Package: MixMashNet (via r-universe)

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Title Tools for Multilayer and Single Layer Network Modeling

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Description Estimation and bootstrap utilities for single layer and multilayer Mixed Graphical Models, including functions for centrality, bridge metrics, membership stability, and plotting (De Martino et al. (2026) <doi:10.48550/arXiv.2602.05716>).

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BugReports https://github.com/ARCbiostat/MixMashNet/issues

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`MixMashNet-package` *Tools for Multilayer and Single Layer Network Modeling*

Description

Tools for estimating and analyzing single layer and multilayer networks using Mixed Graphical Models (MGMs), accommodating continuous, count, and categorical variables. In the multilayer setting, layers may comprise different types and numbers of variables, and users can explicitly impose a predefined multilayer topology to constrain the estimation of inter and intralayer connections. The package implements bootstrap procedures to derive quantile regions for edge weights and node-level centrality and bridge metrics, and provides tools to assess the stability of node community membership. In addition, subject-level community scores can be computed to summarize the latent dimensions identified through network clustering.

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References

De Martino, M., Triolo, F., Perigord, A., Ornago, A. M., Vetrano, D. L., Gregorio, C. (2026). MixMashNet: An R Package for Single and Multilayer Networks. https://arxiv.org/abs/2602.05716

Christensen, A. P., & Golino, H. (2021). Estimating the Stability of Psychological Dimensions via Bootstrap Exploratory Graph Analysis: A Monte Carlo Simulation and Tutorial. *Psych*, 3(3), 479–500. doi:10.3390/psych3030032

Christensen, A. P., Golino, H., Abad, F. J., & Garrido, L. E. (2025). Revised network loadings. *Behavior Research Methods*, 57(4), 114. doi:10.3758/s13428025026403

Epskamp, S., Borsboom, D., & Fried, E. I. (2018). Estimating psychological networks and their accuracy: A tutorial paper. *Behavior Research Methods*, 50(1), 195–212. doi:10.3758/s13428017-08621

Haslbeck, J. M. B., & Waldorp, L. J. (2020). mgm: Estimating Time-Varying Mixed Graphical Models in High-Dimensional Data. *Journal of Statistical Software*, 93(8). doi:10.18637/jss.v093.i08

Jones, P. J., Ma, R., & McNally, R. J. (2021). Bridge Centrality: A Network Approach to Understanding Comorbidity. *Multivariate Behavioral Research*, 56(2), 353–367. doi:10.1080/00273171.2019.1614898

See Also

Useful links:

- https://arcbiostat.github.io/MixMashNet/
- Report bugs at https://github.com/ARCbiostat/MixMashNet/issues

---

`bacteremia` *Bacteremia example dataset for single layer network analysis*

Description

Clinical bacteremia dataset used to illustrate single-layer network estimation with MixMashNet. This dataset contains 7240 patients with clinical suspicion of bacteremia who underwent blood culture testing at the Vienna General Hospital.

Usage

```
data(bacteremia)
```

Format

A data frame with 7420 rows and 16 variables:

AGE Age (numeric).

WBC White blood cell (numeric).

NEU Neutrophil counts (numeric).

HGB Hemoglobin (numeric).

PLT Platelet count (numeric).

CRP C-reactive protein (numeric).

APTT Activated partial thromboplastin time (numeric).

FIB Fibrinogen (numeric).

CREA Creatinine (numeric).

BUN Blood urea nitrogen (numeric).

GLU Glucose (numeric).

ALAT High-sensitivity C-reactive protein (numeric).

GBIL Total bilirubin (numeric).

ALB Albumin (numeric).

SEX Sex with 0=male and 1=female.

BloodCulture Positive blood culture results with 0=no and 1=yes.

References

Ratzinger, F., Dedeyan, M., Rammerstorfer, M., Perkmann, T., Burgmann, H., Makristathis, A., Dorffner, G., Loetsch, F., Blacky, A., & Ramharter, M. (2014). A risk prediction model for screening bacteremic patients: A cross sectional study. *PLoS ONE*, 9(9), e106765. doi:10.1371/journal.pone.0106765

`bridge_metrics` *Bridge metrics for nodes across communities*

Description

Computes bridge centrality measures for nodes with an assigned community. This function is used internally by `mixMN()` and `multimixMN()`. Specifically, the function computes bridge strength as the sum of absolute edge weights connecting a node to nodes in other communities; bridge expected influence of order one (EI1) as the signed sum of direct connections to nodes in other communities; bridge expected influence of order two (EI2) as the signed influence that propagates indirectly to nodes in other communities via one intermediate neighbor (i.e., through paths of length two); bridge betweenness as the number of times a node lies on shortest paths between nodes belonging to different communities; and bridge closeness as the inverse of the mean shortest-path distance to nodes in other communities.

Usage

```
bridge_metrics(g, membership)
```

Arguments

`g`	An igraph object with edge attribute `weight`.
`membership`	Named vector/factor of community labels for a subset of nodes (names must match `V(g)$name`).

Details

Bridge betweenness and closeness are computed on the positive-weight subgraph only, with weights converted to distances as $d = 1/w$.

Value

A data.frame with columns: `node`, `community`, `bridge_strength`, `bridge_ei1`, `bridge_ei2`, `bridge_betweenness`, `bridge_closeness`.

References

Jones, P. J., Ma, R., & McNally, R. J. (2021). Bridge Centrality: A Network Approach to Understanding Comorbidity. *Multivariate Behavioral Research*, 56(2), 353–367. doi:10.1080/00273171.2019.1614898

`bridge_metrics_excluded`

Bridge metrics for nodes excluded from communities

Description

Computes bridge centrality measures for nodes that are not assigned to any community. This function is used internally by `mixMN()` and `multimixMN()`. For these excluded nodes, the function computes bridge strength, bridge closeness, bridge betweenness, and bridge expected influence of order one and two (EI1 and EI2), quantifying their role in connecting nodes across different communities.

Usage

```
bridge_metrics_excluded(g, membership)
```

Arguments

`g`	An igraph object with edge attribute `weight`.
`membership`	Named vector/factor of community labels for a subset of nodes (names must match `V(g)$name`). Nodes not present here are treated as excluded.

Details

Bridge betweenness excluded and closeness excluded are computed on the positive-weight subgraph only, with weights converted to distances as $d = 1/w$.

Value

A data.frame with columns: `node`, `bridge_strength`, `bridge_closeness`, `bridge_betweenness`, `bridge_ei1`, `bridge_ei2`.

References

Jones, P. J. (2025). **networktools**: Tools for identifying important nodes in networks. R package version 1.6.1. https://github.com/paytonjjones/networktools

`community_scores` *Compute community scores from a fitted MixMashNet model*

Description

Computes subject-level community scores. Community scores are obtained as weighted sums of the variables belonging to each detected community, where weights correspond to the standardized community loadings estimated via `EGAnet::net.loads` and stored in the fitted `mixMN_fit` object. Scores are computed using the dataset provided via the `data` argument. If `data = NULL`, the original dataset used to fit the model (`fit$model$data`) is used by default. Errors if both are NULL. Optionally, percentile bootstrap quantile regions for the community scores can be computed if bootstrap community loadings are available in `fit$community_loadings$boot`. Community scores are only available if community loadings were computed in the fitted model. This requires that all variables in the community subgraph are of MGM type Gaussian (`"g"`), Poisson (`"p"`), or binary categorical (`"c"` with `level == 2`).

Usage

```
community_scores(
  fit,
  data = NULL,
  layer = NULL,
  scale = TRUE,
  quantile_level = NULL,
  return_quantile_region = FALSE,
  na_action = c("stop", "omit")
)
```

Arguments

`fit`	A fitted object of class `c("mixMN_fit", "multimixMN_fit")` returned by `mixMN()` or `multimixMN()`.
`data`	Optional data.frame with variables in columns. If `NULL`, uses `fit$model$data`. Errors if both are `NULL`.
`layer`	Optional. If fit is a multimixMN_fit, specify which layer to score (name or index). If NULL, scores are computed for all scoreable layers and returned as a named list. If no layer is scoreable, the function errors.
`scale`	Logical; if `TRUE` (default), z-standardize variables used for scoring, using the mean/SD computed from the dataset used for scoring.
`quantile_level`	Optional numeric from 0 to 1, e.g. 0.95 or 0.99. If provided, percentile bootstrap quantile regions are computed for community scores (requires `fit$community_loadings$boot`).
`return_quantile_region`	Logical; if `TRUE`, return quantile regions.
`na_action`	Character. How to handle missing values in the scoring data: `"stop"` (default) stops if any missing value is present in the required variables; `"omit"` computes scores using row-wise omission within each community (i.e., uses available variables only, re-normalizing weights within community for that row).

Details

The function requires that `fit$community_loadings$true` exists and that the input `data` contains all required variables in `fit$community_loadings$nodes`. It errors otherwise.

The returned object has class `"community_scores"` and implements `print()` and `summary()` methods for quick inspection and descriptive summaries of the scores.

Value

A list with class `"community_scores"` containing:

`call` The matched call.

`settings` List with `scale`, `quantile_level`, and `na_action`.

`ids` Character vector of subject IDs (rownames of `data`).

`communities` Character vector of community score names.

`scores` Numeric matrix of scores (n × K).

`quantile_region` If requested and available, a list with `lower` and `upper` matrices (n × K) for percentile bootstrap quantile regions; otherwise `NULL`.

`details` List containing `nodes_used`, `loadings_true`, `loadings_boot_available`, and scaling parameters (`center`, `scale`).

If `fit` is a `mixMN_fit` (or a `multimixMN_fit` with `layer` specified), returns a `"community_scores"` object. If `fit` is a `multimixMN_fit` and `layer = NULL`, returns a named list of `community_scores` objects for all scoreable layers. If no layer is scoreable, the function errors.

References

Christensen, A. P., Golino, H., Abad, F. J., & Garrido, L. E. (2025). Revised network loadings. *Behavior Research Methods*, 57(4), 114. doi:10.3758/s13428025026403

Examples

```
data(bacteremia)

vars <- c("WBC", "NEU", "HGB", "PLT", "CRP")
df <- bacteremia[, vars]

fit <- mixMN(
  data = df,
  lambdaSel = "EBIC",
  reps = 0,
  seed_model = 42,
  compute_loadings = TRUE,
  progress = FALSE,
  save_data = TRUE
)

# Compute community scores on the original data
scores <- community_scores(fit)
summary(scores)
```

`find_bridge_communities` *Bridge profiles of a node across communities*

Description

Identifies which communities contribute most to the bridge role of a given node, by decomposing its bridge connectivity into community-specific contributions, excluding its own community when assigned. The function is designed as an interpretative companion to `bridge_metrics()` and `bridge_metrics_excluded()`, providing the components underlying the corresponding overall bridge indices.

Bridge connectivity is summarized using five complementary profiles: bridge strength, bridge EI1, bridge EI2, bridge closeness, and bridge betweenness.

For single layer fits (`mixMN_fit`), profiles are computed directly on the supplied fitted object.

For multilayer fits (`multimixMN_fit`), profiles are computed within the selected layer only, by applying the same single layer procedure to the corresponding intralayer fit stored in `fit$layer_fits[[layer]]`.

Usage

```
find_bridge_communities(fit, node, layer = NULL)
```

Arguments

`fit`	An object of class `mixMN_fit` or `multimixMN_fit`.
`node`	Character scalar: node of interest.
`layer`	Character scalar giving the layer of interest for `multimixMN_fit` objects. Ignored for `mixMN_fit` objects.

Details

Bridge profiles are computed using only connections from the focal node to nodes in communities different from its own. If the focal node is not assigned to any community, i.e. excluded, connections to all assigned nodes in communities are considered.

Bridge betweenness is computed by counting all shortest paths between pairs of nodes in different communities that pass through the focal node as an intermediate vertex. When multiple shortest paths exist, each path is counted separately.

The returned object has class `"bridge_profiles"` and provides a dedicated `print()` method. By default, all bridge profiles are displayed; a specific profile can be selected through the `statistic` argument.

Value

An object of class `"bridge_profiles"` (a named list) with the following components:

`bridge_strength` Bridge strength. List with `overall`, the total value across all other communities, and `by_comm`, a tibble with community-specific contributions (`community`, `sum_abs_w`).

`bridge_ei1` Bridge expected influence (order 1). List with `overall` and `by_comm` (`community`, `sum_signed_w`).

`bridge_ei2` Bridge expected influence (order 2). List with `overall` and `by_comm` (`community`, `sum_signed_w2`).

`bridge_closeness` Bridge closeness. List with `overall` and `by_comm` (`community`, `inv_mean_dist`).

`bridge_betweenness` Bridge betweenness. List with `overall` and `by_pair`, a tibble with contributions by community pair (`Ci`, `Cj`, `hits`).

`find_bridge_layers` *Bridge profiles of a node across layers*

Description

Identifies which layers contribute most to the interlayer bridge role of a given node, by decomposing its interlayer connectivity into layer-specific contributions. The function is designed as an interpretative companion to the interlayer node-level indices returned by `multimixMN()`, providing the components underlying the corresponding overall interlayer indices.

Interlayer connectivity is summarized using four complementary profiles: interlayer strength, interlayer expected influence (order 1), interlayer closeness, and interlayer betweenness.

Usage

```
find_bridge_layers(fit, node, layer)
```

Arguments

`fit`	An object of class `multimixMN_fit`.
`node`	Character scalar: node of interest.
`layer`	Character scalar giving the layer of the focal node.

Details

The function operates on the interlayer-only graph, i.e. on the graph containing only edges between nodes belonging to different layers.

For a focal node in the selected `layer`, the function decomposes:

- interlayer strength into contributions toward each layer;
- interlayer expected influence (order 1) into signed contributions toward each layer;
- interlayer closeness into additive harmonic-distance contributions toward each layer;
- interlayer betweenness into additive contributions from shortest paths between layer pairs, using the standard fraction $\sigma_{st}(v)/\sigma_{st}$.

Contributions are defined so that they sum to the corresponding overall interlayer index.

The returned object has class `"bridge_layer_profiles"` and provides a dedicated `print()` method. By default, all interlayer profiles are displayed; a specific profile can be selected through the `statistic` argument.

Value

An object of class "bridge_layer_profiles" (a named list) with the following components:

bridge_strength List with overall and by_layer, where by_layer is a tibble with columns target_layer and sum_abs_w.

bridge_ei1 List with overall and by_layer, where by_layer is a tibble with columns target_layer and sum_signed_w.

bridge_closeness List with overall and by_layer, where by_layer is a tibble with columns target_layer and contribution.

bridge_betweenness List with overall and by_pair, where by_pair is a tibble with columns Li, Lj, and contribution.

---

get_centrality *Extract node-level centrality indices*

Description

Extracts node-level centrality indices from fitted objects returned by mixMN() and multimixMN() in a long-format data frame.

For single layer fits of class "mixMN_fit", only intralayer node-level indices are available.

For multilayer fits of class "multimixMN_fit", what = "intra" returns intralayer node-level indices, whereas what = "inter" returns node-level indices computed on the interlayer-only graph. If what is not specified for a multilayer fit, both intralayer and interlayer node-level indices are returned by default, unless layer or pairs imply a specific scope.

The function returns the original estimates and, when available, bootstrap means, standard errors, and bootstrap quantile regions.

Usage

```
get_centrality(object, ...)

## S3 method for class 'mixMN_fit'
get_centrality(
  object,
  what = "intra",
  statistics = NULL,
  digits = NULL,
  drop_na_boot = TRUE,
  ...
)

## S3 method for class 'multimixMN_fit'
get_centrality(
  object,
  what = c("intra", "inter"),
```

```
  statistics = NULL,
  layer = NULL,
  pairs = NULL,
  digits = NULL,
  drop_na_boot = TRUE,
  ...
)
```

Arguments

object	A fitted object of class "mixMN_fit" or "multimixMN_fit".
...	Further arguments passed to methods.
what	Character string indicating which node-level indices to extract: • "intra": intralayer node-level indices; • "inter": interlayer-only node-level indices (available only for "multimixMN_fit" objects). For single layer fits, only "intra" is allowed. For multilayer fits, if omitted, both scopes are returned by default unless layer or pairs imply a specific scope.
statistics	Character vector specifying which node-level statistics to include.
digits	Optional number of digits used to round numeric columns.
drop_na_boot	Logical. If TRUE (default), bootstrap-related columns that are entirely NA are removed from the output.
layer	Optional character vector of layer names to subset. Relevant for intralayer output in multilayer fits.
pairs	Optional character vector of layer-pair names to subset. Relevant for interlayer output in multilayer fits.

Details

The returned data frame is in long format, with one row per node-statistic combination.

For single layer fits, only what = "intra" is available.

For multilayer fits, layer can be used to subset intralayer output, whereas pairs can be used to subset interlayer output.

The set of admissible statistics depends on what and on the class of object. In particular, bridge-related indices are available only for intralayer output.

Value

A tibble in long format with one row per node-statistic combination. It contains the columns:

- node
- layer
- scope
- metric

- estimated

When available, the output also contains bootstrap summary columns:

- mean.bootstrap
- SE.bootstrap
- quantile.lower.bootstrap
- quantile.upper.bootstrap

The quantile level used to compute the bootstrap quantile region is stored as the "quantile_level" attribute of the returned tibble.

---

get_edges *Extract edge-level summaries*

Description

Extracts edge-level summaries from fitted objects returned by mixMN() and multimixMN() in a long-format data frame.

For single layer fits of class "mixMN_fit", only intralayer edges are available.

For multilayer fits of class "multimixMN_fit", what = "intra" returns intralayer edges, whereas what = "inter" returns interlayer edges. If what is not specified for a multilayer fit, both scopes are returned by default, unless layer or pairs imply a specific scope.

The function returns the original edge weights and, when available, bootstrap means, standard errors, and bootstrap quantile regions.

Usage

```
get_edges(object, ...)

## S3 method for class 'mixMN_fit'
get_edges(object, what = "intra", digits = NULL, drop_na_boot = TRUE, ...)

## S3 method for class 'multimixMN_fit'
get_edges(
  object,
  what = c("intra", "inter"),
  layer = NULL,
  pairs = NULL,
  digits = NULL,
  drop_na_boot = TRUE,
  ...
)
```

Arguments

object	A fitted object of class "mixMN_fit" or "multimixMN_fit".
...	Further arguments passed to methods.
what	Character string indicating which edge-level summaries to extract: • "intra": intralayer edges; • "inter": interlayer edges (available only for "multimixMN_fit" objects). For single layer fits, only "intra" is allowed. For multilayer fits, if omitted, both scopes are returned by default unless layer or pairs imply a specific scope.
digits	Optional number of digits used to round numeric columns.
drop_na_boot	Logical. If TRUE (default), bootstrap-related columns that are entirely NA are removed from the output.
layer	Optional character vector of layer names to subset. Relevant for intralayer output in multilayer fits.
pairs	Optional character vector of layer-pair names to subset. Relevant for interlayer output in multilayer fits.

Details

The returned data frame is in long format, with one row per edge.

For single layer fits, only what = "intra" is available.

For multilayer fits, layer can be used to subset intralayer output, whereas pairs can be used to subset interlayer output.

Value

A tibble in long format with one row per edge. It contains the columns:

- edge
- layer for intralayer edges
- pairs for interlayer edges
- scope
- estimated

When available, the output also contains bootstrap summary columns:

- mean.bootstrap
- SE.bootstrap
- quantile.lower.bootstrap
- quantile.upper.bootstrap

The quantile level used to compute the bootstrap quantile region is stored as the "quantile_level" attribute of the returned tibble.

layer_slice *Extract a single layer from a multilayer MixMashNet object*

Description

Extracts one layer from a fitted multilayer `multimixMN_fit` object returned by `multimixMN()`.

The selected layer is returned as the corresponding single layer `mixMN_fit` object stored in `layer_fits`.

Usage

```
layer_slice(object, ...)

## S3 method for class 'multimixMN_fit'
layer_slice(object, layer, ...)
```

Arguments

`object`	An object of class `"multimixMN_fit"` returned by `multimixMN()`.
`...`	Further arguments passed to methods.
`layer`	Character string giving the layer to extract.

Value

An object of class `"mixMN_fit"` corresponding to the selected layer.

membershipStab *Node stability from bootstrap community assignments*

Description

Computes per-node stability given the empirical community structure and the homogenized bootstrap memberships contained in a `mixMN_fit` object. Stability is expressed as the proportion of bootstrap replications that assign each node to its empirical (original) community.

Usage

```
membershipStab(fit)
```

Arguments

`fit`	An object returned by `mixMN()` (class `mixMN_fit`), containing `$communities$original_membership` and `$communities$boot_memberships`. Bootstrap memberships must be available, i.e. `reps > 0` and `"community" %in% boot_what`.

Details

Bootstrap community labels are first aligned to the empirical solution using `EGAnet::community.homogenize()`. Stability is then computed node-wise as the proportion of bootstrap runs in which the node's community matches its empirical assignment.

The returned object has class `"membershipStab"` and provides `print()`, `summary()`, and `plot()` methods for quick inspection, descriptive summaries, and visualization of node stability.

Value

An object of class `c("membershipStab")`, with components:

`membership` List with:

- `empirical` Named integer vector of empirical community labels
- `bootstrap` Matrix of homogenized bootstrap labels (`reps` × `p`)

`membership.stability` List with:

- `empirical.dimensions` Named numeric vector of node-level stability (proportion assigned to empirical community)
- `all.dimensions` Matrix (`p` × `K`) with proportions of assignment to each community

`community_palette` Named vector of colors for communities, if available

References

Christensen, A. P., & Golino, H. (2021). Estimating the Stability of Psychological Dimensions via Bootstrap Exploratory Graph Analysis: A Monte Carlo Simulation and Tutorial. *Psych*, 3(3), 479–500. doi:10.3390/psych3030032

`mixMN` *Estimate single layer MGM network with bootstrap centrality, bridge metrics, clustering, and (optionally) community score loadings*

Description

Estimates a single layer Mixed Graphical Model (MGM) network on the original data, using the estimation framework implemented in the **mgm** package, and performs non-parametric bootstrap (row resampling) to compute centrality indices, bridge metrics, clustering stability, and quantile regions for node metrics and edge weights. Optionally, the function computes community score loadings (for later prediction on new data) and can bootstrap the corresponding loadings.

Usage

```
mixMN(
  data,
  reps = 100,
  scale = TRUE,
  lambdaSel = c("CV", "EBIC"),
```

```
  lambdaFolds = 5,
  lambdaGam = 0.25,
  alphaSeq = 1,
  alphaSel = "CV",
  alphaFolds = 5,
  alphaGam = 0.25,
  k = 2,
  ruleReg = "AND",
  threshold = "LW",
  overparameterize = FALSE,
  thresholdCat = TRUE,
  quantile_level = 0.95,
  covariates = NULL,
  exclude_from_cluster = NULL,
  treat_singletons_as_excluded = FALSE,
  seed_model = NULL,
  seed_boot = NULL,
  cluster_method = c("louvain", "edge_betweenness", "fast_greedy", "infomap",
   "label_prop", "leading_eigen", "leiden", "optimal", "spinglass", "walktrap"),
  cluster_args = list(),
  compute_loadings = TRUE,
  boot_what = c("general_index", "bridge_index", "excluded_index", "community",
    "loadings"),
  save_data = FALSE,
  progress = TRUE
)
```

Arguments

data	A data.frame (n x p) with variables in columns. Variables may be numeric, integer, logical, or factors. Character and Date/POSIXt variables are not supported and must be converted prior to model fitting. Variable types are internally mapped to MGM types as follows: continuous numeric (double) variables are treated as Gaussian; integer variables are treated as Poisson unless they take only values in {0,1}, in which case they are treated as binary categorical; factors and logical variables are treated as categorical. Binary categorical variables (two-level factors and logical variables) are internally recoded to {0,1} for model fitting. The original input data are not modified.
reps	Integer (>= 0). Number of bootstrap replications.
scale	Logical; if TRUE (default) Gaussian variables (type == "g") are z-standardized internally by mgm(). Use scale = FALSE if your data are already standardized.
lambdaSel	Method for lambda selection: "CV" or "EBIC".
lambdaFolds	Number of folds for CV (if lambdaSel = "CV").
lambdaGam	EBIC gamma parameter (if lambdaSel = "EBIC").
alphaSeq	Alpha parameters of the elastic net penalty (values between 0 and 1).
alphaSel	Method for selecting the alpha parameter: "CV" or "EBIC".

alphaFolds Number of folds for CV (if alphaSel = "CV").

alphaGam EBIC gamma parameter (if alphaSel = "EBIC").

k Integer (>= 1). Order of modeled interactions.

ruleReg Rule to combine neighborhood estimates: "AND" or "OR".

threshold Threshold below which edge-weights are set to zero: Available options are "LW", "HW", or "none". "LW" applies the threshold proposed by Loh & Wainwright; "HW" applies the threshold proposed by Haslbeck & Waldorp; "none" disables thresholding. Defaults to "LW".

overparameterize
Logical; controls how categorical interactions are parameterized in the neighborhood regressions. If TRUE, categorical interactions are represented using a fully over-parameterized design matrix (i.e., all category combinations are explicitly modeled). If FALSE, the standard glmnet parameterization is used, where one category serves as reference. For continuous variables, both parameterizations are equivalent. The default is FALSE. The over-parameterized option may be advantageous when distinguishing pairwise from higher-order interactions.

thresholdCat Logical; if FALSE thresholds of categorical variables are set to zero.

quantile_level Level of the central bootstrap quantile region (default 0.95). Must be a single number between 0 and 1.

covariates Character vector. Variables used as adjustment covariates in model estimation.

exclude_from_cluster
Character vector. Nodes excluded from community detection (in addition to covariates).

treat_singletons_as_excluded
Logical; if TRUE, singleton communities (size 1) are treated as excluded nodes when computing bridge metrics.

seed_model Optional integer seed for reproducibility of the initial MGM fit.

seed_boot Optional integer seed passed to future.apply for reproducibility of bootstrap replications.

cluster_method Community detection method used on the clustering graph. Either a character string naming one of the built-in methods "louvain", "edge_betweenness", "fast_greedy", "infomap", "label_prop", "leading_eigen", "leiden", "optimal", "spinglass", "walktrap", or a user-supplied function.

If a function is supplied, it must accept a graph through argument graph and return either an **igraph** communities object, a list with component membership, or a membership vector of length equal to the number of nodes used for clustering.

cluster_args Named list of additional arguments passed to the selected community detection method. For example, steps for "walktrap", nb.trials for "infomap", spins for "spinglass". Ignored if not relevant for the selected method.

compute_loadings
Logical; if TRUE (default), compute community loadings (EGAnet::net.loads). Only supported for Gaussian, Poisson, and binary categorical nodes; otherwise loadings are skipped and the reason is stored in community_loadings$reason.

boot_what	Character vector specifying which quantities to bootstrap. Valid options are: "general_index" (centrality indices), "bridge_index" (bridge metrics for nodes in communities), "excluded_index" (bridge metrics for nodes treated as excluded), "community" (community memberships), "loadings" (community loadings, only if compute_loadings = TRUE), and "none" (skip all node-level bootstrap: only edge-weight bootstrap is performed if reps > 0).
save_data	Logical; if TRUE, store the original data in the output object.
progress	Logical; if TRUE (default), show a bootstrap progress bar.

Details

This function does **not** call future::plan(). To enable parallel bootstrap, set a plan (e.g. future::plan(multisession)) before calling mixMN(). If boot_what is "none" and reps > 0, node-level metrics are not bootstrapped but edge-weight bootstrap and corresponding quantile regions are still computed.

Value

An object of class "mixMN_fit", that is a list with the following top-level components:

call The matched function call.

settings List of main settings used in the call, including reps, cluster_method, cluster_args, covariates, exclude_from_cluster, treat_singletons_as_excluded, and boot_what.

data_info List with information derived from the input data used for model setup: mgm_type_level (data frame with one row per variable, reporting the original R class and the inferred MGM type and level, as used in the call to mgm::mgm), and binary_recode_map (named list describing the mapping from original binary labels to the internal {0,1} coding used for model fitting).

model List with: mgm (the fitted mgm object), nodes (character vector of all node names), n (number of observations), p (number of variables), and data (if save_data = TRUE).

graph List describing the graph: igraph (an **igraph** object built on keep_nodes_graph, with edge attributes weight, abs_weight, sign and vertex attribute membership for communities), keep_nodes_graph (nodes retained in the graph and all node-level metrics), and keep_nodes_cluster (nodes used for community detection).

communities List describing community structure with: original_membership (integer vector of community labels on keep_nodes_cluster), groups (factor of community labels actually used for bridge metrics, optionally with singletons treated as excluded), palette (named vector of colors per community), and boot_memberships (list of bootstrap memberships if "community" is requested in boot_what, otherwise an empty list).

statistics List with node- and edge-level summaries: node is a list with: true (data frame with one row per node in keep_nodes_graph, containing the node name and metrics strength, ei1, closeness, betweenness, bridge_strength, bridge_betweenness, bridge_closeness, bridge_ei1, bridge_ei2, and for nodes treated as excluded from communities also bridge_strength_excluded, bridge_betweenness_excluded, bridge_closeness_excluded, bridge_ei1_excluded, bridge_ei2_excluded); boot (list of bootstrap matrices for each metric, each of dimension reps x length(keep_nodes_graph), possibly NULL if the metric was not requested or if reps = 0); and quantile_region (list of quantile regions for each node metric, one p x 2 matrix per metric, with columns corresponding to the lower and upper quantile bounds implied by quantile_level, or NULL if no bootstrap was performed).

edge is a list with: true (data frame with columns edge and weight for all unique undirected edges among keep_nodes_graph); boot (matrix of bootstrap edge weights of dimension n_edges x reps); and quantile_region (matrix of quantile regions for edge weights, n_edges x 2, with columns corresponding to the lower and upper bootstrap quantile bounds, or NULL if reps = 0).

community_loadings List containing community-loading information (based on EGAnet::net.loads) for later community-score computation on new data: nodes(nodes used for loadings), wc (factor of community labels aligned with nodes), true (matrix of standardized loadings, nodes x communities, or NULL if loadings were not computed.), boot (list of bootstrap loading matrices, one per replication, or NULL if not bootstrapped), available (logical indicating whether loadings were computed), reason (character string explaining why loadings were not computed, or NULL if available = TRUE), non_scorable_nodes (character vector of nodes in the community subgraph that prevented loadings from being computed (e.g., categorical variables with >2 levels), otherwise empty).

References

Haslbeck, J. M. B., & Waldorp, L. J. (2020). mgm: Estimating Time-Varying Mixed Graphical Models in High-Dimensional Data. *Journal of Statistical Software*, 93(8). doi:10.18637/jss.v093.i08

Loh, P. L., & Wainwright, M. J. (2012). Structure estimation for discrete graphicalmodels: Generalized covariance matrices and their inverses. *NIPS*

Examples

```
data(bacteremia)
df <- bacteremia[, !names(bacteremia) %in% "BloodCulture"]

fit <- mixMN(
  data = df,
  lambdaSel = "EBIC",
  lambdaGam = 0.25,
  reps = 0,
  seed_model = 42,
  cluster_method = "louvain",
  covariates = c("AGE", "SEX"),
  compute_loadings = FALSE,
  progress = FALSE
)
fit

# Plot the estimated network
set.seed(1)
plot(fit)


fit_b <- mixMN(
  data = df,
  lambdaSel = "EBIC",
  lambdaGam = 0.25,
```

```
  reps = 5,
  seed_model = 42,
  seed_boot =42,
  cluster_method = "louvain",
  covariates = c("AGE", "SEX"),
  boot_what = "community",
  compute_loadings = FALSE,
  progress = FALSE
)

# Plot the membership stability
plot(fit_b, what = "stability", cutoff = 0.7)
```

`multimixMN` *Multilayer MGM with bootstrap, intra/interlayer metrics, and quantile regions*

Description

Estimates a multilayer Mixed Graphical Model (MGM) using the estimation framework implemented in the **mgm** package, with a masking scheme that enforces which cross-layer edges are allowed according to `layer_rules`. Within each layer, the function computes community structure and performs non-parametric row-bootstrap to obtain node centrality indices, edge weights, and bridge metrics, including metrics for nodes treated as excluded. Optionally, within-layer community loadings can also be estimated and bootstrapped. The function additionally returns interlayer-only node metrics and summaries of cross-layer edge weights.

Usage

```
multimixMN(
  data,
  layers,
  layer_rules,
  scale = TRUE,
  reps = 100,
  lambdaSel = c("CV", "EBIC"),
  lambdaFolds = 5,
  lambdaGam = 0.25,
  alphaSeq = 1,
  alphaSel = "CV",
  alphaFolds = 5,
  alphaGam = 0.25,
  k = 2,
  ruleReg = "AND",
  threshold = "LW",
  overparameterize = FALSE,
```

```
  thresholdCat = TRUE,
  quantile_level = 0.95,
  covariates = NULL,
  exclude_from_cluster = NULL,
  seed_model = NULL,
  seed_boot = NULL,
  treat_singletons_as_excluded = FALSE,
  cluster_method = c("louvain", "edge_betweenness", "fast_greedy", "infomap",
   "label_prop", "leading_eigen", "leiden", "optimal", "spinglass", "walktrap"),
  cluster_args = list(),
  compute_loadings = TRUE,
 boot_what = c("general_index", "interlayer_index", "bridge_index", "excluded_index",
    "community", "loadings"),
  save_data = FALSE,
  progress = TRUE
)
```

Arguments

data	A data.frame (n x p) with variables in columns. Variables may be numeric, integer, logical, or factors. Character and Date/POSIXt variables are not supported and must be converted prior to model fitting. Variable types are internally mapped to MGM types as follows: continuous numeric (double) variables are treated as Gaussian; integer variables are treated as Poisson unless they take only values in {0,1}, in which case they are treated as binary categorical; factors and logical variables are treated as categorical. Binary categorical variables (two-level factors and logical variables) are internally recoded to {0,1} for model fitting. The original input data are not modified.
layers	A named vector (names = variable names) assigning each node to a layer (character or factor). Must cover all columns of data except variables listed in covariates (treated as adjustment covariates).
layer_rules	A square matrix (L × L), where L is the number of layers. Row and column names must match the layer names. Entries equal to TRUE or 1 allow cross-layer edges between the corresponding pair of layers, while FALSE or 0 disallow them. The matrix is symmetrized internally. Diagonal entries are ignored (intralayer edges are always permitted).
scale	Logical; if TRUE (default) Gaussian variables (type == "g") are z-standardized internally by mgm(). Use scale = FALSE if your data are already standardized.
reps	Integer (>= 0). Number of bootstrap replications (row resampling with replacement). If reps = 0, no bootstrap is performed.
lambdaSel	Method for lambda selection in mgm: "CV" or "EBIC".
lambdaFolds	Number of folds for CV (if lambdaSel = "CV").
lambdaGam	EBIC gamma parameter (if lambdaSel = "EBIC").
alphaSeq	Alpha parameters of the elastic net penalty (values between 0 and 1).
alphaSel	Method for selecting the alpha parameter: "CV" or "EBIC".
alphaFolds	Number of folds for CV (if alphaSel = "CV").

alphaGam — EBIC gamma parameter (if alphaSel = "EBIC").

k — Integer (>= 1). Order of modeled interactions.

ruleReg — Rule to combine neighborhood estimates: "AND" or "OR".

threshold — Threshold below which edge-weights are set to zero: Available options are "LW", "HW", or "none". "LW" applies the threshold proposed by Loh & Wainwright; "HW" applies the threshold proposed by Haslbeck & Waldorp; "none" disables thresholding. Defaults to "LW".

overparameterize — Logical; controls how categorical interactions are parameterized in the neighborhood regressions. If TRUE, categorical interactions are represented using a fully over-parameterized design matrix (i.e., all category combinations are explicitly modeled). If FALSE, the standard glmnet parameterization is used, where one category serves as reference. For continuous variables, both parameterizations are equivalent. The default is FALSE. The over-parameterized option may be advantageous when distinguishing pairwise from higher-order interactions.

thresholdCat — Logical; if FALSE thresholds of categorical variables are set to zero.

quantile_level — Level of the central bootstrap quantile region (default 0.95). Must be a single number between 0 and 1.

covariates — Character vector. Variables used as adjustment covariates in model estimation.

exclude_from_cluster — Character vector of node names. Nodes in this set are excluded from community detection in addition to covariates.

seed_model — Optional integer seed for reproducibility of the initial MGM fit.

seed_boot — Optional integer seed passed to future.apply for reproducibility of bootstrap replications.

treat_singletons_as_excluded — Logical; if TRUE, singleton communities (size 1) are treated as "excluded" when computing bridge metrics and related summaries.

cluster_method — Community detection method used within each layer. Either a character string naming one of the built-in methods "louvain", "edge_betweenness", "fast_greedy", "infomap", "label_prop", "leading_eigen", "leiden", "optimal", "spinglass", "walktrap", or a user-supplied function.

If a function is supplied, it must accept a graph through argument graph and return either an **igraph** communities object, a list with component membership, or a membership vector of length equal to the number of nodes used for clustering.

cluster_args — Named list of additional arguments passed to the selected community detection method. For example, steps for "walktrap", nb.trials for "infomap", spins for "spinglass". Ignored if not relevant for the selected method.

compute_loadings — Logical; if TRUE (default), compute community loadings (EGAnet::net.loads). Only supported for Gaussian, Poisson, and binary categorical nodes; otherwise loadings are skipped and the reason is stored in community_loadings$reason.

boot_what	Character vector specifying which quantities to bootstrap. Valid options are: "general_index" (intralayer centrality indices), "interlayer_index" (interlayer-only node metrics), "bridge_index" (bridge metrics for nodes in communities), "excluded_index" (bridge metrics for nodes treated as excluded), "community" (community memberships), "loadings" (within-layer community loadings, only if compute_loadings = TRUE), and "none" (skip all node-level bootstrap: only edge-weight bootstrap is performed if reps > 0).
save_data	Logical; if TRUE, store the original data in the output object.
progress	Logical; if TRUE (default), show a bootstrap progress bar.

Details

This function does **not** call future::plan(). To enable parallel bootstrap, set a plan (e.g. future::plan(multisession)) before calling multimixMN(). If "none" is the only element of boot_what and reps > 0, node-level metrics are not bootstrapped, but intra and interlayer edge-weight bootstrap and the corresponding quantile regions are still computed.

Value

An object of class "multimixMN_fit". The returned list contains at least the following components:

call The matched function call.

settings List of main settings used in the call, including reps, cluster_method, cluster_args, covariates, exclude_from_cluster, treat_singletons_as_excluded, boot_what).

data_info List with information derived from the input data used for model setup: mgm_type_level (data frame with one row per variable, reporting the original R class and the inferred MGM type and level, as used in the call to mgm::mgm), and binary_recode_map (named list describing the mapping from original binary labels to the internal {0,1} coding used for model fitting).

model List with: mgm (the fitted mgm object), nodes (character vector of all node names), n (number of observations), p (number of variables), and data (if save_data = TRUE))

layers List describing the multilayer structure (assignment of nodes to layers, layer_rules matrix used and color of each layer in palette).

layer_fits Named list (one element per layer) with single layer fits, including community structure, node-level statistics, edge-level statistics, bridge metrics, and (optionally) community loadings with bootstrap information.

interlayer List collecting interlayer-only node metrics (strength, expected influence, closeness, betweenness, with or without bootstrap) and cross-layer edge summaries for each allowed pair of layers.

graph List containing a global **igraph** object built on the retained nodes (keep_nodes_graph), with vertex attributes such as name, layer, membership, and edge attributes such as weight, abs_weight, sign, type (intra vs inter) and layer_pair.

References

Haslbeck, J. M. B., & Waldorp, L. J. (2020). mgm: Estimating Time-Varying Mixed Graphical Models in High-Dimensional Data. *Journal of Statistical Software*, 93(8). doi:10.18637/jss.v093.i08

Examples

```
data(nhanes)

bio_vars  <- c("ALT", "AST", "HDL", "HbA1c")
ant_vars  <- c("BMI", "Waist", "ArmCirc", "LegLength")
life_vars <- c("Smoke", "PhysicalActivity", "Drug")
covs      <- c("Age", "Gender", "MonInc")

df <- nhanes[, c(bio_vars, ant_vars, life_vars, covs)]

# Layer assignment (must cover all columns except covariates)
layers <- c(
  setNames(rep("bio",  length(bio_vars)),  bio_vars),
  setNames(rep("ant",  length(ant_vars)),  ant_vars),
  setNames(rep("life", length(life_vars)), life_vars)
)

# Allow cross-layer edges bio<->ant and ant<->life; disallow bio<->life
layer_rules <- matrix(0, nrow = 3, ncol = 3,
                      dimnames = list(c("bio","ant","life"),
                                      c("bio","ant","life")))
layer_rules["bio","ant"]  <- 1
layer_rules["ant","life"] <- 1

fitM <- multimixMN(
  data = df,
  layers = layers,
  layer_rules = layer_rules,
  covariates = covs,
  lambdaSel = "EBIC",
  lambdaGam = 0.25,
  reps = 5,
  seed_model = 42,
  seed_boot = 42,
  compute_loadings = FALSE,
  progress = FALSE
)
fitM

# Plot the estimated network
set.seed(1)
plot(fitM, color_by = "layer")
```

---

nhanes *NHANES-derived dataset for multilayer network analysis*

Description

Example dataset derived to illustrate multilayer network estimation in MixMashNet. This dataset contains 29 variables derived from the National Health and Nutrition Examination Survey (NHANES)

Usage

```
data(nhanes)
```

Format

A data frame with 2759 rows and 29 variables:

TotChol Total Cholesterol (numeric).

HDL High-density lipoprotein cholesterol (numeric).

Creatinine Creatinine (numeric).

UricAcid Uric acid (numeric).

ALT Alanine aminotransferase (numeric).

AST Aspartate aminotransferase (numeric).

GGT Gamma-glutamyl transferase (numeric).

Bilirubin Bilirubin (numeric).

Albumin Albumin (numeric).

TotProtein Total protein (numeric).

HbA1c Glycated hemoglobin (numeric).

hsCRP High-sensitivity C-reactive protein (numeric).

BMI Body mass index (numeric).

Waist waist circumference (numeric).

Height Height (numeric).

ArmCirc Arm circumference (numeric).

HipCirc Hip circumference (numeric).

LegLength Leg length (numeric).

ArmLength Arm Length (numeric).

TroubleSleep Trouble Sleep with 0=no and 1=yes.

PhysicalActivity Physical Activity with 0=no and 1=yes.

Smoke Smoking with 0=no and 1=yes.

Drug Drug use with 0=no and 1=yes.

Diet Dietary quality with 1=Poor, 2=Fair, 3=Good, 4=Very good, 5=Excellent.

Alcohol Alcohol consumption with 0=no and 1=yes.

Work Employment status with 1=working, 2=employed but absent, 3=seeking work, 4=not working.

MonInc Monthly income category (1–12), where higher values indicate higher income.

Gender Gender with 0=male and 1=female.

Age Age (numeric).

References

Centers for Disease Control and Prevention (CDC) & National Center for Health Statistics (NCHS). (2020). National Health and Nutrition Examination Survey data. https://www.cdc.gov/nchs/nhanes/

`plot.mixMN_fit` *Plot method for single layer MixMashNet objects*

Description

Plotting interface for objects returned by `mixMN()`.

Depending on `what`, the method can:

- `what = "network"`: plot the estimated single-layer network;
- `what = "intra"`: plot node-level metrics or edge weights with bootstrap quantile regions at the level stored in the object;
- `what = "stability"`: plot node stability within communities based on bootstrap community assignments.

Usage

```
## S3 method for class 'mixMN_fit'
plot(x, what = c("network", "intra", "stability"), ...)
```

Arguments

`x`	An object of class `"mixMN_fit"`, as returned by `mixMN()`.
`what`	Type of plot to produce. One of `c("network","intra","stability")`.
`...`	Additional arguments. Supported arguments depend on `what`: see the details below.

Details

Network plots (`what = "network"`): Supported arguments (via `...`):

`layout` Network layout. Either one of `c("fr","kk","circle")` or a numeric matrix with one row per node and at least two columns. If omitted, `"fr"` is used.

`color_by` Node coloring: `c("community","none")`.

`edge_color_by` Edge coloring: `c("sign","none")`.

`edge_scale` Numeric scaling factor for edge widths (multiplied by `abs(weight)`).

`graphics::plot.igraph` **arguments** e.g., `vertex.size`, `vertex.label.cex`, `edge.width`, `vertex.label.color`, etc.

Within-network statistics (`what = "intra"`): Plots node-level metrics or edge weights with bootstrap quantile regions.

Supported arguments (via `...`):

`statistics` Character vector of metrics. Options include: `"strength"`, `"expected_influence"`, `"closeness"`, `"betweenness"`, bridge metrics `"bridge_strength"`, `"bridge_ei1"`, `"bridge_ei2"`, `"bridge_closeness"`, `"bridge_betweenness"`, excluded bridge metrics `"bridge_strength_excluded"`, `"bridge_ei1_excluded"`, `"bridge_ei2_excluded"`, `"bridge_closeness_excluded"`, `"bridge_betweenness_exc` and `"edges"`. Different metric families cannot be mixed in the same call (e.g., `"edges"` cannot be combined with node metrics).

`ordering` Node ordering: `c("value","alphabetical","community")`.

`standardize` Logical; if `TRUE`, z-standardize the displayed values within the panel.

`exclude_nodes` Optional character vector of node names to remove before plotting.

`color_by_community` Logical; if `TRUE`, color nodes by community when available.

`edges_top_n` Integer; when `statistics = "edges"`, keep the top edges by absolute weight.

`title` Optional plot title.

Community membership stability (`what = "stability"`): Plots node stability by community.

Supported arguments (via `...`):

`title` Plot title. Default: `"Node Stability by Community"`.

`cutoff` Optional numeric threshold in $[0, 1]$ shown as a dashed vertical line. Use `NULL` to hide the line. Default: 0.7.

The quantile region level is taken from the fitted object (`x$settings$quantile_level`); if missing or invalid, a default of 0.95 is used.

Value

If `what != "network"`, the function returns a `ggplot` object. If `what = "network"`, the network is plotted directly.

See Also

`mixMN`

`plot.multimixMN_fit` *Plot method for multilayer MixMashNet objects*

Description

Plotting interface for objects returned by `multimixMN()`.

Depending on `what`, the method can:

- `what = "network"`: plot the estimated multilayer network, or a single layer if `layer` is specified;
- `what = "intra"`: plot intralayer node-level metrics or edge weights with bootstrap quantile regions;
- `what = "inter"`: plot interlayer node metrics or interlayer edge weights with bootstrap quantile regions;
- `what = "stability"`: plot node stability within communities based on bootstrap community assignments.

Usage

```
## S3 method for class 'multimixMN_fit'
plot(x, what = c("network", "intra", "inter", "stability"), layer = NULL, ...)
```

Arguments

x	An object of class "multimixMN_fit", as returned by multimixMN().
what	Type of plot to produce. One of c("network","intra","inter","stability").
layer	Optional layer name. For what = "intra" or what = "stability", this selects which layer-specific fit to use. For what = "network", if provided, the selected layer is plotted as a single-layer network; in this case, layout follows the single-layer behavior.
...	Additional arguments. Supported arguments depend on what: see the details below.

Details

Network plots (what = "network"**):** Supported arguments (via ...):

layout Layout used within each layer of the multilayer network. Either one of c("fr","kk","circle") applied to all layers, or a named list specifying a layout for selected layers. List elements can be layout names or numeric matrices with one row per node in the corresponding layer and at least two columns. Layer-specific layouts are then centered around fixed layer centroids. If omitted, "fr" is used.

color_by Node coloring: c("layer","community","none").

edge_color_by Edge coloring: c("sign","none").

edge_scale Numeric scaling factor for edge widths (multiplied by abs(weight)).

graphics::plot.igraph **arguments** e.g., vertex.size, vertex.label.cex, edge.width, vertex.label.color, etc.

Intralayer statistics (what = "intra"**):** Plots node-level metrics or edge weights with bootstrap quantile regions. If layer is provided, only that layer is plotted. If layer is NULL, all layers are plotted, one panel per layer.

Supported arguments (via ...):

statistics Character vector of metrics. Options include: "strength", "expected_influence", "closeness", "betweenness", bridge metrics "bridge_strength", "bridge_ei1", "bridge_ei2", "bridge_closeness", "bridge_betweenness", excluded bridge metrics "bridge_strength_excluded", "bridge_ei1_excluded", "bridge_ei2_excluded", "bridge_closeness_excluded", "bridge_betweenness_exc and "edges". Different metric families cannot be mixed in the same call (e.g., "edges" cannot be combined with node metrics).

ordering Node ordering: c("value","alphabetical","community").

standardize Logical; if TRUE, z-standardize the displayed values within each panel.

exclude_nodes Optional character vector of node names to remove before plotting.

color_by_community Logical; if TRUE, color nodes by community when available.

`edges_top_n` Integer; when `statistics = "edges"`, keep the top edges by absolute weight.

`title` Optional plot title. If omitted and multiple layers are shown, layer-specific titles are added automatically.

Interlayer summaries (`what = "inter"`): Plots interlayer node metrics or interlayer edge weights with bootstrap quantile regions.

Supported arguments (via `...`):

`statistics` Character vector. Node metrics: `c("strength","expected_influence","closeness","betweenness")`, or `"edges"` for interlayer edge weights. Node metrics and `"edges"` cannot be combined.

`pairs` Layer pairs to show. Either `"*"` (all available) or a character vector of pair keys like `"bio_dis"` (order-insensitive).

`edges_top_n` Integer; keep the top interlayer edges by absolute weight.

`ordering` Ordering within panels: `c("value","alphabetical")`.

`standardize` Logical; if `TRUE`, z-standardize values (node metrics by metric, edges by pair).

`exclude_nodes` Optional character vector; removes nodes and incident interlayer edges.

`nodes_layer` Optional layer name to restrict node metrics to nodes belonging to that layer.

`title` Optional plot title.

Community membership stability (`what = "stability"`): Plots node stability by community. If `layer` is provided, only that layer is shown. Otherwise, stability plots are shown for all layers.

Supported arguments (via `...`):

`title` Plot title. Default: `"Node Stability by Community"`.

`cutoff` Optional numeric threshold in $[0, 1]$ shown as a dashed vertical line. Use `NULL` to hide the line. Default: 0.7.

The quantile region level is taken from the fitted object (`x$settings$quantile_level`); if missing or invalid, a default of 0.95 is used.

Value

If `what != "network"`, the function returns a `ggplot` object. If `what = "network"`, the network is plotted directly.

See Also

`multimixMN`

print.mixMN_fit *Print method for single layer MixMashNet objects*

Description

Compact textual summary for objects returned by `mixMN()`.

Usage

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

Arguments

`x`	An object of class `"mixMN_fit"`.
`...`	Additional arguments.

Value

The input object `x`, returned invisibly.

See Also

`mixMN`

print.multimixMN_fit *Print method for multilayer MixMashNet objects*

Description

Compact textual summary for objects returned by `multimixMN()`.

Usage

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

Arguments

`x`	An object of class `"multimixMN_fit"`.
`...`	Additional arguments.

Value

The input object `x`, returned invisibly.

See Also

multimixMN

---

summary.mixMN_fit *Summarize top intralayer edges for single-layer MixMashNet fits*

Description

Returns the top 10 intralayer edges for fitted objects returned by mixMN(), in the same long-format structure used for edge summaries.

Usage

```
## S3 method for class 'mixMN_fit'
summary(object, top_n = 10L, digits = NULL, drop_na_boot = TRUE, ...)
```

Arguments

object	An object of class "mixMN_fit".
top_n	Number of top edges to retain. Default is 10.
digits	Optional number of digits used to round numeric columns.
drop_na_boot	Logical. If TRUE (default), bootstrap-related columns that are entirely NA are removed.
...	Further arguments for S3 compatibility.

Value

An object of class "summary.mixMN_fit" containing the top intralayer edges.

---

summary.multimixMN_fit

Summarize top interlayer edges for multilayer MixMashNet fits

---

Description

Returns the top 10 interlayer edges for fitted objects returned by multimixMN(), in the same long-format structure used for edge summaries.

Usage

```
## S3 method for class 'multimixMN_fit'
summary(object, top_n = 10L, digits = NULL, drop_na_boot = TRUE, ...)
```

Arguments

object	An object of class "multimixMN_fit".
top_n	Number of top edges to retain. Default is 10.
digits	Optional number of digits used to round numeric columns.
drop_na_boot	Logical. If TRUE (default), bootstrap-related columns that are entirely NA are removed.
...	Further arguments for S3 compatibility.

Value

An object of class "summary.multimixMN_fit" containing the top interlayer edges.

---

update_palette *Update community and layer color palettes in MixMashNet objects*

Description

Updates the color palettes associated with communities and/or layers in fitted mixMN_fit and multimixMN_fit objects.

For mixMN_fit objects, community_colors must be a named character vector specifying colors for community labels in object$communities$palette.

For multimixMN_fit objects, community_colors must be a named list whose elements correspond to layer names. Each element must be a named character vector specifying colors for the community labels of that layer. The list may be partial, so only the specified layers are updated.

For multimixMN_fit objects, layer_colors updates the palette stored in object$layers$palette.

The function replaces only the colors corresponding to the provided names, leaving all other colors unchanged. Unknown layer names, community labels, or layer labels are ignored with a warning.

Usage

```
update_palette(object, ...)

## S3 method for class 'mixMN_fit'
update_palette(object, community_colors = NULL, layer_colors = NULL, ...)

## S3 method for class 'multimixMN_fit'
update_palette(object, community_colors = NULL, layer_colors = NULL, ...)
```

Arguments

object	An object of class mixMN_fit or multimixMN_fit.
...	Further arguments passed to methods.

`community_colors`
: For `mixMN_fit` objects, an optional named character vector specifying new colors for communities.
For `multimixMN_fit` objects, an optional named list whose names are layer names and whose elements are named character vectors specifying new colors for communities within each layer.

`layer_colors`
: Optional named character vector specifying new colors for layers. Only applicable to `multimixMN_fit` objects.

Details

For single layer fits, only `community_colors` is used.

For multilayer fits:

- `community_colors` updates community palettes within the specified layers;
- `layer_colors` updates the palette of the layers themselves.

For multilayer fits, `community_colors` can be partial: layers not included in the list are left unchanged.

Value

The input object, with updated community and/or layer palettes.

Examples

```
data(bacteremia)

vars <- c("WBC", "NEU", "HGB", "PLT", "CRP")
df <- bacteremia[, vars]

fit <- mixMN(
  data = df,
  lambdaSel = "EBIC",
  reps = 0,
  seed_model = 42,
  compute_loadings = FALSE,
  progress = FALSE
)

fit$communities$palette

fit2 <- update_palette(
  fit,
  community_colors = c("1" = "red", "2" = "blue")
)

fit2$communities$palette

set.seed(1)
plot(fit2)
```

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