](#), [95](#), [100](#)
  
- FACTOR\_SCORES, [43](#)
- format.EFA (print.EFA), [77](#)
- format.EFA\_POOLED (print.EFA), [77](#)
- format.LOADINGS (print.LOADINGS), [84](#)
- future::plan, [47](#)
- future\_lapply, [66](#)
  
- GPArotation::GPFoblq, [28](#), [35](#)
- GRiPS\_raw, [44](#)
  
- HULL, [20](#), [42](#), [45](#), [50](#), [51](#), [58–60](#), [69](#), [71](#), [82](#), [95](#),  
[100](#)
  
- IDS2\_R, [48](#)
  
- KGC, [20](#), [40–42](#), [48](#), [49](#), [58–60](#), [67](#), [69](#), [71](#), [83](#),  
[100](#)
- KMO, [17](#), [18](#), [52](#), [59](#), [60](#), [83](#)
  
- lavaan, [96](#)
  
- MAP, [53](#), [86](#)
  
- N\_FACTORS, [17–20](#), [42](#), [47](#), [48](#), [50–53](#), [56](#), [57](#),  
[68](#), [69](#), [87](#), [95](#), [99](#), [100](#)
- NEST, [55](#), [58–60](#), [86](#)

- OMEGA, [61](#), [87](#), [96](#)
- PARALLEL, [20](#), [41](#), [42](#), [46–48](#), [50](#), [51](#), [56](#),  
[58–60](#), [66](#), [72](#), [88](#), [95](#), [100](#)
- plot.CD, [69](#)
- plot.EFA\_AVERAGE, [70](#)
- plot.EKC, [70](#)
- plot.HULL, [71](#)
- plot.KGC, [71](#)
- plot.PARALLEL, [72](#)
- plot.SCREEN, [72](#)
- population\_models, [73](#), [100](#), [101](#), [103](#)
- print.BARTLETT, [75](#)
- print.CD, [76](#)
- print.COMPARE, [76](#)
- print.EFA, [77](#)
- print.EFA\_AVERAGE, [81](#)
- print.EFA\_POOLED (print.EFA), [77](#)
- print.EKC, [81](#)
- print.HULL, [82](#)
- print.KGC, [83](#)
- print.KMO, [83](#)
- print.LOADINGS, [79](#), [80](#), [84](#)
- print.MAP, [86](#)
- print.N\_FACTORS, [87](#)
- print.NEST, [86](#)
- print.OMEGA, [87](#)
- print.PARALLEL, [88](#)
- print.SCREEN, [88](#)
- print.SL, [89](#)
- print.SLLOADINGS, [90](#)
- print.SMT, [90](#)
- PROCRUSTES, [91](#)
- psych::cortest.bartlett, [17](#)
- psych::fa, [27](#), [28](#), [34](#), [35](#), [96](#)
- psych::factor.model, [62](#), [63](#)
- psych::factor.scores, [43](#)
- psych::KMO, [52](#)
- psych::omega, [61](#), [63](#)
- psych::schmid, [61–63](#), [95](#)
- residuals.EFA, [93](#)
- RiskDimensions, [93](#)
- round, [84](#), [87](#), [90](#)
- SCREE, [58–60](#), [72](#), [89](#), [94](#)
- SL, [61–63](#), [89](#), [95](#)
- SMT, [20](#), [42](#), [48](#), [50](#), [51](#), [60](#), [69](#), [90](#), [95](#), [98](#)
- SPSS\_23, [100](#)
- SPSS\_27, [101](#)
- stats::cor, [17](#), [19](#), [28](#), [35](#), [41](#), [46](#), [50](#), [52](#), [56](#),  
[58](#), [67](#), [94](#), [98](#)
- stats::factanal, [28](#), [30](#), [35](#), [47](#)
- stats::na.omit, [19](#)
- stats::varimax, [28](#), [30](#), [34](#)
- stats:optim, [30](#), [37](#)
- test\_models, [100](#), [101](#), [103](#)
- UPPS\_raw, [103](#)
- WJIV\_ages\_14\_19, [104](#)
- WJIV\_ages\_20\_39, [106](#)
- WJIV\_ages\_3\_5, [108](#)
- WJIV\_ages\_40\_90, [109](#)
- WJIV\_ages\_6\_8, [111](#)
- WJIV\_ages\_9\_13, [113](#)