Package: rSpectral (via r-universe)

October 18, 2024

Type Package

Title Spectral Modularity Clustering

Version 1.0.0.10

Description Implements the network clustering algorithm described in
Newman (2006) <doi:10.1103/PhysRevE.74.036104>. The complete
iterative algorithm comprises of two steps. In the first step,
the network is expressed in terms of its leading eigenvalue and
eigenvector and recursively partition into two communities.
Partitioning occurs if the maximum positive eigenvalue is
greater than the tolerance (10e-5) for the current partition,
and if it results in a positive contribution to the Modularity.
Given an initial separation using the leading eigen step,
'rSpectral' then continues to maximise for the change in
Modularity using a fine-tuning step - or variate thereof. The
first stage here is to find the node which, when moved from one
community to another, gives the maximum change in Modularity.
This node's community is then fixed and we repeat the process
until all nodes have been moved. The whole process is repeated
from this new state until the change in the Modularity, between
the new and old state, is less than the predefined tolerance. A
slight variant of the fine-tuning step, which can improve speed
of the calculation, is also provided. Instead of moving each
node into each community in turn, we only consider moves of
neighbouring nodes, found in different communities, to the
community of the current node of interest. The two steps
process is repeatedly applied to each new community found,
subdivided each community into two new communities, until we
are unable to find any division that results in a positive
change in Modularity.

URL https://github.com/cmclean5/rSpectral

BugReports https://github.com/cmclean5/rSpectral/issues/

License GPL-2

Encoding UTF-8

1

RoxygenNote 7.2.1

Depends R (>= 3.5.0)

Imports Rcpp (>= 1.0.8.3), Rdpack, igraph, graph

RdMacros Rdpack

LinkingTo Rcpp, RcppArmadillo(>= 0.11.2.0.0)

Suggests RColorBrewer, Rgraphviz, igraphdata, testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation yes

Author Colin Mclean [aut] (algorithm implementation in Rcpp functions), Anatoly Sorokin [aut, cre] (R functions, cranification, documentation, testing, maintenance)

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Repository CRAN

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Contents

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rSpectral   *rSpectral*

Description

This package implements the Spectral Modularity clustering algorithm for igraph and graphNEL graphs. The algorithm was proposed in (Newman 2006) and an example of its application to the real biological network could be found in (Roy et al. 2018).

Author(s)

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References

Newman MEJ (2006). "Finding community structure in networks using the eigenvectors of matrices." *Phys. Rev. E*, **74**(3), 036104. doi:10.1103/PhysRevE.74.036104, https://link.aps.org/doi/10.1103/PhysRevE.74.036104.

Roy M, Sorokina O, McLean C, Tapia-González S, DeFelipe J, Armstrong JD, Grant SGN (2018). "Regional Diversity in the Postsynaptic Proteome of the Mouse Brain." *Proteomes*, **6**(3), 31. ISSN 2227-7382, doi:10.3390/proteomes6030031, https://www.mdpi.com/2227-7382/6/3/31.

See Also

Useful links:

- <https://github.com/cmclean5/rSpectral>

- Report bugs at <https://github.com/cmclean5/rSpectral/issues/>

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spectral_graphNEL   *Spectral clustering for* [graphNEL](#) *objects*

Description

Spectral clustering for [graphNEL](#) objects

Usage

```
spectral_graphNEL(g, Cn_min = 1L, tol = 1e-05, names = 1L, fix_neig = 0L)
```

Arguments

g	[graphNEL](#) object
Cn_min	minimum cluster size
tol	tolerance
names	are we dealing with alphaNumeric (1) or numeric (!1) ids
fix_neig	whether to fix neighbouring nodes found in same community

Value

data.frame with node names and membership information

See Also

[spectral_igraph_membership](#)

Examples

```
library(graph)
V = letters[1:12]
g2 = randomEGraph(V, edges=20)
mem.df = spectral_graphNEL(g2)
head(mem.df)
```

spectral_igraph_communities

Spectral clustering for igraph *objects*

Description

This function invoke [spectral_igraph_membership](#) to calculate clustering and convert it into [communities](#) object for seamless work with native [igraph](#) clustering functions.

Usage

```
spectral_igraph_communities(
  g,
  Cn_min = 1L,
  tol = 1e-05,
  names = 1L,
  fix_neig = 0L
)
```

Arguments

g	igraph object
Cn_min	minimum cluster size
tol	tolerance
names	are we dealing with alphaNumeric (1) or numeric (!1) ids
fix_neig	whether to fix neighbouring nodes found in same community

Value

[communities](#) object

Examples

```
data(karate,package='igraphdata')
c<-spectral_igraph_communities(karate)
```

---

spectral_igraph_membership

Spectral clustering for igraph *objects*

Description

This function implements the network clustering algorithm described in (M. E. J. Newman, 2006).

Usage

```
spectral_igraph_membership(
  g,
  Cn_min = 1L,
  tol = 1e-05,
  names = 1L,
  fix_neig = 0L
)
```

Arguments

g	igraph object
Cn_min	minimum cluster size
tol	tolerance
names	are we dealing with alphaNumeric (1) or numeric (!1) ids
fix_neig	whether to fix neighbouring nodes found in same community

Details

The complete iterative algorithm comprises of two steps. In the first step, the network is expressed in terms of its leading eigenvalue and eigenvector and recursively partition into two communities. Partitioning occurs if the maximum positive eigenvalue is greater than the tolerance (tol=10-5) for the current partition, and if it results in a positive contribution to the Modularity.

Given an initial separation using the leading eigen step, the function then continues to maximise for the change in Modularity using a fine-tuning step - or variate thereof. The first stage here is to find the node which, when moved from one community to another, gives the maximum change in Modularity. This node's community is then fixed and we repeat the process until all nodes have been moved. The whole process is repeated from this new state until the change in the Modularity, between the new and old state, is less than the predefined tolerance (tol).

A slight variant of the fine-tuning step, which can reduce execution time by factor 2 to 5, is also provided. Instead of moving each node into each community in turn, we only consider moves of neighbouring nodes, found in different communities, to the community of the current node of interest. This variant of the node-moving algorithm effectively 'fixes' neigbouring nodes fix_neig in the community being considered.

The two steps process is repeatedly applied to each new community found, subdivided each community into two new communities, until we are unable to find any division that results in a positive

change in Modularity. An additional stopping criteria, based on the minimum cluster size `Cn_min`, is also provided.

Value

`data.frame` with node names and membership information

Examples

```
data(karate,package='igraphdata')
df.mem<-spectral_igraph_membership(karate)
```

Index