Package ‘EBSeqHMM’

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Type Package

Title Bayesian analysis for identifying gene or isoform expression changes in ordered RNA-seq experiments

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Author Ning Leng, Christina Kendziorski

Depends EBSeq

Maintainer Ning Leng <lengning1@gmail.com>

Description
The EBSeqHMM package implements an auto-regressive hidden Markov model for statistical analysis in ordered RNA-seq experiments (e.g. time course or spatial course data). The EBSeqHMM package provides functions to identify genes and isoforms that have non-constant expression profile over the time points/positions, and cluster them into expression paths.

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‘EBHMMNBMultiEM_2chain.R’ ‘f0.R’ ‘LikefunNBHMM.R’ ‘beta.mom.R’
‘GetAllPaths.R’ ‘PlotExp.R’

BuildVignettes yes

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R topics documented:

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EBSeqHMM-package

EBSeqHMM: A Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments

Description

The EBSeqHMM package implements an auto-regressive hidden Markov model for statistical analysis in ordered RNA-seq experiments (e.g. time course or spatial course data). The EBSeqHMM package provides functions to identify genes and isoforms that have non-constant expression profile over the time points/positions, and cluster them into expression paths.

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Author(s)

Ning Leng, Christina Kendziorski
Maintainer: Ning Leng <nleng@wisc.edu>

References


See Also

EBSeq

Examples

data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
EBSeqHMMGeneOut <- EBSeqHMMTest(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions, UpdateRd=2)
**beta.mom**

*Method of moments estimation (beta distribution)*

**Description**

Method of moments estimation (beta distribution)

**Usage**

```
beta.mom(qs.in)
```

**Arguments**

- `qs.in`: A vector contains the numbers that will be fitted with a beta distribution.

**Details**

The `beta.mom()` function can be used to estimate parameters in a Beta function using method of moments.

**Value**

- `alpha.hat`, `beta.hat`: Returns the estimation of alpha and beta.

**Author(s)**

Ning Leng

**Examples**

```
beta.mom(rbeta(10,1,1))
```

---

**EBHMMNBfun**

*Baum-Welch algorithm for a single hidden markov chain*

**Description**

Baum-Welch algorithm for a single hidden markov chain

**Usage**

```
EBHMMNBfun(Data,NgVector=NULL,Conditions, sizeFactors,
PriorFC=1.5,homo=TRUE, maxround=5,
Pi0=NULL, Tran=NULL,NoTrend=FALSE, NumTranStage=3,
FCParam=NULL, AlphaIn=NULL,BetaIn=NULL,
StateNames=c("Up","NC","Down"),
EM=TRUE, UpdateParam=TRUE, Print=TRUE,
OnlyQ=FALSE,WithinCondR=TRUE,
PenalizeLowMed=TRUE, PenalizeLowMedQt=.2,PenalizeLowMedVal=10)
```
Arguments

Data: input data, rows are genes/isoforms and columns are samples
NgVector: Ng vector; NULL for gene level data
Conditions: A factor indicates the condition (time/spatial point) which each sample belongs to.
sizeFactors: a vector indicates library size factors
Tran: initial values for transition matrices
Pi0: initial values for starting probabilities
NumTranStage: number of states
PriorFC: target FC for gridient change
StateNames: name of the hidden states
homo: whether the chain is assumed to be homogenous
maxround: max number of iteration
AlphaIn, BetaIn: If the parameters are known and the user doesn’t want to estimate them from the data, user may specify them here.
NoTrend: if NoTrend=TRUE, initial transition probabilities will be set to be equal
FCParam: not in use
EM: Whether estimate the prior parameters of the beta distribution by EM
UpdateParam: Whether update starting probabilities and transition probabilities
OnlyQ: If OnlyQ=TRUE, the function will only return estimated q’s.
WithinCondR: By defining WithinCondR=TRUE, estimation of r’s are obtained within each condition. (WithinCondR=FALSE is not suggested here)
Print: Whether print the elapsed-time while running the test.
PenalizeLowMed, PenalizeLowMedQt, PenalizeLowMedVal: Transcripts with median quantile <= PenalizeLowMedQt will be penalized

Details

EBHMMNBfun() function implements the Balm-Welch algorithm that estimates the starting probabilities and transition probabilities of a single hidden Markov model. Here the emission distribution of each gene is assumed to be a Beta-Negative Binomial distribution with parameters \((r_{g}, \alpha, \beta)\), in which \(\alpha\) and \(\beta\) are shared by all the genes and \(r_{g}\) is gene specific. If not specified, \(r_{g}\), \(\alpha\) and \(\beta\) will be estimated using method of moments. For isoform data, we assume isoforms from the same Ig group share the same beta^Ig. \(\alpha\) is shared by all the isoforms and \(r_{gi}\) is isoform specific. The user also needs to specify an expected FC.

Value

MAPTerm: the most likely path of each gene/isoform. MAPTermNum: numeric version of MAPTerm.
AllTerm: all possible expression paths considered in the model. PP: posterior probability of being each expression path.
WhichMax: index of the most likely path. Allf: prior probability of being each path.
Pi0Track: estimated starting probabilities of each iteration.
TranTrack: estimated transition probabilities of each iteration.
AlphaTrack, BetaTrack: estimated alpha and beta(s).
LLAll=PostSumForLL.Sum: log likelihood of the model.
EBHMMNBFunForMulti

Author(s)
Ning Leng

Examples
data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
tmp <- EBHMMNBFun(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions,
maxround=2, OnlyQ=TRUE)

EBHMMNBFunForMulti  Baum-Welch algorithm for multiple hidden markov chains

Description
Baum-Welch algorithm for multiple hidden markov chains

Usage

EBHMMNBFunForMulti(Data,PPIn,
NgVector=NULL,Conditions, sizeFactors,
PriorFC=1.5,homo=TRUE, maxround=5,
Pi0=NULL, Tran=NULL, NumTranStage=3,
FCPParam=NULL, AlphaIn=NULL,BetaIn=NULL,
StateNames=c("Up","NC","Down"),
EM=TRUE, UpdateParam=TRUE, Print=TRUE,WithinCondR=TRUE,
PenalizeLowMed=TRUE, PenalizeLowMedQt=.2,PenalizeLowMedVal=10)

Arguments

Data  input data, rows are genes/isoforms and columns are samples
PPIn  PPDE for all adjacent comparisons
NgVector  Ng vector; NULL for gene level data
Conditions  A factor indicates the condition (time/spatial point) which each sample belongs to.
sizes  a vector indicates library size factors
Tran  initial values for transition matrices
Pi0  initial values for starting probabilities
NumTranStage  number of states in two chains
PriorFC  target FC for gridient change
StateNames  name of the hidden states
homo  whether the chain is assumed to be homogenious
maxround  max number of iteration
AlphaIn,BetaIn  If the parameters are known and the user doesn’t want to estimate them from the data, user may specify them here.
EBHMMNBfunForMulti

FCParam not in use
EM Whether estimate the prior parameters of the beta distribution by EM
UpdateParam Whether update starting probabilities and transition probabilities
WithinCondR By defining WithinCondR=TRUE, estimation of r’s are obtained within each condition. (WithinCondR=FALSE is not suggested here)
Print Whether print the elapsed-time while running the test.
PenalizeLowMed, PenalizeLowMedQt, PenalizeLowMedVal

Transcripts with median quantile <= PenalizeLowMedQt will be penalized

Details

EBHMMNBfunForMulti() function implements the Balm-Welch algorithm that estimates the starting probabilities and transition probabilities of a hidden Markov model with multiple chains. Here the emission distribution of each gene is assumed to be a Beta-Negative Binomial distribution with parameters (r_g, alpha, beta), in which alpha and beta are shared by all the genes and r_g is gene specific. If not specified, r_g, alpha and beta will be estimated using method of moments. For isoform data, we assume isoforms from the same Ig group share the same beta^Ig. alpha is shared by all the isoforms and r_gi is isoform specific. The user also needs to specify an expected FC.

Value

MAPTerm: the most likely path of each gene/isoform.
MAPTermNum: numeric version of MAPTerm.
AllTerm: all possible expression paths considered in the model.
PP: posterior probability of being each expression path.
WhichMax: index of the most likely path.
Allf: prior probability of being each path.
Pi0Track: estimated starting probabilities of each iteration.
TranTrack: estimated transition probabilities of each iteration.
AlphaTrack, BetaTrack: estimated alpha and beta(s).
LLAll=PostSumForLL.Sum: log likelihood of the model.

Author(s)

Ning Leng

Examples

data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
tmp <- EBHMMNBfunForMulti(Data=GeneExampleData, PPIn=matrix(1,ncol=15, nrow=100), sizeFactors=Sizes, Conditions=Conditions, maxround=2)
EBHMMNBMultiEM_2chain  Run EBSeqHMM model with a fixed expected FC

Description

Run EBSeqHMM model with a fixed expected FC

Usage

```R
EBHMMNBMultiEM_2chain(Data,
NgVector=NULL, Conditions, AllTran=NULL,
AllPi0=NULL, Terms=NULL,
sizeFactors, NumTranStage=c(3,2),PriorFC=2,
StateNames=c("Up","Down"),homo=FALSE,
UpdateRd=5, PIBound=.9, UpdatePI=FALSE,Print=FALSE,
WithinCondR=TRUE,
PenalizeLowMed=TRUE, PenalizeLowMedQt=.1,PenalizeLowMedVal=10)
```

Arguments

- **Data**: input data, rows are genes and columns are samples
- **NgVector**: Ng vector; NULL for gene level data
- **Conditions**: A factor indicates the condition (time/spatial point) which each sample belongs to.
- **AllTran**: initial values for transition matrices
- **AllPi0**: initial values for starting probabilities
- **Terms**: Terms
- **sizeFactors**: a vector indicates library size factors
- **StateNames**: names of the hidden states
- **NumTranStage**: number of states in two chains
- **PriorFC**: target FC for gradient change
- **homo**: whether the chain is assumed to be homogenous
- **UpdateRd**: max number of iteration
- **UpdatePI**: whether update the mixture proportion of two chains
- **PIBound**: upper bound of the mixture proportion of the two chains
- **Print**: Whether print the elapsed-time while running the test.
- **WithinCondR**: By defining WithinCondR=TRUE, estimation of r’s are obtained within each condition. (WithinCondR=FALSE is not suggested here)
- **PenalizeLowMed, PenalizeLowMedQt, PenalizeLowMedVal**: Transcripts with median quantile \(\leq\) PenalizeLowMedQt will be penalized
Details

EBHMMNBMultiEM_2chain() function implements the EBSeqHMM model to perform statistical analysis in an RNA-seq experiment with ordered conditions. EBHMMNBMultiEM_2chain() calls EBHMMNBfunForMulti() function to perform Balm-Welch algorithm that estimates the starting probabilities and transition probabilities. Here the emission distribution of each gene is assumed to be a Beta-Negative Binomial distribution with parameters \((r_g, \alpha, \beta)\), in which \(\alpha\) and \(\beta\) are shared by all the genes and \(r_g\) is gene specific. If not specified, \(r_g\), \(\alpha\) and \(\beta\) will be estimated using method of moments. For isoform data, we assume isoforms from the same Ig group share the same \(\alpha^\text{Ig}\). \(\alpha\) is shared by all the isoforms and \(r_{gi}\) is isoform specific. The user also needs to specify an expected FC. Function EBSeqHMMTest() runs several models with varying FCs and returns the model with maximum likelihood.

Value

- **Pi0Out**: estimated starting probabilities of each iteration.
- **TranOut**: estimated transition probabilities of each iteration.
- **Pi**: estimated probability of being each chain.
- **Alpha, Beta**: estimated \(\alpha\) and \(\beta\)(s).
- **LLSum**: log likelihood of the model.
- **QList**: estimated q’s.
- **MgAllPP**: marginal PP for all paths.
- **MgAllMAPChar**: Most likely path based on MgAllPP.
- **MgAllMaxVal**: Highest PP based on MgAllPP.
- **PPMatW**: Posterior probabilities of being each of the chains.

Author(s)

Ning Leng

Examples

```r
data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
tmp <- EBHMMNBMultiEM_2chain(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions, UpdateRd=2)
```

**EBSeqHMMTest**

*Identify DE genes and classify them into their most likely path in an RNA-seq experiment with ordered conditions*

Description

Identify DE genes and classify them into their most likely path in an RNA-seq experiment with ordered conditions
Usage

EBSeqHMMTest(Data,
NgVector=NULL, Conditions, AllTran=NULL,
AllPi0=NULL, Terms=NULL,
sizeFactors, NumTranStage=c(3,2), FCV=2,
home=FALSE, UpdateRd=10, PIBound=.9, UpdatePI=FALSE,
Print=FALSE, WithinCondR=TRUE, Qtrm=.75, QtrmCut=10,
PenalizeLowMed=TRUE, PenalizeLowMedQt=.1, PenalizeLowMedVal=10)

Arguments

Data input data, rows are genes and columns are samples
NgVector Ng vector; NULL for gene level data
Conditions A factor indicates the condition (time/spatial point) which each sample belongs to.
AllTran initial values for transition matrices
AllPi0 initial values for starting probabilities
Terms Terms
FCV candidate values for expected FC. Default is 2. If user wants to search through a list of candidate FCs, he/she may define FCV as a vector. e.g. By defining FCV=seq(1.4,2,.2), the function will search over (1.4 1.6 1.8 2.0). Note that searching over a number of candidate FCs will increase the running time.
sizeFactors a vector indicates library size factors
NumTranStage number of states in two chains
homo whether the chain is assumed to be homogenous
UpdateRd max number of iteration
UpdatePI whether update the mixture proportion of two chains
PIBound upper bound of the mixture proportion of the two chains
Qtrm,QtrmCut Transcripts with Qtrm th quantile \leq QtrmCut will be removed before testing. The default value is Qtrm = 0.75 and QtrmCut=10. By default setting, transcripts that have >75% of the samples with expression less than 10 won’t be tested.
WithinCondR By defining WithinCondR=TRUE, estimation of r’s are obtained within each condition. (WithinCondR=FALSE is not suggested here)
Print Whether print the elapsed-time while running the test.
PenalizeLowMed,PenalizeLowMedQt,PenalizeLowMedVal Transcripts with median quantile \leq PenalizeLowMedQt will be penalized

Details

EBSeqHMMTest() function applies EBSeqHMM model with different expected FC’s and select the optimal FC that maximizes the log likelihood. EBSeqHMMTest() calls EBHMMNBMultiEM_2chain() function which implements the EBSeqHMM model to perform statistical analysis in an RNA-seq experiment with ordered conditions based on a fixed expected FC. EBSeqHMMTest() runs EBHMMNBMultiEM_2chain() with varying FCs (default is seq(1.4,2,.2)). And it will return the results of the model with optimal FC. Here the emission distribution of each gene is assumed to be a Beta-Negative Binomial distribution with parameters \( r_g, \alpha, \beta \), in which \( \alpha \) and \( \beta \) are shared by all the genes and \( r_g \) is gene specific. If not specified, \( r_g, \alpha \) and \( \beta \) will be estimated using method of moments. For isoform data, we assume isoforms from the same Ig group share the same \( \beta^Ig \). \( \alpha \) is shared by all the isoforms and \( r_gi \) is isoform specific. The user also needs to specify an expected FC.
Value

- Pi0Out: estimated starting probabilities of each iteration.
- TranOut: estimated transition probabilities of each iteration.
- Pi: estimated probability of being each chain.
- Alpha, Beta: estimated alpha and beta(s).
- LLSum: log likelihood of the model.
- QList: estimated q’s.
- MgAllPP: marginal PP for all paths.
- MgAllMAPChar: Most likely path based on MgAllPP.
- MgAllMaxVal: Highest PP based on MgAllPP.
- PPMatW: Posterior probabilities of being each of the chains.
- FCLikelihood: log likelihood of each FC.

Author(s)

Ning Leng

Examples

```r
data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
EBSeqHMMGeneOut <- EBSeqHMMTest(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions, UpdateRd=2)
```

Description

Extented EBTest function

Usage

```
EBTest_ext(Data,NgVector=NULL,Conditions,
sizeFactors, maxround, Pool=FALSE, NumBin=1000,
ApproxVal=10^-10, Alpha=NULL, Beta=NULL,
PInput=NULL,RInput=NULL,PoolLower=.25,
PoolUpper=.75,OnlyCalcR=FALSE,Print=TRUE)
```

Arguments

- **Data**: Input data, rows are genes/isoforms and columns are samples. Data should come from a two condition experiment.
- **NgVector**: Ng vector; NULL for gene level data
- **Conditions**: A factor indicates the condition (time/spatial point) which each sample belongs to. Only two levels are allowed.
sizeFactors  a vector indicates library size factors
maxround  number of iteration
Pool  While working without replicates, user could define the Pool = TRUE in the EBTest function to enable pooling.
NumBin  By defining NumBin = 1000, EBSeq will group the genes with similar means together into 1,000 bins.
PoolLower,PoolUpper  
With the assumption that only subset of the genes are DE in the data set, we take genes whose FC are in the PoolLower - PoolUpper quantile of the FCs as the candidate genes (default is 25 bin, the bin-wise variance estimation is defined as the median of the cross condition variance estimations of the candidate genes within that bin. We use the cross condition variance estimations for the candidate genes and the bin-wise variance estimations of the host bin for the non-candidate genes.
ApproxVal  The variances of the transcripts with mean < var will be approximated as \( \text{mean} / (1 - \text{ApproxVal}) \).
Alpha,Beta,PInput,RInput  If the parameters are known and the user doesn’t want to estimate them from the data, user may specify them here.
Print  Whether print the elapsed-time while running the test.
OnlyCalcR  if OnlyCalcR=TRUE, the function will only return estimation of r's.

Details

EBSeq_ext() function is an extension of EBTest() function, which is used to calculate the conditional probability \( P(X_{g,t} | X_{g,t-1}) \). In EBSeqHMM, we assume the conditional distribution is Beta-Negative Binomial.

Value

See EBTest

Author(s)

Ning Leng

Examples

data(GeneExampleData)
Data=GeneExampleData[,1:6]
CondVector <- rep(paste("t",1:2,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2"))
Sizes <- MedianNorm(Data[1:10,])
Out <- EBTest_ext(Data=Data[1:10,], sizeFactors=Sizes, Conditions=Conditions,
maxround=1)
Calculate the prior predictive distribution of the Beta-Negative Binomial model

Usage

f0(Input, AlphaIn, BetaIn, EmpiricalR, NumOfGroups, log)

Arguments

- Input: expression values
- AlphaIn, BetaIn, EmpiricalR: The parameters estimated from last iteration of EM.
- NumOfGroups: How many transcripts within each Ng group
- log: If set as TRUE, the output will in log scale.

Details

Function f0() will calculate the Beta-Negative Binomial prior predictive probability for a given set of parameters.

Value

output a numeric vector, each element shows the prior predictive probability of one gene/isoform

Author(s)

Ning Leng

Examples

f0(matrix(rnorm(100,100,1),ncol=10), .5, .6, matrix(rnorm(100,200,1),ncol=10), 100, TRUE)

GeneExampleData

Simulated gene level data set with 5 ordered conditions

Description

'GeneExampleData' gives the gene level simulated data with 5 ordered conditions, triplicates for each condition. The data set was simulated following the Negative Binomial distribution. The parameters of each gene (mean and overdispersion) were sampled from the empirical estimates from an empirical RNA-Seq data set from Thomson lab at Morgridge Institute for Research.
GetAllPaths

Format
GeneExampleData is a matrix with 100 genes (rows) and 15 samples (columns).

See Also
IsoExampleList

Examples

data(GeneExampleData)
str(GeneExampleData)

| GetAllPaths | Obtain all possible gene paths for an RNA-seq experiments with ordered conditions |

Description
Obtain all possible gene paths for an RNA-seq experiments with ordered conditions

Usage
GetAllPaths(EBSeqHMMOut, OnlyDynamic=TRUE)

Arguments

| EBSeqHMMOut | output from EBSeqHMMTest function |
| OnlyDynamic | if specifies as TRUE, only dynamic paths will be shown |

Details
GetAllPaths() function may be used to generate all possible expression paths of a particular design.

Value
output: a vector of paths. For example, Up-Up-Up-Up, Up-Up-EE-EE, Up-Down-Up-EE, etc.

Author(s)
Ning Leng

Examples

data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
EBSeqHMMGeneOut <- EBSeqHMMTest(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions, UpdateRd=2)
AllPaths <- GetAllPaths(EBSeqHMMGeneOut)
GetConfidentCalls can be used to obtain a list of DE genes/isoforms with user specific cutoffs. To obtain a list of DE genes/isoforms with a target FDR alpha, the user may specify FDR=alpha. To further choose genes/isoforms with high posterior probability of being its most likely path, the user may specify the option cutoff (default is 0.5). Then genes or isoforms with PP(most likely path ) >= 0.5 will be selected.

Value

Overall: a list of genes/isoforms that are identified as DE under the target FDR, shown are their names and PPs; EachPath: a list object, each sublist contains confident calls (genes/isoforms) that have PP(path)>=cutoff for a particular expression path, shown are their names and PPs; NumEach: length of each sublist in EachPath. EachPathName: gene/isoform names in each of the sublists in EachPath.

Note

Output: output a list of genes that are classified to a expression path as a confident assignment.

Author(s)

Ning Leng
GetDECalls

Examples

data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
EBSeqHMMGeneOut <- EBSeqHMMTest(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions,
UpdateRd=2)
GeneDECalls <- GetDECalls(EBSeqHMMGeneOut, FDR=.05)
GeneConfCalls <- GetConfidentCalls(EBSeqHMMGeneOut, FDR=.05,cutoff=.5, OnlyDynamic=TRUE)

GetDECalls

Obtain DE gene/isoform list at a certain FDR

Description

Obtain DE gene/isoform list at a certain FDR

Usage

GetDECalls(EBSeqHMMOut,FDR=.05)

Arguments

EBSeqHMMOut output from EBSeqHMMTest function
FDR Target FDR; default is 0.05

Details

Function GetDECalls() can be used to obtain a list of DE genes/isoforms with user specific cutoffs. To obtain a list of DE genes/isoforms with a target FDR alpha, the user may specify FDR=alpha.

Value

a list of genes/isoforms that are identified as DE under the target FDR, shown are their names and PPs;

Note

Output: output a list of genes that are DE in at least one condition in an RNA-seq experiment with multiple ordered conditions

Author(s)

Ning Leng

Examples

data(GeneExampleData)
CondVector <- rep(paste("t",1:5,sep=""),each=3)
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))
Sizes <- MedianNorm(GeneExampleData)
EBSeqHMMGeneOut <- EBSeqHMMTest(Data=GeneExampleData, sizeFactors=Sizes, Conditions=Conditions,
UpdateRd=2)
GeneDECalls <- GetDECalls(EBSeqHMMGeneOut, FDR=.05)
IsoExampleList

Simulated isoform level data set with 5 ordered conditions

Description

'IsoExampleList' gives the isoform level simulated data with 5 ordered conditions, triplicates for each condition. The data set was simulated following the Negative Binomial distribution. The parameters of each isoform (mean and overdispersion) were sampled from the isoform level empirical estimates from an empirical RNA-Seq data set from Thomson lab at Morgridge Institute for Research.

Format

IsoExampleList is a list with three components. IsoExampleList$IsoExampleData contains a matrix with 200 isoform (rows) and 15 samples (columns). IsoExampleList$IsoNames contains a vector of isoform names. IsoformExampleList$IsosGeneNames contains a vector indicating the gene each isoform belongs to.

See Also

GeneExampleData

Examples

data(IsoExampleList)
str(IsoExampleList)

LikefunNBHMM

Likelihood function of the Beta-Negative Binomial HMM Model

Description

Likelihood function of the Beta-Negative Binomial HMM Model

Usage

LikefunNBHMM(ParamPool, InputPool)

Arguments

ParamPool The parameters that will be estimated in EM.
InputPool The control parameters that will not be estimated in EM

Details

The likelihood function of the Beta-Negative Binomial HMM model used in EBSeqHMM. EBSeqHMM uses optim() function to obtain the optimal estimates that minimizes the likelihood.

Value

optimal estimates of the parameters of interest
**Author(s)**  
Ning Leng

**Examples**

data(GeneExampleData)  
tmp <- GeneExampleData[1:10,]  
In <- list(tmp,1,5,10,3,tmp,rep(1,15),as.factor(rep(1:5,each=3)), 10,cbind(rep(.5,10),rep(1,10),rep(2,10)))  
Start <- c(1,1)  
LikeFunNBHMM(Start,In)

---

**PlotExp**  
Plot expression of a single gene

**Description**
Plot expression of a single gene

**Usage**

PlotExp(NormalizedData, Conditions, Name)

**Arguments**

- **NormalizedData**: Expression data after adjusting for library size factors
- **Conditions**: sample conditions
- **Name**: name of the gene/isoform of interest

**Details**
PlotExp() function will generate line plots for genes or isoforms of interest.

**Value**
PlotExp() function will generate line plots for genes or isoforms of interest.

**Author(s)**
Ning Leng

**Examples**

data(GeneExampleData)  
CondVector <- rep(paste("t",1:5,sep=""),each=3)  
Conditions <- factor(CondVector, levels=c("t1","t2","t3","t4","t5"))  
Sizes <- MedianNorm(GeneExampleData)  
NormData <- GetNormalizedMat(GeneExampleData, Sizes)  
PlotExp(NormData, Conditions, "Gene_1")
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