

Package: dynamicmultiplex (via r-universe)

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Title Community Detection for Evolving Multiplex Networks

Version 1.3.1

Description Multiplex temporal community detection with customizable interlayer coupling. Runs Louvain or Leiden community detection on each network layer and constructs interlayer ties using Jaccard similarity, overlap coefficient, node-strength weighted variants, or direct node identity links, and also provides a two-stage snapshot-and-match tracker that aligns independently detected per-layer communities across time with the Hungarian assignment algorithm. Supports user-specified layer connectivity via the `layer_links` argument, enabling adjacent-only temporal coupling that avoids the long-range pooling problem in standard multislice approaches.

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animate_multilayer_gif
<i>Animate multiplex networks as a GIF by layer</i>

Description

Creates one frame per layer and colors nodes by community using colorblind-friendly ColorBrewer palettes (Set2 or Dark2).

Usage

```
animate_multilayer_gif(  
  layers,  
  fit = NULL,  
  community_memberships = NULL,  
  output_file,  
  directed = FALSE,  
  fps = 2,  
  width = 800,  
  height = 600,  
  layout = "layout_with_fr",  
  palette = "Dark2"  
)
```

Arguments

layers	List of igraph objects or square adjacency matrices.
fit	Optional fit object from <code>fit_multilayer_jaccard()</code> , <code>fit_multilayer_overlap()</code> , or <code>fit_multilayer_identity_ties()</code> .
community_memberships	Optional list of membership vectors (one per layer). Ignored when <code>fit</code> is provided.
output_file	Output GIF file path. Required; the function writes the animation to this location and nowhere else. Use <code>tempfile(fileext = ".gif")</code> to write to the session temporary directory.
directed	Logical; if TRUE, adjacency matrices are treated as directed.
fps	Frames per second.
width	Width of GIF in pixels.
height	Height of GIF in pixels.
layout	igraph layout function name. Defaults to "layout_with_fr".
palette	ColorBrewer qualitative palette, one of "Set2" or "Dark2".

Value

The path to the created GIF.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("gganimate", quietly = TRUE) &&
    requireNamespace("gifski", quietly = TRUE)) {
  set.seed(123)
  layers <- lapply(1:3, function(i) {
    m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
    m <- pmax(m, t(m))
    diag(m) <- 0
    m
  })
  fit <- fit_multilayer_jaccard(layers, algorithm = "louvain")
  gif_path <- animate_multilayer_gif(
    layers,
    fit = fit,
    output_file = tempfile(fileext = ".gif"),
    fps = 2,
    width = 200,
    height = 150
  )
}
```

bootstrap_multilayer *Bootstrap confidence intervals for multilayer community detection*

Description

Quantifies the uncertainty of multilayer community detection by refitting communities on `n_boot` resampled networks, using a parametric network bootstrap: within- and between-community edge probabilities (and, for weighted networks, edge-weight pools) are estimated from the observed network using the point-estimate partition, and each replicate redraws the full edge set from those estimates. This reproduces the variability of fresh data, including which edges exist.

Uncertainty is quantified on the cross-layer *meta-communities* (the tracked partition from the second-stage detection), not the independently-detected per-layer communities. Co-assignment therefore answers "do these two nodes belong to the same persistent community," and the community count is the number of meta-communities per layer.

Versions before 1.1.0 instead used a Bayesian bootstrap on edge weights (Exponential(1) multipliers on a fixed topology). That scheme was removed: because it never varies which edges exist, it understates the variability of fresh data, and in simulation studies confidence intervals built from it undercovered substantially (pairwise co-assignment intervals covered ~45-48 percent at a nominal 95 percent).

Usage

```
bootstrap_multilayer(
  layers,
  fit_type = c("jaccard", "overlap", "weighted_jaccard", "weighted_overlap", "identity"),
  algorithm = c("louvain", "leiden"),
  n_boot = 100,
  layer_links = NULL,
  min_similarity = 0,
  resolution_parameter = 1,
  directed = FALSE,
  seed = NULL,
  objective = NULL
)
```

Arguments

<code>layers</code>	List of adjacency matrices or igraph objects.
<code>fit_type</code>	One of "jaccard", "overlap", "weighted_jaccard", "weighted_overlap", "identity".
<code>algorithm</code>	Community detection algorithm: "louvain" or "leiden".
<code>n_boot</code>	Number of bootstrap replicates.
<code>layer_links</code>	Optional data.frame defining layer connectivity.
<code>min_similarity</code>	Minimum weighted similarity for interlayer ties.

resolution_parameter	Resolution parameter for community detection.
directed	Logical; if TRUE, treat networks as directed.
seed	Optional random seed for reproducibility.
objective	One of "cpm" or "modularity" for directed networks only

Value

A list of class "multilayer_bootstrap" with components:

n_boot Number of completed bootstrap replicates.

co_assignment Per-layer co-assignment probability matrices on the meta-communities (probability two nodes share a persistent community).

node_stability Per-layer vectors giving the fraction of replicates in which each node was assigned to its modal community.

modularity_samples Per-layer vectors of bootstrap modularity values.

community_count_reproducibility Per-layer numeric vector: the share of completed replicates whose meta-community count equals the observed-network count. A descriptive stability measure. The raw per-replicate community counts are intentionally not returned.

stability_samples List with matrices nmi and ari (completed replicates x layers): agreement of each replicate's meta-partition with the point-estimate partition. Summarised by [partition_stability](#).

node_jaccard_stability Per-layer vectors: for each node, the mean Jaccard overlap between its replicate community and its point-estimate community.

point_estimate The fit result from the original data.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
boot <- bootstrap_multilayer(
  layers,
  fit_type = "jaccard",
  algorithm = "louvain",
  n_boot = 5,
  seed = 123
)
names(boot)
```

co_assignment_ci

Descriptive Monte Carlo interval for node-pair co-assignment

Description

For every pair of nodes in every layer, returns the bootstrap co-assignment share (the fraction of replicates in which the pair landed in the same meta-community) with a Wilson score interval treating the replicates as binomial draws.

Read this interval as a diagnostic, not as a calibrated confidence interval. In the package's simulation study its width shrinks with the number of replicates while its coverage of the fresh-data co-assignment propensity was near nominal only for pairs whose share is close to 0 or 1 and fell to 0.03-0.15 for ambiguous pairs (share between 0.3 and 0.8). No conditioning or alternative bootstrap repaired this, so versions from 1.3.0 no longer offer a "calibrated" pair interval. The validated reliability product is [partition_stability](#): a stability score for the tracked partition with a calibrated lower bound on its accuracy, plus a decided / undetermined flag for each pair.

Usage

```
co_assignment_ci(
  boot_result,
  alpha = 0.05,
  method = c("wilson", "calibrated"),
  calibration_table = NULL
)
```

Arguments

boot_result	Output from bootstrap_multilayer .
alpha	Significance level; alpha = 0.05 gives 95 percent Wilson intervals.
method	"wilson". "calibrated" is accepted only to raise an informative error pointing to partition_stability() .
calibration_table	Ignored; retained for backward compatibility.

Value

A list with one element per layer. Each element is a list with components:

estimate n x n matrix of co-assignment shares.

lower n x n matrix of interval lower bounds.

upper n x n matrix of interval upper bounds.

Diagonals are 1 by construction. The list carries the attribute "method".

See Also

[partition_stability](#) for the calibrated reliability score; [community_est](#) for community-count summaries.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
boot <- bootstrap_multilayer(
  layers,
  fit_type = "jaccard",
  algorithm = "louvain",
  n_boot = 5,
  seed = 123
)
pci <- co_assignment_ci(boot)
pci[[1]]$estimate[1:4, 1:4]
```

community_est	<i>Summarize bootstrap community-count reproducibility (meta-communities)</i>
---------------	---

Description

Reports, for each layer, the community count from the observed network together with its *bootstrap reproducibility*: the proportion of bootstrap replicates in which the fitted number of communities equals the observed-network count. It also returns mean node stability, per-node stability, and the co-assignment matrices.

Usage

```
community_est(boot_result)
```

Arguments

boot_result Output from [bootstrap_multilayer](#).

Value

A list with components:

community_count Data frame with columns layer, estimate (the observed-network meta-community count), and reproducibility (share of bootstrap replicates whose community count equals estimate, in [0, 1]).

report Character vector, one plain-language sentence per layer.

mean_node_stability Data frame with columns layer, mean_stability.

node_stability Per-layer stability vectors.

co_assignment Per-layer co-assignment matrices.

Why this is not a confidence interval

Earlier versions returned a percentile `community_count_ci`. It was replaced in version 1.1.0 with a reproducibility summary because the interval's coverage is not robust to model misspecification. In a large simulation study the nominal 95 percent community-count interval covered the truth at or above the nominal level on well-specified planted-partition networks (about 0.99 for $n \geq 100$ nodes), but coverage collapsed to about 0.62 when community sizes were strongly skewed, and no observable diagnostic reliably separated the trustworthy cases from the rest. Rather than ship an interval that silently undercovers, the function now reports how often the community count reproduces under resampling. This is a descriptive stability measure, not a calibrated interval: it makes no claim about the probability that any range contains the true community count. For a calibrated reliability measure use [partition_stability](#), which bounds the accuracy of the tracked partition from below. The raw per-replicate community counts are intentionally not exposed anywhere in the package output; only this reproducibility summary is returned.

See Also

[partition_stability](#) for the calibrated reliability score of the tracked partition.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
boot <- bootstrap_multilayer(
  layers,
  fit_type = "jaccard",
  algorithm = "louvain",
  n_boot = 5,
  seed = 123
)
est <- community_est(boot)
est$community_count
est$report
```

`extract_meta_membership`*Extract cross-layer meta-community membership*

Description

Returns the tracked (cross-layer) community assignment produced by the second-stage detection: for each layer, a vector giving every node's meta-community. Unlike the per-layer `layer_communities` (detected independently, ignoring the coupling), the meta-communities are the partition that reflects the interlayer ties and any custom `layer_links`. This is the membership that `bootstrap_multilayer` validates.

Usage

```
extract_meta_membership(fit)
```

Arguments

`fit` A fit object from one of the `fit_multilayer_*` functions.

Value

A list with one integer vector per layer giving each node's meta-community assignment (node order).

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m)); diag(m) <- 0; m
})
fit <- fit_multilayer_jaccard(layers, algorithm = "leiden")
extract_meta_membership(fit)
```

`fit_multilayer_hungarian`*Fit multilayer communities with Hungarian snapshot matching*

Description

Detects communities independently in each layer and then tracks them across time by matching community labels between consecutive layers with the Hungarian (optimal linear-sum assignment) algorithm applied to the community overlap (contingency) matrix. This is a two-stage *snapshot-and-match* tracker: unlike the coupling-based fits ([fit_multilayer_jaccard](#), [fit_multilayer_overlap](#), [fit_multilayer_identity_ties](#)), communities are found per layer and aligned *post hoc*, not jointly optimised on a coupled supra-graph. It provides the common "independent detection + optimal label matching" baseline (e.g. per-layer Leiden matched with the Hungarian algorithm) as a first-class method with the same interface as the other fits.

Usage

```
fit_multilayer_hungarian(
  layers,
  algorithm = c("louvain", "leiden"),
  resolution_parameter = 1,
  directed = FALSE,
  objective = NULL,
  seed = NULL
)
```

Arguments

layers	List of igraph objects or square adjacency matrices.
algorithm	Community algorithm: "louvain" or "leiden".
resolution_parameter	Leiden resolution parameter.
directed	Logical; if TRUE, build directed graphs from adjacency matrices (collapsed to undirected for detection, as elsewhere in the package).
objective	One of "cpm" or "modularity" (directed networks only).
seed	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call <code>set.seed()</code> beforehand for reproducibility).

Details

Matching is sequential: layer t is aligned to layer $t - 1$. For each adjacent pair the community overlap matrix is completed to a square cost matrix and [solve_LSAP](#) maximises total overlap; unmatched current communities receive fresh labels. The result is a consistently-labelled sequence suitable for [extract_meta_membership](#), [bootstrap_multilayer](#), and the plotting helpers.

Value

A list of class "multilayer_community_fit" with components:

layer_communities Per-layer community detection (each with membership and communities), detected independently.

meta_communities The tracked partition: one integer vector per layer where labels are aligned across consecutive layers by Hungarian matching on community overlap. A community with no positive-overlap match is given a new label (a birth); labels not carried forward are treated as deaths. See [extract_meta_membership](#).

interlayer_ties NULL - no coupled supra-graph is built.

method "hungarian".

layer_links Sequential adjacent-layer links (the chain the matcher walks).

See Also

[fit_multilayer_jaccard](#), [fit_multilayer_overlap](#), [fit_multilayer_identity_ties](#) for coupling-based tracking.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m)); diag(m) <- 0; m
})
fit <- fit_multilayer_hungarian(layers, algorithm = "leiden")
extract_meta_membership(fit)
```

fit_multilayer_identity_ties

Fit multilayer communities with identity interlayer ties

Description

Runs Louvain or Leiden community detection for each layer and creates interlayer ties between the same node in selected adjacent layers. With `allow_unequal_nodes = TRUE`, layers may contain different node sets; only nodes present in both layers of a linked pair receive interlayer edges. Nodes are matched by $V(g)$name when available, or by vertex index otherwise.$

For this specification the cross-layer meta_communities are obtained by **Mucha et al. (2010) multislice modularity**: each layer keeps its own configuration null model ($k_{is}k_{js}/2m_s$), interlayer identity ties (each node to its copies in the coupled layers, weight = layer-link weight times omega) carry no null term, and the objective is optimised with a generalized Louvain (local moving + aggregation, random restarts). Versions before 1.2.1 ran plain single-graph modularity on the stacked supra-graph, which is a different objective and returns each layer as one community at $\omega \leq 1$.

Usage

```
fit_multilayer_identity_ties(
  layers,
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
  resolution_parameter = 1,
  omega = 1,
  directed = FALSE,
  objective = NULL,
  seed = NULL,
  allow_unequal_nodes = FALSE
)
```

Arguments

layers	List of igraph objects or square adjacency matrices.
algorithm	Community algorithm for the per-layer (first-stage) partitions: "louvain" or "leiden". The multislice meta-communities always use the generalized Louvain optimiser.
layer_links	Optional data.frame defining which layers to connect, with columns from, to, and optional weight. If NULL, adjacent layers are connected in sequence.
resolution_parameter	Leiden resolution parameter. Also forwarded to the multislice supra-graph detection as Mucha's modularity resolution (larger values yield more, smaller meta-communities).
omega	Interlayer coupling strength for the multislice supra-graph (Mucha's omega). Multiplies the interlayer identity-edge weights on top of any layer_links weights. Larger omega couples layers more strongly and, past a point, collapses everything into one meta-community; smaller omega decouples toward independent per-layer detection. Use to probe the omega-sensitivity / resolution-limit behavior of multislice modularity.
directed	Logical; if TRUE, build directed graphs from adjacency matrices. Directed layers are collapsed to undirected weighted graphs before community detection (igraph supports Leiden on undirected graphs only; a warning is issued for algorithm = "leiden").
objective	One of "cpm" or "modularity" for directed networks only
seed	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call set.seed() beforehand for reproducibility).
allow_unequal_nodes	Logical; if TRUE, layers may contain different node sets (nodes entering or exiting the system), and only nodes present in both layers of a linked pair receive interlayer edges. Defaults to FALSE: layers must share the same node universe, as in the other fit functions.

Value

A list of class "multilayer_community_fit" with components:

layer_communities Per-layer community detection (each with membership and communities). Detected independently per layer.

meta_communities The cross-layer tracked partition from the second-stage detection: one integer vector per layer giving each node's meta-community. This is the membership that reflects the interlayer ties and any custom layer_links, and the one validated by [bootstrap_multilayer](#). See [extract_meta_membership](#).

interlayer_ties Interlayer similarity edges between communities (plus self-loops).

layer_links The layer connectivity used.

Directed networks

Directed layers are stored as directed graphs and the interlayer self-loop weighting is directed-aware, but community *detection* collapses directed layers to weighted undirected graphs on both Louvain and Leiden (igraph's detectors are undirected-only). For detection that respects edge direction, use the Python package with algorithm = "leiden".

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
fit <- fit_multilayer_identity_ties(layers, algorithm = "louvain")
names(fit)
```

fit_multilayer_jaccard

Fit multilayer communities and interlayer weighted Jaccard ties

Description

Runs Louvain or Leiden community detection for each layer and creates interlayer ties between communities in selected layer pairs using weighted Jaccard similarity.

Usage

```
fit_multilayer_jaccard(
  layers,
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
```

```

    min_similarity = 0,
    resolution_parameter = 1,
    directed = FALSE,
    add_self_loops = TRUE,
    self_loop_multiplier = 1,
    objective = NULL,
    seed = NULL,
    allow_unequal_nodes = FALSE
)

```

Arguments

<code>layers</code>	List of igraph objects or square adjacency matrices.
<code>algorithm</code>	Community algorithm: "louvain" or "leiden".
<code>layer_links</code>	Optional data.frame defining which layers to connect, with columns from, to, and optional weight. If NULL, adjacent layers are connected in sequence.
<code>min_similarity</code>	Minimum weighted similarity required to keep an interlayer tie.
<code>resolution_parameter</code>	Leiden resolution parameter.
<code>directed</code>	Logical; if TRUE, build directed graphs from adjacency matrices. Directed layers are collapsed to undirected weighted graphs before community detection (igraph supports Leiden on undirected graphs only; a warning is issued for <code>algorithm = "leiden"</code>).
<code>add_self_loops</code>	Logical; if TRUE, add intra-layer community self-loop ties after similarity computation to mimic aggregation behavior.
<code>self_loop_multiplier</code>	Numeric multiplier applied to self-loop weighted ties. The default 1 yields self-loop weighted similarity of $2 * \text{layer_weight}$ for undirected or $1 * \text{layer_weight}$ for directed networks, following the Louvain/Leiden community aggregation convention.
<code>objective</code>	One of "cpm" or "modularity" for directed networks only
<code>seed</code>	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call <code>set.seed()</code> beforehand for reproducibility).
<code>allow_unequal_nodes</code>	Logical; if TRUE, layers may contain different node sets (nodes entering or exiting the system). Layers must then carry vertex names (or row names on the adjacency matrices) so nodes can be matched across layers; only nodes present in both layers of a linked pair contribute to the interlayer similarity. Defaults to FALSE: layers must share the same node universe.

Value

A list of class "multilayer_community_fit" with components:

layer_communities Per-layer community detection (each with membership and communities).
Detected independently per layer.

meta_communities The cross-layer tracked partition from the second-stage detection: one integer vector per layer giving each node's meta-community. This is the membership that reflects the interlayer ties and any custom layer_links, and the one validated by [bootstrap_multilayer](#). See [extract_meta_membership](#).

interlayer_ties Interlayer similarity edges between communities (plus self-loops).

layer_links The layer connectivity used.

Directed networks

Directed layers are stored as directed graphs and the interlayer self-loop weighting is directed-aware, but community *detection* collapses directed layers to weighted undirected graphs on both Louvain and Leiden (igraph's detectors are undirected-only). For detection that respects edge direction, use the Python package with `algorithm = "leiden"`.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
fit <- fit_multilayer_jaccard(layers, algorithm = "louvain")
names(fit)
fit$layer_communities[[1]]$membership
```

fit_multilayer_overlap

Fit multilayer communities and interlayer weighted overlap ties

Description

Runs Louvain or Leiden community detection for each layer and creates interlayer ties between communities in selected layer pairs using a weighted overlap coefficient.

Usage

```
fit_multilayer_overlap(
  layers,
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
  min_similarity = 0,
  resolution_parameter = 1,
  directed = FALSE,
  add_self_loops = TRUE,
  self_loop_multiplier = 1,
  objective = NULL,
  seed = NULL,
  allow_unequal_nodes = FALSE
)
```

Arguments

layers	List of igraph objects or square adjacency matrices.
algorithm	Community algorithm: "louvain" or "leiden".
layer_links	Optional data.frame defining which layers to connect, with columns from, to, and optional weight. If NULL, adjacent layers are connected in sequence.
min_similarity	Minimum weighted similarity required to keep an interlayer tie.
resolution_parameter	Leiden resolution parameter.
directed	Logical; if TRUE, build directed graphs from adjacency matrices. Directed layers are collapsed to undirected weighted graphs before community detection (igraph supports Leiden on undirected graphs only; a warning is issued for algorithm = "leiden").
add_self_loops	Logical; if TRUE, add intra-layer community self-loop ties after similarity computation to mimic aggregation behavior.
self_loop_multiplier	Numeric multiplier applied to self-loop weighted ties. The default 1 yields self-loop weighted similarity of $2 * \text{layer_weight}$ for undirected or $1 * \text{layer_weight}$ for directed networks, following the Louvain/Leiden community aggregation convention.
objective	One of "cpm" or "modularity" for directed networks only
seed	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call <code>set.seed()</code> beforehand for reproducibility).
allow_unequal_nodes	Logical; if TRUE, layers may contain different node sets (nodes entering or exiting the system). Layers must then carry vertex names (or row names on the

adjacency matrices) so nodes can be matched across layers; only nodes present in both layers of a linked pair contribute to the interlayer similarity. Defaults to FALSE: layers must share the same node universe.

Value

A list of class "multilayer_community_fit" with components:

layer_communities Per-layer community detection (each with membership and communities). Detected independently per layer.

meta_communities The cross-layer tracked partition from the second-stage detection: one integer vector per layer giving each node's meta-community. This is the membership that reflects the interlayer ties and any custom layer_links, and the one validated by [bootstrap_multilayer](#). See [extract_meta_membership](#).

interlayer_ties Interlayer similarity edges between communities (plus self-loops).

layer_links The layer connectivity used.

Directed networks

Directed layers are stored as directed graphs and the interlayer self-loop weighting is directed-aware, but community *detection* collapses directed layers to weighted undirected graphs on both Louvain and Leiden (igraph's detectors are undirected-only). For detection that respects edge direction, use the Python package with algorithm = "leiden".

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
  m <- pmax(m, t(m))
  diag(m) <- 0
  m
})
fit <- fit_multilayer_overlap(layers, algorithm = "louvain")
names(fit)
```

fit_multilayer_weighted_jaccard

Fit multilayer communities and interlayer node-strength weighted Jaccard ties

Description

Runs Louvain or Leiden community detection for each layer and creates interlayer ties between communities in selected layer pairs using node-strength weighted Jaccard similarity.

Usage

```
fit_multilayer_weighted_jaccard(
  layers,
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
  min_similarity = 0,
  resolution_parameter = 1,
  directed = FALSE,
  add_self_loops = TRUE,
  self_loop_multiplier = 1,
  objective = NULL,
  seed = NULL,
  allow_unequal_nodes = FALSE
)
```

Arguments

<code>layers</code>	List of igraph objects or square adjacency matrices.
<code>algorithm</code>	Community algorithm: "louvain" or "leiden".
<code>layer_links</code>	Optional data.frame defining which layers to connect, with columns from, to, and optional weight. If NULL, adjacent layers are connected in sequence.
<code>min_similarity</code>	Minimum weighted similarity required to keep an interlayer tie.
<code>resolution_parameter</code>	Leiden resolution parameter.
<code>directed</code>	Logical; if TRUE, build directed graphs from adjacency matrices.
<code>add_self_loops</code>	Logical; if TRUE, add intra-layer community self-loop ties.
<code>self_loop_multiplier</code>	Numeric multiplier applied to self-loop weighted ties.
<code>objective</code>	One of "cpm" or "modularity" for directed networks only
<code>seed</code>	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call <code>set.seed()</code> beforehand for reproducibility).
<code>allow_unequal_nodes</code>	Logical; if TRUE, layers may contain different node sets (nodes entering or exiting the system). Layers must then carry vertex names (or row names on the adjacency matrices) so nodes can be matched across layers; only nodes present in both layers of a linked pair contribute to the interlayer similarity. Defaults to FALSE: layers must share the same node universe.

Value

A list of class "multilayer_community_fit" with components:

layer_communities Per-layer community detection (each with membership and communities). Detected independently per layer.

meta_communities The cross-layer tracked partition from the second-stage detection: one integer vector per layer giving each node's meta-community. This is the membership that reflects the interlayer ties and any custom layer_links, and the one validated by [bootstrap_multilayer](#). See [extract_meta_membership](#).

interlayer_ties Interlayer similarity edges between communities (plus self-loops).

layer_links The layer connectivity used.

Directed networks

Directed layers are stored as directed graphs and the interlayer self-loop weighting is directed-aware, but community *detection* collapses directed layers to weighted undirected graphs on both Louvain and Leiden (igraph's detectors are undirected-only). For detection that respects edge direction, use the Python package with algorithm = "leiden".

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  w <- matrix(runif(64), 8, 8) * matrix(rbinom(64, 1, 0.35), 8, 8)
  w <- (w + t(w)) / 2
  diag(w) <- 0
  w
})
fit <- fit_multilayer_weighted_jaccard(layers, algorithm = "louvain")
names(fit)
```

fit_multilayer_weighted_overlap

Fit multilayer communities and interlayer node-strength weighted overlap ties

Description

Runs Louvain or Leiden community detection for each layer and creates interlayer ties between communities in selected layer pairs using node-strength weighted overlap coefficient.

Usage

```
fit_multilayer_weighted_overlap(
  layers,
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
  min_similarity = 0,
  resolution_parameter = 1,
```

```

    directed = FALSE,
    add_self_loops = TRUE,
    self_loop_multiplier = 1,
    objective = NULL,
    seed = NULL,
    allow_unequal_nodes = FALSE
)

```

Arguments

layers	List of igraph objects or square adjacency matrices.
algorithm	Community algorithm: "louvain" or "leiden".
layer_links	Optional data.frame defining which layers to connect, with columns from, to, and optional weight. If NULL, adjacent layers are connected in sequence.
min_similarity	Minimum weighted similarity required to keep an interlayer tie.
resolution_parameter	Leiden resolution parameter.
directed	Logical; if TRUE, build directed graphs from adjacency matrices.
add_self_loops	Logical; if TRUE, add intra-layer community self-loop ties.
self_loop_multiplier	Numeric multiplier applied to self-loop weighted ties.
objective	One of "cpm" or "modularity" for directed networks only
seed	Optional integer seed for reproducible community detection. When supplied, the global RNG state is saved, the RNG is seeded for the duration of the call, and the previous state is restored on exit, so the caller's random number stream (e.g. bootstrap resampling) is unaffected. Defaults to NULL (detection inherits the caller's RNG stream, matching previous behavior; call <code>set.seed()</code> beforehand for reproducibility).
allow_unequal_nodes	Logical; if TRUE, layers may contain different node sets (nodes entering or exiting the system). Layers must then carry vertex names (or row names on the adjacency matrices) so nodes can be matched across layers; only nodes present in both layers of a linked pair contribute to the interlayer similarity. Defaults to FALSE: layers must share the same node universe.

Value

A list of class "multilayer_community_fit" with components:

- layer_communities** Per-layer community detection (each with membership and communities). Detected independently per layer.
- meta_communities** The cross-layer tracked partition from the second-stage detection: one integer vector per layer giving each node's meta-community. This is the membership that reflects the interlayer ties and any custom `layer_links`, and the one validated by [bootstrap_multilayer](#). See [extract_meta_membership](#).
- interlayer_ties** Interlayer similarity edges between communities (plus self-loops).
- layer_links** The layer connectivity used.

Directed networks

Directed layers are stored as directed graphs and the interlayer self-loop weighting is directed-aware, but community *detection* collapses directed layers to weighted undirected graphs on both Louvain and Leiden (igraph's detectors are undirected-only). For detection that respects edge direction, use the Python package with `algorithm = "leiden"`.

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  w <- matrix(runif(64), 8, 8) * matrix(rbinom(64, 1, 0.35), 8, 8)
  w <- (w + t(w)) / 2
  diag(w) <- 0
  w
})
fit <- fit_multilayer_weighted_overlap(layers, algorithm = "louvain")
names(fit)
```

partition_stability	<i>Stability score and calibrated accuracy floor for a tracked partition</i>
---------------------	--

Description

Summarises a `bootstrap_multilayer` result into one reliability report for the recovered (tracked) partition:

1. **Stability score** *s*: the mean agreement (NMI by default, or ARI) between each bootstrap replicate's meta-partition and the point-estimate meta-partition, averaged over layers.
2. **Accuracy floor**: a calibrated lower bound on the accuracy of the point-estimate partition against the (unknown) truth. In the package's simulation study, fits were binned by *s* and the 5th percentile of accuracy (NMI or ARI to the planted partition) recorded in each bin on a calibration half of the configurations. On the held-out half, accuracy exceeded the floor in 95 percent of fits, in every bin. The floor is therefore read as "with this stability, partition accuracy was at least this value 95 percent of the time in calibration".
3. **Node-level stability**: per node, the mean Jaccard overlap between its replicate community and its point-estimate community, with a calibrated floor on node-level accuracy that is reported only above stability 0.9 (below that the floor is uninformative).
4. **Decided pairs**: per layer, node pairs whose bootstrap co-assignment share is below `decided[1]` (decidedly apart) or above `decided[2]` (decidedly together); everything in between is undetermined. No interval is attached to pairs: pair-level intervals were found not to be calibratable for ambiguous pairs.

The calibration is within the simulated family (planted-partition networks with node switching, sizes 50-400, 3-10 communities, 5-15 layers). On networks whose structure the planted-partition model does not describe, a stable but wrong partition could receive a floor it does not deserve; the accompanying paper reports the degree-corrected and weighted robustness arms.

Usage

```
partition_stability(
  boot_result,
  metric = c("nmi", "ari"),
  decided = c(0.1, 0.9),
  calibration_table = NULL
)
```

Arguments

<code>boot_result</code>	Output from bootstrap_multilayer (version 1.3.0 or later, which records <code>stability_samples</code>).
<code>metric</code>	"nmi" (default) or "ari": the agreement measure for the partition-level score and floor.
<code>decided</code>	Length-2 numeric: co-assignment shares at or below the first value are "apart", at or above the second are "together".
<code>calibration_table</code>	Optional path or data frame overriding the bundled table (<code>inst/extdata/stability_calibration_table</code>); columns <code>level</code> , <code>stab_lo</code> , <code>stab_hi</code> , <code>n_calib</code> , <code>acc_median</code> , <code>acc_q05</code> .

Value

A list of class "partition_stability":

stability Partition stability score s (mean over replicates and layers).

stability_by_layer Per-layer mean agreement.

stability_mc_se Monte Carlo standard error of s from the replicate spread (about 0.02 at 100 replicates).

floor Calibrated 5th-percentile accuracy for the bin containing s ; `floor_median` is the median accuracy in that bin.

bin The stability bin used, as "[lo, hi)".

node Per-layer data frames with `node`, `stability` (Jaccard) and `floor` (NA below 0.9).

pairs Per-layer integer matrices: 1 = decidedly together, -1 = decidedly apart, 0 = undetermined; `pair_summary` gives the shares.

report One-sentence plain-language summary.

See Also

[bootstrap_multilayer](#), [community_est](#)

Examples

```
set.seed(123)
layers <- lapply(1:3, function(i) {
  m <- matrix(rbinom(400, 1, 0.3), nrow = 20)
  m <- pmax(m, t(m)); diag(m) <- 0; m
})
boot <- bootstrap_multilayer(layers, fit_type = "jaccard",
```

```

                                algorithm = "leiden", n_boot = 10, seed = 123)
ps <- partition_stability(boot)
ps$stability; ps$floor; ps$report

```

plot_multilayer_alluvial

Plot an alluvial view of community transitions over time

Description

Plot an alluvial view of community transitions over time

Usage

```
plot_multilayer_alluvial(fit, max_nodes = NULL, palette = "Dark2")
```

Arguments

fit	Fit object from fit_multilayer_jaccard(), fit_multilayer_overlap(), or fit_multilayer_identity_ties().
max_nodes	Optional cap on number of nodes to include for readability.
palette	ColorBrewer qualitative palette, one of "Set2" or "Dark2".

Value

A ggplot object.

Examples

```

if (requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("ggalluvial", quietly = TRUE)) {
  set.seed(123)
  layers <- lapply(1:3, function(i) {
    m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
    m <- pmax(m, t(m))
    diag(m) <- 0
    m
  })
  fit <- fit_multilayer_jaccard(layers, algorithm = "louvain")
  p <- plot_multilayer_alluvial(fit)
}

```

plot_multilayer_series

Plot multiplex networks as wrapped panels

Description

Draws one panel per layer with nodes colored by community assignment, using a faceted/wrapped layout.

Usage

```
plot_multilayer_series(
  layers,
  fit = NULL,
  community_memberships = NULL,
  directed = FALSE,
  layout = "layout_with_fr",
  ncol = 3,
  palette = "Dark2"
)
```

Arguments

layers	List of igraph objects or square adjacency matrices.
fit	Optional fit object from <code>fit_multilayer_jaccard()</code> , <code>fit_multilayer_overlap()</code> , or <code>fit_multilayer_identity_ties()</code> .
community_memberships	Optional list of membership vectors (one per layer). Ignored when <code>fit</code> is provided.
directed	Logical; if TRUE, adjacency matrices are treated as directed.
layout	igraph layout function name. Defaults to "layout_with_fr".
ncol	Number of wrap columns in the panel layout.
palette	ColorBrewer qualitative palette, one of "Set2" or "Dark2".

Value

A ggplot object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  set.seed(123)
  layers <- lapply(1:3, function(i) {
    m <- matrix(rbinom(64, 1, 0.35), nrow = 8)
    m <- pmax(m, t(m))
    diag(m) <- 0
  })
}
```

```

      m
    })
    fit <- fit_multilayer_jaccard(layers, algorithm = "louvain")
    p <- plot_multilayer_series(layers, fit = fit)
  }

```

simulate_and_fit_multilayer

Simulate multiplex layers and fit interlayer models

Description

Generates synthetic multiplex network layers using a planted partition model, then fits one of the provided interlayer tie strategies.

Usage

```

simulate_and_fit_multilayer(
  n_nodes = 100,
  n_layers = 4,
  n_communities = 4,
  p_in = 0.2,
  p_out = 0.05,
  fit_type = c("jaccard", "overlap", "weighted_jaccard", "weighted_overlap", "identity"),
  algorithm = c("louvain", "leiden"),
  layer_links = NULL,
  min_similarity = 0,
  seed = NULL,
  directed = FALSE
)

```

Arguments

n_nodes	Number of nodes per layer.
n_layers	Number of temporal layers.
n_communities	Number of latent communities.
p_in	Probability of an in-community edge.
p_out	Probability of an out-community edge.
fit_type	One of "jaccard", "overlap", or "identity".
algorithm	Community algorithm for fitting: "louvain" or "leiden".
layer_links	Optional layer connectivity specification.
min_similarity	Minimum similarity threshold for overlap-based methods.
seed	Optional random seed.
directed	Logical; if TRUE, simulate directed adjacency matrices.

Value

A list containing simulated layers, true memberships, and fit results.

Examples

```
sim <- simulate_and_fit_multilayer(  
  n_nodes = 30,  
  n_layers = 3,  
  n_communities = 3,  
  fit_type = "jaccard",  
  algorithm = "louvain",  
  seed = 123  
)  
names(sim)
```

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