Package 'CormotifExample'

May 3, 2015

Type Package
Title Simulation result for the Correlation Motifs model
Version 1.0
Depends R (>= 2.12.0), Cormotif
Date 2015-05-03
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Description The CormotifExample package comtains the simulation raw data and the simulation result. The user can have a quick look at the Correlation Motifs result or run the simulation themselves using the raw simulation data.
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CormotifExample Simulation results for Correlation Moitfs model
Description
This is the result for Correlation Motifs model using simulated data. The raw simulated data are also available in this demo package.
Usage
<pre>data(CormotifExample)</pre>
Details
More usage see the examples

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Source

Wei, Yingying, Toyoaki Tenzen, and Hongkai Ji. "Joint analysis of differential gene expression in multiple studies using correlation motifs." *Biostatistics* 16.1 (2015): 31-46.

Examples

```
library(Cormotif)
#1. Correlation Motifs model can be build from the raw simulated data
data(simulationData)
data(groupid)
data(compid)
exprs <- as.matrix(simulationData[,2:ncol(simulationData)])</pre>
#Correlation Motif simulation result
result <- cormotiffit(exprs, groupid, compid, K = 1:10, max.iter = 1000, BIC = TRUE)
#Optimal cluster number K is obtained by BIC
K <- which.min(result$bic[,'bic'])</pre>
#The posterior probability for each gene in each study to bedifferential expressed.
posterior <- result$bestmotif$p.post</pre>
cutoff <- 0.5
diffExprs <- (posterior > cutoff)
#Rank the gene by the posterior probability
topgenelist <- generank(posterior)</pre>
#2. Correlation Motifs model result can be loaded directly
data(CormotifExample)
#3. Visual result
plotMotif(result)
head(diffExprs)
head(topgenelist)
```

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