Package ‘leiden’

November 17, 2023

Type Package

Title R Implementation of Leiden Clustering Algorithm

Version 0.4.3.1

Date 2023-11-08

Description Implements the 'Python leidenalg' module to be called in R.

   Enables clustering using the leiden algorithm for partition a graph into communities.

   See the 'Python' repository for more details: <https://github.com/vtraag/leidenalg>


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URL https://github.com/TomKellyGenetics/leiden

BugReports https://github.com/TomKellyGenetics/leiden/issues

Imports methods, reticulate, Matrix, igraph (>= 1.2.7)

Encoding UTF-8

RoxygenNote 7.2.3

Suggests bipartite, covr, data.table, devtools, graphsim, knitr, markdown, multiplex, multinet, network, qpdf, RColorBrewer, remotes, rmarkdown, spelling, testthat, tibble

Language en-US

VignetteBuilder knitr

Collate 'find_partition.R' 'leiden.R' 'py_objects.R'

NeedsCompilation no

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Repository CRAN

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\begin{tabular}{ll}
\texttt{leiden} & \textit{Run Leiden clustering algorithm} \\
\end{tabular}

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\textbf{Description}

Implements the Leiden clustering algorithm in R using reticulate to run the Python version. Requires the python "leidenalg" and "igraph" modules to be installed. Returns a vector of partition indices. Windows users can still this with devtools::install_github("rstudio/reticulate", ref = "86ebb56"); reticulate::use_condaenv("r-reticulate"); reticulate::conda_install("r-reticulate", "leidenalg", channel = "vtraag")

\textbf{Usage}

leiden(
  object,
  initial_membership = NULL,
  weights = NULL,
  node_sizes = NULL,
  resolution_parameter = 1,
  seed = NULL,
  n_iterations = 2L,
  max_comm_size = 0L,
  degree_as_node_size = FALSE,
  laplacian = FALSE,
  legacy = FALSE
)

\textbf{Arguments}

\begin{itemize}
  \item \texttt{object} An adjacency matrix compatible with \texttt{igraph} object or an input graph as an \texttt{igraph} object (e.g., shared nearest neighbours). A list of multiple graph objects can be passed for multiplex community detection.
  \item \texttt{partition_type} Type of partition to use. Defaults to \texttt{RBConfigurationVertexPartition}. Options include: \texttt{ModularityVertexPartition}, \texttt{RBERVertexPartition}, \texttt{CPMVertexPartition}, \texttt{MutableVertexPartition}, \texttt{SignificanceVertexPartition}, \texttt{SurpriseVertexPartition}, \texttt{ModularityVertexPartition.Bipartite}, \texttt{CPMVertexPartition.Bipartite} (see the Leiden python module documentation for more details)
\end{itemize}
initial_membership, weights, node_sizes
Parameters to pass to the Python leidenalg function (defaults initial_membership=None, weights=None). Weights are derived from weighted igraph objects and non-zero integer values of adjacency matrices.

resolution_parameter
A parameter controlling the coarseness of the clusters

seed
Seed for the random number generator. By default uses a random seed if nothing is specified.

n_iterations
Number of iterations to run the Leiden algorithm. By default, 2 iterations are run. If the number of iterations is negative, the Leiden algorithm is run until an iteration in which there was no improvement.

max_comm_size (non-negative int) – Maximal total size of nodes in a community. If zero (the default), then communities can be of any size.

degree_as_node_size
(defaults to FALSE). If True use degree as node size instead of 1, to mimic modularity for Bipartite graphs.

laplacian
(defaults to FALSE). Derive edge weights from the Laplacian matrix.

legacy
(defaults to FALSE). Force calling python implementation via reticulate. Default behaviour is calling cluster_leiden in igraph with Modularity (for undirected graphs) and CPM cost functions.

Value
A partition of clusters as a vector of integers

Examples

```r
#check if python is available
modules <- reticulate::py_module_available("leidenalg") && reticulate::py_module_available("igraph")
if(modules){
  #generate example data
  adjacency_matrix <- rbind(cbind(matrix(round(rbinom(4000, 1, 0.8)), 20, 20),
                           matrix(round(rbinom(4000, 1, 0.3)), 20, 20),
                           matrix(round(rbinom(400, 1, 0.1)), 20, 20)),
                          cbind(matrix(round(rbinom(400, 1, 0.3)), 20, 20),
                                matrix(round(rbinom(400, 1, 0.8)), 20, 20),
                                matrix(round(rbinom(4000, 1, 0.2)), 20, 20)),
                          cbind(matrix(round(rbinom(400, 1, 0.3)), 20, 20),
                                matrix(round(rbinom(4000, 1, 0.1)), 20, 20),
                                matrix(round(rbinom(4000, 1, 0.9)), 20, 20)))
  rownames(adjacency_matrix) <- 1:60
colnames(adjacency_matrix) <- 1:60
  #generate partitions
  partition <- leiden(adjacency_matrix)
table(partition)

  #generate partitions at a lower resolution
  partition <- leiden(adjacency_matrix, resolution_parameter = 0.5)
table(partition)
```
#generate example weights
weights <- sample(1:10, sum(adjacency_matrix!=0), replace=TRUE)
partition <- leiden(adjacency_matrix, weights = weights)
table(partition)

#generate example weighted matrix
adjacency_matrix[adjacency_matrix == 1] <- weights
partition <- leiden(adjacency_matrix)
table(partition)

# generate (unweighted) igraph object in R
library("igraph")
adjacency_matrix[adjacency_matrix > 1] <- 1
my_graph <- graph_from_adjacency_matrix(adjacency_matrix)
partition <- leiden(my_graph)
table(partition)

# generate (weighted) igraph object in R
library("igraph")
adjacency_matrix[adjacency_matrix >= 1] <- weights
my_graph <- graph_from_adjacency_matrix(adjacency_matrix, weighted = TRUE)
partition <- leiden(my_graph)
table(partition)

# pass weights to python leidenalg
adjacency_matrix[adjacency_matrix >= 1] <- 1
my_graph <- graph_from_adjacency_matrix(adjacency_matrix, weighted = NULL)
weights <- sample(1:10, sum(adjacency_matrix!=0), replace=TRUE)
partition <- leiden(my_graph, weights = weights)
table(partition)

# run only if python is available (for testing)
}
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