Package 'mcPAFit'

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Type Package

Title Estimating Preferential Attachment from a Single Network Snapshot by Markov Chain Monte Carlo

Version 0.1.3

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Description A Markov chain Monte Carlo method is provided to estimate the preferential attachment function from a single network snapshot. Conventional methods require the complete information about the appearance order of all nodes and edges in the network. This package incorporates the appearance order into the state space and estimates it together with the preferential attachment function. Auxiliary variables are introduced to facilitate fast Gibbs sampling.

License GPL-3

Depends R(>= 2.10.0)

Imports Rcpp (>= 0.11.3) , grDevices, graphics, stats, RColorBrewer, PAFit

LinkingTo Rcpp

LazyData True

NeedsCompilation yes

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mcPAFit-package *Estimating Preferential Attachment from a Single Network Snapshot by Markov Chain Monte Carlo*

Description

A Markov chain Monte Carlo method is provided to estimate the preferential attachment function from a single network snapshot. Conventional methods require the complete information about the appearance order of all nodes and edges in the network. This package incorporates the appearance order into the state space and estimates it together with the preferential attachment function. Auxiliary variables are introduced to facilitate fast Gibbs sampling.

Details

Package:	mcPAFit
Type:	Package
Version:	0.1.3
Date:	2016-05-25
License:	GPL-3

- mcPAFit: estimates the Preferential Attachment function in a temporal complex network without temporal information.
- create_sim_data: generate simulation data.

Author(s)

Thong Pham, Paul Sheridan, Hidetoshi Shimodaira. Maintainer: Thong Pham <thongpham@thongpham.net>

References

1. Pham, T. and Sheridan, P. and Shimodaira, H. (2015). mcPAFit: Nonparametric Measurement of Preferential Attachment and Fitness from a Single Network Snapshot. Conference on Complex Systems 2015, September 2015, Arizona.

Examples

```
## Not run:
library("mcPAFit")

## End(Not run)
```

create_sim_data *Generating simulated networks*

Description

A function generates a complex network from the Bianconi-Barabasi model and a random order to create a random network.

Usage

```
create_sim_data(mode = 1, sat_at = 10, alpha = 0.5, beta = 1, N = 200)
```

Arguments

mode	Integer. Indicates the attachment function to be used in generating the network. If mode == 1, the attachment function is $A_k = k^\alpha$. If mode == 2, the attachment function is $A_k = min(k, sat_at)^\alpha$. If mode == 3, the attachment function is $A_k = \alpha log(k)^\beta$. Default value is 1.
sat_at	Integer. This is the saturation position sat_at in the attachment function $A_k = min(k, sat_at)^\alpha$.
alpha	Numeric. If mode == 1, this is the attachment exponent in the attachment function $A_k = k^\alpha$. If mode == 2, this is the attachment exponenet in the attachment function $A_k = min(k, sat_at)^\alpha$. If mode == 3, this is the alpha in the attachment function $A_k = \alpha log(k)^\beta$ + 1.
beta	Numeric. This is the beta in the attachment function $A_k = \alpha log(k)^\beta$ + 1.
N	Integer. Number of nodes in the final network.

Value

An object of class mcPAFit.Sim containing the true network as well as the random-shuffled final snapshot together with the true timeline.

Author(s)

Thong Pham <thongpham@thongpham.net>

References

1. Pham, T. and Sheridan, P. and Shimodaira, H. (2015). mcPAFit: Nonparametric Measurement of Preferential Attachment and Fitness from a Single Network Snapshot. Conference on Complex Systems 2015, September 2015, Arizona.

Examples

```
library("mcPAFit")
data <- create_sim_data(N = 100)
```

`mcPAFit` *estimates the Preferential Attachment function in a temporal complex network without temporal information.*

Description

This function takes an input file name and then output the MCMC results into files.

Usage

```
mcPAFit(file_name, burn_in = 1000,
        needed_sample = 1000,
        skip = 1, B = 1,
        step_s = 0.1, lambda = 1, G = 10000, s = 1,
        h_s_shape = 5, h_s_rate = 5,
        not_start_A = 1, file_A = "", not_start_f = 1,
        file_f = "", filename = "network", only_active_node = 1, random = 0)
```

Arguments

`file_name`	String. Name of the file containing the network snapshot.
`burn_in`	Integer. Number of burn-in steps. Default is 1000.
`needed_sample`	Integer. Number of needed sample. Number of iterations = Skip * needed_sample + burn_in. Default is 1000.
`skip`	Integer. Number of skips. Large skips reduce correleration between successive samples. Default is 1.
`B`	Integer. Number of combinations of odd-sweep and even-sweep inside a complete sweep. Default is 1.
`step_s`	Numeric. Step size for the Metropolis-Hastings random walk for s.
`lambda`	Integer. Mean parameter of the Poisson prior of number of edges at a time.
`G`	Integer. Number of bins. Default value is 10000.
`s`	Numeric. Parameter of the gamma distribution of PA.
`h_s_shape`	Numeric. The shape of the prior for s.
`h_s_rate`	Numeric. The rate of the prior for s.
`not_start_A`	Integer. Indicates whether to use a custom PA function supplied by user. 1 is not to use. Default is 1.
`file_A`	String. Name of the file containing the custom PA function in the case not_start_A == 0. Default is "".
`not_start_f`	Integer. Indicates whether to use a custom starting position for f. 1 is not to use. Default is 1.
`file_f`	String. Name of the file containing the custom fitness in the case not_start_f == 0. Default is "".

`filename` String. Main part of names of the output files. Default is "network".

`only_active_node`
Integer. If 1, then only nodes with degrees greater than 0 are considered. Default is 1.

`random` Integer. If 1, then the program randomizes the order of edges for starting value. Default is 0.

Value

The function writes directly to output files.

Author(s)

Thong Pham <thongpham@thongpham.net>

References

1. Pham, T. and Sheridan, P. and Shimodaira, H. (2015). mcPAFit: Nonparametric Measurement of Preferential Attachment and Fitness from a Single Network Snapshot. Conference on Complex Systems 2015, September 2015, Arizona.

Examples

```
library(mcPAFit)
N      <- 1000 #number of nodes in the network
M      <- 500  #number of needed sample
lag   <-  1
start <-  100

data   <- create_sim_data(N = N, alpha = 1)
write.table(data$random[,1:2], row.names = FALSE,
            col.names = FALSE, file = "input.txt")
system.time(mcPAFit(file_name = "input.txt",burn_in = 0, s = 5, skip = 1,
            needed_sample = M, G = 20,only_active_node = 1, random = 0))
# plot log posterior
to.read = file("log_pos_network.binary","rb")
log_pos = readBin(to.read, numeric(),n = M);
plot(log_pos,type = "l",xlab = "Iteration", ylab = "Log Posterior",cex.axis = 1.5, cex.lab = 1.5);
########

########
#plot b
to.read = file("b_out_network.binary","rb")
b = readBin(to.read, numeric(),n = M);
used  <- seq(start,M,1)
plot(b[used],type = "l", xlab = "Iteration", ylab = "b", cex.lab =2 , cex.axis =2);
acf(b[used])
mean(b[used])
```

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