

Package ‘lute’

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Version 1.0.0

Title Framework for cell size scale factor normalized bulk transcriptomics deconvolution experiments

Description Provides a framework for adjustment on cell type size when performing bulk transcriptomics deconvolution. The main framework function provides a means of reference normalization using cell size scale factors. It allows for marker selection and deconvolution using non-negative least squares (NNLS) by default. The framework is extensible for other marker selection and deconvolution algorithms, and users may reuse the generics, methods, and classes for these when developing new algorithms.

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Encoding UTF-8

URL <https://github.com/metamaden/lute>

BugReports <https://github.com/metamaden/lute/issues>

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'referencebasedParam-class.R' 'independentbulkParam-class.R'
'bisqueParam-class.R' 'typemarkersParam-class.R'
'findmarkersParam-class.R' 'globals.R'
'lute_cellScaleFactors.R' 'lute_classes.R' 'lute_conversions.R'
'lute_framework.R' 'lute_metadata.R' 'lute_randomized-data.R'
'lute_rmse.R' 'lute_rnf.R' 'lute_utilities.R'
'nnlsParam-class.R'

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| | |
|-------------|---|
| bisqueParam | <i>Make new object of class bisqueParam</i> |
|-------------|---|

Description

Main constructor for class [bisqueParam](#).

Usage

```
bisqueParam(
  bulkExpression = NULL,
  bulkExpressionSet = NULL,
  bulkExpressionIndependent = NULL,
  referenceExpression = NULL,
  cellScaleFactors = NULL,
  scData = NULL,
  assayName = "counts",
  batchVariable = "batch.id",
  cellTypeVariable = "celltype",
  useOverlap = FALSE,
```



```
useOverlap=FALSE)  
  
## get predicted proportions  
res <- deconvolution(newBisqueParameter)
```

cellProportionsPredictions

Make new cellProportionsPredictions object.

Description

Make new cellProportionsPredictions object.

Usage

```
cellProportionsPredictions(  
  predictionsTable,  
  cellTypeVector = NULL,  
  sampleIdVector = NULL  
)
```

Arguments

predictionsTable Table of cell type predictions.
cellTypeVector Character vector of cell type labels.
sampleIdVector Character vector of sample id labels.

Value

New cellProportionsPredictions object.
New cellProportionsPredictions object.

Examples

```
exampleData <- getDeconvolutionExampleData()
```

cellProportionsPredictions-class
cellProportionsPredictions-class

Description

Class for cell type predictions.

Arguments

predictionsTable Table containing cell type predictions.
cellTypeVector Character vector of cell type labels.
sampleIdVector Character vector of sample id labels.

Details

Main constructor for class [cellProportionsPredictions](#).

Value

New cellProportionsPredictions object.

Examples

```
new("cellProportionsPredictions")
predictionsTable <- matrix(sample(100,50),nrow=10)
colnames(predictionsTable) <- paste0("cell_type", seq(ncol(predictionsTable)))
rownames(predictionsTable) <- paste0("sample", seq(nrow(predictionsTable)))
cellProportionsPredictions(predictionsTable)
```

deconvolution *deconvolution*

Description

Get predicted cell type proportions using a deconvolution method.

Usage

```
deconvolution(object)
```

Arguments

object A [deconvolutionParam](#)-type object (see `?`deconvolutionParam-class``).

Details

This generic maps standard deconvolution inputs to the parameters of the specified deconvolution method for which a subclass of type [deconvolutionParam](#) exists. This generic uses a similar approach to the bluster R/Bioconductor package.

Value

By default, return named numeric vector of predicted proportions for each cell type.

If returnInfo == TRUE, instead returns a list including proportions, results object returned from specified method, and additional metadata.

Author(s)

Sean Maden

References

Aaron Lun. bluster: Clustering Algorithms for Bioconductor. (2022) Bioconductor, R package version 1.6.0.

See Also

[deconvolutionParam](#), [referencebasedParam](#), [independentbulkParam](#), [nnlsParam](#), [musicParam](#), [bisqueParam](#)

Examples

```
## get param object
exampleList <- getDeconvolutionExampleData()
param <- nnlsParam(cellScaleFactors=exampleList[["cellScaleFactors"]],
                  bulkExpression=exampleList[["bulkExpression"]],
                  referenceExpression=exampleList[["referenceExpression"]])

## run deconvolution
deconvolution(param)
```

deconvolution,bisqueParam-method

Deconvolution method for bisqueParam

Description

Main method to access the Bisque deconvolution method from the main lute deconvolution generic.

Usage

```
## S4 method for signature 'bisqueParam'
deconvolution(object)
```


Arguments

object Object of type `bisqueParam` (see `?bisqueParam`).

Details

Takes an object of class `bisqueParam` as input, returning a list.

Value

Either a vector of predicted proportions, or a list containing predictions, metadata, and original outputs.

References

Brandon Jew and Marcus Alvarez (2021). BisqueRNA: Decomposition of Bulk Expression with Single-Cell Sequencing. CRAN, R package version 1.0.5. URL: <https://CRAN.R-project.org/package=BisqueRNA>

Brandon Jew et al. Accurate estimation of cell composition in bulk expression through robust integration of single-cell information. *Nat Commun* 11, 1971 (2020). <https://doi.org/10.1038/s41467-020-15816-6>

Examples

```
## get data
exampleList <- getDeconvolutionExampleDataBisque()
bulkExpressionSet <- exampleList[["bulkExpressionSet"]][,seq(10)]
bulkExpression <- exprs(exampleList[["bulkExpressionSet"]])
bulkExpression <- bulkExpression[,c(11:ncol(bulkExpression))]

## get param object
newBisqueParameter <- bisqueParam(bulkExpressionSet=bulkExpressionSet,
                                   bulkExpressionIndependent=bulkExpression,
                                   scData=exampleList[["singleCellExpressionSet"]],
                                   batchVariable="SubjectName",
                                   cellTypeVariable="cellType",
                                   useOverlap=FALSE)

## get predicted proportions
deconvolutionResult <- deconvolution(newBisqueParameter)
```

deconvolution,deconvolutionParam-method

Deconvolution generic behavior for object of class `deconvolutionParam`

Description

Deconvolution generic behavior for object of class `deconvolutionParam`

Usage

```
## S4 method for signature 'deconvolutionParam'  
deconvolution(object)
```

Arguments

object An object of class [deconvolutionParam](#) (see ?deconvolutionParam).

Details

Method for behavior of deconvolution generic when called for object of class [deconvolutionParam](#).

Value

Null method.

Examples

```
param <- new("deconvolutionParam")  
deconvolution(param)
```

deconvolution,independentbulkParam-method

Deconvolution method for class [independentbulkParam](#)

Description

Function to perform standard operations prior to deconvolution (a.k.a. "deconvolution prep") for an object of class [independentbulkParam](#).

Usage

```
## S4 method for signature 'independentbulkParam'  
deconvolution(object)
```

Arguments

object An object of class [independentbulkParam](#).

Details

Takes an object of [independentbulkParam](#) class as input, and returns a list with the filtered/checked/parsed experiment objects.

Value

Method results.

Examples

```
new("independentbulkParam")
```

deconvolution, nlsParam-method

Deconvolution method for nlsParam

Description

Defines the deconvolution method for [nlsParam](#).

Usage

```
## S4 method for signature 'nlsParam'  
deconvolution(object)
```

Arguments

object An object of class [nlsParam](#) (see ?nlsParam).

Details

Takes an object of class [nlsParam](#) as input, returning either a list containing proportions, return info, and metadata, or a vector of predicted cell type proportions.

The key term mappings for this method include: * A : bulkExpression, bulk signals matrix (Y). * b : referenceExpression, signature matrix (Z).

Value

Either a vector of predicted proportions, or a list containing predictions, metadata, and original outputs.

References

Katharine M. Mullen and Ivo H. M. van Stokkum (2012). "nnls: The Lawson-Hanson algorithm for non-negative least squares (NNLS)." CRAN, R package version 1.4. URL: <https://cran.r-project.org/web/packages/nnls/index.html>

Examples

```
exampleList <- getDeconvolutionExampleData()  
param <- nlsParam(  
  cellScaleFactors=exampleList[["cellScaleFactors"]],  
  bulkExpression=exampleList[["bulkExpression"]],  
  referenceExpression=exampleList[["referenceExpression"]])  
  
## return only predicted proportions
```

```
deconvolution(param)

# return full results
param@returnInfo <- TRUE
names(deconvolution(param))
```

deconvolution,referencebasedParam-method

Deconvolution generic behavior for object of class [referencebased-Param](#)

Description

Deconvolution generic behavior for object of class [referencebasedParam](#)

Usage

```
## S4 method for signature 'referencebasedParam'
deconvolution(object)
```

Arguments

object An object of class [referencebasedParam](#) (see `?referencebasedParam`).

Details

Method for behavior of deconvolution generic when called for object of class [referencebasedParam](#).

Value

Method results.

Examples

```
exampleList <- getDeconvolutionExampleData()
referencebasedParam(
  bulkExpression=exampleList$bulkExpression,
  referenceExpression=exampleList$referenceExpression,
  cellScaleFactors=exampleList$cellScaleFactors)
```

 deconvolutionParam-class

deconvolutionParam-class

Description

Defines the principal parent class for all deconvolution method parameters.

Details

Defines the parent class for deconvolution method parameters. Since all deconvolution runs require a y signals matrix, whether from experiment data or simulations such as pseudobulking, this parent class manages the bulk signals matrix. For this class, the deconvolution generic performs basic summaries of the bulk signals matrix.

Value

New deconvolutionParam object.

See Also

deconvolution

Examples

```
param <- new("deconvolutionParam")
deconvolution(param)
```

 eset_to_sce

eset_to_sce Convert ExpressionSet to SingleCellExperiment.

Description

eset_to_sce Convert ExpressionSet to SingleCellExperiment.

Usage

```
eset_to_sce(expressionSet, assayName = "counts")
```

Arguments

expressionSet Object of type ExpressionSet (see ?ExpressionSet).
 assayName Name of new assay in new SingleCellExperiment object.

Value

ExpressionSet.

Examples

```
expressionSet <- getDeconvolutionExampleDataBisque()$singleCellExpressionSet
eset_to_sce(expressionSet)
```

eset_to_se

eset_to_se

Description

Convert ExpressionSet to SummarizedExperiment.

Usage

```
eset_to_se(expressionSet, assayName = "counts")
```

Arguments

expressionSet Object of type ExpressionSet (see ?ExpressionSet).

assayName Name of assay to store in new SummarizedExperiment object.

Value

New object of type SummarizedExperiment.

Examples

```
expressionSet <- getDeconvolutionExampleDataBisque()$singleCellExpressionSet
eset_to_se(expressionSet, "counts")
```

| | |
|------------------|--|
| findmarkersParam | <i>Make new object of class findmarkersParam</i> |
|------------------|--|

Description

Main constructor for class [findmarkersParam](#).

Usage

```
findmarkersParam(  
  singleCellExperiment,  
  assayName = "counts",  
  cellTypeVariable = "cellType",  
  testType = "wilcox",  
  markersPerType = 20,  
  returnInfo = FALSE  
)
```

Arguments

| | |
|----------------------|---|
| singleCellExperiment | Object of type <code>SingleCellExperiment</code> (see <code>?SingleCellExperiment</code>). |
| assayName | Name of expression matrix in <code>SingleCellExperiment</code> assays (e.g. "counts"). |
| cellTypeVariable | Name of cell type variable in <code>SingleCellExperiment</code> coldata. |
| testType | Test type (see <code>?findMarkers</code> for options). |
| markersPerType | Number of top markers to get per cell type. |
| returnInfo | Whether to return metadata and original method outputs with predicted proportions. |

Details

Main class for mapping arguments to the `findMarkers` method implemented as `scran::findMarkers()`.

Value

Object of class [findmarkersParam](#)

See Also

[typemarkersParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
singleCellExperimentExample <- randomSingleCellExperiment()
newParam <- findmarkersParam(singleCellExperiment=singleCellExperimentExample,
cellTypeVariable="celltype", markersPerType=5)
markers <- typemarkers(newParam)
```

findmarkersParam-class

findmarkersParam-class

Description

class definition for findmarkersParam, which uses scanr::findMarkers()

Arguments

assayName Name of expression matrix in SingleCellExperiment assays (e.g. "counts").
singleCellExperiment Object of type SingleCellExperiment (see ?SingleCellExperiment).
cellTypeVariable Name of cell type variable in SingleCellExperiment coldata.
testType Test type (see ?findMarkers for options).

Details

Main constructor for class [findmarkersParam](#).

Value

New object.

See Also

[typemarkersParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
singleCellExperimentExample <- randomSingleCellExperiment()
newParam <- findmarkersParam(singleCellExperiment=singleCellExperimentExample,
cellTypeVariable="celltype", markersPerType=5)
markers <- typemarkers(newParam)
```

```
getDeconvolutionExampleData  
  getDeconvolutionExampleData
```

Description

Make example data for deconvolution.

Usage

```
getDeconvolutionExampleData(  
  cellScaleFactors = c(1, 10),  
  numberBulkSamples = 2,  
  numberMarkers = 10,  
  numberTypes = 2  
)
```

Arguments

| | |
|--------------------------------|------------------------------|
| <code>cellScaleFactors</code> | Vector of cell scale factors |
| <code>numberBulkSamples</code> | Number of bulk samples. |
| <code>numberMarkers</code> | Number of cell type markers. |
| <code>numberTypes</code> | Number of cell types. |

Value

Example data as list.

Examples

```
exampleData <- getDeconvolutionExampleData()
```

```
getDeconvolutionExampleDataBisque  
  getDeconvolutionExampleDataBisque
```

Description

Get example data for Bisque algorithm.

Usage

```
getDeconvolutionExampleDataBisque(  
  numberBulkSamples = 100,  
  numberMarkers = 1000,  
  numberCells = 1000,  
  numberTypes = 2  
)
```

Arguments

| | |
|--------------------------------|------------------------------|
| <code>numberBulkSamples</code> | Number of bulk samples. |
| <code>numberMarkers</code> | Number of cell type markers. |
| <code>numberCells</code> | Number of cells. |
| <code>numberTypes</code> | Number of cell types. |

Value

Example data as list.

Examples

```
exampleData <- getDeconvolutionExampleDataBisque()
```

```
getDeconvolutionExampleDataSCDC  
  getDeconvolutionExampleDataSCDC
```

Description

Get example data for SCDC

Usage

```
getDeconvolutionExampleDataSCDC()
```

Value

Example data as list.

Examples

```
exampleData <- getDeconvolutionExampleDataSCDC()
```

```
get_celltypes_from_sce  
    get_celltypes_from_sce
```

Description

Extract cell type values from SingleCellExperiment.

Usage

```
get_celltypes_from_sce(singleCellExperiment, cellTypeVariable = "celltype")
```

Arguments

`singleCellExperiment`
A SingleCellExperiment object.

`cellTypeVariable`
Variable containing cell type labels (e.g. "type1", "type2", etc.).

Value

List of cell type variable metadata and values.

Examples

```
exampleList <- getDeconvolutionExampleData()
```

```
get_csf_reference    get_csf_reference
```

Description

Retrieves the cell scale factors (csf) reference from the cellScaleFactors package.

Usage

```
get_csf_reference(userCellTypesVector = NULL, preferOrthogonal = TRUE)
```

Arguments

`userCellTypesVector`
Vector of user-specified cell types.

`preferOrthogonal`
Whether to prefer expression-orthogonal values (if TRUE, removes expression-based values, but only if alternative value types are available).

Details

Returns a table of cell scale factors from various data sources. The cell scale factors reference table has the following columns:

1. `cell_type` : Label of the cell type for the scale factor (e.g. neuron, T cell, etc.)
2. `tissue` : Label of the tissue of origin (e.g. brain, blood, etc.)
3. `scale.factor.value` : Point scale factor value prior to additional normalization
4. `scale.factor.type` : Label for scale factor type (e.g. cell or nuclear area, etc.)
5. `scale.factor.data.source` : Label for scale factor source (e.g. osmFISH, housekeeping gene expression, etc.)
6. `citation.s` : Citation(s) of source studies from which original measures or measure summaries were made.

Further details about the reference table can be found in the `cellScaleFactors` package.

Value

Table of type "data.frame" or "tibble".

Examples

```
example.data <- getDeconvolutionExampleData()
```

`get_eset_from_matrix` *get_eset_from_matrix*

Description

Makes an ExpressionSet from a matrix.

Usage

```
get_eset_from_matrix(inputMatrix, batchVariable = "SampleName")
```

Arguments

`inputMatrix` User-specified expression matrix.
`batchVariable` Name of the batch variable.

Value

ExpressionSet.

Examples

```
exampleList <- getDeconvolutionExampleData()
```

independentbulkParam *Make a new [independentbulkParam](#) object*

Description

Function to make a new object of class [independentbulkParam](#)

Usage

```
independentbulkParam(  
  bulkExpression = NULL,  
  bulkExpressionIndependent = NULL,  
  referenceExpression = NULL,  
  cellScaleFactors = NULL,  
  returnInfo = FALSE  
)
```

Arguments

bulkExpression Bulk mixed signals matrix of samples, which can be matched to single-cell samples.

bulkExpressionIndependent Bulk mixed signals matrix of independent samples, which should not overlap samples in y.

referenceExpression Signature matrix of cell type-specific signals. If not provided, can be computed from a provided ExpressionSet containing single-cell data.

cellScaleFactors Cell size scale factor transformations of length equal to the K cell types to deconvolve.

returnInfo Whether to return metadata and original method outputs with predicted proportions.

Value

New object.

Examples

```
new("independentbulkParam")
```

independentbulkParam-class

independentbulkParam-class

Description

Class and methods for managing methods requiring independent bulk samples.

Arguments

bulkExpressionIndependent

Bulk mixed signals matrix of independent samples, which should not overlap samples in y.

Details

The main purpose of this class is to compare bulk sample data between the passed objects y and yi. Since we assume yi contains the independent bulk samples, it should not have overlapping sample IDs (colnames), and it should have overlapping marker IDs (rownames) compared to the reference bulk samples y.

Value

New object.

See Also

[deconParam](#), [referencebasedParam](#)

Examples

```
new("independentbulkParam")
```

lute

lute framework

Description

Obtain cell type markers and proportion predictions from various algorithms. Allows flexible data types and standard application of cell size scale factors.

Usage

```

lute(
  singleCellExperiment = NULL,
  referenceExpression = NULL,
  bulkExpression = NULL,
  bulkSummarizedExperiment = NULL,
  cellScaleFactors = NULL,
  returnInfo = FALSE,
  markersPerType = 20,
  assayName = "counts",
  cellTypeVariable = "celltype",
  typemarkerAlgorithm = "findmarkers",
  deconvolutionAlgorithm = "nnls",
  verbose = TRUE
)

```

Arguments

singleCellExperiment Object of type `SingleCellExperiment`. Optional (see argument `z`).

referenceExpression Signature matrix of cell type-specific signals. Optional (see argument `singleCellExperiment`).

bulkExpression Bulk mixed signals matrix of samples, which can be matched to single-cell samples. Optional (see argument `y.se`).

bulkSummarizedExperiment `SummarizedExperiment` or similar data type containing the bulk signals matrix in its assays (e.g. accessible with `assays(y.se)[[assayName]]`) using the provided `assayName` argument). Optional (see argument `y`).

cellScaleFactors Cell size factor transformations of length equal to the `K` cell types to deconvolve. Optional, if not provided, uses equal weights for types.

returnInfo Whether to return metadata and original method outputs with predicted proportions.

markersPerType Number of top markers to get per cell type.

assayName Name of expression matrix in `singleCellExperiment`, and optionally `y.se`, `assays`. Optional (e.g. "counts"; see arguments `singleCellExperiment`, `y.se`).

cellTypeVariable Name of cell type variable in `singleCellExperiment` `coldata`.

typemarkerAlgorithm Which type-specific marker selection algorithm to use. If `NULL`, skips type marker analyses.

deconvolutionAlgorithm Where deconvolution algorithm to use. If `NULL`, skips deconvolution.

verbose Whether to show verbose status messages.

Details

Main function to use the lute deconvolution framework. Manages data conversions and mappings to deconvolution experiment steps, including setup, gene marker identification, and main deconvolution runs.

Support is provided for [SummarizedExperiment](#)-type or matrix-type inputs for the Z signature matrix (see `referenceExpression` argument) and Y bulk signals matrix (see `bulkExpression` arguments). Note, both Z and Y need to be provided or derivable in order to run deconvolution.

Value

A list containing results returned from type marker selection and deconvolution runs, with additional information returned if `returnInfo == TRUE`.

Examples

```
# get example bulk data
bulkExpression <- getDeconvolutionExampleData()$reference

# get example singleCellExperiment
singleCellExperiment <- randomSingleCellExperiment()[seq(10),]

# get framework results
experiment.results <- lute(
  singleCellExperiment=singleCellExperiment,
  bulkExpression=bulkExpression, typemarkerAlgorithm=NULL
)
```

`luteSupportedDeconvolutionAlgorithms`

luteSupportedDeconvolutionAlgorithms

Description

View details about supported deconvolution algorithms.

Usage

```
luteSupportedDeconvolutionAlgorithms()
```

Value

Table of supported deconvolution algorithms.

Examples

```
luteSupportedDeconvolutionAlgorithms()
```

| | |
|--------------------|---------------------------|
| new_workflow_table | <i>new_workflow_table</i> |
|--------------------|---------------------------|

Description

Makes a new experiment table for r-nf_deconvolution runs.

Usage

```
new_workflow_table(  
  singleCellExperimentNames = NULL,  
  dataDirectory = "data",  
  trueProportionsFilenameStem = "true_proportions_",  
  cellTypeVariable = "celltype",  
  tableDirectory = ".",  
  tableFileName = "workflow_table.csv",  
  save = TRUE,  
  overwrite = TRUE,  
  verbose = FALSE  
)
```

Arguments

| | |
|-----------------------------|---|
| singleCellExperimentNames | Names of SingleCellExperiment files to load. |
| dataDirectory | Directory containing datasets to load. |
| trueProportionsFilenameStem | File name stem of true proportions values. |
| cellTypeVariable | Name of variable containing cell type labels. |
| tableDirectory | Directory to write table. |
| tableFileName | The file name of the new table to write. |
| save | Whether to save the new table. |
| overwrite | Whether to overwrite old table files. |
| verbose | Whether to show verbose messages (T/F). |

Details

Makes and returns/saves a r-nf_deconvolution experiment table. Checks for existence of provided files.

Value

New r-nf_deconvolution compatible table of experiment/run metadata.

Examples

```
new_workflow_table(save=FALSE)
```

nnlsParam

Make new object of class nnlsParam

Description

Main constructor for class [nnlsParam](#).

Usage

```
nnlsParam(
  bulkExpression,
  referenceExpression,
  cellScaleFactors,
  returnInfo = FALSE
)
```

Arguments

bulkExpression Bulk mixed signals matrix of samples, which can be matched to single-cell samples.

referenceExpression Signature matrix of cell type-specific signals. If not provided, can be computed from a provided [ExpressionSet](#) containing single-cell data.

cellScaleFactors Cell size factor transformations of length equal to the K cell types to deconvolve.

returnInfo Whether to return metadata and original method outputs with predicted proportions.

Details

Main parameter class for mapping inputs to the non-negative least squares (NNLS) deconvolution algorithm, implemented as `nnls::nnls()`.

Value

Object of class [nnlsParam](#)

See Also

[referencebasedParam](#), [deconvolutionParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
param <- nplsParam(cellScaleFactors=exampleList[["cellScaleFactors"]],
  bulkExpression=exampleList[["bulkExpression"]],
  referenceExpression=exampleList[["referenceExpression"]])

## return only predicted proportions
deconvolution(param)

# return full results
param@returnInfo <- TRUE
names(deconvolution(param))
```

nplsParam-class

nplsParam-class

Description

Uses `npls::npls()`.

Details

Main constructor for class [nplsParam](#).

Value

New object.

See Also

[deconParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
param <- nplsParam(cellScaleFactors=exampleList[["cellScaleFactors"]],
  bulkExpression=exampleList[["bulkExpression"]],
  referenceExpression=exampleList[["referenceExpression"]])

## return only predicted proportions
deconvolution(param)

# return full results
param@returnInfo <- TRUE
names(deconvolution(param))
```

```
parseDeconvolutionPredictionsResults
      parseDeconvolutionPredictionsResults
```

Description

Gets formatted predicted cell type proportions table from deconvolution results list.

Usage

```
parseDeconvolutionPredictionsResults(listPred, columnLabels, rowLabels)
```

Arguments

| | |
|---------------------------|---|
| <code>listPred</code> | List of cell type proportions predictions. |
| <code>columnLabels</code> | Vector of cell type labels (e.g. "type1", "type2", etc.). |
| <code>rowLabels</code> | Vector of sample id labels (e.g. "sample1", "sample2", etc.). |

Value

Example data as list.

Examples

```
exampleData <- getDeconvolutionExampleData()
```

```
proportionsVectorsList
      proportionsVectorsList
```

Description

Get complementary proportions for k types. The first type `k1` is the vector of proportions for the first type. The remaining types up to `totalCellTypesK` are based on the reverse of `k1`. Types `k > 1` are assumed to have equal proportions complementary to `k1`.

Usage

```
proportionsVectorsList(totalCellTypesK = 2, firstCellTypeProportions = NULL)
```

Arguments

| | |
|---------------------------------------|---|
| <code>totalCellTypesK</code> | Total number of cell types to simulate. |
| <code>firstCellTypeProportions</code> | Vector of first cell type proportions. If NULL, uses <code>seq(1e-3, 1-1e-3, 1e-3)</code> . |

Details

For $k1=c(0, 0.5, 1)$, $totalCellTypesK=2$ will generate an additional type with proportions $c(1, 0.5, 0)$.

For the same $k1$ above, $totalCellTypesK=3$, will generate 2 types with the same proportions as $c(0.5, 0.25, 0)$.

Value

`lpv`, a list of proportions vectors for simulation iterations.

Examples

```
proportionsVectorsList(firstCellTypeProportions=c(0, 0.5, 1))
```

```
randomMarkersVectorsList
      randomMarkersVectorsList
```

Description

Get randomized markers using Poisson distribution sampling. For a given K , we assume "positive" markers have higher values than for non- K types, and thus we sample from 2 different Poisson distributions defined by different λ values (e.g. arguments `lambdaMean`, `lambdaMeanNegative`). WE also use argument `markerIndexVector` to define total markers as `length(markerIndexVector)` and the marker balance as relative counts of each type index.

Usage

```
randomMarkersVectorsList(
  markerIndexVector,
  numberIterations = 1,
  lambdaMean = 25,
  lambdaMeanNegative = 2,
  method = "nbinom",
  gammaSize = 10,
  gammaSizeNegative = 10
)
```

Arguments

`markerIndexVector`

Vector of marker indices. Index values correspond to the k types, and each index position represents a marker (e.g. $c(1,2,2)$ means two markers for the second type, etc.).

`numberIterations`

Total simulation iterations.

| | |
|---------------------------------|---|
| <code>lambdaMean</code> | Value of lambda (Poisson dist. mean) for "positive" marker status (e.g. mean of dist. for k when marker is positive for k, negative for not-k). This is passed to the argument mu when method is "nbinom". |
| <code>lambdaMeanNegative</code> | Value of lambda (Poisson dist. mean) for "negative" marker status (e.g. mean of dist. for k when marker is positive for not-k, negative for k). This is passed to the argument mu when method is "nbinom". |
| <code>method</code> | Type of randomization method to use. Accepts either "poisson" for poisson distribution (see <code>?rpois</code> for details), or "nbinom" for the negative binomial (a.k.a. <code>gamm poisson</code>) distribution (see <code>?rnbinom</code> for details). |
| <code>gammaSize</code> | The gamma distribution magnitude for "positive" markers. This is applied when the "nbinom" method is used. |
| <code>gammaSizeNegative</code> | The gamma distribution magnitude for "negative" markers. This is applied when the "nbinom" method is used. |

Details

For example, if `gindex` is `c(1, 1, 2)`, we define 3 total markers, 2 positive markers for type 1 (negative for type 2) and a single positive marker for type 2 (negative for type 1).

Value

Listed `Igv` object containing the randomized marker values across types.

Examples

```
randomMarkersVectorsList(markerIndexVector=c(rep(1, 10), rep(2, 5)))
```

```
randomSingleCellExperiment
      randomSingleCellExperiment
```

Description

Make a random object of type `SingleCellExperiment`. Uses the negative binomial distribution to randomly generate gene expression data for simulated cells.

Usage

```
randomSingleCellExperiment(
  numberGenes = 20,
  numberCells = 12,
  numberTypes = 2,
  fractionTypes = NULL,
  dispersion = NULL,
```

```

    expressionMean = 10,
    naInclude = FALSE,
    naFraction = 0.2,
    zeroInclude = FALSE,
    zeroFraction = 0.2,
    verbose = FALSE,
    seedNumber = 0
)

```

Arguments

| | |
|----------------|---|
| numberGenes | Number of genes to randomize. |
| numberCells | Number of cells to randomize. |
| numberTypes | Number of cell types to annotate. |
| fractionTypes | Vector of fractions by type. |
| dispersion | Dispersion of gene expression. If NULL, uses the mean from expressionMean |
| expressionMean | Poisson dist mean for random expression data. |
| naInclude | Whether to include random NA values. |
| naFraction | Fraction of NA values to include. |
| zeroInclude | Whether to include random zero-count values. |
| zeroFraction | Fraction of zero-count values to include. |
| verbose | Whether to show verbose status messages. |
| seedNumber | Seed value for randomization of expression data. |

Value

New randomized SingleCellExperiment object.

Examples

```
singleCellExperiment <- randomSingleCellExperiment()
```

referencebasedParam *Make new object of class referencebasedParam*

Description

Main constructor for class [referencebasedParam](#).

Usage

```
referencebasedParam(
  bulkExpression,
  referenceExpression,
  cellScaleFactors,
  returnInfo = FALSE
)
```

Arguments

bulkExpression Bulk mixed signals matrix of samples, which can be matched to single-cell samples.

referenceExpression Signature matrix of cell type-specific signals. If not provided, can be computed from a provided ExpressionSet containing single-cell data.

cellScaleFactors Cell size factor transformations of length equal to the K cell types to deconvolve.

returnInfo Whether to return metadata and original method outputs with predicted proportions.

Details

Takes standard inputs for reference-based deconvolution algorithms.

Value

New object of class [referencebasedParam](#).

New object.

Examples

```
exampleList <- getDeconvolutionExampleData()
referencebasedParam(
  bulkExpression=exampleList$bulkExpression,
  referenceExpression=exampleList$referenceExpression,
  cellScaleFactors=exampleList$cellScaleFactors
)
```

referencebasedParam-class

referencebasedParam-class

Description

Class and methods for managing reference-based deconvolution methods.

Details

This is a parent class to manage reference-based deconvolution algorithms.

Child/sub-classes of this are distinguished by their use of either an explicit or implied z signature matrix (i.e. $Z[G,K]$ of dimensions G markers by K cell types). These also have an implied cell size term for biases from systematic cell size differences. If no cell size transformation is intended, this is the equivalent of passing equal size scales, (e.g. a K-length vector of equal values). See ‘vignette(package="lute")’ for details about experiment terms.

Value

New object.

Examples

```
exampleList <- getDeconvolutionExampleData()
referencebasedParam(
  bulkExpression=exampleList$bulkExpression,
  referenceExpression=exampleList$referenceExpression,
  cellScaleFactors=exampleList$cellScaleFactors)
```

referenceFromSingleCellExperiment

referenceFromSingleCellExperiment

Description

Makes the Z cell atlas reference from a SingleCellExperiment.

Usage

```
referenceFromSingleCellExperiment(
  singleCellExperiment,
  assayName = "counts",
  cellTypeVariable = "celltype"
)
```

Arguments

singleCellExperiment

A SingleCellExperiment object.

assayName Name of expression assay type (e.g. "counts").

cellTypeVariable

Name of variable containing cell type labels (e.g. "type1", "type2", etc.).

Value

Matrix of cell summary values (Z reference atlas).

Examples

```
exampleList <- getDeconvolutionExampleData()
```

rmse

rmse

Description

Takes 2 vectors of numerics

Usage

```
rmse(proportionsTrue, proportionsPred, summaryType = "mean")
```

Arguments

proportionsTrue
cell type proportions taken as true

proportionsPred
cell type proportions taken as false

summaryType Toggle summary type (either "mean" or "median")

Details

Calculates the root mean squared error (RMSE) for specified true and predicted cell type proportions.

Function does not distinguish between true and predicted status, variable labels provided for convenience.

Value

single numeric

Examples

```
proportionsVectorPred <- seq(1e-10, 2e-10, 1e-11)  
proportionsVectorTrue <- rev(proportionsVectorPred)  
rmse(proportionsVectorTrue, proportionsVectorPred)
```

| | |
|----------|-----------------|
| rmseTest | <i>rmseTest</i> |
|----------|-----------------|

Description

Takes 2 vectors of numerics

Usage

```
rmseTest(firstVector, secondVector)
```

Arguments

| | |
|--------------|------------------------|
| firstVector | First numeric vector. |
| secondVector | Second numeric vector. |

Details

Tests the rmse function for rounding imprecision.
Function to test RMSE values (`./unitTests/test_rmse.R`).

Value

Single numeric value

Examples

```
proportionsVectorPred <- seq(1e-10, 2e-10, 1e-11)
proportionsVectorTrue <- rev(proportionsVectorPred)
rmseTest(proportionsVectorTrue, proportionsVectorPred)
```

| | |
|-------------|---|
| sce_to_eset | <i>sce_to_eset Convert SingleCellExperiment to ExpressionSet.</i> |
|-------------|---|

Description

sce_to_eset Convert SingleCellExperiment to ExpressionSet.

Usage

```
sce_to_eset(singleCellExperiment, assayName = "counts")
```

Arguments

| | |
|----------------------|--|
| singleCellExperiment | Object of type SingleCellExperiment (see <code>?SingleCellExperiment</code>). |
| assayName | Name of assay to store in new eset. |

Value

ExpressionSet.

Examples

```
sce <- randomSingleCellExperiment()
sce_to_eset(sce, "counts")
```

| | |
|-------------|--|
| sce_to_eset | <i>sce_to_eset</i> Convert SingleCellExperiment to SummarizedExperiment. |
|-------------|--|

Description

sce_to_eset Convert SingleCellExperiment to SummarizedExperiment.

Usage

```
sce_to_eset(singleCellExperiment)
```

Arguments

singleCellExperiment
Object of type SingleCellExperiment (see ?SingleCellExperiment).

Value

SummarizedExperiment.

Examples

```
sce <- randomSingleCellExperiment()
sce_to_eset(sce)
```

| | |
|------------|-------------------|
| se_to_eset | <i>se_to_eset</i> |
|------------|-------------------|

Description

Convert SummarizedExperiment to ExpressionSet.

Usage

```
se_to_eset(summarizedExperiment, assayName = "counts")
```

Arguments

summarizedExperiment
Object of type SummarizedExperiment (see ?SummarizedExperiment).

assayName
Name of assay to store in new ExpressionSet object.

Value

New object of type ExpressionSet.

Examples

```
summarizedExperiment <- sce_to_se(randomSingleCellExperiment())
se_to_eset(summarizedExperiment)
```

| | |
|-----------|------------------|
| se_to_sce | <i>se_to_sce</i> |
|-----------|------------------|

Description

Convert SummarizedExperiment to SingleCellExperiment.

Usage

```
se_to_sce(summarizedExperiment)
```

Arguments

summarizedExperiment
Object of type SummarizedExperiment (see ?SummarizedExperiment).

Value

New SingleCellExperiment object.

Examples

```
se_to_sce(SummarizedExperiment())
```

show,bisqueParam-method

Show generic behavior for object of class bisqueParam

Description

Show generic behavior for object of class bisqueParam

Usage

```
## S4 method for signature 'bisqueParam'  
show(object)
```

Arguments

object Object of class [bisqueParam](#) (see ?bisqueParam).

Value

Prints data summary messages to console.

Examples

```
## get data  
exampleList <- getDeconvolutionExampleDataBisque()  
bulkExpressionSet <- exampleList[["bulkExpressionSet"]][,seq(10)]  
bulkExpression <- exprs(exampleList[["bulkExpressionSet"]])  
bulkExpression <- bulkExpression[,c(11:ncol(bulkExpression))]  
  
## get param object  
newBisqueParameter <- bisqueParam(bulkExpressionSet=bulkExpressionSet,  
                                  bulkExpressionIndependent=bulkExpression,  
                                  scData=exampleList[["singleCellExpressionSet"]],  
                                  batchVariable="SubjectName",  
                                  cellTypeVariable="cellType",  
                                  useOverlap=FALSE)  
  
## show  
newBisqueParameter
```

show,cellProportionsPredictions-method
Inspect cellProportionsPredictions object.

Description

Inspect cellProportionsPredictions object.

Usage

```
## S4 method for signature 'cellProportionsPredictions'  
show(object)
```

Arguments

object Object of type cellProportionsPredictions (see ?cellProportionsPredictions).

Details

Method behavior for show.

Value

Shows object summaries.

Examples

```
exampleData <- getDeconvolutionExampleData()
```

show,deconvolutionParam-method
Show generic behavior for object of class [deconvolutionParam](#)

Description

Show generic behavior for object of class [deconvolutionParam](#)

Usage

```
## S4 method for signature 'deconvolutionParam'  
show(object)
```

Arguments

object An object of class [deconvolutionParam](#) (see ?deconvolutionParam).

Details

Method for behavior of show generic when called for object of class [deconvolutionParam](#)

Value

Shows object summaries.

Examples

```
param <- new("deconvolutionParam")
deconvolution(param)
```

show,findmarkersParam-method

Show generic behavior for object of class [findmarkersParam](#)

Description

Show generic behavior for object of class [findmarkersParam](#)

Usage

```
## S4 method for signature 'findmarkersParam'
show(object)
```

Arguments

object An object of class [findmarkersParam](#) (see ?findmarkersParam).

Details

Method for behavior of show generic when called for object of class [findmarkersParam](#)

Value

Shows object summaries.

Examples

```
exampleList <- getDeconvolutionExampleData()
singleCellExperimentExample <- randomSingleCellExperiment()
newParam <- findmarkersParam(singleCellExperiment=singleCellExperimentExample,
cellTypeVariable="celltype", markersPerType=5)
markers <- typemarkers(newParam)
```

show,independentbulkParam-method

Method for [independentbulkParam](#)

Description

Method for [independentbulkParam](#)

Usage

```
## S4 method for signature 'independentbulkParam'  
show(object)
```

Arguments

object An object of class [independentbulkParam](#) (see ?independentbulkParam).

Details

Display data summaries for an object of class [independentbulkParam](#).

Value

Shows object summaries.

Examples

```
new("independentbulkParam")
```

show,nlsParam-method *Show generic behavior for object of class nlsParam*

Description

Show generic behavior for object of class [nlsParam](#)

Usage

```
## S4 method for signature 'nlsParam'  
show(object)
```

Arguments

object Object of class [nlsParam](#) (see ?nlsParam).

Value

Prints data summary messages to console.

Examples

```
exampleList <- getDeconvolutionExampleData()
referencebasedParam(
  bulkExpression=exampleList$bulkExpression,
  referenceExpression=exampleList$referenceExpression,
  cellScaleFactors=exampleList$cellScaleFactors)
```

show,referencebasedParam-method

Show generic behavior for object of class referencebasedParam

Description

Show generic behavior for object of class referencebasedParam

Usage

```
## S4 method for signature 'referencebasedParam'
show(object)
```

Arguments

object Object of class [referencebasedParam](#) (see ?referencebasedParam).

Value

Prints data summary messages to console.

Examples

```
exampleList <- getDeconvolutionExampleData()
referencebasedParam(
  bulkExpression=exampleList$bulkExpression,
  referenceExpression=exampleList$referenceExpression,
  cellScaleFactors=exampleList$cellScaleFactors)
```

 show, typemarkersParam-method

Show generic behavior for object of class [typemarkersParam](#)

Description

Show generic behavior for object of class [typemarkersParam](#)

Usage

```
## S4 method for signature 'typemarkersParam'
show(object)
```

Arguments

object An object of class [typemarkersParam](#) (see ?[typemarkersParam](#)).

Details

Method for behavior of show generic when called for object of class [typemarkersParam](#)

Value

Shows object summaries.

Examples

```
exampleList <- getDeconvolutionExampleData()
```

 typemarkers

typemarkers

Description

Get cell type gene markers using standard accessors to supported functions.

Usage

```
typemarkers(object)
```

Arguments

object A [typemarkersParam](#)-type object (see ?[typemarkersParam](#)).

Details

This generic manages tasks for marker gene identification. In particular, it takes a specified amount of marker genes to return per type.

Value

By default, return a vector of marker genes.

If returnInfo == TRUE, provides detailed results, including original outputs.

Author(s)

Sean Maden

See Also

[typemarkersParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
```

typemarkers,findmarkersParam-method

Cell type markers method for findmarkersParam

Description

Defines the typemarkers method for [findmarkersParam](#).

Usage

```
## S4 method for signature 'findmarkersParam'  
typemarkers(object)
```

Arguments

object An object of class [findmarkersParam](#) (see ?findmarkersParam).

Details

Takes an object of class [findmarkersParam](#) as input, returning either a vector of cell type gene markers, or (if returnInfo == TRUE) a list containing such a vector along with original function outputs.

Value

Returns the top available markers, with type-specific marker filters, as either a vector of marker IDs or a results list.

Examples

```
exampleList <- getDeconvolutionExampleData()
singleCellExperimentExample <- randomSingleCellExperiment()
newParam <- findmarkersParam(singleCellExperiment=singleCellExperimentExample,
  cellTypeVariable="celltype", markersPerType=5)
markers <- typemarkers(newParam)
```

typemarkers, typemarkersParam-method

Method for class [typemarkersParam](#)

Description

Method for class [typemarkersParam](#)

Usage

```
## S4 method for signature 'typemarkersParam'
typemarkers(object)
```

Arguments

object An object of class [typemarkersParam](#).

Value

Info related to gene markers for cell types.

Examples

```
example.data <- getDeconvolutionExampleData()
```

| | |
|------------------|--|
| typemarkersParam | <i>Make new object of class typemarkersParam</i> |
|------------------|--|

Description

Main constructor for class [typemarkersParam](#).

Usage

```
typemarkersParam(markersPerType = 20, returnInfo = FALSE)
```

Arguments

| | |
|----------------|---|
| markersPerType | Bulk mixed signals matrix of samples, which can be matched to single-cell samples. |
| returnInfo | Whether to return metadata and original marker selection method outputs with predicted proportions. |

Details

This is the main parent class for cell type gene marker identification methods. Currently supported methods and their child classes include:

1. Mean Ratios: The method `DeconvoBuddies::get_mean_ratios2()`, supported by the class `mean-ratiosParam`.

Value

New object of class [typemarkersParam](#).

Examples

```
example.data <- getDeconvolutionExampleData()
```

| | |
|------------------------|-------------------------------|
| typemarkersParam-class | <i>typemarkersParam-class</i> |
|------------------------|-------------------------------|

Description

Main constructor for class to manage mappings to the `typemarkers()` generic.

Arguments

| | |
|----------------|--|
| markersPerType | Number of top markers to get per cell type. |
| returnInfo | Whether to return metadata and original method outputs with predicted proportions. |

Details

Main constructor for class [typemarkersParam](#).

Value

New object.

See Also

[meanratiosParam](#)

Examples

```
exampleList <- getDeconvolutionExampleData()
```

| | |
|---------------------------|---------------------------|
| <code>ypb_from_sce</code> | <code>ypb_from_sce</code> |
|---------------------------|---------------------------|

Description

Get pseudobulk from a `SingleCellExperiment` object.

Usage

```
ypb_from_sce(  
  singleCellExperiment,  
  assayName = "counts",  
  cellTypeVariable = "celltype",  
  sampleIdVariable = NULL,  
  cellScaleFactors = NULL  
)
```

Arguments

| | |
|-----------------------------------|--|
| <code>singleCellExperiment</code> | An object of type SingleCellExperiment . |
| <code>assayName</code> | Name of expression matrix in <code>singleCellExperiment</code> assays. |
| <code>cellTypeVariable</code> | Variable name for cell type labels in <code>singleCellExperiment</code> coldata. |
| <code>sampleIdVariable</code> | Variable name for sample/group ID labels in <code>singleCellExperiment</code> coldata. |
| <code>cellScaleFactors</code> | Vector of cell type size scale factors. Optional. |

Value

Matrix of simulated bulk convoluted signals.

Examples

```
singleCellExperimentExample <- randomSingleCellExperiment()
ypb_from_sce(singleCellExperimentExample)
```

z_matrix_from_sce *z_matrix_from_sce*

Description

Calculate a Z signature matrix (referenceExpression) from object of type [SingleCellExperiment](#).

Usage

```
z_matrix_from_sce(
  singleCellExperiment,
  cellTypeVariable = "celltype",
  summaryMethod = "mean",
  assayName = "counts"
)
```

Arguments

`singleCellExperiment` An object of type [SingleCellExperiment](#).

`cellTypeVariable` Variable name for cell type labels in `singleCellExperiment` coldata (e.g. "type1", "type2", etc.).

`summaryMethod` Summary statistic function to use.

`assayName` Name of expression matrix in `singleCellExperiment` assays (e.g. "counts").

Details

Calculate a Z signature matrix from object of type [SingleCellExperiment](#).

Value

New Z signature matrix.

Examples

```
singleCellExperiment.example <- randomSingleCellExperiment()
z_matrix_from_sce(singleCellExperiment.example)
```

[[,deconvolutionParam,ANY,ANY-method

Inspect slot in [deconvolutionParam](#) object

Description

Inspect slot in [deconvolutionParam](#) object

Usage

```
## S4 method for signature 'deconvolutionParam,ANY,ANY'  
x[[i]]
```

Arguments

| | |
|---|-------------------|
| x | Object to access. |
| i | Slot to access. |

Details

Inspect slot in [deconvolutionParam](#) object

Value

Contents of specified slot.
Object slot contents.

Examples

```
param <- new("deconvolutionParam")  
deconvolution(param)
```

[[,typemarkersParam,ANY,ANY-method

Inspect slot in [typemarkersParam](#) object

Description

Inspect slot in [typemarkersParam](#) object

Usage

```
## S4 method for signature 'typemarkersParam,ANY,ANY'  
x[[i]]
```

Arguments

x Object to access.
i Slot to access.

Details

Inspect slot in [typemarkersParam](#) object

Value

Contents of specified slot.

Examples

```
example.data <- getDeconvolutionExampleData()
```

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