Package ‘modMax’

July 24, 2015

Type Package
Title Community Structure Detection via Modularity Maximization
Version 1.1
Date 2015-07-24
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Depends gtools, igraph
Description The algorithms implemented here are used to detect the community structure of a network. These algorithms follow different approaches, but are all based on the concept of modularity maximization.
License GPL-2
NeedsCompilation no
Repository CRAN
Date/Publication 2015-07-24 18:21:32

R topics documented:

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modMax-package  Calculate network modularity via maximization algorithms

Description
Calculation of modularity and detection of the community structure of a given network depicted by an (nonnegative symmetric) adjacency matrix using different modularity maximization algorithms.

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The modMax package implements 38 algorithms of 6 major categories maximizing modularity, including the greedy approach, simulated annealing, extremal optimization, genetic algorithm, mathematical programming and the usage of local modularity.

All algorithms work on connected (consisting of only one connected component), undirected graphs given by their adjacency matrix.

Most algorithms also provide the possibility to compare the estimated modularity of the identified community structure with the modularity for random networks generated by null models with the number of vertices and edges conserved.

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extremalOptimization  Extremal optimization (EO) algorithms

Description
extremalOptimization is a function executing the extremal optimization approach and its modifications for calculating modularity and detecting communities (modules of nodes) of a network via modularity maximization.

pceoss is a function which uses extremal optimization, but also considers pairwise constraints when calculating the fitness function and the modularity. The violation of constraints is punished, leading to smaller fitness and modularity values for community structures that violate many pairwise constraints. The constraints are predefined as two matrices separately for must-links and cannot-links with punishment for violation.
Usage

```r
extremalOptimization(adjacency, numRandom = 0,
    refine = c("none", "agents"),
    tau = FALSE, alpha_max = length(adjacency[1,]), steps = 3)
```

pcseoss(adjacency, constraints_ml, constraints_cl)

Arguments

- `adjacency`: A nonnegative symmetric adjacency matrix of the network whose community structure will be analyzed.
- `numRandom`: The number of random networks with which the modularity of the resulting community structure should be compared (default: no comparison). See details below for further explanation of the used null model.
- `refine`: Specify whether or not a refinement step is needed, the default option is `none`. See details below.
- `tau`: If `TRUE`, τ-EO is executed where the vertices are ranked according to their fitness values and chosen by a probability depending on this ranking.
- `alpha_max`: It gives the maximum number of iteration steps. If the community structure could not be improved for this number of steps, the algorithm terminates. It is 1 for the normal EO-algorithm and \( n \) for the \( \tau \)-EO where \( n \) is the number of vertices in the network.
- `steps`: The number of iteration steps for the random local search agent algorithm. The algorithm terminates, if the clusters have not changed for this number of steps. Ignored if `refine` is `none`.
- `constraints_ml`: The matrix where each column is a must-link constraint given by two vertices in the first two rows which have to be in the same community and a punishment for the violation of the constraint in the third row.
- `constraints_cl`: The matrix where each column is a cannot-link constraint given by two vertices in the first two rows which cannot be in the same community and a punishment for the violation of the constraint in the third row.

Details

The used random networks have the same number of vertices and the same degree distribution as the original network.

The EO algorithm can be run with a certain refinement step, the local random search agent algorithm, applied at the end of one round of extremal where all communities have been split once.

This refinement algorithm is executed if `refine` equals `agents`, otherwise the generic EO algorithm is executed.

Value

The result of the extremal optimization algorithms is a list with the following components:

- `number of communities`: The number of communities detected by the algorithm.
modularity  The modularity of the detected community structure
mean  The mean of the modularity values for random networks, only computed if numRandom>0
standard deviation  The standard deviation of the modularity values for random networks, only computed if numRandom>0
community structure  The community structure of the examined network given by a vector assigning each vertex its community number
random modularity values  The list of the modularity values for random networks, only computed if numRandom>0

Author(s)
Maria Schelling, Cang Hui

References

Examples

#weighted network
randomgraph <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

#to ensure that the graph is connected
vertices <- which(clusters(randomgraph)$membership==1)
graph <- induced.subgraph(randomgraph, vertices)
graph <- set.edge.attribute(graph, "weight", value=runif(ecount(graph),0,1))

adj <- get.adjacency(graph, attr="weight")
result <- extremalOptimization(adj)
**geneticAlgorithm**  

*Genetic algorithm*

**Description**

`geneticAlgorithm` is a function executing the genetic algorithm and its modifications for identifying the community structure of a network via modularity maximization.

**Usage**

```r
geneticAlgorithm(adjacency, numRandom = 0,  
initial = c("general", "cluster", "own"), p, g,  
mutRat = 0.5, crossOver = 0.2, beta = 0.1, alpha = 0.4,  
n_l = 4, local = FALSE)
```

**Arguments**

- `adjacency`  
  A nonnegative symmetric adjacency matrix of the network whose community structure will be analyzed.

- `numRandom`  
  The number of random networks with which the modularity of the resulting community structure should be compared (default: no comparison). See details below for further explanation of the used null model.

- `initial`  
  Specify the community structure to use as initial partition in the algorithm. See details below.

- `p`  
  Population size.

- `g`  
  Number of generations.

- `mutRat`  
  Mutation rate. Default is 0.5.

- `crossOver`  
  Crossing over rate. Default is 0.2.

- `beta`  
  The fraction of chromosomes to save. The top $\beta p$ chromosomes are saved in each generation to ensure that the fitness scores of the top $\beta p$ chromosomes of the child generation are at least as good as the parent population. Default is 0.1.

- `alpha`  
  The fraction of repetitions for the identification of an initial partition according to `cluster`. Default is 0.4. Ignored if `initial` is not `cluster`.

- `n_l`  
  The number of copies of a chromosome made by the local search operator. Default is 4. Ignored if `local` is `FALSE`.

- `local`  
  If `TRUE`, local search operator is applied at the end of each iteration in the genetic algorithm.
Details
The used random networks have the same number of vertices and the same degree distribution as the original network.

The initial partition used in the genetic algorithm can either be the generic one where all vertices are put in their own community (initial=general) or the initial partition can be identified by randomly picking a vertex \(\alpha\) times and assigning its cluster to all its neighbours (initial=cluster) or the initial partition can be given by the user (initial=own). In this case, the user needs to add a last column to the adjacency matrix indicating the initial partition. Hence, the adjacency matrix has to have one column more than the network has vertices.

Value
The result of the genetic algorithm is a list with the following components

```
number of communities
The number of communities detected by the algorithm
modularity
The modularity of the detected community structure
mean
The mean of the modularity values for random networks, only computed if numRandom>0
standard deviation
The standard deviation of the modularity values for random networks, only computed if numRandom>0
community structure
The community structure of the examined network given by a vector assigning each vertex its community number
random modularity values
The list of the modularity values for random networks, only computed if numRandom>0
```

Author(s)
Maria Schelling, Cang Hui

References


Examples
```
#unweighted network
randomgraph <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

#to ensure that the graph is connected
vertices <- which(clusters(randomgraph)$membership==1)
graph <- induced.subgraph(randomgraph,vertices)
```
**Greedy algorithms**

**Description**

Greedy algorithms execute the general CNM algorithm and its modifications for modularity maximization.

- `rgplus` uses the randomized greedy approach to identify core groups (vertices which are always placed into the same community) and uses these core groups as initial partition for the randomized greedy approach to identify the community structure and maximize the modularity.
- `msgvm` is a greedy algorithm which performs more than one merge at one step and applies fast greedy refinement at the end of the algorithm to improve the modularity value.
- `cd` iteratively performs complete greedy refinement on a certain partition and then, moves vertices with a probability $p$ to another community to avoid the greedy algorithm getting trapped in a local optimum.
- `louvain` performs fast greedy refinement and uses the resulting community structure to build a new network where vertices in the new network are the communities in the original network. For this new network, all vertices are assigned to their own community, and the fast greedy refinement is applied again.
- `vertexSim` uses a vertex similarity measure to identify the initial partition and further improves this community structure by merging neighbouring communities.
- `mome` consists of the two phases of coarsening and uncoarsening with refinement. In the coarsening phase, two vertices are collapsed into one vertex for which the increase in modularity is maximal. In the uncoarsening phase, each intermediate graph of the coarsening phase is revisited and its community structure is refined by applying fast greedy refinement. After revisiting the different steps, the community structure for the original graph can be reconstructed from different coarsening levels.

**Usage**

```r
adj <- get.adjacency(graph)
result <- geneticAlgorithm(adj, p=4, g=6)
```

```r
greedy(adjacency, numRandom = 0,
      q = c("general", "danon", "wakita1", "wakita2", "wakita3"),
      initial = c("general", "prior", "walkers", "subgraph", "adclust", "own"),
      randomized = 0, refine = c("none", "complete", "fast", "kernighan"),
      coarse = 0)
rgplus(adjacency, numRandom=0, z, randomized)
msgvm(adjacency, numRandom=0, initial=c("general","own"), parl)
```

```r
cd(adjacency, numRandom=0, initial=c("general","own"), maxC=length(adjacency[,1]),
    iter,p)
```

```r
louvain(adjacency, numRandom=0, initial=c("general","own"))
```

```r
vertexSim(adjacency, numRandom=0, frac=0.5)
```

```r
mome(adjacency, numRandom=0)
```
Arguments

adjacency  A nonnegative symmetric adjacency matrix of the network whose community
structure will be analyzed

numRandom  The number of random networks with which the modularity of the resulting
community structure should be compared (default: no comparison). See details
below for further explanation of the used null model.

q  Specify whether the general $\Delta Q$ value or a modification should be used. See
details below.

initial  Specify the community structure to be used as initial partition in the algorithm.
See details below.

z  The number of executions of the randomized greedy approach to identify the
core groups.

randomized  The number of rows to use for the randomized greedy approach. Ignored when
set to 0 (default)

refine  specifies which refinement algorithm should be used. See details below.

coarse  Define the percentage by which the number of communities has to be decreased
since the last coarsening level to consider the current clustering as a new coarsen-
ing level and apply refinement on this clustering

parL  The number of merges at one step in the msgvm algorithm

maxC  The maximum number of communities for the initial partition used in the cd
algorithm

iter  The number of iterations in the cd algorithm

p  The probability with which a vertex is moved into another community in the
dilation step of the cd algorithm

frac  The fraction of iteration steps for which "pairwise" merging is performed in the
vertexSim algorithm. Remaining iteration steps are "single neighbour" merges.

Details

The used random networks have the same number of vertices and the same degree distribution as
the original network.

For the identification of the best merging event leading to a maximum increase in modularity, dif-
ferent values of the modularity were proposed. Which modularity value to use is specified by the
parameter $q$. The options are general where the normal value for $\Delta Q$ is used, danon where $\Delta Q$ is
normalized by the number of overall edges of vertices in a community and wakita1, wakita2 and
wakita3 where $\Delta Q$ is multiplied by the consolidation ratio.

The greedy algorithms can be run on different initial partitions. The used initial partition is speci-
ied by parameter initial. The options are general where all vertices are assigned to their own
community, prior where the initial community structure is identified by using prior knowledge,
walkers where the initial community structure is identified by using random walkers, subgraph
where the initial community structure is identified by using subgraph similarity, adclust where the
general initial partition is refined using fast greedy refinement and own where the user can specify
an initial partition to use with the greedy approach. In this case, the user needs to add a last column
to the adjacency matrix indicating the initial partition. Hence, the adjacency matrix has to have one column more than the network has vertices.

The community structure identified by the CNM algorithm can be refined by applying a refinement step at the end of the algorithm. The used refinement algorithm is specified by the parameter refine. The options are none where no refinement algorithm is applied, complete where the complete greedy refinement is applied, fast where the fast greedy refinement is applied, kernighan where the adapted Kernighan-Lin refinement is applied. Besides, if initial is set to adclust, fast greedy refinement is applied to the community structure after each merging event. If coarse ! = 0, the refinement algorithm specified by refine is not only applied at the end of the algorithm, but at each coarsening level where coarsening levels are defined according to coarse.

**Value**

The result of the greedy algorithms is a list with the following components

- **number of communities**
  The number of communities detected by the algorithm

- **modularity**
  The modularity of the detected community structure

- **mean**
  The mean of the modularity values for random networks, only computed if numRandom>0

- **standard deviation**
  The standard deviation of the modularity values for random networks, only computed if numRandom>0

- **community structure**
  The community structure of the examined network given by a vector assigning each vertex its community number

- **random modularity values**
  The list of the modularity values for random networks, only computed if numRandom>0

**Author(s)**

Maria Schelling, Cang Hui

**References**


### Examples

```
# unweighted network
randomgraph1 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

# to ensure that the graph is connected
vertices1 <- which(clusters(randomgraph1)$membership==1)
graph1 <- induced.subgraph(randomgraph1, vertices1)
adj1 <- get.adjacency(graph1)
result1 <- greedy(adj1, refine = "fast")

# weighted network
randomgraph2 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

# to ensure that the graph is connected
vertices2 <- which(clusters(randomgraph2)$membership==1)
graph2 <- induced.subgraph(randomgraph2, vertices2)
graph2 <- set.edge.attribute(graph2, "weight", value=runif(ecount(graph2),0,1))
adj2 <- get.adjacency(graph2, attr="weight")
result2 <- louvain(adj2)
```
localModularity

**Description**

localModularity uses the local modularity to identify the local community structure around a certain vertex.

localModularityWang uses the local modularity to identify the community structure of the entire network.

**Usage**

localModularity(adjacency, srcV, k)
localModularityWang(adjacency, numRandom=0)

**Arguments**

- **adjacency**: A nonnegative symmetric adjacency matrix of the network whose community structure will be analyzed.
- **srcV**: A given vertex whose local community structure should be determined by localModularity.
- **k**: The maximum number of vertices to add to the local community of srcV.
- **numRandom**: The number of random networks with which the modularity of the resulting community structure should be compared (default: no comparison). See details below for further explanation of the used null model.

**Details**

The used random networks have the same number of vertices and the same degree distribution as the original network.

**Value**

The result for localModularity is returned as a list with the following components:

- **local community structure**: Vertices assigned to the same community as the source vertex srcV.
- **local modularity**: The local modularity value for the determined local community.

The result for localModularityWang is returned as a list with the following components:

- **number of communities**: The number of communities detected by the algorithm.
- **modularity**: The modularity of the detected community structure.
localModularity

mean The mean of the modularity values for random networks, only computed if numRandom>0

standard deviation The standard deviation of the modularity values for random networks, only computed if numRandom>0

community structure The community structure of the examined network given by a vector assigning each vertex its community number

random modularity values The list of the modularity values for random networks, only computed if numRandom>0

Author(s)

Maria Schelling, Cang Hui

References


Examples

#unweighted network
randomgraph1 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

# to ensure that the graph is connected
vertices1 <- which(clusters(randomgraph1)$membership==1)
graph1 <- induced.subgraph(randomgraph1, vertices1)

adj1 <- get.adjacency(graph1)
result1 <- localModularity(adj1, srcV=1, k=4)

# weighted network
randomgraph2 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

# to ensure that the graph is connected
vertices2 <- which(clusters(randomgraph2)$membership==1)
graph2 <- induced.subgraph(randomgraph2, vertices2)

graph2 <- set.edge.attribute(graph2, "weight", value=runif(ecount(graph2),0,1))

adj2 <- get.adjacency(graph2, attr="weight")
result2 <- localModularityWang(adj2)
Simulated Annealing

Description

The functions presented here are based on simulated annealing and identify the community structure and maximize the modularity. simulatedAnnealing is only based on moving a single vertex from one community to another, while saIndividualCollectiveMoves considers movements of vertices, merging of communities and splitting of communities as alternatives to increase the modularity.

Usage

simulatedAnnealing(adjacency, numRandom = 0,
initial = c("general", "random","greedy", "own"),
beta = length(adjacency[1,])/2, alpha = 1.005, fixed)
saIndividualCollectiveMoves(adjacency,numRandom=0,initial=c("general","own"),
beta=length(adjacency[1,])/2,alpha=1.005,
fixed=25,numIter=1.0)

Arguments

adjacency A nonnegative symmetric adjacency matrix of the network whose community structure will be analyzed.
numRandom The number of random networks with which the modularity of the resulting community structure should be compared (default: no comparison). see details below for further explanation of the used null model.
initial Specify the community structure to use as the initial partition in the algorithm. See details below.
beta Define the initial inverse temperature. Default is (network size)/2
alpha Define the cooling parameter. Default is 1.005
fixed If the community structure has not changed for this specified number of steps, the algorithm is terminated.
numIter Define the iteration factor. At each temperature, the algorithm performs $fu^2$ individual moves (movement of a single vertex) and $fn$ collective moves (merge or split of a community) where $n$ is the number of vertices in the network.

Details

The used random networks have the same number of vertices and the same degree distribution as the original network.

The initial partition used in the simulated annealing algorithms can either be the generic one where all vertices are put in their own community (initial=general) or the initial partition can be identified by randomly identifying the initial number of communities and randomly assigning the vertices
to one of these communities (initial=random) or the initial partition can be the community structure identified by the greedy algorithm (initial=greedy) or the initial partition can be given by the user (initial=own). In this case, the user needs to add a last column to the adjacency matrix indicating the initial partition. Hence, the adjacency matrix has to have one column more than the network has vertices.

Value

The result of the simulated annealing algorithms is a list with the following components

- **number of communities**
  - The number of communities detected by the algorithm
- **modularity**
  - The modularity of the detected community structure
- **mean**
  - The mean of the modularity values for random networks, only computed if numRandom>0
- **standard deviation**
  - The standard deviation of the modularity values for random networks, only computed if numRandom>0
- **community structure**
  - The community structure of the examined network given by a vector assigning each vertex its community number
- **random modularity values**
  - The list of the modularity values for random networks, only computed if numRandom>0

Author(s)

Maria Schelling, Cang Hui

References


Examples

```r
#unweighted network
randomgraph <- erdos.renyi.game(10L, 0.3L, type="gnp",directed = FALSE, loops = FALSE)

#to ensure that the graph is connected
vertices <- which(clusters(randomgraph)$membership==1)
graph <- induced.subgraph(randomgraph,vertices)

adj <- get.adjacency(graph)
```
spectralOptimization

result <- simulatedAnnealing(adj, fixed=10)

description

spectralOptimization uses the leading eigenvector to recursively split the communities of a network into two until no further improvement of modularity is possible.

multiWay, spectral1 and spectral2 use $k-1$ leading eigenvectors to split the network into $k$ communities. The value for $k$ leading to the best community structure is chosen as the final number of communities and the resulting split of the network into $k$ communities as the final community structure. The 3 functions implement slightly different approaches leading to possibly different results.

Usage

spectralOptimization(adjacency, numRandom = 0, initial = c("general", "own"), refine = FALSE)
multiWay(adjacency, numRandom=0, maxComm=length(adjacency[1,]))
spectral1(adjacency, numRandom=0, maxComm=(length(adjacency[1,])-1))
spectral2(adjacency, numRandom=0, maxComm=(length(adjacency[1,])-1))

Arguments

adjacency: A nonnegative symmetric adjacency matrix of the network whose community structure will be analyzed.
numRandom: The number of random networks with which the modularity of the resulting community structure should be compared (default: no comparison). see details below for further explanation of the used null model.
initial: Specify the community structure to use as initial partition in the algorithm. See details below.
refine: If TRUE, Kernighan-Lin refinement is applied after splitting a community into two communities only on this part of the network.
maxComm: The maximum number of communities that the network allows.

Details

The used random networks have the same number of vertices and the same degree distribution as the original network.

The initial partition used in the spectral optimization algorithm can either be the generic one where all vertices are put in their own community (initial=general) or the initial partition can be given by the user (initial=own). In this case, the user needs to add a last column to the adjacency matrix indicating the initial partition. Hence, the adjacency matrix has to have one column more than the network has vertices.
Value

The result of the spectral optimization algorithms is a list with the following components:

- **number of communities**
  - The number of communities detected by the algorithm.

- **modularity**
  - The modularity of the detected community structure.

- **mean**
  - The mean of the modularity values for random networks, only computed if `numRandom>0`.

- **standard deviation**
  - The standard deviation of the modularity values for random networks, only computed if `numRandom>0`.

- **community structure**
  - The community structure of the examined network given by a vector assigning each vertex its community number.

- **random modularity values**
  - The list of the modularity values for random networks, only computed if `numRandom>0`.

Author(s)

Maria Schelling, Cang Hui

References


Examples

```
#unweighted network
randomgraph1 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)

#to ensure that the graph is connected
vertices1 <- which(clusters(randomgraph1)$membership==1)
graph1 <- induced.subgraph(randomgraph1,vertices1)
adj1 <- get.adjacency(graph1)
result1 <- spectralOptimization(adj1, refine = TRUE)

#weighted network
randomgraph2 <- erdos.renyi.game(10, 0.3, type="gnp", directed = FALSE, loops = FALSE)
```
spectralOptimization

# to ensure that the graph is connected
vertices2 <- which(clusters(randomgraph2)$membership==1)
graph2 <- induced.subgraph(randomgraph2, vertices2)
graph2 <- set.edge.attribute(graph2, "weight", value=runif(ecount(graph2), 0, 1))

adj2 <- get.adjacency(graph2, attr="weight")
result2 <- multiWay(adj2, maxComm=3)
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