

Package ‘ackwards’

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Title Bass-Ackwards Hierarchical Structural Analysis

Version 0.2.0

Description Implements Goldberg's (2006) <[doi:10.1016/j.jrp.2006.01.001](https://doi.org/10.1016/j.jrp.2006.01.001)> bass-ackwards method and modern descendants for hierarchical structural analysis. Extracts solutions from 1 to k factors using principal component analysis (PCA), exploratory factor analysis (EFA), or exploratory structural equation modeling (ESEM) engines, then characterizes the hierarchy via between-level factor-score correlations computed via exact linear algebra (Waller, 2007, <[doi:10.1016/j.jrp.2006.08.005](https://doi.org/10.1016/j.jrp.2006.08.005)>) or materialized scores. Includes the Forbes (2023) <[doi:10.1037/met0000546](https://doi.org/10.1037/met0000546)> extension for redundancy pruning and all-levels cross-correlations.

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Description

Extracts factor/component solutions at levels 1 through k, then characterises the hierarchy by computing between-level factor-score correlations. The "hierarchy" is descriptive: edges are score correlations, not a fitted higher-order SEM.

Usage

```
ackwards(
  data,
  k_max,
  engine = "pca",
  cor = "pearson",
  fm = "minres",
  estimator = NULL,
  missing = "pairwise",
  n_obs = NULL,
  align_signs = TRUE,
  keep_scores = FALSE,
  keep_fits = FALSE,
  seed = NULL,
  pairs = "adjacent",
  cut_show = 0.3,
  correct = 0.5,
  ...
)
```

Arguments

data	A data frame or numeric matrix of observed variables (items in columns, observations in rows). Alternatively, a pre-computed correlation matrix may be supplied (a square, symmetric, numeric matrix with unit diagonal). When a correlation matrix is supplied, engine must be "pca" or "efa" (ESEM requires raw data), and the missing and cor arguments are ignored. See the <i>Correlation-matrix input</i> section below.
k_max	Maximum number of factors/components to extract. Required; use suggest_k() if uncertain. Sets the <i>depth</i> of the hierarchy: levels 1 through k_max are all extracted and retained. (Note: suggest_k()'s k_max means something related but distinct – the max number of factors/components it <i>evaluates</i> when recommending a depth, not a depth itself; see that function's docs.)
engine	Extraction engine: "pca" (default), "efa", or "esem". "esem" uses lavaan::efa() with rotation-aware SEs and per-level fit indices; recommended for the clinical/HiTOP workflow (Kim & Eaton, 2015; Forbush et al., 2024). Requires lavaan >= 0.6-13.

cor	Correlation basis: "pearson" (default), "spearman", or "polychoric". For PCA/EFA, "polychoric" computes a polychoric correlation matrix via <code>psych::polychoric()</code> (requires <code>psych</code>). For ESEM, it triggers WLSMV estimation via <code>lavaan</code> . A cli warning is emitted when ordinal-looking columns are detected and <code>cor</code> is not "polychoric".
fm	Factor extraction method passed to <code>psych::fa()</code> ; only used when <code>engine = "efa"</code> . One of "minres" (default, robust OLS), "ml" (maximum likelihood, gives chi-square fit but converges less reliably at deep levels), or "pa" (principal axis). Ignored for <code>engine = "pca"</code> .
estimator	Estimation method for the ESEM engine. NULL (default) auto-selects: "WLSMV" when <code>cor = "polychoric"</code> , "ML" otherwise. Pass explicitly to override: "ULSMV" (unweighted WLS), "MLR" (robust ML). <code>cor = "polychoric"</code> with <code>estimator = "ML"/"MLR"</code> errors (<code>lavaan</code> itself does not support ML/MLR on ordered indicators); "WLSMV"/"ULSMV" with a continuous <code>cor</code> is allowed (a valid, if atypical, continuous WLS/ADF estimator). Ignored for PCA and EFA engines. The effective value (after auto-selection) is recorded in <code>x\$meta\$estimator</code> (NA for PCA/EFA).
missing	How to handle missing item responses. One of: "pairwise" (default) – use all available observations pairwise. For PCA/EFA this feeds <code>stats::cor(use = "pairwise.complete.obs")</code>. For ESEM with WLSMV/ULSMV (ordinal), <code>lavaan</code> uses <code>available.cases</code>, which computes polychoric thresholds and correlations from all rows that contribute to each pair – MCAR-valid and uses the full N. For ESEM with ML/MLR (continuous), <code>lavaan</code> uses listwise deletion internally while edges are computed from a pairwise correlation matrix; this minor inconsistency is documented in <code>\$meta</code>. A warning is emitted when incomplete rows are detected. "listwise" – only complete rows are used. Reduces data to <code>stats::complete.cases()</code> before fitting, so the correlation matrix, the engine fit, and the edges are all consistent. <code>n_obs</code> in the result reflects the reduced N. "fiml" – Full Information Maximum Likelihood. For <code>engine = "esem"</code> (with <code>estimator = "ML"/"MLR"</code>), passes <code>missing = "fiml"</code> to <code>lavaan::efa()</code> and derives edge correlations from <code>lavaan</code>'s FIML-estimated saturated model. For <code>engine = "pca"/"efa"</code> (M38), the correlation matrix is estimated via <code>psych::corFiml()</code> and fed to the usual $W'RW$ algebra; this requires <code>cor = "pearson"</code> (<code>corFiml</code> estimates a multivariate-normal matrix) and the route is announced via a cli message. Errors for WLSMV/ULSMV and for a non-Pearson PCA/EFA basis. Note: FIML improves estimation under missingness but does not impute item responses; score materialisation (<code>keep_scores = TRUE</code>) still produces NA rows for incomplete observations. See <code>n_obs</code> for the fit-index sample size on the PCA/EFA path.
n_obs	Number of observations, or (on the raw-data FIML path) a string selecting which N feeds the fit indices. Correlation-matrix input: a positive integer. Required for <code>engine = "efa"</code> (<code>psych::fa()</code> needs N for chi-square / RMSEA / TLI); optional for "pca" (stored as <code>NA_integer_</code> if omitted). For PCA it is recorded in the result

metadata and feeds the N-based sampling-adequacy checks only – PCA level fit is eigenvalue-based and computes no N-dependent fit statistics.

- **Raw data:** N is normally taken from `nrow(data)` and a numeric `n_obs` is ignored (with a warning). The exception is `missing = "fiml"` with `engine = "pca"/"efa"` (M38): because `psych::corFiml()` estimates the correlation matrix from incomplete rows, `n_obs` may be `"total"` (default – every row contributing to the FIML likelihood, matching the FIML convention; Enders, 2010) or `"complete"` (complete-case N, a conservative lower bound). Point estimates (loadings, edges) do not depend on this choice; only the EFA fit indices do, and those are *approximate* under this two-step (FIML matrix into normal-theory EFA) route regardless of N (Zhang & Savalei, 2020). A string `n_obs` is accepted only on this path.

<code>align_signs</code>	Logical; sign-align factors to primary-parent lineage? Default TRUE.
<code>keep_scores</code>	Logical; store factor scores in the result? Default FALSE (recomputable via <code>augment.ackwards()</code>). When TRUE, per-observation scores are stored in <code>x\$scores</code> as a named list of <code>n x k_j</code> matrices, one per level, standardized by real score SDs (see <code>augment.ackwards()</code>).
<code>keep_fits</code>	Logical; store raw engine fit objects? Default FALSE. When TRUE, the per-level fit objects (psych or lavaan) are stored in <code>x\$fits</code> as a named list indexed by level.
<code>seed</code>	Integer seed for stochastic engines (not used by PCA but captured for reproducibility metadata). Default NULL.
<code>pairs</code>	Which level pairs to compute edges for: <code>"adjacent"</code> (default, classic Goldberg – only consecutive levels) or <code>"all"</code> (Forbes extension – every pair of levels, including skip-level correlations). <code>prune()</code> recomputes its own all-pairs edges on demand regardless of this setting, so pruning does not require <code>pairs = "all"</code> here.
<code>cut_show</code>	Edges with $ r \geq \text{cut_show}$ are flagged above_cut in <code>tidy()</code> output. Default 0.3.
<code>correct</code>	Continuity correction passed to <code>psych::polychoric()</code> on the PCA/EFA polychoric path (<code>engine = "pca"/"efa"</code> with <code>cor = "polychoric"</code>). Default 0.5 (psych's own default), which adds that value to zero cells before estimating thresholds. Set <code>correct = 0</code> if <code>psych::polychoric()</code> fails on your data (its error suggests exactly this) – this typically happens when an item has a near-empty response category or when items with unequal category counts produce a sparse cross-cell. Ignored on other paths: ESEM computes its own polychoric correlations inside lavaan, and the Pearson/Spearman bases do not use it.
<code>...</code>	Reserved for future arguments.

Value

An object of class `"ackwards"`. See `print.ackwards()`, `tidy.ackwards()`, `glance.ackwards()`, and `augment.ackwards()` for output methods.

Defaults and why

- `engine = "pca"` – the original Goldberg (2006) method; fastest; never fails to converge; the Waller (2007) algebra is exact for components.

- `rotation = "varimax"` – varimax keeps the within-level factors mutually uncorrelated (orthogonal), so each between-level edge reflects only the cross-level relationship; an oblique rotation's correlated within-level factors would leak into the between-level edges and confound the between-level signal that is the method's core output. The closed-form $W'RW$ edge algebra is itself exact for any fixed linear scoring, orthogonal or not, so the choice is interpretive, not a numerical necessity. Matches Goldberg (2006), Kim & Eaton (2015), and Forbush et al. (2024); varimax is the only supported rotation.
- `cor = "pearson"` – no silent basis switching. If your items look ordinal (≤ 7 distinct integer values), a cli warning will suggest `cor = "polychoric"`, which is available for all three engines.
- `align_signs = TRUE` – unaligned signs make the output unreadable. Anchor: `m1f1` is oriented toward the positive manifold; each subsequent factor is flipped so its edge to its primary parent is positive.
- `keep_scores = FALSE / keep_fits = FALSE` – memory and privacy. Scores are $O(n \times \text{Sigmak})$ and often sensitive; raw engine fits can be large. Both are recomputable from the stored `r` matrix.

Performance (ESEM, large item sets)

The ESEM engine fits a separate lavaan model at every level `1..k_max`. For ordinal data (`cor = "polychoric"`, WLSMV) the costly sample statistics lavaan derives from the raw data – thresholds, the polychoric correlation matrix, and the asymptotic weight matrix – depend only on the data, not on the number of factors, so they are **computed once** at the first level and **reused** for every deeper level (identical solutions, much less work). This matters most when you have many items (hundreds), where recomputing those statistics at each level dominated the run time.

The per-level model fits are mutually independent and are dispatched through the **future** framework when **future.apply** is installed. By default the plan is sequential (no behaviour change). To run the levels in parallel, set a plan once before calling `ackwards()`:

```
future::plan(future::multisession, workers = 4) # or multicore on Unix
x <- ackwards(items, k_max = 8, engine = "esem", cor = "polychoric")
```

Parallelism pays off when the per-level fits are heavy (large `p`, several levels); for small problems the worker startup cost can outweigh it. Results are reproducible across plans when seed is supplied. PCA and EFA already compute their correlation matrix once and are unaffected.

Correlation-matrix input

When data is a pre-computed correlation matrix (square, symmetric, unit diagonal), `ackwards()` runs entirely from that matrix using the $W'RW$ algebra – no raw item responses are needed. This is useful when you have a published correlation table or a polychoric matrix computed externally.

Constraints and behaviour when a correlation matrix is supplied:

- **Engine:** only `"pca"` and `"efa"` are supported. `"esem"` requires raw data (for lavaan's own polychoric computation, WLSMV estimation, and per-level fit indices) and will error clearly.
- `n_obs:` required for `"efa"` (psych needs `N` for chi-square / RMSEA / TLI); optional for `"pca"` (stored as `NA` if omitted; used for the `N`-based sampling-adequacy checks and result metadata only – PCA computes no `N`-dependent fit statistics).

- **cor argument:** ignored – the basis is already determined by the matrix you supply. A warning is emitted if you set cor explicitly.
- **missing argument:** ignored – missingness was handled when computing the matrix. A warning is emitted if you set missing explicitly.
- **Factor scores:** keep_scores = TRUE will error; augment() and tidy(what = "scores") will also error because individual-level scores require row-level item responses.
- **\$cor field:** stored as NA_character_; printed as "(user-supplied matrix)".

When to trust the result

ackwards() raises diagnostics as it fits. They fall into three tiers by what they mean for whether you should trust and report the solution:

Fatal – fix before trusting. The result is undefined or rests on a broken correlation matrix:

- **A constant item** (no variance) errors – drop it (see [check_items\(\)](#)).
- **psych::polychoric() fails** – usually a near-empty response category; set correct = 0 or collapse rare categories.
- **A level fails to converge** – the hierarchy is truncated to the deepest level that did; do not interpret beyond it.
- **A near-singular correlation matrix** (smallest eigenvalue < 1e-4, recorded in meta\$near_singular / meta\$min_eigenvalue and re-surfaced by print()/summary()) means per-level fit indices and factor scores are unreliable and the loadings/edges rest on a rank-deficient matrix. (For EFA the residual-based fallback inflates TLI/RMSEA; for ESEM CFI comes back NA.) Trim redundant items, use missing = "listwise", or – on the polychoric basis – collapse sparse categories or set correct = 0.

Caution – interpret carefully. The solution exists but may be unstable:

- **A Heywood case** (communality > 1 / negative uniqueness) at a level – check that level's loadings make substantive sense; consider fewer factors.
- **A near-constant item** (one response category dominates) can drive a meaningless factor – inspect it with [check_items\(\)](#).
- **Ordinal data on a Pearson basis** attenuates correlations – fine for a quick look or suggest_k() screening, but report the final model on cor = "polychoric".

Informational – usually fine. Proceed, just be aware: the pairwise-missing note, a merely *sparse* (rare-but-present) response category, and the ordinal-detection warning when you did intend Pearson.

References

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See Also

`print.ackwards()`, `tidy.ackwards()`, `glance.ackwards()`, `prune()` (Forbes-extension redundancy/artifact flagging, piped off the result of this function)

Examples

```
# sim16 is continuous with a known 1 -> 2 -> 4 hierarchy, so the default
# pearson basis is appropriate. For ordinal items (e.g. bfi25), fit on the
# polychoric basis instead -- see `cor = "polychoric"` and the ordinal
# vignette.
x <- ackwards(sim16, k_max = 4)
print(x)
tidy(x)
glance(x)

# Correlation-matrix input (PCA engine; n_obs optional)
R <- cor(sim16)
x_R <- ackwards(R, k_max = 4)
print(x_R)
```

augment.ackwards

Augment data with factor scores from an ackwards object

Description

Appends per-observation factor scores for every level to a data frame. Score columns are named `.m{k}f{j}` (e.g., `.m1f1`, `.m2f1`, `.m2f2`), matching the factor labels used throughout the object.

Usage

```
## S3 method for class 'ackwards'
augment(
  x,
  data = NULL,
  append = TRUE,
  id_cols = NULL,
  scaling = c("fit", "sample"),
  ...
)
```

Arguments

x	An ackwards object.
data	A data frame or numeric matrix with the same variables (columns) used to fit x. When NULL (default), uses pre-stored scores if available (requires keep_scores = TRUE at fit time).
append	Logical. When TRUE (default) the score columns are appended to data (or to a .obs index when data is NULL). When FALSE only the score columns are returned (plus any id_cols).
id_cols	Optional character vector naming columns of data to carry through alongside the scores when append = FALSE (for example a subject identifier, so scores can be rejoined after filtering). Ignored – and an error – when append = TRUE (all columns are already kept) or when data is NULL (there are no source columns to carry). NULL (default) returns the bare score columns.
scaling	Which item means/SDs standardize data before the weights are applied. "fit" (default) uses the fit-time moments stored in the object – the correct choice for scoring new observations (e.g. a cross-validation test split) or subsets on the training metric. "sample" standardizes by the supplied data's own moments (the only option for objects fit from a correlation matrix, which carry no raw-data moments). Only used when data is supplied; passing it without data is an error (stored scores are returned exactly as computed at fit time).
...	Ignored.

Details

Score computation. Scores are $S = Z W / \sqrt{\text{score_var}}$, where Z is the item z-scores, W is the per-level weight matrix stored in the object, and $\sqrt{\text{score_var}}$ standardizes by the real score standard deviations (Invariant 1: never assume unit variance). For PCA the method is "components"; for EFA/ESEM it is "tenBerge". The scaling argument controls which means/SDs build Z: by default the **fit-time** moments stored in the object, so any data you score — the training data, a subset of it, or entirely new observations — lands on the same metric the model was estimated in.

Scoring new observations (cross-validation). Because scoring only needs the stored weight matrices and the fit-time moments, you can fit `ackwards()` on a training split and score a held-out test split *without retraining*: `augment(x, data = test_set)` (or, equivalently, `predict.ackwards()`). Under the default `scaling = "fit"` the test observations are standardized by the *training* means/SDs,

which is what "applying the trained model" means: a test observation's score does not depend on which other observations happen to share its split, and train and test scores are directly comparable. `scaling = "sample"` instead re-standardizes by the supplied data's own moments — a deliberate choice when scoring a sample from a different population in its own metric, and the only option for objects fit from a correlation matrix (which carry no raw-data moments). For non-Pearson bases (polychoric, Spearman) the usual caveat applies either way: the weights derive from the non-Pearson R while Z is a linear standardization, so empirical score SDs are close to but not exactly 1 (a one-time warning says so); train/test comparability under `scaling = "fit"` is unaffected. For objects fit with `missing = "fiml"` (PCA/EFA), the stored moments are the observed (`na.rm`) means/SDs of the training items — the correlation matrix was FIML-estimated, but scoring operates on observed responses, so the observed moments are the consistent frame; incomplete rows still score NA (scoring does not impute).

Missing data. Score projection applies weights row-wise and propagates NAs listwise: any observation with at least one missing item variable will produce NA scores at every level. This differs from fitting, which uses pairwise-complete correlations. A warning is issued if NA rows are detected. Use `na.omit(data)` before scoring if NA rows are unwanted.

Data source. If data is supplied, scores are always recomputed from it using the stored weights — this is how to score new observations. If data is NULL and `keep_scores = TRUE` was set at fit time, the stored scores are returned. If neither is available an informative error is raised.

Scores-only output (`append = FALSE`). By default (`append = TRUE`) the scores are appended to the supplied data, following the broom convention. Set `append = FALSE` to return *only* the score columns — convenient for feeding scores straight into `cor()`, `lm()`, or a clustering call without dragging the item columns along. Because `augment()` always preserves row order and row count, `cbind(data, augment(x, data, append = FALSE))` reproduces the appended output exactly. A row that scores NA (because it is missing an item — see *Missing data* above) is still returned in place, so the positional alignment holds even with NA scores. For a rejoin that survives *filtering* the scores afterwards, name identifier columns with `id_cols` so they travel with the scores.

Value

A data frame. With `append = TRUE`: the supplied data (or a `.obs` index when data is NULL) with score columns appended. With `append = FALSE`: only the score columns, optionally prefixed by the `id_cols`. Row order and count always match the input.

See Also

`ackwards()`, `tidy.ackwards()`

Examples

```
# Score the training data on the fly (no keep_scores = TRUE needed)
x <- ackwards(sim16, k_max = 5)
scores_df <- augment(x, data = sim16)
head(scores_df[, startsWith(names(scores_df), ".m")])

# Scores-only: just the .m{k}f{j} columns, ready for cor()/lm()
scores_only <- augment(x, data = sim16, append = FALSE)
round(cor(scores_only[, c(".m5f1", ".m5f2")]), 2)
```

```

# Carry an identifier through for a safe post-filter rejoin
df <- data.frame(id = seq_len(nrow(sim16)), sim16)
scored <- augment(x, data = df, append = FALSE, id_cols = "id")
head(scored[, c("id", ".m5f1")])

# Store at fit time and augment without re-supplying data
x2 <- ackwards(sim16, k_max = 5, keep_scores = TRUE)
scores_df2 <- augment(x2)

# Cross-validation: fit on a training split, score the test split on the
# training metric (no retraining; see also predict.ackwards())
train_idx <- seq_len(500)
x_train <- ackwards(sim16[train_idx, ], k_max = 5)
test_scores <- augment(x_train, data = sim16[-train_idx, ], append = FALSE)
head(test_scores)

```

autoplot

autoplot generic

Description

Create ggplot2-based visualisations from model objects.

This generic is defined in **ackwards** so that `autoplot.ackwards()` is available without requiring `library(ggplot2)`. When **ggplot2** is also loaded its own `autoplot` generic takes over in the search path, but S3 dispatch still finds `autoplot.ackwards` correctly via either route. Defining our own generic is intentional – it avoids putting `ggplot2` in Imports while keeping the `autoplot(x)` ergonomic without a `library()` call.

Usage

```
autoplot(object, ...)
```

Arguments

<code>object</code>	An object to visualise.
<code>...</code>	Additional arguments passed to methods.

Value

A ggplot object.

autoplot.ackwards	<i>Plot a bass-ackwards diagram or per-level fit index chart</i>
-------------------	--

Description

When `what = "hierarchy"` (default), renders the layered bass-ackwards hierarchy as a `ggplot2` diagram. Factors appear as labelled boxes arranged in levels (level 1 at top, level `k` at bottom by default; set `direction = "horizontal"` for a left-to-right layout). Between-level edges below `cut_show` are hidden. Two aesthetics carry the edge information, each explained by its own legend: **sign** (positive/negative) is shown by `sign_by` (edge colour by default) and **magnitude** ($|r|$) by `magnitude_by` (line thickness by default). No aesthetic is ever mapped without a matching legend.

Usage

```
## S3 method for class 'ackwards'
autoplot(
  object,
  what = c("hierarchy", "fit"),
  sign_by = c("color", "linetype", "both", "none"),
  magnitude_by = c("linewidth", "none"),
  cut_show = NULL,
  color_pos = "#2166AC",
  color_neg = "#D6604D",
  color_edge = "black",
  colour_pos = NULL,
  colour_neg = NULL,
  colour_edge = NULL,
  node_width = 0.8,
  node_height = 0.4,
  min_sep = 1,
  order = NULL,
  show_items = FALSE,
  n_items = 5,
  item_cut = 0.3,
  show_skip = NULL,
  curvature = 0.2,
  color_pruned = "grey80",
  colour_pruned = NULL,
  show_r = FALSE,
  r_digits = 2L,
  r_label_size = 2.5,
  mono = FALSE,
  edge_linewidth = NULL,
  cut_strong = NULL,
  direction = c("vertical", "horizontal"),
  show_level_labels = TRUE,
  level_label_size = 3,
```

```

    node_labels = NULL,
    primary_only = FALSE,
    drop_pruned = FALSE,
    compress_levels = FALSE,
    show_secondary = FALSE,
    show_arrows = TRUE,
    legend = TRUE,
    ...
)

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

```

Arguments

object	An ackwards object.
what	One of "hierarchy" (default) or "fit". Controls which visualisation is produced. All other parameters are ignored when what = "fit".
sign_by	How edge sign (positive vs negative correlation) is encoded. One of "color" (default; positive = color_pos, negative = color_neg), "linetype" (positive = solid, negative = dashed), "both" (colour <i>and</i> linetype, with negative drawn as a distinct double-dash so it reads clearly in greyscale), or "none" (sign not encoded; all edges color_edge and solid). Whichever channel is used gets a "Direction" legend. Colour is the default because it reads sign pre-attentively and leaves linetype free; switch to "linetype" or "both" for greyscale or colour-blind-safe figures.
magnitude_by	How edge magnitude ($ r $) is encoded. One of "linewidth" (default; thicker = stronger, with a $ r $ legend) or "none" (constant width). A numeric edge_linewidth also forces constant width at that value.
cut_show	Edges with $ r < \text{cut_show}$ are not drawn. Defaults to the value used when the object was created (x\$meta\$cut_show, typically 0.3).
color_pos, colour_pos	Colour for positive edges when sign_by uses colour. Default "#2166AC" (blue). colour_pos is an accepted British alias.
color_neg, colour_neg	Colour for negative edges when sign_by uses colour. Default "#D6604D" (red). colour_neg is an accepted British alias.
color_edge, colour_edge	Single colour for all edges when sign_by does not use colour ("linetype" or "none"). Default "black". colour_edge is an accepted British alias.
node_width	Width of factor boxes in layout units. Either a single value applied to every box (default 0.8), or a named numeric vector keyed by factor ID (e.g. c(m5f1 = 1.6)) giving a per-box width; boxes not named fall back to the 0.8 default. Use a per-box width to fit a long manual node_labels string. Names matching no factor ID warn.
node_height	Height of factor boxes in layout units. Either a single value applied to every box (default 0.4), or a named numeric vector keyed by factor ID for a per-box height

	(unnamed boxes fall back to 0.4); useful for multi-line manual labels. Names matching no factor ID warn.
min_sep	Minimum horizontal separation between nodes; passed to <code>ba_layout()</code> . Default 1.0.
order	Optional manual left-to-right ordering of the deepest (<code>k_max</code>) level, passed to <code>ba_layout()</code> ; a character vector of that level's factor IDs (or a named list keyed by the level number) fixes the leaf order and every upper factor re-centres above its primary children. Use it to untangle a figure by hand. NULL (default) uses the automatic ordering.
show_items	When TRUE, lists the salient observed items beneath each deepest-level (<code>k_max</code>) factor box, so a publication figure shows what each most-granular factor is made of. Items are the top <code>n_items</code> by <code> loading </code> at or above <code>item_cut</code> , using the same extraction as <code>top_items()</code> (variable labels are shown when the fit carried them, else the item IDs). Listed below the boxes in a vertical layout, to their right in a horizontal one. Default FALSE.
n_items	Maximum number of items listed per deepest-level factor when <code>show_items = TRUE</code> . NULL lists every item meeting <code>item_cut</code> . Default 5.
item_cut	Absolute-loading threshold for <code>show_items</code> : only items with <code> loading >= item_cut</code> are listed. Default 0.3.
show_skip	Whether to draw skip-level (non-adjacent) edges. NULL (default) auto-detects: TRUE when the object was run with <code>pairs = "all"</code> , FALSE otherwise. Ignored when <code>drop_pruned = TRUE</code> .
curvature	Curvature of skip-level edge arcs. Passed to <code>ggplot2::geom_curve()</code> . Positive values curve right; default 0.2. Ignored when <code>drop_pruned = TRUE</code> .
color_pruned, colour_pruned	Fill colour for nodes flagged as pruned/redundant. Default "grey80". Only applied when the object carries pruning annotations (<code>x\$prune</code> is non-NULL) and <code>drop_pruned = FALSE</code> (pruned nodes are omitted entirely when <code>drop_pruned = TRUE</code>). <code>colour_pruned</code> is an accepted British alias.
show_r	Whether to label each drawn edge with its correlation coefficient. Default FALSE. When TRUE, labels are formatted in APA style (leading zero stripped, e.g. .23, -.30) and placed beside each edge using a white-background label that clears the arrowhead.
r_digits	Number of decimal places for edge labels when <code>show_r = TRUE</code> . Default 2L.
r_label_size	Font size for edge correlation labels when <code>show_r = TRUE</code> . Passed to <code>ggplot2::geom_label()</code> as <code>size</code> . Default 2.5.
mono	Monochrome convenience wrapper. When TRUE, equivalent to <code>sign_by = "linetype"</code> with black edges (it overrides <code>sign_by</code> and the colour arguments). <code>magnitude_by</code> still applies. Default FALSE.
edge_linewidth	NULL (default) uses <code>magnitude_by</code> to decide edge width. A numeric value forces every edge to that constant width (implying <code>magnitude_by = "none"</code>) and drops the <code> r </code> legend. Forbes figures use uniform thin lines (~ 0.5 – 0.6).
cut_strong	Deprecated in M35 and ignored (with a warning). Edge magnitude is now shown by <code>magnitude_by</code> (linewidth) and sign by <code>sign_by</code> ; the old strong/weak linetype split double-encoded magnitude. Retained only so existing calls do not error.

direction	Layout orientation. "vertical" (default) stacks levels top-to-bottom (level 1 at top); "horizontal" lays them out left-to-right (level 1 at left), which suits wide slides or posters. Level-axis labels move to the bottom margin under "horizontal".
show_level_labels	Whether to draw level axis labels ("1 factor", "2 factors", ...) to the left of the diagram. Default TRUE. When the object carries pruning annotations (<code>x\$prune</code> non-NULL) and <code>drop_pruned = FALSE</code> , a level whose factors are <i>all</i> pruned has its axis label rendered in italic to denote its status (matching the grey node fill); partially-pruned levels keep a plain label.
level_label_size	Font size for level axis labels. Default 3.
node_labels	A named character vector mapping factor IDs (e.g. "m5f1") to custom display strings (e.g. "General"). Unspecified factors keep any label attached with <code>set_factor_labels()</code> , falling back to the default <code>m{k}f{j}</code> ID. Entries here override a stored factor label for that node, so this argument is a per-call last word over the persistent labels. A warning is issued for names that match no factor ID in the object. Default NULL.
primary_only	When TRUE, only primary-parent edges (<code>is_primary == TRUE</code>) are drawn. Because skip-level edges are never primary, this also suppresses skip arcs. Ignored when <code>drop_pruned = TRUE</code> . Default FALSE.
drop_pruned	When TRUE, activates the Forbes (2023) pruned-view rendering path: pruned nodes are removed from the diagram entirely and each retained node is connected to its single strongest kept ancestor by a straight arrow (even across level gaps). Requires the object to carry pruning annotations (piped through <code>prune()</code>); errors if not. Overrides <code>show_skip</code> , <code>curvature</code> , and <code>primary_only</code> . Default FALSE.
compress_levels	When TRUE under <code>drop_pruned = TRUE</code> , closes vertical gaps left by pruned levels so retained levels are evenly spaced; level axis labels (d) still show the original level numbers. Ignored when <code>drop_pruned = FALSE</code> . Default FALSE.
show_secondary	When TRUE under <code>drop_pruned = TRUE</code> , also draws the between-level correlation edges the single-strongest-ancestor primary view hides: every kept cross-level factor pair with $ r \geq \text{cut_show}$ that is not already a primary edge. This includes cross-branch second parents <i>and</i> same-lineage skip arcs (a direct skip-level r is a distinct, non-transitive fact, not implied by the primary path). Secondary edges render in a channel deliberately distinct from the primary edges – dimmed (reduced opacity) and thinner, with plain line ends – while still inheriting the sign encoding (<code>sign_by</code>), so the sign colour/linetype is never conflated with the secondary channel. By construction each node's secondaries are weaker than its primary edge, so a secondary edge never appears while that node's primary is below <code>cut_show</code> . Ignored when <code>drop_pruned = FALSE</code> . Default FALSE.
show_arrows	When FALSE, edges are drawn with plain line ends instead of closed arrowheads (<code>arrow = NULL</code>). Applies to both straight and curved edge layers. Default TRUE. Forbes (2023) figures use plain line ends.
legend	When FALSE, suppresses all plot legends (<code>legend.position = "none"</code>). Useful when <code>color_pos == color_neg</code> (e.g. both "black") to remove an otherwise redundant Direction key. Default TRUE.

...	Ignored.
x	An ackwards object.

Details

When `what = "fit"`, renders a two-panel line plot of per-level fit indices (CFI/TLI in the top panel; RMSEA/SRMR in the bottom panel) with horizontal reference lines at conventional Hu & Bentler (1999) thresholds. The anchor level ($k = 1$, saturated and always fits perfectly) is excluded. Requires an EFA or ESEM engine; returns an informative empty plot for PCA (which has no model-fit indices).

Requires the **ggplot2** package.

Value

A **ggplot** object.

Saving plots

`autoplot()` returns a standard **ggplot** object, so save it with `ggplot2::ggsave()`:

```
p <- autoplot(x)
ggplot2::ggsave("hierarchy.png", p, width = 8, height = 6, dpi = 300)
```

`ggsave()` is not re-exported by **ackwards** (that would move **ggplot2** from Suggests into Imports); call it from **ggplot2** directly. For a wide slide or poster, pair it with `direction = "horizontal"`.

See Also

[ba_layout\(\)](#), [plot.ackwards\(\)](#)

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  # sim16 has a known 1 -> 2 -> 4 hierarchy (continuous; pearson basis)
  x <- ackwards(sim16, k_max = 5)
  autoplot(x)
  autoplot(x, color_pos = "steelblue")

  # Encode sign by linetype instead of colour, or by both
  autoplot(x, sign_by = "linetype")
  autoplot(x, sign_by = "both")

  # Left-to-right layout (wide slides / posters)
  autoplot(x, direction = "horizontal")

  # List the top items under each deepest-level factor
  autoplot(x, show_items = TRUE, n_items = 4)

  # Per-level fit index chart (EFA or ESEM only)
  x_efa <- ackwards(sim16, k_max = 5, engine = "efa")
  autoplot(x_efa, what = "fit")
}
```



```
# Monochrome with correlation labels (for greyscale figures)
autoplot(x, mono = TRUE, show_r = TRUE)

# Custom node labels for the 5-factor level
autoplot(x, node_labels = c(m5f1 = "Factor A", m5f2 = "Factor B"))

# Widen two boxes to fit long manual labels (per-box sizing)
autoplot(x,
  node_labels = c(m5f1 = "Conscientiousness"),
  node_width = c(m5f1 = 1.8)
)

# Primary links only -- clean hierarchy tree
autoplot(x, primary_only = TRUE)

# Manually order the deepest level to untangle the figure by hand
ids5 <- paste0("m5f", c(2, 1, 3, 5, 4))
autoplot(x, order = ids5)

# Forbes pruned view: omit redundant nodes, straight spanning arrows
xp <- backwards(sim16, k_max = 5) |> prune("redundant")
autoplot(xp, drop_pruned = TRUE)
autoplot(xp, drop_pruned = TRUE, show_r = TRUE)
autoplot(xp, drop_pruned = TRUE, compress_levels = TRUE)

# Add the secondary between-level correlations the primary view hides
# (dimmed + thinner, drawn beneath the primary edges)
autoplot(xp, drop_pruned = TRUE, show_secondary = TRUE)

# Plain line ends without arrowheads
autoplot(x, show_arrows = FALSE)

# Uniform edge width (no |r| scaling)
autoplot(x, edge_linewidth = 0.5)

# Suppress legend
autoplot(x, legend = FALSE)

# Forbes (2023) publication style: black lines, uniform width, no arrowheads
autoplot(xp,
  drop_pruned = TRUE,
  color_pos = "black", color_neg = "black",
  edge_linewidth = 0.6, show_arrows = FALSE, legend = FALSE
)
}
```

autoplot.comparability

Plot a comparability diagnostic

Description

Renders a two-panel ggplot2 diagnostic for a `comparability()` object: score comparability (r) and loading congruence (Tucker's ϕ) for every factor at every level. Grey points are individual splits; black points are the per-factor medians. Dashed and dotted reference lines mark the conventional .90 / .95 benchmarks – visual guides, not tests.

Usage

```
## S3 method for class 'comparability'
autoplot(object, ...)
```

Arguments

<code>object</code>	A comparability object.
<code>...</code>	Ignored.

Details

Requires the **ggplot2** package.

Value

A ggplot object.

See Also

`comparability()`

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  cmp <- comparability(sim16, k_max = 5, n_splits = 5, seed = 1)
  autoplot(cmp)
}
```

autoplot.suggest_k	<i>Plot a suggest_k diagnostic</i>
--------------------	------------------------------------

Description

Renders a ggplot2 diagnostic for a suggest_k object. The plot shows one panel for each criterion group that was requested: Scree/PA (if "pa_pc" or "pa_fa" were requested), MAP (if "map"), VSS (if "vss"), and CD RMSE (if "cd" and **EFAtools** was available). When four panels are shown the layout is a 2x2 grid; otherwise a single-column layout is used. The recommended k for each criterion is marked with a star-shaped point.

Usage

```
## S3 method for class 'suggest_k'
autoplot(object, ...)
```

Arguments

object	A suggest_k object.
...	Ignored.

Details

The scree panel shows both PC and FA observed eigenvalues alongside their respective random-data thresholds (for whichever PA bases were requested). PA-PC compares the blue "Observed (PC)" line to the dashed PA-PC threshold; PA-FA compares the teal "Observed (FA)" line to the dotted PA-FA threshold.

The CD panel plots the mean RMSE between observed and comparison-data eigenvalues at each k. CD uses a sequential one-sided Wilcoxon test (Ruscio & Roche, 2012): a factor is retained while adding it significantly reduces RMSE (default $\alpha = 0.30$); the starred k is the last retained factor. The curve is shown only over the levels that were actually computed; the starred k need not be the visible minimum of the plotted curve.

Requires the **ggplot2** package.

Value

A ggplot object.

See Also

[suggest_k\(\)](#)

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  sk <- suggest_k(sim16, n_iter = 5)
  autoplot(sk)
}
```

ba_layout

Compute a layered layout for a bass-ackwards diagram

Description

Returns tidy node coordinates and the edge table needed to render a bass-ackwards diagram. The layout is a layered (Sugiyama-style) barycenter algorithm in two stages:

Usage

```
ba_layout(x, min_sep = 1, order = NULL)
```

Arguments

x	An ackwards object.
min_sep	Minimum horizontal separation between adjacent nodes at the same level. Default 1.0. Increase for wider diagrams.
order	Optional manual left-to-right ordering of the deepest (k_max) level, overriding Stage 1. Supply either a character vector of the deepest level's factor IDs in the desired order, or a named list with an entry for the deepest level (keyed by the level number as a string, e.g. <code>list("5" = c("m5f2", "m5f1", ...))</code>). Fixing the leaf order propagates upward: every upper factor stays at the mean-x of its primary children, so any arrangement of the primary forest is reachable from the leaf order. Entries for non-deepest levels are ignored with a warning (an upper factor's position is derived, not free). The vector must be a permutation of the deepest level's IDs. NULL (default) uses the automatic ordering.

Details

1. **Ordering** – determines the left-to-right *order* of factors at each level. Two candidate orderings are scored and the crossing-minimising one kept: a single top-down lr-weighted barycenter sweep (the historical order), and a **primary-forest traversal** – each factor has exactly one primary parent, so the primary edges form a forest, and a depth-first, subtree-contiguous leaf order lays every subtree out as an unbroken run. In deep hierarchies (k >= 10) the traversal drives primary-tree crossings to zero (the "bent levels" a single pass leaves behind); keep-best scoring (lexicographic: primary crossings, then all crossings) means shallow layouts are never made worse.

2. **X-assignment** – assigns actual x coordinates bottom-up. The deepest level is spread evenly; every upper-level factor is placed at the simple mean x of its **primary** children: a factor with one primary child lands directly above it; a factor with two primary children lands exactly halfway between them. Falls back to lrl-weighted mean of all children for factors with no primary children. Spreading resolves any remaining overlaps.

After both stages the layout is shifted so that the single level-1 node is always at x = 0. The result is fully deterministic.

Value

A list with two data frames:

nodes	One row per factor: id, level, x, y, label. y = -level so level 1 is at the top.
edges	The tidy edge table from x\$edges\$tidy.

See Also

`autoplot.ackwards()`, `tidy.ackwards()`

Examples

```
x <- ackwards(sim16, k_max = 5)
lay <- ba_layout(x)
head(lay$nodes)
```

bfi25	<i>Big Five Inventory – 25-item IPIP example dataset</i>
-------	--

Description

A 1 000-row subset of the 25 IPIP Big Five personality-marker items from Revelle’s psych package (psych::bfi). Included so that package examples and vignettes run without reaching into psych’s namespace directly.

Usage

bfi25

Format

A data frame with 1 000 rows and 25 integer columns (Likert responses scored 1–6, with some NAs reflecting genuine missing values in the original survey). The 25 items span the Big Five personality domains:

Columns	Domain
A1–A5	Agreeableness
C1–C5	Conscientiousness

E1–E5	Extraversion
N1–N5	Neuroticism
O1–O5	Openness

Details

Derived from `psych::bfi[, 1:25]` by sampling 1 000 rows with `set.seed(42)`. Missing values are preserved as in the original data. The full dataset (`psych::bfi`) contains responses from 2 800 participants collected via the SAPA project.

Each item column carries its public-domain IPIP stem (Goldberg, 1999) as a label attribute, so `ackwards()` captures it at fit time and `top_items()` prints the wording as `code: label` (e.g. E4: Make friends easily) with no setup. These are plain attributes: base row-subsetting (e.g. `na.omit(bfi25)`, `bfi25[rows, ]`) drops them, as base R does for any non-labelled-class vector, so fit on `bfi25` **directly** – its NAs are handled by the missing argument of `ackwards()` – to keep the labels.

To regenerate this dataset, run `source("data-raw/bfi25.R")` from the package root.

Source

Revelle, W. (2026). *psych: Procedures for Psychological, Psychometric, and Personality Research*. Northwestern University, Evanston, Illinois. R package. <https://CRAN.R-project.org/package=psych>

Data collected via the SAPA (Synthetic Aperture Personality Assessment) project (<https://www.sapa-project.org/>). Items are public-domain IPIP (International Personality Item Pool) markers developed by Goldberg (1999):

Goldberg, L. R. (1999). A broad-bandwidth, public domain, personality inventory measuring the lower-level facets of several five-factor models. In I. Mervielde, I. Deary, F. De Fruyt, & F. Ostendorf (Eds.), *Personality Psychology in Europe*, Vol. 7, pp. 7–28. Tilburg University Press.

Examples

```
dim(bfi25)
head(bfi25)
attr(bfi25$E4, "label") # public-domain IPIP item stem
```

boot_edges	<i>Bootstrap confidence intervals for between-level edges</i>
------------	---

Description

Attaches nonparametric bootstrap standard errors and percentile confidence intervals to every between-level correlation (edge) of a fitted bass-ackwards hierarchy. Every edge `ackwards()` reports is a point estimate; `boot_edges()` quantifies its sampling uncertainty, which matters most where a hard threshold consumes the estimate – `prune()`'s `|r| >= redundancy_r` redundancy rule, and the Forbes (2023) practice of interpreting the strongest all-pairs edge.

Usage

```
boot_edges(x, ...)

## S3 method for class 'ackwards'
boot_edges(x, data, n_boot = 1000L, conf = 0.95, seed = NULL, ...)
```

Arguments

x	An <code>ackwards</code> object fit with <code>engine = "pca"</code> or <code>"efa"</code> on a "pearson" or "spearman" basis. ESEM objects are not supported (refitting <code>n_boot</code> lavaan hierarchies needs its own performance treatment), nor are polychoric-basis objects (estimating a polychoric matrix in every resample is slow and unstable) or objects fit from a correlation matrix (resampling needs rows).
...	Reserved for future arguments.
data	The raw item data the model was fit on. Required – the <code>ackwards</code> object deliberately does not store raw data (light core), so it must be re-supplied here. Columns are matched by name against the fit; a warning is issued if the data do not look like the fit data.
n_boot	Number of bootstrap replicates. Default 1000L; larger values (2000+) are advisable for published interval endpoints (Efron & Tibshirani, 1993). Each replicate refits the full hierarchy, so cost scales linearly.
conf	Confidence level for the percentile intervals. Default 0.95.
seed	Integer seed for reproducible resampling. NULL (default) uses the current RNG state.

Details

For each of `n_boot` replicates, `n` rows are resampled with replacement, the correlation matrix is recomputed with the same basis and missing-data routine used at fit time, and the full hierarchy is refit. Each replicate level is then **anchored to the full-sample solution** – its factors matched (greedy max-`lrl` with removal) and sign-oriented against the full-sample factors on the full-sample correlation matrix – before its edges are computed. Without anchoring, factor label switching and sign flipping across replicates would corrupt the pooled edge distributions; this is the same matching machinery `comparability()` uses.

All resample indices are drawn upfront from `seed`, so results are reproducible and identical whether replicates run serially or in parallel. Replicate fits are dispatched through **`future.apply`** when it is installed and the user has set a `future::plan()` (serial otherwise, as in `ackwards()`'s ESEM engine).

Value

`x`, invisibly modified: the `$boot` element is populated with

edges	Data frame with one row per edge (aligned with <code>tidy(x, what = "edges")</code>): <code>from</code> , <code>to</code> , <code>level_from</code> , <code>level_to</code> , <code>r</code> (the full-sample point estimate), <code>se</code> (bootstrap standard error), <code>lo</code> , <code>hi</code> (percentile interval endpoints), and <code>n_boot_ok</code> (usable replicates for that edge).
-------	--

n_boot, conf, seed

The request.

After calling `boot_edges()`, `tidy(x, what = "edges")` gains `se`, `lo`, and `hi` columns, and `print(x)/summary(x)` note the interval coverage.

What the intervals do and do not fix

Per-edge intervals make sampling uncertainty **visible**: an edge whose interval straddles `prune()`'s `redundancy_r` threshold should not be treated as decisively above or below it. They do **not** correct the selection bias of scanning many edges for the strongest one – the maximum of hundreds of correlations capitalizes on chance even when every individual interval is honest. Treat the intervals as per-edge error bars, not a familywise inference.

Failed replicates

A replicate whose hierarchy fails to converge (in full or at some levels) contributes NA to the affected edges and is dropped from their distributions – convergence is data, not an error. The usable replicate count is reported per edge in `n_boot_ok`, and a message summarises any shortfall.

References

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

Forbes, M. K. (2023). Improving hierarchical models of individual differences: An extension of Goldberg's bass-ackward method. *Psychological Methods*. doi:10.1037/met0000546

See Also

`prune()` for the thresholded rules the intervals contextualise, `comparability()` for split-half replicability of the factors themselves, `tidy.ackwards()` for the augmented edge table.

Examples

```
x <- ackwards(sim16, k_max = 3)
x <- boot_edges(x, sim16, n_boot = 100, seed = 1)
x$boot$edges
head(tidy(x)) # now carries se / lo / hi
```


Description

Real-world item sets often contain columns that break or *silently* degrade a factor analysis: an item everyone answered the same way (no variance), an item dominated by one response with a couple of stray answers, or an item with heavy missingness. On the polychoric basis these are especially costly – a near-empty response category can make `psych::polychoric()` fail outright (see the correct argument of `ackwards()`), and a near-constant item can produce a plausible-looking but meaningless factor with no warning.

`check_items()` reports these problems *before* you fit, one row per item, so you can collapse rare categories, drop degenerate items, or set `cor/correct` deliberately rather than debugging a cryptic error. It only reports; it never changes your data. `ackwards()` runs the same screen internally: it **errors** on a constant item and **warns** on a near-degenerate one, naming the offenders.

Usage

```
check_items(data, cor = c("polychoric", "pearson", "spearman"))
```

Arguments

<code>data</code>	A data frame or numeric matrix (items in columns).
<code>cor</code>	The correlation basis you plan to use: "polychoric" (default), "pearson", or "spearman". Only affects which problems are flagged – sparse response categories destabilise the polychoric basis but not the others.

Value

A data frame (class `check_items`) with one row per item and columns `item`, `n_valid`, `pct_missing`, `n_distinct`, `min_count` (smallest observed category count), `top_prop` (proportion of valid responses in the most common value), and `flag` – one of "ok", "constant", "near-constant", "sparse category", or "high missing". Print it for a grouped summary with guidance; treat it as a plain data frame for the full per-item table.

See Also

`ackwards()` and its correct argument (the polychoric failure this screens for); `factorability()`, `suggest_k()`, and `comparability()`, the other pre-analysis diagnostics.

Examples

```
# sim16 is clean continuous data -> nothing flagged
check_items(sim16, cor = "pearson")

# An item dominated by one response with a couple of stray answers is flagged
d <- sim16
d$bad <- c(rep(1L, nrow(d) - 2L), 2L, 3L)
check_items(d)
```

comparability

*Split-half factor comparability***Description**

Measures how well each factor at each level of a bass-ackwards hierarchy **replicates** across random split-halves of the sample – Everett’s (1983) factor comparability coefficients, reviving the split-half replication gate of the research program that produced the bass-ackwards method: Saucier (1997) screened factor solutions by their split-half stability, and Saucier, Georgiades, Tsaoasis, and Goldberg (2005) chose the optimal hierarchical level by requiring split-half replication above a .90 threshold. It is also the direct instrument for the overextraction caution in [suggest_k\(\)](#): non-replicable structure concentrates in the deeper levels of an overextracted hierarchy (Forbes, 2023).

Usage

```
comparability(
  data,
  k_max,
  engine = "pca",
  cor = "pearson",
  fm = "minres",
  n_splits = 10L,
  seed = NULL,
  ...
)
```

Arguments

data	A data frame or numeric matrix of observed variables (items in columns, observations in rows). Raw data only – splitting needs rows, so a correlation matrix is not accepted. Missing values are handled pairwise throughout (as in ackwards() ’s default).
k_max	Maximum number of factors/components to evaluate – normally the same value (or one or two above it) you intend to pass to ackwards() . Required.
engine	Extraction engine: "pca" (default) or "efa". "esem" is not yet supported here (fitting $2 * n_splits$ lavaan hierarchies needs its own performance treatment); for ESEM workflows, run <code>comparability()</code> with <code>engine = "efa"</code> as a structural screen.
cor	Correlation basis: "pearson" (default) or "spearman". As with suggest_k() , "polychoric" is not supported (estimating polychoric matrices in every half-sample is slow and unstable); users analysing ordinal data should screen replicability on the Pearson basis and fit the final model with <code>cor = "polychoric"</code> in ackwards() .
fm	Factor extraction method passed to psych::fa() ; only used when <code>engine = "efa"</code> . One of "minres" (default), "ml", or "pa".

<code>n_splits</code>	Number of random split-half replicates. Default 10L. The published precedents used a single split (Saucier et al., 2005); repeating the split guards against the luck of one draw and is this implementation's robustness choice. Each replicate fits $2 * k_max$ solutions, so the default costs 20 hierarchy fits; PCA and EFA are fast enough that this is typically a few seconds.
<code>seed</code>	Integer seed for reproducible splits. NULL (default) uses the current RNG state.
<code>...</code>	Reserved for future arguments.

Details

For each of `n_splits` random half-splits, solutions at every level $1..k_max$ are fit independently in each half. Each half-solution's factors are matched to the **full-sample** solution's factors (so coefficients are reported under the same `m{k}f{j}` labels you get from `ackwards()`), and the comparability coefficient for a factor is the correlation between its two matched half-solution scores, computed on the pooled correlation matrix via the same $W'RW$ algebra used for between-level edges – applying both halves' scoring weights to the full sample, exactly Everett's procedure. Tucker's congruence coefficient (ϕ) between the matched half-solution loading columns is reported alongside: comparability asks whether the two halves' *scores* agree; ϕ asks whether their *loading patterns* agree.

Value

An object of class "comparability". Print it for a per-level summary; call `autoplot()` on it for a diagnostic plot. The list contains:

<code>coefficients</code>	Data frame with one row per split x level x factor: <code>split</code> , <code>level</code> , <code>factor</code> (full-sample <code>m{k}f{j}</code> label), <code>r</code> (score comparability), <code>phi</code> (Tucker's congruence of the matched loading columns). NA when the level did not converge in one of the halves.
<code>summary</code>	Data frame with one row per level x factor: <code>level</code> , <code>factor</code> , <code>r_median</code> , <code>r_min</code> , <code>phi_median</code> , <code>phi_min</code> (across splits), and <code>n_splits_ok</code> (splits in which both halves converged).
<code>k_max</code>	Deepest level evaluated. Can be lower than the <code>k_max</code> you asked for when the full-sample fit truncated (non-convergence at deep levels); the original request is kept in <code>k_requested</code> .
<code>k_requested</code> , <code>n_splits</code> , <code>n_half</code> , <code>engine</code> , <code>cor</code> , <code>fm</code> , <code>n_obs</code> , <code>n_vars</code> , <code>seed</code>	Metadata.

Interpreting the output

Coefficients near 1 mean the factor re-emerges in independent half-samples; a factor whose comparability is low is sample-idiosyncratic and should not anchor substantive interpretation. Conventional benchmarks: **.90** is the split-half replication threshold of Goldberg's lexical research program (Saucier et al., 2005) and follows from Everett's (1983) rationale (split-half factors sharing at least 81% of their variance); **.95** is the stricter bound at which two factors are conventionally treated as interchangeable (Lorenzo-Seva & ten Berge, 2006). These are conventions, not tests, so `comparability()` reports every coefficient and flags nothing. The deepest level at which all factors replicate is a natural **hierarchy floor** for `ackwards()`'s `k_max`; see `vignette("ackwards-girard")` for the full workflow.

A level that fails to converge in a half-sample yields NA coefficients for that split (convergence is data, not an error); the number of usable splits per factor is reported in `summary$n_splits_ok` and a message summarises any shortfall.

References

- Everett, J. E. (1983). Factor comparability as a means of determining the number of factors and their rotation. *Multivariate Behavioral Research*, 18(2), 197–218. doi:[10.1207/s15327906mbr1802_5](https://doi.org/10.1207/s15327906mbr1802_5)
- Saucier, G. (1997). Effects of variable selection on the factor structure of person descriptors. *Journal of Personality and Social Psychology*, 73(6), 1296–1312. doi:[10.1037/00223514.73.6.1296](https://doi.org/10.1037/00223514.73.6.1296)
- Saucier, G., Georgiades, S., Tsaousis, I., & Goldberg, L. R. (2005). The factor structure of Greek personality adjectives. *Journal of Personality and Social Psychology*, 88(5), 856–875. doi:[10.1037/00223514.88.5.856](https://doi.org/10.1037/00223514.88.5.856)
- Lorenzo-Seva, U., & ten Berge, J. M. F. (2006). Tucker’s congruence coefficient as a meaningful index of factor similarity. *Methodology*, 2(2), 57–64. doi:[10.1027/16142241.2.2.57](https://doi.org/10.1027/16142241.2.2.57)
- Forbes, M. K. (2023). Improving hierarchical models of individual differences: An extension of Goldberg’s bass-ackward method. *Psychological Methods*. doi:[10.1037/met0000546](https://doi.org/10.1037/met0000546)

See Also

[suggest_k\(\)](#) for the plausible depth *range* (eigenstructure), [factorability\(\)](#) for sampling adequacy before you fit, [prune\(\)](#) for factors that perpetuate without differentiating (redundancy), and [ackwards\(\)](#) for the extraction itself.

Examples

```
cmp <- comparability(sim16, k_max = 5, n_splits = 5, seed = 1)
cmp
cmp$summary
```

factorability

Screen a dataset for factorability and sampling adequacy

Description

Before extracting a hierarchy, it is worth asking two prior questions: *is this correlation matrix even worth factoring*, and *is the sample large enough to trust the answer*. `factorability()` reports the standard diagnostics for both, one object you can print or pull values from:

- **KMO** – the Kaiser-Meyer-Olkin measure of sampling adequacy, overall and per variable (via `psych::KMO()`). It contrasts correlations with partial correlations: a low value means the variables share little common variance once other variables are partialled out, so a factor model has little to recover.

- **Bartlett's test of sphericity** – tests whether the correlation matrix differs from the identity (via `psych::cortest.bartlett()`). Needs N; a non-significant result says the correlations are too weak to factor.
- **Sample size** – N, the number of variables p, and the N:p ratio.
- **Ledermann bound** – the largest number of *common factors* identifiable from p variables (a hard limit for EFA/ESEM, though not for PCA).

Read these as conventions, not verdicts. Every cutoff here – Kaiser's KMO bands, the 5:1 / 10:1 N:p rules of thumb, Bartlett significance at .05 – is a widely repeated *rule of thumb*, not a settled threshold, and each is contested in the methodological literature (the required N in particular depends on communalities and factor overdetermination far more than on any fixed ratio; MacCallum et al. 1999). `factorability()` deliberately reports the numbers and their conventional bands rather than returning a pass/fail flag. `ackwards()` runs the same screen internally and warns only at the genuinely consequential extreme ($KMO < 0.5$, $N:p < 5$).

Usage

```
factorability(data, cor = c("pearson", "spearman", "polychoric"), n_obs = NULL)
```

Arguments

data	A data frame or numeric matrix of item responses, or a correlation matrix (detected automatically). KMO and Bartlett are computed on the correlation matrix in the basis you name via cor.
cor	The correlation basis to screen on: "pearson" (default), "spearman", or "polychoric". Ignored when data is already a correlation matrix. Use the same basis you plan to pass to <code>ackwards()</code> .
n_obs	Number of observations. Taken from <code>nrow(data)</code> for raw data (a supplied value is ignored with a warning). Required for the N-based diagnostics (Bartlett, N:p) when data is a correlation matrix; those are reported as NA when it is absent.

Value

An object of class `factorability` (a named list): `cor`, `n_obs`, `n_vars`, `np_ratio`, `kmo_overall`, `kmo_items` (a data frame of per-item MSA), `bartlett` (a list of `chisq/df/p_value`, or NULL when N is unknown), and `ledermann` (the bound). Print it for a banded summary; index the list for the raw values.

References

- Kaiser, H. F. (1974). An index of factorial simplicity. *Psychometrika*, 39(1), 31–36.
- MacCallum, R. C., Widaman, K. F., Zhang, S., & Hong, S. (1999). Sample size in factor analysis. *Psychological Methods*, 4(1), 84–99.

See Also

`check_items()` (per-item screening), `suggest_k()` (how many factors), and `comparability()` (split-half replicability) – the other pre-analysis diagnostics; `ackwards()`, which runs this screen internally.

Examples

```
# Continuous data, Pearson basis
factorability(sim16)

# From a correlation matrix: supply n_obs for the N-based diagnostics
R <- cor(sim16)
factorability(R, n_obs = nrow(sim16))
```

factor_labels	<i>Read the factor labels stored on an ackwards object</i>
---------------	--

Description

Read the factor labels stored on an ackwards object

Usage

```
factor_labels(x)
```

Arguments

x An ackwards object.

Value

The named character vector of factor labels (names are factor IDs), or NULL if none have been set. See [set_factor_labels\(\)](#) to attach them.

See Also

[set_factor_labels\(\)](#)

Examples

```
x <- ackwards(sim16, k_max = 4, engine = "pca")
factor_labels(x) # NULL -- none set yet
x <- set_factor_labels(x, c(m4f1 = "Alpha"))
factor_labels(x)
```

forbes2023	<i>Assessing Mental Health symptom correlation matrix (Forbes 2023 applied example)</i>
------------	---

Description

The 155 x 155 Spearman correlation matrix among 155 mental-health symptom variables that forms the applied example in Forbes (2023). It is a real, deep hierarchy: `ackwards(forbes2023, k_max = 10)` unfolds a general factor of psychopathology at the top down to 10 fine-grained components, the worked example that motivates the Forbes extension (`pairs = "all"`, `prune()`).

Usage

`forbes2023`

Format

A 155 x 155 numeric matrix of Spearman correlations: symmetric, unit diagonal, correlations in roughly 0.01–0.94. Row and column names are the 155 symptom-variable labels (e.g. Impulsivity, Blurting).

Details

Where `sim16` and `bfi25` are teaching foils, `forbes2023` is a fidelity/reproduction dataset: a large, messy, published case bundled so the package can reproduce the exact applied example analyzed in Forbes's paper.

The correlations come from the Assessing Mental Health (AMH) study – the Australian general-population sample ($N = 3,175$) of Forbes et al. (2021) – spanning symptoms of 18 DSM disorders. Being a correlation matrix, it carries no per-variable sample size; supply `n_obs = 3175` to `ackwards()` if you want EFA/ESEM fit statistics scaled to the original sample.

This matrix reproduces Forbes's published results exactly: the package regression test `test-forbes-fidelity.R` runs `ackwards()` on this exported `forbes2023` and matches her reference implementation's between-level correlations to $1.3e-14$ across all 45 level-pairs at `k_max = 10`.

To regenerate this dataset, run `source("data-raw/forbes2023.R")` from the package root (downloads the source CSV from OSF).

Source

Forbes's OSF project for the 2023 paper (file `corSpearman_AMH.csv`), <https://osf.io/pcwm8/>, redistributed here under its Creative Commons Attribution 4.0 International (CC-BY 4.0) license (see the package's `LICENSE.note`). The underlying data are from the Assessing Mental Health study (Forbes et al., 2021).

References

Forbes, M. K. (2023). Improving hierarchical models of individual differences: An extension of Goldberg's bass-ackward method. *Psychological Methods*. doi:10.1037/met0000546

Forbes, M. K., Sunderland, M., Rapee, R. M., Batterham, P. J., Caltar, A. L., Carragher, N., Ruggero, C., Zimmerman, M., Baillie, A. J., Lynch, S. J., Mewton, L., Slade, T., & Krueger, R. F. (2021). A detailed hierarchical model of psychopathology: From individual symptoms up to the general factor of psychopathology. *Clinical Psychological Science*, 9(2), 139–168. doi:10.1177/2167702620954799

See Also

vignette("ackwards-forbes2023") for a full reproduction of the Forbes (2023) applied example on this dataset, and vignette("ackwards-forbes") for the method extension itself.

Examples

```
dim(forbes2023)
forbes2023[1:3, 1:3]

# The Forbes (2023) applied example: a 10-level hierarchy from 155 symptoms.
x <- ackwards(forbes2023, k_max = 10, pairs = "all")
x
```

glance.ackwards

Glance at an ackwards object

Description

Returns a one-row data frame of top-level model metadata. For EFA and ESEM objects, fit indices at the deepest converged level are included. The same five columns (CFI, TLI, RMSEA, SRMR, BIC) are present across all engines; columns unavailable for a given engine or estimator are NA (e.g., CFI and SRMR are NA for EFA; all five are NA for PCA; for ESEM, BIC is NA under estimator = "WLSMV"/"ULSMV" – these limited-information estimators have no proper log-likelihood – and populated under "ML"/"MLR"). Under a scaled-test estimator ("WLSMV"/"ULSMV"/"MLR") the CFI/TLI/RMSEA reported here are the scaled variants (see [tidy.ackwards\(\)](#) for the rationale).

Usage

```
## S3 method for class 'ackwards'
glance(x, ...)
```

Arguments

x	An ackwards object.
...	Ignored.

Value

A one-row data.frame.

See Also

[tidy.ackwards\(\)](#), [print.ackwards\(\)](#)

Examples

```
x <- ackwards(sim16, k_max = 5)
glance(x)
```

label_template	<i>Generate a node-label scaffold for autoplot</i>
----------------	--

Description

Returns a named character vector covering all factor IDs in the object, ready to pass to `autoplot(x, node_labels = ...)`. Printing the result shows an editable `c(...)` literal so you can copy it into a script, fill in substantive labels, and use it directly; assigning the result (`labs <- label_template(x)`) produces no console output.

Usage

```
label_template(x, style = c("id", "forbes", "blank"))
```

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

Arguments

<code>x</code>	An <code>ackwards</code> object.
<code>style</code>	One of "id" (default), "forbes", or "blank". See Style options above.
<code>...</code>	Ignored; included for S3 method consistency.

Details

The factor IDs are returned in the same left-to-right, top-to-bottom order used by [ba_layout\(\)](#) and [autoplot.ackwards\(\)](#), so the printed literal maps directly onto the diagram.

Value

A named character vector of class "ackwards_labels": names are factor IDs (`"m{k}f{j}"`), values are the label strings for the chosen style. The vector is suitable for direct use as the `node_labels` argument to [autoplot.ackwards\(\)](#). Its `print()` method renders the vector as an editable `c(...)` literal for copy-paste.

Style options

- "id" (*default*) – every value equals the factor ID ("m1f1", "m2f1", ...). This is a round-trip no-op: passing the result to node_labels without editing reproduces the default labels exactly. Useful as the starting point for adding substantive labels.
- "forbes" – values follow the Forbes (2023) convention: level-letter + within-level index ("A1", "B1", "B2", ...). Level 1 -> A, level 2 -> B, level 3 -> C, and so on. Within-level indices are assigned in canonical layout order (left to right). Requires k_max <= 26 (LETTERS has 26 entries); an error is raised for deeper objects.
- "blank" – all values are empty strings. Useful as a starting scaffold when you want to supply every label from scratch with no defaults showing through.

See Also

[autoplot.ackwards\(\)](#), [top_items\(\)](#), [ba_layout\(\)](#)

Examples

```
x <- ackwards(sim16, k_max = 5)

# Start from ID defaults, then fill in your own labels:
labs <- label_template(x)
labs["m5f1"] <- "My factor name"

# Forbes letter convention:
label_template(x, style = "forbes")
```

predict.ackwards

Score new observations with a fitted ackwards model

Description

Applies a fitted bass-ackwards model to new data — for example the held-out test split of a cross-validation design — producing factor scores for every level **without retraining**. This is the idiomatic predict() front door to the same machinery as [augment.ackwards\(\)](#): the call predict(object, newdata) returns exactly augment(object, data = newdata, append = FALSE), a data frame holding only the .m{k}f{j} score columns, one row per row of newdata.

Usage

```
## S3 method for class 'ackwards'
predict(object, newdata, scaling = c("fit", "sample"), ...)
```

Arguments

object	An ackwards object.
newdata	A data frame or numeric matrix with the same variables (columns) used to fit object. Required — to retrieve scores stored at fit time, use <code>augment(object)</code> instead.
scaling	Which item means/SDs standardize newdata: "fit" (default, the training moments) or "sample" (newdata's own moments). See augment.ackwards() .
...	Ignored.

Details

Under the default `scaling = "fit"`, newdata is standardized by the **fit-time** item means/SDs stored in the object before the stored weight matrices are applied, so the new scores land on the same metric as the training solution: an observation's score does not depend on which other observations share its split, and train and test scores are directly comparable. See [augment.ackwards\(\)](#) (section *Scoring new observations*) for the full semantics, the `scaling = "sample"` alternative, and the non-Pearson-basis caveat.

newdata must contain the variables the model was fit on (matched by column name, with extra columns ignored; a bare unnamed matrix is matched positionally). Rows with missing items produce NA scores (scoring does not impute).

Value

A data frame of factor scores (columns `.m{k}f{j}`, one per factor per level), with one row per row of newdata in the original order.

See Also

[augment.ackwards\(\)](#) for appending scores to the data (and the full scoring documentation), [ackwards\(\)](#).

Examples

```
# Cross-validation: fit on a training split, score the test split
train <- sim16[1:500, ]
test <- sim16[501:1000, ]
x <- ackwards(train, k_max = 5)
test_scores <- predict(x, test)
head(test_scores)

# Identical to the augment() spelling:
identical(test_scores, augment(x, data = test, append = FALSE))
```

print.ackwards	<i>Print an ackwards object</i>
----------------	---------------------------------

Description

Displays a compact summary of the bass-ackwards result using cli formatting. No matrix dumps – use `tidy.ackwards()` to access values programmatically.

Usage

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

Arguments

x	An ackwards object.
...	Ignored.

Value

x invisibly.

See Also

`tidy.ackwards()`, `glance.ackwards()`

print.check_items	<i>Print an item quality check</i>
-------------------	------------------------------------

Description

Print an item quality check

Usage

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

Arguments

x	A check_items object (produced by <code>check_items()</code>).
...	Ignored.

Value

x invisibly.

`print.comparability` *Print a comparability object*

Description

Print a comparability object

Usage

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

Arguments

<code>x</code>	A comparability object.
<code>...</code>	Ignored.

Value

`x` invisibly.

`print.factorability` *Print a factorability screen*

Description

Print a factorability screen

Usage

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

Arguments

<code>x</code>	A factorability object (produced by factorability()).
<code>...</code>	Ignored.

Value

`x` invisibly.

print.suggest_k	<i>Print a suggest_k object</i>
-----------------	---------------------------------

Description

Print a suggest_k object

Usage

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

Arguments

x	A suggest_k object.
...	Ignored.

Value

x invisibly.

print.summary_ackwards	<i>Print a summary_ackwards object</i>
------------------------	--

Description

Print a summary_ackwards object

Usage

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

Arguments

x	A summary_ackwards object (produced by summary()).
...	Ignored.

Value

x invisibly.

print.top_items	<i>Print a top_items object</i>
-----------------	---------------------------------

Description

Print a top_items object

Usage

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

Arguments

x	A top_items object (produced by top_items()).
...	Ignored.

Value

x invisibly.

prune	<i>Flag redundant or artifactual factors (Forbes 2023 extension)</i>
-------	--

Description

`prune()` never removes anything from an `ackwards` object – it only annotates factors with `pruned/prune_reason` flags in `x$prune$nodes` (flag-only, never removes; the object keeps every level). Because it is a separate, cheap step from extraction, you can re-prune with new thresholds without re-running [ackwards\(\)](#):

```
x <- ackwards(bfi25, k_max = 6, engine = "esem") # expensive
x |> prune("redundant")                        # cheap, repeatable
x |> prune("redundant", redundancy_r = 0.95)    # no re-extraction
```

`prune()` is an S3 generic (rather than a plain function) so it coexists with the `prune` generics already defined by recursive-partitioning packages (e.g. `rpart::prune`) regardless of package load order.

Usage

```
prune(x, ...)

## S3 method for class 'ackwards'
prune(
  x,
  rules = "none",
  manual = NULL,
  redundancy_r = 0.9,
  redundancy_phi = NULL,
  redundancy_criterion = c("direct", "adjacent"),
  min_items = 3L,
  orphan_r = 0.5,
  near_margin = 0.1,
  ...
)
```

Arguments

x	An ackwards object.
...	Reserved for future methods/arguments.
rules	Character vector controlling which auto-rules run. Default "none" (no auto rule; combine with manual for pure manual pruning, or call <code>prune(x)</code> with no arguments to clear any existing pruning). Options: "redundant" – identify chains of factors connected by score correlations $r \geq \text{redundancy_r}$ (and optionally $\phi > \text{redundancy_phi}$), using <code>redundancy_criterion</code> (default "direct", faithful to Forbes). Applies Forbes's (2023) retention rule: keep the bottom node when the chain reaches level <code>k_max</code> (most specific); keep the top node otherwise. Flagged nodes get <code>pruned = TRUE</code> and <code>prune_reason = "redundant"</code> in <code>x\$prune\$nodes</code>. "artifact" (or the alias "artefact", normalized to "artifact") – compute Tucker's congruence coefficient (ϕ) for all cross-level factor pairs and store in <code>x\$prune\$phi</code>, structural signals (<code>few_items</code>/<code>orphan</code>/<code>split_merge</code>) in <code>x\$prune\$structural</code>, and the near-redundant band (<code>near_margin</code>, see Details) in <code>x\$prune\$near_redundant</code>. No factors are auto-flagged; artifact identification requires judgment (Forbes, 2023; Wicherts et al., 2016).
manual	Character vector of factor labels (e.g. <code>c("m4f3", "m4f4")</code>) to flag directly, in addition to or instead of an auto rule. Standalone manual pruning is supported: <code>prune(x, manual = c("m4f3"))</code> . Unknown labels error. A node already flagged by an auto rule keeps that <code>prune_reason</code> ; only otherwise-unflagged manual nodes get <code>prune_reason = "manual"</code> .
redundancy_r	Scalar in $(0, 1]$. Score-correlation $ r $ threshold for redundancy chains. Default 0.9 (Forbes, 2023).
redundancy_phi	Scalar in $(0, 1]$, NULL (default, auto), or NA (explicit opt-out). When NULL: <code>x\$engine == "pca"</code> – no phi filter. Component scores are <i>determinate</i> (exact linear functions of the data, with no factor-score indeterminacy), so the

score correlation $|r|$ is the true correlation between the components themselves; phi adds nothing that $|r|$ does not already capture.

- `x$engine` is "efa" or "esem" – automatically set to 0.95 (Lorenzo-Seva & ten Berge, 2006). Factor-score indeterminacy off-PCA means $|r|$ -alone is liberal; the conjunctive phi criterion is the conservative default. A cli message announces the resolved value. Pass NA to disable phi filtering regardless of engine. Pass a numeric value to override on any engine.

redundancy_criterion

How redundancy chains are traced. One of:

- "direct" (default) – chase upward via the **direct (skip-level)** correlation between a factor and each ancestor level, continuing while $|r| \geq \text{redundancy_r}$ contiguously. This is Forbes's (2023) published ChaseCorrPaths rule and the honest operationalization of "the same construct" (two factor scores share $\geq \text{redundancy_r}^2$ variance *directly*). It reproduces her AMH applied example exactly.
- "adjacent" – trace **adjacent primary-parent** links only (each consecutive level $|r| \geq \text{redundancy_r}$). This was the pre-M53 default; because correlation is non-transitive it can both over- and under-flag versus "direct" in deep (many-level) hierarchies, so it is retained only as an opt-in. On shallow/transitive hierarchies the two agree.

min_items

Minimum number of items for which a factor must be the primary loader (highest $|loading|$). Factors with fewer than `min_items` primary items are flagged `few_items = TRUE` in `x$prune$structural`. Only used when rules includes "artifact". Default 3L – a factor defined by one or two items is under-identified and frequently an extraction artifact rather than a replicable construct (the classic "three-indicator rule"; Forbes, 2023, Fig. 2).

orphan_r

Threshold for the orphan structural signal. A factor whose maximum **adjacent-level** $|r|$ (to the immediately shallower and deeper levels) falls below `orphan_r` is flagged `orphan = TRUE` in `x$prune$structural` – it does not connect to the neighbouring solutions and so does not replicate across the hierarchy. Only used when rules includes "artifact". Default 0.5 – a moderate correlation; a factor that shares less than a quarter of its variance with every neighbour is a structural outlier worth inspecting.

near_margin

Scalar in $(0, 1]$. Width of the **near-redundant band** reported by "artifact" mode (see Details). A cross-level pair is flagged near-redundant when its direct $|r|$ sits in $[\text{redundancy_r} - \text{near_margin}, \text{redundancy_r})$ **or** its Tucker phi sits in $[\text{redundancy_phi} - \text{near_margin}, \text{redundancy_phi})$ – i.e. within `near_margin` *below* a redundancy threshold – while the pair is not itself fully redundant. Only used when rules includes "artifact". Default 0.1.

Details

The "direct" criterion is a star anchored on the leaf, not a walk. Take a three-level chain candidate with deepest leaf `m3f1` and shallower factors `m2f1` (level 2) and `m1f1` (level 1). Under the default "direct" criterion the chain `m1f1 -> m2f1 -> m3f1` forms when **both** direct-to-leaf correlations $|r(m1f1, m3f1)|$ and $|r(m2f1, m3f1)|$ meet `redundancy_r` – every member is judged by its own direct correlation to the *same* deepest factor (a star centred on the leaf). It does **not** require

the adjacent hop $|r(m1f1, m2f1)|$ to meet the threshold (that is the "adjacent" criterion), and it does **not** screen every ancestor pair against every other (there is no all-pairs test). So an ancestor can join on a strong direct link to the leaf even where its adjacent hop to the next chain member is weak – which is exactly why `r_to_prev` (below) can sit under `redundancy_r`.

Reading `x$prune$chains` under `redundancy_criterion = "direct"`. The `r_to_prev` and `phi_to_prev` columns report the **adjacent-level** correlation and congruence between consecutive chain members (for continuity of display), but chain *membership* is decided by the **direct (skip-level)** correlation to the chain's deepest factor. A direct chain can therefore legitimately contain a link whose `r_to_prev` is *below* `redundancy_r` – the stronger direct link is what justified it. The `endpoint_r` column gives the direct root-to-leaf correlation as an at-a-glance cross-check. Under `redundancy_criterion = "adjacent"`, `r_to_prev` is the criterion and always meets `redundancy_r`.

The near-redundant band ("artifact" mode). `prune("redundant")` drops *full* redundancy – pairs at or above the thresholds. Forbes (2023) uses the artifact flags mainly for the messier band *just below* them: a pair that correlates, say, $|r| = 0.89$ and shares a loading pattern $\phi = 0.93$ is not quite redundant but is a candidate re-rotation worth a second look. Artifact mode surfaces this as `x$prune$near_redundant` – a data frame of every cross-level pair that is **not** itself fully redundant yet has its direct (skip-level) $|r|$ **or** its Tucker ϕ within `near_margin` *below* the corresponding threshold (`redundancy_r / redundancy_phi`). Columns: `from`, `to`, `level_from`, `level_to`, `r` (direct score correlation), `phi` (loading congruence), and the logical band flags `near_r / near_phi`. Under the PCA engine `redundancy_phi` is NULL (component scores are determinate), so only the $|r|$ band applies; under EFA/ESEM `redundancy_phi` auto-resolves to 0.95 (announced via cli) and the ϕ band is active too. Like ϕ and the structural signals, the band is **report-only** – it never drops or mutates the kept node set.

Value

`x`, with `$prune` populated (replacing any prior pruning).

References

- Forbes, M. K. (2023). Improving hierarchical models of individual differences: An extension of Goldberg's bass-ackward method. *Psychological Methods*. doi:10.1037/met0000546
- Lorenzo-Seva, U., & ten Berge, J. M. F. (2006). Tucker's congruence coefficient as a meaningful index of factor similarity. *Methodology*, 2(2), 57–64. doi:10.1027/16142241.2.2.57

See Also

`ackwards()`, `tidy.ackwards()` (what = "nodes"), `autoplot.ackwards()` (drop_pruned)

Examples

```
# sim16 has a planted redundant chain + overextraction artifact at k = 5,
# so the prune rules always have a finding to show (and no ordinal warning).
x <- ackwards(sim16, k_max = 5)

xp <- prune(x, "redundant")
xp$prune$nodes

# Re-prune with a new threshold -- no re-extraction needed
```

```
prune(x, "redundant", redundancy_r = 0.95)

# Manual pruning: standalone, or mixed with an auto rule
prune(x, manual = "m4f2")
prune(x, "redundant", manual = "m4f2")
```

set_factor_labels	<i>Attach persistent factor labels to an awkward object</i>
-------------------	---

Description

Store substantive names for factors (e.g. "Neuroticism" for "m5f1") on the object itself, so that [print\(\)](#), [summary\(\)](#), [tidy\(\)](#), [autoplot\(\)](#), and [top_items\(\)](#) display them without re-supplying the labels each time. This is the *factor*-label counterpart to item / variable labels (see [top_items\(\)](#) and [?ackwards](#)); the two are distinct and never interchanged.

Usage

```
set_factor_labels(x, labels)
```

Arguments

x	An awkward object.
labels	A named character vector mapping factor IDs ("m{k}f{j}") to label strings, or NULL to clear all stored labels. Every name must match a factor ID in x (an unknown ID is an error, not a warning – the object's IDs are knowable up front; see factor_labels() to read the current set).

Details

Labels are display only – they never change a factor's stable ID (m{k}f{j}), and every lineage / edge / score column continues to key on the ID. A factor with no label falls back to its ID everywhere. The stored labels ride along through [prune\(\)](#), [boot_edges\(\)](#), [augment\(\)](#), and [predict\(\)](#) unchanged.

Value

The awkward object, with meta\$factor_labels updated. Pipeable.

Updating and clearing

[set_factor_labels\(\)](#) **merges** into any labels already stored, so you can build them up incrementally. Within a single call:

- a normal string sets (or overwrites) that factor's label;
- an NA or "" value **removes** just that factor's label;
- passing labels = NULL clears **all** labels at once.

The scaffold printed by [label_template\(\)](#) is a convenient starting point: copy its c(...) literal, fill in the substantive names, and pass it here.

See Also

`factor_labels()` to read them back, `label_template()` for a ready-to-edit scaffold, `autoplot.ackwards()` (`node_labels` overrides a stored label per node).

Examples

```
x <- ackwards(sim16, k_max = 4, engine = "pca")

# Start from a scaffold, fill in names, attach them:
x <- set_factor_labels(x, c(m4f1 = "Alpha", m4f2 = "Beta"))
factor_labels(x)

# Merge in more; remove one; everything downstream now shows the labels:
x <- set_factor_labels(x, c(m2f1 = "Broad", m4f2 = NA))
summary(x)
```

sim16	<i>Simulated continuous bass-ackwards teaching example (16 items, known hierarchy)</i>
-------	--

Description

A 1 000-row, fully continuous dataset simulated from a population model with a known 1 -> 2 -> 4 bass-ackwards hierarchy, for showcasing the default `cor = "pearson"` extraction path without the ordinal-detection warning that `bf125`'s Likert items trigger.

Usage

```
sim16
```

Format

A data frame with 1 000 rows and 16 numeric columns (`i1–i16`, continuous, no missing values).

Details

Population model. $\Sigma = \Lambda \Phi \Lambda^T + \Psi$, an oblique common-factor model with 4 true group factors, sampled via a Cholesky factorization (base R; no MASS dependency):

Factor	Items	Metatrait
f1	i1–i4	1 (with f2)
f2	i5–i8	1 (with f1)
f3	i9–i12	2 (with f4)
f4	i13–i16	2 (with f3)

All items load 0.75 on their true factor (no cross-loadings). Factor correlations: 0.45 within a metatrait (f1-f2, f3-f4), 0.15 between metatraits. Uniquenesses are 1 - communality (uniform 0.4375 by the symmetry of the design above).

Ground-truth hierarchy (verified against `ackwards(engine = "efa")`): k=1 recovers a single general factor across all 16 items; k=2 splits along the metatrait line (i1-i8 vs. i9-i16); k=4 recovers the 4 true group factors exactly; all six `suggest_k()` recommendations (five criteria - VSS reports at complexities 1 and 2) reach a consensus of k = 4.

Idealized by design. The planted signal is strong and clean, so all six `suggest_k()` recommendations converge on k = 4 - deliberately the *easy* case, for building intuition about what recovering a known hierarchy looks like. Real data rarely agree this cleanly: on `bfi25` the same criteria span k = 4-6. The two datasets are complementary teaching foils - `sim16` for "watch the method recover a structure we planted," `bfi25` for "reason about a hierarchy when the criteria disagree." Present `sim16`'s consensus as the ideal, not the norm.

Deliberate overextraction artifact at k=5. The population has exactly 4 factors, so requesting a 5th finds no real dimension: EFA produces an orphan factor with zero primary-loading items. With `prune(x, "artifact")` (default `min_items = 3`, `orphan_r = 0.5`), that factor is flagged both `few_items` and `orphan`. Because the true (non-splitting) factors persist essentially unchanged from k=3 onward, their parent-child score correlations approach 1 and are flagged by `prune(x, "redundant")` ($|r| \geq .9$ and, under the EFA auto-default, Tucker's $\phi > .95$). This is a textbook overextraction artifact, included so the Forbes/redundancy examples have a guaranteed finding to teach against (unlike `bfi25`, which does not reliably trigger one).

To regenerate this dataset, run `source("data-raw/sim16.R")` from the package root (`set.seed(42)`).

Source

Simulated; see `data-raw/sim16.R` for the full generative model.

Examples

```
dim(sim16)
head(sim16)
```

suggest_k

Suggest a maximum number of factors for bass-ackwards analysis

Description

Runs complementary factor-retention criteria and reports their recommendations. No single criterion is definitive; the goal is a consensus range to inform your choice of k in `ackwards()`.

Usage

```
suggest_k(
  data,
  k_max = NULL,
  criteria = c("pa_pc", "pa_fa", "map", "vss", "cd"),
```

```

cor = "pearson",
n_obs = NULL,
n_iter = 20L,
seed = NULL,
...
)

```

Arguments

data	A data frame or numeric matrix (items in columns, observations in rows). Alternatively, a pre-computed correlation matrix may be supplied (a square, symmetric, numeric matrix with unit diagonal). When a correlation matrix is supplied, <code>n_obs</code> is required (PA and VSS need N), the <code>cor</code> argument is ignored, and the Comparison Data (CD) criterion is skipped (CD requires raw item distributions for resampling).
k_max	Maximum number of factors/components to <i>evaluate</i> when recommending a depth – not a depth itself. Defaults to <code>min(ncol(data) - 1, 8)</code> . Increase if you expect a deeper hierarchy. (Note: this is a distinct meaning from <code>ackwards()</code> 's <code>k_max</code> , which <i>is</i> the extraction depth; the two share a name because they're the same dial in the <code>suggest_k()</code> -> <code>ackwards()</code> workflow, just applied at different stages.)
criteria	Character vector of criteria to compute. Any subset of <code>c("pa_pc", "pa_fa", "map", "vss", "cd")</code> ; default is all five. "pa_pc" and "pa_fa" share one parallel-analysis call (both or neither are fast); "map" and "vss" share one VSS call. Criteria not requested are skipped entirely (no computation) and their <code>k_*</code> fields in the result are NA. "vss" selects both VSS-1 and VSS-2 as a unit.
cor	Correlation basis: "pearson" (default) or "spearman". Should match the <code>cor</code> argument you plan to use in <code>ackwards()</code> . Ignored when data is a correlation matrix (the basis is already fixed).
n_obs	Number of observations. Required when data is a pre-computed correlation matrix (PA and VSS need N). Ignored when raw data are supplied (N is determined from <code>nrow(data)</code>).
n_iter	Number of Monte Carlo iterations for parallel analysis. Default 20. Reduce to 5 for fast/exploratory runs; increase to 100+ for publication.
seed	Integer seed passed to <code>set.seed()</code> before the Comparison Data (CD) step. NULL (default) uses the current RNG state. Note: the parallel-analysis step uses <code>psych::fa.parallel()</code> , which does not respond reliably to <code>set.seed()</code> – PA simulation results will vary across calls regardless of seed.
...	Reserved for future arguments.

Details

Criteria available (controlled by the `criteria` argument):

- **PA-PC** ("pa_pc") – Horn (1965) parallel analysis on PC eigenvalues. Compares observed eigenvalues to those from random correlation matrices; suggests retaining components whose eigenvalues exceed the 95th percentile of chance. Tends to overextract; treat as an upper bound.

- **PA-FA** ("pa_fa") – Horn (1965) parallel analysis using common-factor eigenvalues. More conservative than PA-PC and the better match for the EFA and ESEM engines in [ackwards\(\)](#). Shares one `psych::fa.parallel()` call with PA-PC.
- **MAP** ("map") – Velicer (1976) Minimum Average Partial criterion. Finds the k that minimises the average squared partial correlation remaining after extracting k components. Usually conservative. Shares one `psych::vss()` call with VSS.
- **VSS** ("vss") – Revelle & Rocklin (1979) Very Simple Structure fit at complexities 1 and 2 (VSS-1 and VSS-2). Finds the k maximising the fit of a very simple loading structure. Shares one `psych::vss()` call with MAP.
- **CD** ("cd") – Ruscio & Roche (2012) Comparison Data. Resamples from the observed item distributions to generate comparison eigenvalue profiles; retains factors until adding one no longer improves RMSE beyond chance. Requires the **EFAtools** package (install separately). Skipped with an informational message when **EFAtools** is absent or when a correlation matrix is supplied.

PA (both bases), MAP, and VSS share the same correlation matrix as [ackwards\(\)](#). CD operates on the raw data matrix directly (required for resampling).

Value

An object of class "suggest_k". Print it for a formatted summary; call [autoplot\(\)](#) on it for a diagnostic scree/criteria plot. The list contains:

k_parallel_pc	Recommended k from PC-based parallel analysis (NA_integer_ when "pa_pc" not in criteria).
k_parallel_fa	Recommended k from FA-based parallel analysis (NA_integer_ if no FA factor exceeded the random threshold, or when "pa_fa" not in criteria).
k_map	Recommended k from MAP (NA_integer_ when "map" not in criteria).
k_vss1	Recommended k from VSS complexity-1 (NA_integer_ when "vss" not in criteria).
k_vss2	Recommended k from VSS complexity-2 (NA_integer_ when "vss" not in criteria).
k_cd	Recommended k from Comparison Data (NA_integer_ when "cd" not in criteria, EFAtools is not installed, or CD fails).
cd_available	Logical; TRUE when "cd" was requested, EFAtools was found, and CD ran successfully.
criteria	Data frame with one row per k: k, ev_obs (observed PC eigenvalue), ev_obs_fa (observed FA eigenvalue), pa_pc_quant / pa_fa_quant (95th-pct simulated eigenvalue for each basis), pa_pc_suggested / pa_fa_suggested (logical retention), map, vss1, vss2. Columns for non-requested criteria are NA.
criteria_requested	Character vector of the criteria that were requested (and therefore computed).
k_max, n_obs, n_vars, cor	Metadata.

Interpreting the output

k in `ackwards()` is a **maximum depth**, not a claim that exactly k factors exist. Users commonly set k one or two levels above the consensus to watch higher-level factors fragment – this is a feature of the method, not overextraction.

Treating retention estimates as a range rather than a verdict has direct support in the parallel-analysis literature: Lim and Jahng (2019) recommend interpreting the PA estimate as a range of roughly plus or minus one factor, resolved by interpretability, and Achim (2021) argues that even that overstates PA's precision – the disagreement itself is why `suggest_k()` reports several criteria and a consensus range, never a single number.

Ordinal (Likert) data

`suggest_k()` screens on the Pearson or Spearman basis by design and never computes polychoric correlations itself, so when the raw data look ordinal (at most 7 distinct integer values per column) it emits a one-per-session warning – the same `detect_ordinal()` signal `ackwards()` and `comparability()` use (Invariant 6: announce consequential defaults loudly). Crucially, the advice points at the *final* `ackwards()` fit (`cor = "polychoric"`), **not** at `suggest_k()` itself: the screening basis is intentional. The plausible-k *range* is robust to the Pearson-vs-polychoric choice, so screening on Pearson and fitting the final model polychoric is the recommended workflow – computing polychoric correlations at the screening stage would only add cost and NPD risk without changing the range. The warning is skipped for correlation-matrix input (there are no items to inspect).

A note on overextraction

PA-PC in particular tends to recommend more factors than replicate across independent samples, especially with correlated items (Forbes, 2023). This is a long-standing observation in practice: Saucier (1997, footnote 14) reported parallel analysis suggesting as many as 30 factors in wide lexical item sets. PA-FA and CD are more conservative. Treat the full set of criteria as a range: the true k is likely somewhere in the middle.

References

- Achim, A. (2021). Determining the number of factors using parallel analysis and its recent variants: Comment on Lim and Jahng (2019). *Psychological Methods*, 26(1), 69–73. doi:10.1037/met0000269
- Forbes, M. K. (2023). Improving hierarchical models of individual differences: An extension of Goldberg's bass-ackward method. *Psychological Methods*. doi:10.1037/met0000546
- Tong, L., Qu, W., & Zhang, Z. (2025). Comparison of the K1 rule, parallel analysis, and the Bass-Ackward method on identifying the number of factors in factor analysis. *Fudan Journal of the Humanities and Social Sciences*, 18(1), 17–44. doi:10.1007/s40647024004232
- Horn, J. L. (1965). A rationale and test for the number of factors in factor analysis. *Psychometrika*, 30, 179–185.
- Lim, S., & Jahng, S. (2019). Determining the number of factors using parallel analysis and its recent variants. *Psychological Methods*, 24(4), 452–467. doi:10.1037/met0000230
- Revelle, W., & Rocklin, T. (1979). Very simple structure: An alternative procedure for estimating the optimal number of interpretable factors. *Multivariate Behavioral Research*, 14(4), 403–414.

Ruscio, J., & Roche, B. (2012). Determining the number of factors to retain in an exploratory factor analysis using comparison data of a known factorial structure. *Psychological Assessment*, 24(2), 282–292.

Saucier, G. (1997). Effects of variable selection on the factor structure of person descriptors. *Journal of Personality and Social Psychology*, 73(6), 1296–1312. doi:10.1037/00223514.73.6.1296

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

See Also

`ackwards()`, `factorability()`, `check_items()`, and `comparability()`, the other pre-analysis diagnostics.

Examples

```
sk <- suggest_k(sim16)
sk
autoplot(sk)

# Run only MAP (fast; skips parallel analysis and CD)
suggest_k(sim16, criteria = "map")

# Run only the parallel-analysis criteria
suggest_k(sim16, criteria = c("pa_pc", "pa_fa"), n_iter = 5)

# Faster exploratory run
suggest_k(sim16, k_max = 6, n_iter = 5)

# Correlation-matrix input (CD is skipped; n_obs required)
R <- cor(sim16)
suggest_k(R, n_obs = nrow(sim16))
```

summary.ackwards

Summarise an ackwards object

Description

Returns a structured `summary_ackwards` object that, when printed, shows per-level variance and fit indices, a readable lineage list, and (when present) pruning annotations. More verbose than `print.ackwards()`; designed for inspection and reporting.

Usage

```
## S3 method for class 'ackwards'
summary(object, ...)
```

Arguments

object	An ackwards object.
...	Ignored.

Value

An object of class "summary_ackwards", printed via `print.summary_ackwards()`.

See Also

`print.ackwards()`, `tidy.ackwards()`, `glance.ackwards()`

Examples

```
x <- ackwards(sim16, k_max = 5)
summary(x)
```

tidy.ackwards	<i>Tidy an ackwards object into a long data frame</i>
---------------	---

Description

Returns structured data from an ackwards object in tidy format. The default (what = "edges") returns the graph edge list that drives diagrams.

Usage

```
## S3 method for class 'ackwards'
tidy(
  x,
  what = c("edges", "loadings", "variance", "fit", "nodes", "scores"),
  primary_only = FALSE,
  sort = c("none", "strength"),
  format = c("long", "wide"),
  conf_level = 0.95,
  ...
)
```

Arguments

x	An ackwards object.
what	What to extract: "edges" (<i>default</i>) – one row per directed between-level edge: from, to, level_from, level_to, r, is_primary, above_cut. If <code>boot_edges()</code> has been run on the object, four bootstrap columns are appended: se, lo, hi (bootstrap standard error and percentile confidence-interval endpoints), and n_boot_ok (usable replicates).

- "loadings" – one row per item x factor x level: level, factor, item, loading, se, ci_lower, ci_upper. se, ci_lower, and ci_upper are populated only for engine = "esem" (which produces rotation-aware loading SEs); they are NA for PCA and EFA. The confidence level is controlled by conf_level.
- "variance" – one row per factor x level: level, factor, proportion, cumulative. Both are proportions of total item variance on a 0-1 scale (multiply by 100 for a percentage).
- "fit" – one row per fit statistic x level: level, statistic, value. For PCA objects the statistics are eigenvalues; for EFA objects they are chi, dof, p_value, RMSEA, TLI, BIC – where chi is the likelihood-ratio chi-square (`psych::fa()`'s STATISTIC), so chi, dof, p_value, RMSEA, and TLI all share one statistical framing (psych's residual-based *empirical* chi-square is a different statistic and is not reported); for ESEM they are chi, dof, p_value, CFI, TLI, RMSEA, SRMR, BIC. For ESEM under a scaled-test estimator ("WLSMV"/"ULSMV" for ordinal data, "MLR" for continuous), the whole row – chi/dof/ p_value **and** CFI/TLI/RMSEA – reports lavaan's mean-and-variance-adjusted ("scaled") variant, so every quantity shares one scaling. This matters most for WLSMV/ULSMV: the naive chi-square has no valid reference distribution (lavaan's own `summary()` labels its p-value "Unknown"), and the naive CFI/TLI are badly optimistic for ordinal data (Xia & Yang, 2019). "ML" has no scaled variant, so it reports the naive values (the correct ones for ML). SRMR has no scaled variant and is reported as-is. BIC is NA under WLSMV/ULSMV (no proper log-likelihood for a limited-information estimator) and populated under ML/MLR. Use format = "wide" for one row per **non-anchor** level ($k \geq 2$; the saturated 1-factor anchor is dropped, matching `summary()` and `autoplot(what = "fit")`), one column per statistic. Conventional fit cutoffs (Hu & Bentler 1999) are shown as reference lines in `autoplot(what = "fit")` and inline in `summary()`, but are not returned as a pass/fail column here – they are contested thresholds, report-only, and never gate anything (see those functions' docs). format is oriented to the EFA/ESEM model-fit statistics; for PCA the "statistics" are per-component eigenvalues.
- "nodes" – Forbes-extension pruning annotations (requires prune != "none" when the object was created). One row per factor across all levels: id, level, pruned, prune_reason. Returns an empty data frame with the same columns when no pruning was applied.
- "scores" – long-format per-observation factor scores (requires keep_scores = TRUE at fit time or use `augment.ackwards()` for on-the-fly computation). Columns: obs (row index), level, factor, score.

primary_only	For what = "edges" only. When TRUE, returns just each factor's primary-parent edge (<code>is_primary == TRUE</code>) – the lineage tree that the diagram draws as solid arrows. Default FALSE (all edges). Errors for any other value of what.
sort	For what = "edges" only. One of "none" (default, natural order) or "strength" (descending $ r $). Ignored for all other values of what.
format	For what = "fit" only. One of "long" (default, one row per statistic x level) or "wide" (one row per level, one column per statistic). Errors for all other values of what.

conf_level	For what = "loadings" only. Confidence level for the loading intervals; default 0.95. The intervals are computed as loading ± qnorm((1 + conf_level) / 2) * se and are NA for engines that carry no SEs (PCA, EFA). Errors for all other values of what.
...	Ignored.

Value

A data frame (class data.frame).

Factor labels

If [factor labels](#) have been attached to the object, the output gains display-only label columns: factor_label for what = "loadings", "variance", or "scores", and from_label/to_label for what = "edges". Each carries the label for a labeled factor and NA otherwise. These columns are **absent** when no labels are set, so an unlabeled object's output is unchanged; the ID columns (factor, from, to) are never altered.

See Also

[glance.ackwards\(\)](#), [print.ackwards\(\)](#), [set_factor_labels\(\)](#)

Examples

```
x <- ackwards(sim16, k_max = 5)
tidy(x) # edges in natural order
tidy(x, sort = "strength") # strongest edges first
tidy(x, primary_only = TRUE) # just the primary-parent lineage
tidy(x, what = "loadings")
tidy(x, what = "variance")
tidy(x, what = "fit")
tidy(x, what = "fit", format = "wide")
```

top_items	<i>Display the salient items for each factor</i>
-----------	--

Description

Returns, per level and factor, the items whose absolute loading meets or exceeds cut, sorted by descending absolute loading. This gives a concise reading of "what each factor is about" without printing a full item-by-factor matrix, which does not scale well to large k or many items.

Usage

```
top_items(
  x,
  level = NULL,
  cut = 0.3,
  n = NULL,
  sort = TRUE,
  by = c("factor", "item"),
  show_labels = TRUE
)
```

Arguments

x	An <i>ackwards</i> object.
level	Integer vector selecting which level(s) to include. <code>NULL</code> (default) returns all levels.
cut	Absolute-loading threshold. Items with <code> loading >= cut</code> are shown. Default <code>0.3</code> , matching the <code>cut_show</code> plotting default.
n	Maximum number of items to show per factor. <code>NULL</code> (default) shows all items meeting the cut. When set, the top- <code>n</code> items by <code> loading </code> are kept after applying the cut.
sort	Logical. When <code>TRUE</code> (default), items within each group are ordered by descending <code> loading </code> . Set to <code>FALSE</code> to keep the original order (useful when items have a meaningful sequence).
by	One of "factor" (default) or "item". "factor" groups the listing by factor (the salient items <i>of</i> each factor – "what is this factor about?"). "item" inverts the grouping to list, for each item, the factors it loads on – which makes cross-loadings legible ("where does this item go?"). <code>n</code> and <code>sort</code> apply within whichever unit by selects.
show_labels	Logical. When <code>TRUE</code> (default) and the data carried a variable-label attribute at fit time (see ackwards()), items are shown as <code>id: label</code> ; items without a label fall back to the bare id. Set to <code>FALSE</code> to always show the bare <code>m{k}f{j}</code> -style item ids.

Details

Loadings are signed and reflect the object's primary-parent sign alignment (see [ackwards\(\)](#)). Items near the cut threshold may appear for one sign orientation but not the other; this is expected and informative.

If [factor labels](#) have been attached, the factor dimension is shown as `label (id)` wherever it appears – the group headers under `by = "factor"` and the body entries under `by = "item"`.

Value

An object of class "top_items". Print it for a grouped cli listing. The underlying data frame (one row per selected item) is accessible via `$data` and contains columns `level`, `factor`, `item`,

and loading (plus label when labels are available). The values equal the corresponding tidy(x, what = "loadings") rows (after filtering and optional sorting).

See Also

[tidy.ackwards\(\)](#), [label_template\(\)](#), [set_factor_labels\(\)](#), [autoplot.ackwards\(\)](#)

Examples

```
# Fit the raw dataset (not na.omit(), which would drop the column
# attributes): bfi25's IPIP item labels are then captured and printed as
# `code: label`. `missing = "listwise"` handles the NAs cleanly. A 10-item
# subset keeps the example fast; use all items in practice.
x <- ackwards(bfi25[, 1:10], k_max = 3, cor = "polychoric", missing = "listwise")
top_items(x)
top_items(x, level = 3, cut = 0.4, n = 5)

# Invert the grouping to read cross-loadings item-by-item
top_items(x, level = 3, cut = 0.25, by = "item")
```

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