

Package ‘MLRClust’

July 22, 2025

Type Package

Title Randomized spectral clustering for large-scale multi-layer networks

Version 0.1

Date 2025-07-20

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Description This package implements spectral clustering for large-scale multi-layer directed and undirected networks using randomization techniques.

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Encoding UTF-8

Imports Rcpp, stats, Matrix, irlba, gtools

LinkingTo Rcpp, RcppEigen

SystemRequirements C++11

RoxygenNote 7.3.2

NeedsCompilation yes

Suggests knitr,
rmarkdown

VignetteBuilder knitr

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MathOverflow

MathOverflow multilayer network data

Description

A directed multilayer network of interactions on the stack exchange website Math Overflow, with 3 layers corresponding to users' answers to questions(a2q), comments to questions(c2q), and comments to answers(c2a). The network includes 23,654 users, i.e., the multilayer network consists of 23,654 nodes.

Usage

```
data(MathOverflow)
```

Format

The MathOverflow object is a list of sparse matrices representing the adjacency matrices of the MathOverflow interaction network. All matrices share the same node set with consistent node IDs and dimnames.

References

Paranjape, A., Benson, A. R., and Leskovec, J. (2017). *Motifs in temporal networks.*, In *Proceedings of the tenth ACM International Conference on Web Search and Data Mining*.

Examples

```
data(MathOverflow)
m1A <- MathOverflow
timing <- system.time({
  cluster <- mrcoclust(m1A, rank.r = 2, rank.c = 3, kr = 2, kc = 3, q = 4, p = 0.9)
})
print(timing)
```

mIn_generator

Generate multilayer networks from multilayer stochastic block models and multilayer stochastic co-block models.

Description

Generate adjacency matrices of multilayer undirected networks from multilayer stochastic block models and multilayer directed networks from multilayer stochastic co-block models.

Usage

```
mIn_generator(row.label, col.label, probmat, directed = FALSE, sparse = TRUE)
```

Arguments

row.label	The row community vector (from 1:kr) with the numbers indicating which row community each node is assigned.
col.label	The column community vector (from 1:kc) with the numbers indicating which column community each node is assigned. row.label and col.label must have the same length but not necessarily indicate the same communities and community numbers. Only required when directed = TRUE.
probmats	List of link probability matrices with dimension c(kr, kc). probmat[l][i, j] is proportional to the probability of an edge from nodes in row community i to nodes in column community j in layer l.
directed	If TRUE, the multilayer directed networks is generated from the multilayer stochastic co-block model. If FALSE, the multilayer undirected networks is generated from the multilayer stochastic block model. Default is FALSE.
sparse	Logical indicating whether to return sparse matrices (dgCMatrix) for network adjacency matrices. Default is TRUE.

Details

This function generates multilayer undirected (directed) networks using multilayer stochastic block (co-block) models. In the multilayer stochastic block (co-block) models, all layers share common row and column communities but with possibly different edge densities. The layer-wise networks are generated independently from the stochastic block (co-block) model.

Value

A list of adjacency matrices representing the generated multilayer networks.

References

W. Su, X. Guo, X. Chang and Y. Yang. (2024) *Spectral co-clustering in multi-layer directed networks*, *Computational Statistics & Data Analysis*, Vol. 198, 107987
<https://doi.org/10.1016/j.csda.2024.107987>

Examples

```
# The multilayer stochastic block model
n <- 300
kr <- 2
row.label <- sample(rep(1:kr, each = n/kr), n)
probmats <- list(matrix(0.05, kr, kr) + diag(c(0.1, 0.05)),
                 matrix(0.01, kr, kr) + diag(c(0.05, 0.02)))
mIn1 <- mIn_generator(row.label = row.label, probmat = probmats, directed = FALSE)

# The multilayer stochastic co-block model
n <- 300
kr <- 2
kc <- 3
row.label <- sample(rep(1:kr, each = n/kr), n)
col.label <- sample(rep(1:kc, each = n/kc), n)
probmats <- list(matrix(0.05, kr, kc),
                 matrix(0.05, kr, kc))
mIn1 <- mIn_generator(row.label = row.label, col.label = col.label, probmat = probmats, directed = FALSE)
```

```

probm1[2,2] <- 0.1
probm2 <- matrix(0.01, kr, kc)
probm1[1,1] <- 0.05
probm1[2,3] <- 0.03
probmats <- list(probm1, probm2, probm2)
mln2 <- mln_generator(row.label, col.label, probmats, directed = TRUE)

```

mrclust

Randomized spectral clustering for multilayer stochastic block models

Description

Randomized spectral clustering for multilayer undirected networks. Randomized clustering uses both the random sampling strategy and the random projection strategy. Can deal with very large networks.

Usage

```

mrclust(
  mlA,
  rank.t,
  k,
  q = 2,
  p = 0.7,
  iter.max = 50,
  nstart = 10,
  nthread = 1
)

```

Arguments

mlA	The adjacency matrices list of a multilayer undirected network consists of "dgCMatrix" types.
rank.t	The target rank of the low-rank decomposition.
k	The number of clusters.
q	The power parameter. It need to be a positive integer number. Default is 2.
p	The sampling probability. Should be between 0 and 1. Default is 0.7.
iter.max	Maximum number of iterations in the kmeans . Default is 50.
nstart	The number of random sets in kmeans . Default is 10.
nthread	Maximum number of threads for specific computations which could be implemented in parallel. Default is 1.

Details

This function computes the clusters of multilayer undirected networks using randomized spectral clustering algorithms. Random sampling is first performed on the adjacency matrices, then the random projection-based eigendecomposition is performed on the aggregated matrix. The k-means is then performed on the randomized eigenvectors.

Value

cluster The cluster vector (from 1:k) with the numbers indicating which cluster each node is assigned.

Examples

```
# example 1
n <- 500
k <- 2
label.true <- sample(rep(1:k, each = n/k), n)
probm1 <- matrix(0.05, k, k) + diag(c(0.1, 0.05))
probm2 <- matrix(0.01, k, k) + diag(c(0.05, 0.02))
probmats <- list(probm1, probm2, probm2)
mlA <- mln_generator(row.label = label.true, probmat = probmats, directed = FALSE)
rank.t <- 2
q <- 2
p <- 0.7
mrclust(mlA, rank.t, k = k, q = q, p = p)

# example 2
# The effect of power parameter.
U <- matrix(c(1/2, 1/2, -sqrt(2)/2, 1/2, 1/2, sqrt(2)/2, sqrt(2)/2, -sqrt(2)/2, 0), nrow=3, byrow=TRUE)
Lambda1 <- diag(c(1.5, 0.2, 0.4))
Lambda2 <- diag(c(1.5, 0.2, -0.4))
B_1 <- U %%% Lambda1 %%% t(U)
B_2 <- U %%% Lambda2 %%% t(U)
layer <- 20
density <- 0.1
probmats <- lapply(1:layer, function(l) {if (l <= floor(layer / 2)) B_1 * density else B_2 * density})
k <- 3
p <- 0.7 # sampling probability
nodes_list <- seq(400, 2000, 200)
mr.result <- matrix(0, length(nodes_list), 4) # misclassification rates
for (i in 1:length(nodes_list)) {
  n_nodes <- nodes_list[i]
  size_communities <- c(0.3, 0.4, 0.3) * n_nodes
  true_label <- sample(rep(seq_len(k), times=size_communities), n_nodes)
  for (j in 1:5){
    mlA <- mln_generator(row.label = true_label, probmat = probmats, directed = FALSE)
    # randomized spectral clustering q = 2
    cluster.r.q2 <- mrclust(mlA, rank.t = k, k = k, q = 2, p = p)
    mr.result[i, 1] <- mr.result[i, 1] + min_mis_error(true_label, cluster.r.q2, k_clusters = k) / 5
    # randomized spectral clustering q = 4
    cluster.r.q4 <- mrclust(mlA, rank.t = k, k = k, q = 4, p = p)
    mr.result[i, 2] <- mr.result[i, 2] + min_mis_error(true_label, cluster.r.q4, k_clusters = k) / 5
    # randomized spectral clustering q = 6
    cluster.r.q6 <- mrclust(mlA, rank.t = k, k = k, q = 6, p = p)
    mr.result[i, 3] <- mr.result[i, 3] + min_mis_error(true_label, cluster.r.q6, k_clusters = k) / 5
    # original spectral clustering
    cluster.sc <- dsos(mlA, rank.t = k, k = k)
    mr.result[i, 4] <- mr.result[i, 4] + min_mis_error(true_label, cluster.sc, k_clusters = k) / 5
  }
}
line_labels <- c("RSC q = 2", "RSC q = 4", "RSC q = 6", "SC")
matplot(nodes_list, mr.result, type = "l", lty = 1, col = 1:4, xlab = "Number of nodes (n)", ylab = "Misclassification rate")
```

```
legend("topright", legend = line_labels, col = 1:4, lty = 1)
```

mrcoclust	<i>Randomized spectral co-clustering for multilayer stochastic co-block models</i>
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Description

Randomized spectral co-clustering for multilayer directed networks. Randomized clustering uses both the random sampling strategy and the random projection strategy. Can deal with very large networks.

Usage

```
mrcoclust(
  mlA,
  rank.r,
  rank.c,
  kr,
  kc,
  q = 2,
  p = 0.7,
  iter.max = 50,
  nstart = 10,
  nthread = 1
)
```

Arguments

mlA	The adjacency matrices list of a multilayer directed network consists of "dgCMatrix" types.
rank.r	The target row rank of the low-rank decomposition.
rank.c	The target column rank of the low-rank decomposition.
kr	The number of row clusters.
kc	The number of column clusters.
q	The power parameter. It need to be a positive integer number. Default is 2.
p	The sampling probability. Should be between 0 and 1. Default is 0.7.
iter.max	Maximum number of iterations in the kmeans . Default is 50.
nstart	The number of random sets in kmeans . Default is 10.
nthread	Maximum number of threads for specific computations which could be implemented in parallel. Default is 1.

Details

This function computes the clusters of multilayer directed networks using randomized spectral co-clustering algorithms. Random sampling is first performed on the adjacency matrices, then the random projection-based eigendecomposition is performed on the aggregated matrix. The k-means is then performed on the randomized eigenvectors.

Value

row.cluster	The row cluster vector (from 1:kr) with the numbers indicating which row cluster each node is assigned.
col.cluster	The column cluster vector (from 1:kc) with the numbers indicating which column cluster each node is assigned.

Examples

```
n <- 600
kr <- 2
kc <- 2
row.label.true <- sample(rep(1:kr, each = n/kr), n)
col.label.true <- sample(rep(1:kc, each = n/kc), n)
probm1 <- matrix(0.05, kr, kc) + diag(c(0.1, 0.05))
probm1[1,2] <- 0.08
probm2 <- matrix(0.01, kr, kc) + diag(c(0.05, 0.02))
probm2[2,1] <- 0.1
probmats <- list(probm1, probm2, probm2)
mlA <- mln_generator(row.label.true, col.label.true, probmats, directed = TRUE)
rank.r <- 2
rank.c <- 2
q <- 2
p <- 0.7
cc <- mrcoclust(mlA, rank.r, rank.c, kr, kc, q = q, p = p)
```

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