Package ‘bayNorm’

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Author Wenhao Tang [aut, cre], François Bertaux [aut], Philipp Thomas [aut], Claire Stefanelli [aut], Malika Saint [aut],
AdjustSIZE_fun

Adjust MME size estimate

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)

asMatrix

Rcpp version: as.matrix

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:
### Description

Transform sparse matrix to matrix.

### Usage

```r
as_matrix(mat)
```

### Arguments

- **mat**: Sparse matrix.

### Value

Matrix.

### Examples

```r
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

**A wrapper function of prior estimation and bayNorm function**

### 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

```r
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 divided 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 likelihood, 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 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_sff1 (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)

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_sffl, 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.
**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 Shahrezai
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 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)

#Now if you want to generate 2D matrix using the same prior estimates as generated before:
bayNorm_2D<-bayNorm_2D_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,
BB_Fun

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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data</td>
<td>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 &quot;Counts&quot;), just matrix or sparse matrix.</td>
</tr>
<tr>
<td>MeanBETA</td>
<td>Mean capture efficiency of the scRNAseq data. This can be estimated via spike-ins or other methods.</td>
</tr>
</tbody>
</table>

**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

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
Binomial 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

```
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 \( \text{size} \) 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 \( \text{size} \) for each gene.

Examples

```
data('EXAMPLE_DATA_list')
# Return estimated \( \mu \) and \( \text{size} \) for each gene using MME method.
MME_est<-EstPrior(Data=EXAMPLE_DATA_list$inputdata[,seq(1,30)], verbose=TRUE)
```
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 $mu + mu^2/size$ 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:
```

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)
EXAMPLE_DATA_list

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:

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

data(EXAMPLE_DATA_list)
NOISY_FUN

| 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

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

```
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`.
**Prior_fun**

**Description**

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)], 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**

```r
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.

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**

```
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**

```
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**

```
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:
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