Package ‘bayNorm’

February 2, 2024

Type Package
Title Single-cell RNA sequencing data normalization
Version 1.20.0
Description bayNorm is used for normalizing single-cell RNA-seq data.
License GPL (>= 2)
Encoding UTF-8
RoxygenNote 7.0.2
Depends R (>= 3.5),
Imports Rcpp (>= 0.12.12), BB, foreach, iterators, doSNOW, Matrix, parallel, MASS, locfit, fitdistrplus, stats, methods, graphics, grDevices, SingleCellExperiment, SummarizedExperiment, BiocParallel, utils
LinkingTo Rcpp, RcppArmadillo, RcppProgress
Suggests knitr, rmarkdown, BiocStyle, devtools, testthat
VignetteBuilder knitr
biocViews ImmunoOncology, Normalization, RNASEq, SingleCell, Sequencing
URL https://github.com/WT215/bayNorm
BugReports https://github.com/WT215/bayNorm/issues
git_url https://git.bioconductor.org/packages/bayNorm
git_branch RELEASE_3_18
git_last_commit 29ecf00
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-02-02
Author Wenhao Tang [aut, cre], François Bertaux [aut], Philipp Thomas [aut], Claire Stefanelli [aut], Malika Saint [aut],
AdjustSIZE_fun

Description

This function adjusts MME estimated size parameter of prior, which is a negative binomial distribution, using estimates from maximizing marginal distribution (BB_SIZE). Simulation studies have shown this hybrid method of using adjusted MME size estimates is the most robust (see bayNorm paper). Hence, this is the default option for estimating size in bayNorm.

Usage

AdjustSIZE_fun(BB_SIZE, MME_MU, MME_SIZE)

Arguments

- BB_SIZE: size estimated from BB_Fun.
- MME_MU: mu estimated from EstPrior.
- MME_SIZE: size estimated from EstPrior.
Value

MME_SIZE_adjust: A vector of estimated size. Adjusted MME_SIZE based on BB_SIZE (size estimated by maximizing marginal distribution)

Examples

data('EXAMPLE_DATA_list')
MME_MU<-rlnorm(100,meanlog=5,sdlog=1)
MME_SIZE<-rlnorm(100,meanlog=1,sdlog=1)
BB_SIZE<-rlnorm(100,meanlog=0.5,sdlog=1)
adjustt<-AdjustSIZE_fun(BB_SIZE, MME_MU, MME_SIZE)

Description

Rcpp version: as.matrix

Usage

asMatrix(rp, cp, z, nrows, ncols)

Arguments

rp vector
cp vector
z vector
nrows nrows
ncols ncols

Details

Rcpp version: as.matrix

Value

Matrix object in R.

Examples

data("EXAMPLE_DATA_list")
#Should not run by the users, it is used in prior estimation.
## Not run:
as_matrix

Description
Transform sparse matrix to matrix.

Usage
as_matrix(mat)

Arguments
mat Sparse matrix.

Value
Matrix.

Examples
aa=matrix(seq(1,6),nrow=2,ncol=3)
qq=as(as.matrix(aa), "dgCMatrix")
all.equal(unname(as_matrix(qq)),unname(as.matrix(qq)))

bayNorm

Description
This is the main wrapper function for bayNorm. The input is a matrix of raw scRNA-seq data and a vector of capture efficiencies of cells. You can also specify the condition of cells for normalizing multiple groups of cells separately.

Usage
bayNorm(
  Data,
  BETA_vec = NULL,
  Conditions = NULL,
  UMI_sffl = NULL,
  Prior_type = NULL,
  mode_version = FALSE,
  mean_version = FALSE,
  S = 20,
  parallel = TRUE,
bayNorm

NCores = 5,
FIX_MU = TRUE,
GR = FALSE,
BB_SIZE = TRUE,
verbose = TRUE,
out.sparse = FALSE
)

Arguments

Data A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.

BETA_vec A vector of capture efficiencies (probabilities) of cells. If it is null, library size (total count) normalized to 0.06 will be used as the input BETA_vec. BETA_vec less and equal to 0 or greater and equal to 1 will be replaced by the minimum and maximum of the BETA_vec which range between (0,1) respectively.

Conditions vector of condition labels, this should correspond to the columns of the Data. Default is NULL, which assumes that all cells belong to the same group.

UMI_sffl Scaling factors are required only for non-UMI based data for which Data is devided by UMI_sffl. If non-null and Conditions is non-null, then UMI_sffl should be a vector of length equal to the number of groups. Default is NULL.

Prior_type Determines what groups of cells is used in estimating prior using Conditions. Default is NULL. If Conditions is NULL, priors are estimated based on all cells. If Conditions is not NULL and if Prior_type is LL, priors are estimated within each group respectively. If Prior_type is GG, priors are estimated based on cells from all groups. LL is suitable for DE detection. GG is preferred if reduction of batch effect between samples are desired for example for technical replicates (see bayNorm paper).

mode_version If TRUE, bayNorm return modes of posterior estimates as normalized data which is a 2D matrix rather than samples from posterior which is a 3D array. Default is FALSE.

mean_version If TRUE, bayNorm return means of posterior estimates as normalized data, which is a 2D matrix rather than samples from posterior which is a 3D array. Default is FALSE.

S The number of samples you would like to generate from estimated posterior distribution (The third dimension of 3D array). Default is 20. S needs to be specified if mode_version=FALSE.

parallel If TRUE, NCores cores will be used for parallelization. Default is TRUE.

NCores number of cores to use, default is 5. This will be used to set up a parallel environment using either MulticoreParam (Linux, Mac) or SnowParam (Windows) with NCores using the package BiocParallel.

FIX_MU Whether fix mu (the mean parameter of prior distribution) to its MME estimate, when estimating prior parameters by maximizing marginal distribution. If TRUE, then 1D optimization is used, otherwise 2D optimization for both mu and size is used (slow). Default is TRUE.
GR
If TRUE, the gradient function will be used in optimization. However since
the gradient function itself is very complicated, it does not help too much in
speeding up. Default is FALSE.

BB_SIZE
If TRUE, estimate size parameter of prior using maximization of marginal like-
lihood, and then use it for adjusting MME estimate of SIZE. Default is TRUE.

verbose
print out status messages. Default is TRUE.

out.sparse
Only valid for mean version: Whether the output is of type dgCMatrix or not.
Default is FALSE.

Details
A wrapper function of prior estimation and bayNorm function.

Value
List containing 3D arrays of normalized expression (if mode_version=FALSE) or 2D matrix of nor-
malized expression (if mode_version=TRUE or mean_version=TRUE), a list contains estimated
priors and a list contains input parameters used: BETA_vec, Conditions (if specified), UMI_sfl1
(if specified), Prior_type, FIX_MU, BB_SIZE and GR.

References
Wenhao Tang, Francois Bertaux, Philipp Thomas, Claire Stefanelli, Malika Saint, Samuel Blaise
Marguerat, Vahid Shahrezaei bayNorm: Bayesian gene expression recovery, imputation and nor-
malisation for single cell RNA-sequencing data Bioinformatics, btz726; doi: 10.1093/bioinformat-
ics/btz726

Examples
data('EXAMPLE_DATA_list')
#Return 3D array normalzied data:
bayNorm_3D<-bayNorm(
 Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)],
 BETA_vec = EXAMPLE_DATA_list$inputbeta[seq(1,30)],
 mode_version=FALSE,parallel =FALSE)

bayNorm_sup
bayNorm with estimated parameters as input

Description
This is a supplementary wrapper function for bayNorm. It is useful if one has already estimated
prior parameters and wants to simulate 2D or 3D normalized output using the same prior estimates.
Usage

bayNorm_sup(
  Data,
  PRIORS = NULL,
  input_params = NULL,
  mode_version = FALSE,
  mean_version = FALSE,
  S = 20,
  parallel = TRUE,
  NCores = 5,
  BB_SIZE = TRUE,
  verbose = TRUE,
  out.sparse = FALSE
)

Arguments

Data                   A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.
PRIORS                 A list of estimated prior parameters obtained from bayNorm.
input_params           A list of input parameters which have been used: BETA_vec, Conditions, UMI_sff1, Prior_type, FIX_MU, BB_SIZE and GR.
mode_version           If TRUE, bayNorm return mode version normalized data which is of 2D matrix instead of 3D array. Default is FALSE.
mean_version           If TRUE, bayNorm return mean version normalized data which is of 2D matrix instead of 3D array. Default is FALSE.
S                      The number of samples you would like to generate from estimated posterior distribution (The third dimension of 3D array). Default is 20. S needs to be specified if mode_version=FALSE.
parallel               If TRUE, NCores cores will be used for parallelization. Default is TRUE.
NCores                 number of cores to use, default is 5. This will be used to set up a parallel environment using either MulticoreParam (Linux, Mac) or SnowParam (Windows) with NCores using the package BiocParallel.
BB_SIZE                If TRUE (default), use adjusted size for normalization. The adjusted size is obtained by adjusting MME estimated size by a factor. The factor is calculated based on both MME estimated size and BB estimated size. If FALSE, use MME estimated SIZE.
verbose                print out status messages. Default is TRUE.
out.sparse             Only valid for mean version: Whether the output is of type dgCMatrix or not. Default is FALSE.

Details

If you have run bayNorm before and obtained a list of estimated prior parameters, then you may not want to run parameter estimation again. You can just use previous estimated parameters for obtaining 3D or 2D normalized data.
BB_Fun

Value
List containing 3D arrays of normalized expression (if mode_version=FALSE) or 2D matrix of normalized expression (if mode_version=TRUE or mean_version=TRUE), a list contains estimated priors and a list contains input parameters used: BETA_vec, Conditions (if specified), UMI_sffl (if specified), Prior_type, FIX_MU, BB_SIZE and GR.

References
Wenhao Tang, Francois Bertaux, Philipp Thomas, Claire Stefanelli, Malika Saint, Samuel Blaise Marguerat, Vahid Shahrezaei bayNorm: Bayesian gene expression recovery, imputation and normalisation for single cell RNA-sequencing data Bioinformatics, btz726; doi: 10.1093/bioinformatics/btz726

Examples
data('EXAMPLE_DATA_list')
#Return 3D array normalized data:
bayNorm_3D<-bayNorm(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)], BETA_vec = EXAMPLE_DATA_list$inputbeta[seq(1,30)], mode_version=FALSE,parallel =FALSE)

#Now if you want to generate 2D matrix using the same prior estimates as generated before:
bayNorm_2D<-bayNorm_sup(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)], PRIORS=bayNorm_3D$PRIORS, input_params = bayNorm_3D$input_params, mode_version=TRUE)

BB_Fun

Estimating size for each gene by either 1D or 2D maximization of marginal distribution

Description
Estimating parameters of the prior distribution for each gene by maximizing marginal distribution: 1D (optimize with respect to size using MME estimate of mu, 2D (optimize with respect to both mu and size)

Usage
BB_Fun(
Data,
BETA_vec,
INITIAL_MU_vec,
INITIAL_SIZE_vec,
MU_lower = 0.01,
MU_upper = 500,
SIZE_lower = 0.01,
SIZE_upper = 30,
parallel = FALSE,
NCores = 5,
FIX_MU = TRUE,
GR = FALSE
)

Arguments

Data A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.

BETA_vec A vector of capture efficiencies (probabilities) of cells.

INITIAL_MU_vec Mean expression of genes, can be estimated from EstPrior.

INITIAL_SIZE_vec size of genes (size is a parameter in NB distribution), can come from EstPrior.

MU_lower The lower bound for the mu. (Only need it when you want to do 2D optimization). Default is 0.01.

MU_upper The upper bound for the mu. (Only need it when you want to do 2D optimization). Default is 500.

SIZE_lower The lower bound for the size. Default is 0.01.

SIZE_upper The upper bound for the size. Default is 30.

parallel If TRUE, NCores cores will be used for parallelization. Default is TRUE.

NCores number of cores to use, default is 5. This will be used to set up a parallel environment using either MulticoreParam (Linux, Mac) or SnowParam (Windows) with NCores using the package BiocParallel.

FIX_MU If TRUE, then 1D optimization, otherwise 2D optimization (slow).

GR If TRUE, the gradient function will be used in optimization. However since the gradient function itself is very complicated, it does not help too much in speeding up. Default is FALSE.

Value

BB estimated size (1D optimization) or size and mu (2D optimization).

Examples

data('EXAMPLE_DATA_list')
BB_RESULT<-BB_Fun(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)],
BETA_vec = EXAMPLE_DATA_list$inputbeta[seq(1,30)],
INITIAL_MU_vec=EXAMPLE_DATA_list$mu,
INITIAL_SIZE_vec=EXAMPLE_DATA_list:size,
MU_lower=0.01,MU_upper=500,SIZE_lower=0.01,
BetaFun

Estimate capture efficiency for cells

Description
This function estimates cell specific capture efficiencies (BETA_vec) using mean raw counts of a subset of genes that is an input for bayNorm. A specific method is used to exclude genes with high expression or high drop-out are excluded.

Usage

BetaFun(Data, MeanBETA)

Arguments

Data
A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.

MeanBETA
Mean capture efficiency of the scRNAseq data. This can be estimated via spike-ins or other methods.

Value
List containing: BETA: a vector of capture efficiencies, which is of length number of cells; Selected_genes: a subset of genes that are used for estimating BETA.

Examples

data('EXAMPLE_DATA_list')
BETA_out<-BetaFun(Data=EXAMPLE_DATA_list$inputdata,
MeanBETA=0.06)
Check_input

Description
Check input

Usage
Check_input(Data)

Arguments
Data Input data.

Value
Matrix (of type matrix in R).

Examples
aa<-matrix(seq(1,6),nrow=2,ncol=3)
Check_input(aa)

DownSampling

Description
For each element in the Data, randomly generate a number using Binomial distribution with probability equal to the specific capture efficiency.

Usage
DownSampling(Data, BETA_vec)

Arguments
Data raw count Data
BETA_vec A vector of capture efficiencies of cells

Value
A matrix of binomial downsampling data.
EstPrior

Estimate size and \( \mu \) for Negative Binomial distribution for each gene using MME method

**Description**

Input raw data and return estimated size and \( \mu \) for each gene using the MME method.

**Usage**

```r
EstPrior(Data, verbose = TRUE)
```

**Arguments**

- **Data**
  
  A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class `SummarizedExperiment` (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.
  
  - **verbose**
    
    print out status messages. Default is TRUE.

**Details**

\( \mu \) and size are two parameters of the prior that need to be specified for each gene in bayNorm. They are parameters of negative binomial distribution. The variance is \( \mu + \mu^2/size \) in this parametrization.

**Value**

List containing estimated \( \mu \) and size for each gene.

**Examples**

```r
data('EXAMPLE_DATA_list')
MME_est<-EstPrior(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)],
                  verbose=TRUE)
```

---

**Examples**

```r
data("EXAMPLE_DATA_list")
Downsample_data <- DownSampling(Data=EXAMPLE_DATA_list$inputdata,
      BETA_vec = EXAMPLE_DATA_list$inputbeta)
```
EstPrior_rcpp

Estimate size and mu for Negative Binomial distribution for each gene using MME method (Rcpp version)

Description
Input raw data and return estimated size and mu for each gene using the MME method.

Usage
EstPrior_rcpp(Data)

Arguments
Data A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix and is named "Counts") or just matrix.

Details
mu and size are two parameters of the prior that need to be specified for each gene in bayNorm. They are parameters of negative binomial distribution. The variance is $\mu + \mu^2/\text{size}$ in this parametrization.

Value
List containing estimated mu and size for each gene.

Examples

data("EXAMPLE_DATA_list")
#Should not run by the users, it is used in prior estimation.
## Not run:

EstPrior_sprcpp

Estimate size and mu for Negative Binomial distribution for each gene using MME method (Rcpp version, sp_mat)

Description
Input raw data and return estimated size and mu for each gene using the MME method.

Usage
EstPrior_sprcpp(Data)
Arguments

Data A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix and is named "Counts") or just matrix.

Details

mu and size are two parameters of the prior that need to be specified for each gene in bayNorm. They are parameters of negative binomial distribution. The variance is $\mu + \mu^2/\text{size}$ in this parametrization.

Value

List containing estimated mu and size for each gene.

Examples

```r
data("EXAMPLE_DATA_list")
# Should not run by the users, it is used in prior estimation.
## Not run:
```

EXAMPLE_DATA_list A subset of Grun et al (2014) data: 2i samples

Description

Small extract (20 genes and 74 cells) from the Grun et al (2014) data: 2i samples

Usage

EXAMPLE_DATA_list

Format

A list: EXAMPLE_DATA_list[1]: inputdata, EXAMPLE_DATA_list[2]: inputbeta (a vector of probabilities with length equal to the number of cells), EXAMPLE_DATA_list[3]: mu (MME method estimated mean expression for each gene), EXAMPLE_DATA_list[4]: size (adjusted MME size for each gene).

References


Examples

```r
data(EXAMPLE_DATA_list)
```
**NOISY_FUN**

**Noisy gene detection**

**Description**

This function detects noisy genes using trends observed in a set of synthetic controls. Input bayNorm normalized data of real data (bay_array_N) and synthetic control (bay_array_C) respectively.

**Usage**

```r
NOISY_FUN(bay_array_N, bay_array_C, plot.out = FALSE)
```

**Arguments**

- `bay_array_N`: A 2D matrix or 3D array of normalized data (real cells).
- `bay_array_C`: A 2D matrix or 3D array of normalized data (synthetic control).
- `plot.out`: If TRUE, show CV^2 vs Mean expression plot. Default is FALSE.

**Details**

bay_array_N and bay_array_C should be of the same dimension.

**Value**

A vector of adjusted P-values.

**Examples**

```r
bay_array_N<-array(rpois(1000*50*2,17),dim=c(1000,50,2))
bay_array_C<-array(rpois(1000*50*2,58),dim=c(1000,50,2))
noisy_output<-NOISY_FUN(bay_array_N,bay_array_C)
```

---

**noisy_gene_detection**

A wrapper function for noisy gene detection from raw data. This produces synthetic control, performs bayNorm on both real cell data and synthetic controls and does noisy gene detection.

**Description**

A wrapper function for noisy gene detection from raw data. This produces synthetic control, performs bayNorm on both real cell data and synthetic controls and does noisy gene detection.
Usage

```r	noisy_gene_detection(  
  Data,  
  BETA_vec = NULL,  
  mode_version = FALSE,  
  mean_version = FALSE,  
  S = 20,  
  parallel = TRUE,  
  NCores = 5,  
  FIX_MU = TRUE,  
  GR = FALSE,  
  BB_SIZE = TRUE,  
  verbose = TRUE,  
  plot.out = FALSE,  
  PRIORS = NULL,  
  input_params = NULL  
)
```

Arguments

- **Data**: A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class `SummarizedExperiment` (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.

- **BETA_vec**: A vector of capture efficiencies of cells.

- **mode_version**: If TRUE, bayNorm return mode version normalized data which is of 2D matrix instead of 3D array. Default is FALSE.

- **mean_version**: If TRUE, bayNorm return mean version normalized data which is of 2D matrix instead of 3D array. Default is FALSE.

- **S**: The number of samples you would like to generate from estimated posterior distribution (The third dimension of 3D array). Default is 20. S needs to be specified if mode_version=FALSE.

- **parallel**: If TRUE, NCores cores will be used for parallelization. Default is TRUE.

- **NCores**: number of cores to use, default is 5. This will be used to set up a parallel environment using either MulticoreParam (Linux, Mac) or SnowParam (Windows) with NCores using the package BiocParallel.

- **FIX_MU**: Whether fix mu when estimating parameters by maximizing marginal distribution. If TRUE, then 1D optimization, otherwise 2D optimization (slow).

- **GR**: If TRUE, the gradient function will be used in optimization. However since the gradient function itself is very complicated, it does not help too much in speeding up. Default is FALSE.

- **BB_SIZE**: If TRUE, estimate BB size, and then use it for adjusting MME SIZE. Use the adjusted MME size for bayNorm. Default is TRUE.

- **verbose**: Print out status messages. Default is TRUE.

- **plot.out**: If TRUE, show CV\(^2\) vs Mean expression plot. Default is FALSE.
PRIORS (Need to be specified for efficiency if bayNorm has already been applied) A list of estimated prior parameters obtained from bayNorm. Default is NULL.

input_params (Need to be specified for efficiency if bayNorm has already been applied) A list of input parameters which have been used: BETA_vec, Conditions, UMI_sff1, Prior_type, FIX_MU, BB_SIZE and GR.

Details

A wrapper function for noisy gene detection from raw scRNA-seq data.

Value

A list of objects.

Examples

```r
data("EXAMPLE_DATA_list")
noisy_out<-noisy_gene_detection(Data=
EXAMPLE_DATA_list$inputdata[,seq(1,30)],BETA_vec
=EXAMPLE_DATA_list$inputbeta[seq(1,30)], mode_version = FALSE,
mean_version=FALSE,
S = 20,parallel = FALSE, NCores = 5,
FIX_MU = TRUE, GR = FALSE,
PRIORS=NULL,
BB_SIZE = TRUE,
verbose = TRUE, plot.out = TRUE)
```

Prior_fun  

A wrapper function of EstPrior and AdjustSIZE_fun

Description

A wrapper function for estimating the parameters of prior using the hybrid method adjusted MME estimates based on maximization of marginal likelihood. Input raw data and a vector of capture efficiencies of cells.

Usage

```
Prior_fun(
  Data,
  BETA_vec,
  parallel = TRUE,
  NCores = 5,
  FIX_MU = TRUE,
  GR = FALSE,
  BB_SIZE = TRUE,
  verbose = TRUE
)
```
Arguments

Data  A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class SummarizedExperiment (the assays slot contains the expression matrix, is named "Counts"), just matrix or sparse matrix.

BETA_vec  A vector of capture efficiencies of cells.

parallel  If TRUE, 5 cores will be used for parallelization. Default is TRUE.

NCores  number of cores to use, default is 5. This will be used to set up a parallel environment using either MulticoreParam (Linux, Mac) or SnowParam (Windows) with NCores using the package BiocParallel.

FIX_MU  If TRUE, then 1D optimization, otherwise 2D optimization (slow). Default is TRUE.

GR  If TRUE, the gradient function will be used in optimization. However since the gradient function itself is very complicated, it does not help too much in speeding up. Default is FALSE.

BB_SIZE  If TRUE, estimate BB size, and then use it for adjusting MME SIZE. Use the adjusted MME size for bayNorm. Default is TRUE.

darkgray

verbose  Print out status messages. Default is TRUE.

Details

By Default, this function will estimate mu and size for each gene using MME method. If BB_size is enable, spectral projected gradient method from BB package will be implemented to estimate 'BB size' by maximizing marginal likelihood function. MME estimated size will be adjusted according to BB size. BB size itself will not be used in bayNorm this is because that in our simulation we found that MME estimated mu and size have more accurate relationship, but MME estimated size deviates from the true value. BB size is overall more close to the true size but it does not possess a reasonable relationship with either MME estimated mu or BB estimated mu.

Value

List of estimated parameters: mean expression of genes and size of each gene.

Examples

data('EXAMPLE_DATA_list')
PRIOR_RESULT<-Prior_fun(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)],
BETA_vec = EXAMPLE_DATA_list$inputbeta[seq(1,30)],parallel=FALSE,
NCores=5,FIX_MU=TRUE,GR=FALSE,BB_SIZE=TRUE,verbose=TRUE)
**SyntheticControl**

*Generate synthetic control*

**Description**

Input raw data and a vector of capture efficiencies of cells.

**Usage**

```r
SyntheticControl(Data, BETA_vec)
```

**Arguments**

- **Data**: A matrix of single-cell expression where rows are genes and columns are samples (cells). `Data` can be of class `SummarizedExperiment` (the assays slot contains the expression matrix and is named "Counts") or just matrix.
- **BETA_vec**: A vector of capture efficiencies (probabilities) of cells.

**Details**

Simulate control data (based on Poisson distribution).

**Value**

List containing 2D matrix of synthetic control, `BETA_vec` used and `lambda` used in `rpois`.

**Examples**

```r
data("EXAMPLE_DATA_list")
SC_output<-SyntheticControl(Data = EXAMPLE_DATA_list$inputdata,
BETA_vec = EXAMPLE_DATA_list$inputbeta)
```

**t_sp**

*Transpose of sparse matrix*

**Description**

Transpose of sparse matrix

**Usage**

```r
t_sp(Data)
```
Arguments

Data  
A matrix of single-cell expression where rows are genes and columns are samples (cells). Data can be of class `SummarizedExperiment` (the assays slot contains the expression matrix and is named "Counts") or just matrix.

Details

Transpose of sparse matrix.

Value

Transpose of sparse matrix.

Examples

data("EXAMPLE_DATA_list")
#Should not run by the users, it is used in prior estimation.
## Not run:
Index

* datasets
  EXAMPLE_DATA_list, 14

AdjustSIZE_fun, 2
as_matrix, 4
asMatrix, 3

bayNorm, 4
bayNorm_sup, 6
BB_Fun, 8
BetaFun, 10

Check_input, 11

DownSampling, 11

EstPrior, 12
EstPrior_rcpp, 13
EstPrior_sprcpp, 13
EXAMPLE_DATA_list, 14

NOISY_FUN, 15
noisy_gene_detection, 15

Prior_fun, 17

SyntheticControl, 19

t_sp, 19