Package ‘networkABC’

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Type Package

Title Network Reverse Engineering with Approximate Bayesian Computation

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Depends R (>= 3.0.0)

Imports RColorBrewer, network, sna

Suggests ggplot2, knitr

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Description

We developed an inference tool based on approximate Bayesian computation to decipher network data and assess the strength of the inferred links between network's actors. It is a new multi-level approximate Bayesian computation (ABC) approach. At the first level, the method captures the global properties of the network, such as scale-freeness and clustering coefficients, whereas the second level is targeted to capture local properties, including the probability of each couple of genes being linked. Up to now, Approximate Bayesian Computation (ABC) algorithms have been scarcely used in that setting and, due to the computational overhead, their application was limited to a small number of genes. On the contrary, our algorithm was made to cope with that issue and has low computational cost. It can be used, for instance, for elucidating gene regulatory network, which is an important step towards understanding the normal cell physiology and complex pathological phenotype. Reverse-engineering consists in using gene expressions over time or over different experimental conditions to discover the structure of the gene network in a targeted cellular process. The fact that gene expression data are usually noisy, highly correlated, and have high dimensionality explains the need for specific statistical methods to reverse engineer the underlying network.

NeedsCompilation yes

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abc

ABC algorithm for network reverse-engineering

**Description**

ABC algorithm for network reverse-engineering

**Usage**

```r
abc(
  data,
  clust_coeffs = c(0.33, 0.66, 1),
  tolerance = NA,
  number_hubs = NA,
  iterations = 10,
  number_networks = 1000,
  hub_probs = NA,
  neighbour_probs = NA,
)```
is_probs = 1
)

**Arguments**

- **data**: Any microarray data in the form of a matrix (rows are genes and columns are time points)
- **clust_coeffs**: one dimensional array of size clust_size of clustering coefficients (these clustering coefficient are tested in the ABC algorithm).
- **tolerance**: a real value based for the tolerance between the generated networks and the reference network
- **number_hubs**: number of hubs in the network
- **iterations**: number of times to repeat ABC algorithm
- **number_networks**: number of generated networks in each iteration of the ABC algorithm
- **hub_probs**: one-dimensional array of size number_genes for the each label to be in the role of a hub
- **neighbour_probs**: this is the matrix of neighbour probabilities of size number_nodes*number_nodes
- **is_probs**: this needs to be set either to one (if you specify hub_probs and neighbour_probs) or to zero (if neither probabilities are specified). Attention: you should specify both hub_probs and neighbour_probs if is_probs is one. If is_prob is zero these arrays should simply indicate an array of a specified size.

**Examples**

```R
M<-matrix(rnorm(30),10,3)
result<-abc(data=M)
```

---

**clusteringCoefficient**  *Calculate the clustering coefficient*

**Description**

Calculate the clustering coefficient for an adjacency matrix. By default, the local clustering coefficient is calculated. From the PCIT package after it was archived on the CRAN.

**Usage**

```R
clusteringCoefficient(adj, FUN = "localClusteringCoefficient", ...)
```

**Arguments**

- **adj**: An adjacency matrix. Calculating the clustering coefficient only makes sense if some connections are zero i.e. no connection.
- **FUN**: The function for calculating the clustering coefficient.
- **...**: Arguments to pass to FUN
Value

The clustering coefficient(s) for the adjacency matrix.

Author(s)

Nathan S. Watson-Haigh

See Also

localClusteringCoefficient

Examples

clusteringCoefficient(network_gen(50,.33)$network)

localClusteringCoefficient

Calculate the local clustering coefficient

Description

Calculate the local clustering coefficient for each node in an adjacency matrix. The clustering coefficient is defined as the proportion of existing connections from the total possible (Watts and Strogatz, 1998).

Usage

localClusteringCoefficient(adj)

Arguments

adj An adjacency matrix. Calculating the clustering coefficient only makes sense if some connections are zero i.e. no connection.

Value

A vector of local clustering coefficients for each node/gene of the adjacency matrix.

Author(s)

Nathan S. Watson-Haigh

References

netsimul

See Also

clusteringCoefficient

Examples

localClusteringCoefficient(network_gen(50,.33)$network)

netsimul  Simulated network

Description

Result of the use of the network_gen function.

Usage

netsimul

Format

A list of three objects:

number_genes  The number of genes in the network
clust_coef  The clustering coefficient
network  The simulated network

networkABC  networkABC

Description

An inference tool based on approximate Bayesian computations to decipher network data and assess the strength of their inferred links.

References

networkABC: An inference tool for networks based on approximate Bayesian computation, Myriam Maumy-Bertrand, Frédéric Bertrand, preprint.
network_gen

*Random scale-free network generation.* This function is used intensively in the `abc` function.

**Description**

Generate random network topology

**Usage**

```r
network_gen(number_genes, clust_coef)
```

**Arguments**

- `number_genes`: A number
- `clust_coef`: A number

**Value**

A list with the number of genes, the targeted clustering coefficient and the resulting network

**Examples**

```r
network_gen(10, 1)
```

---

resabc

*Result of an ABC inference*

**Description**

Result for the reverse engineering of a simulated Cascade network

**Usage**

```r
resabc
```

**Format**

A list of 14 objects:

- `data`: The microarray data used, rows are genes and columns are time points.
- `ngenes`: The number of genes.
- `ntimes`: The number of timepoints
- `clust_size`: The size of clusters
- `clust_coeffs`: The clustering coefficient
showHp

**tolerance** : the tolerance between the generated networks and the reference network

**number_hubs** : number of hubs in the network

**iterations** : number of times to repeat ABC algorithm

**number_networks** : number of generated networks in each iteration of the ABC algorithm

**hub_probs** : one-dimensional array of size number_genes for the each label to be in the role of a hub

**neighbour_probs** : matrix of neighbour probabilities of size number_nodes*number_nodes

**is_probs** : is equal to 1 since hub_probs and neighbour_probs were specified

---

**showHp**

*Plot for the hub probabilities*

---

**Description**

Plot for the hub probabilities; there is one probability for each node in the network.

**Usage**

showHp(result)

**Arguments**

result : The result of the abc algorithm.

**Examples**

data(resabc)
showHp(resabc)

---

**showNetwork**

*Plot the final network.*

---

**Description**

Plot the final network.

**Usage**

showNetwork(res, min_prob)

**Arguments**

res : The result of the abc algorithm.

min_prob : numeric; under this probability value, the link between two genes is set to 0.
Examples

data(resabc)
showNetwork(resabc,.2)

---

showNp  

*Plot for the neighbourhood probabilities*

Description

Plot for the neighbourhood probabilities; there is one probability for each pair of node in the network.

Usage

showNp(result)

Arguments

result : The result of the abc algorithm.

Examples

data(resabc)
showNp(resabc)
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