Package 'lute'

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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 transcripomics 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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`bisqueParam` *Make new object of class bisqueParam*

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,
  returnInfo = FALSE
)
```

Arguments

`bulkExpression` Bulk expression matrix.

`bulkExpressionSet`
: ExpressionSet of bulk mixed signals.

`bulkExpressionIndependent`
: Bulk expression matrix of independent samples.

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

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

`scData`
: SummarizedExperiment-type object of single-cell transcriptomics data. Accepts ExpressionSet, SummarizedExperiment, and SingleCellExperiment object types.

`assayName`
: Expression data type (e.g. counts, logcounts, tpm, etc.).

`batchVariable`
: Name of variable identifying the batches in scData pData/coldata.

`cellTypeVariable`
: Name of cell type labels variable in scData pData/coldata.

`useOverlap`
: Whether to deconvolve samples overlapping bulk and sc esets (logical, FALSE).

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

Details

Takes standard inputs for the Bisque method. If user provides matrices, will convert these into ExpressionSet objects compatible with the main bisque method.

Value

New object of class bisqueParam.

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)
```

bisqueParam-class *bisqueParam-class*

Description

Applies the BisqueRNA::ReferenceBasedDecomposition() implementation of the Bisque deconvolution algorithm.

Details

Main constructor for class bisqueParam.

Value

New object of class bisqueParam.

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

See Also

deconvolutionParam, referencebasedParam, independentbulkParam

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
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,nnlsParam-method

Deconvolution method for nnlsParam

Description

Defines the deconvolution method for nnlsParam.

Usage

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

Arguments

object	An object of class nnlsParam (see ?nnlsParam).

Details

Takes an object of class nnlsParam 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 <- nnlsParam(
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 referencebasedParam

---

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` *Make new object of class findmarkersParam*

Description

Main constructor for class findmarkersParam.

Usage

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

Arguments

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

cellScaleFactors	Vector of cell scale factors
numberBulkSamples	Number of bulk samples.
numberMarkers	Number of cell type markers.
numberTypes	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

numberBulkSamples	Number of bulk samples.
numberMarkers	Number of cell type markers.
numberCells	Number of cells.
numberTypes	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 *new_workflow_table*

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 <- nnlsParam(cellScaleFactors=exampleList[["cellScaleFactors"]],
bulkExpression=exampleList[["bulkExpression"]],
referenceExpression=exampleList[["referenceExpression"]])

## return only predicted proportions
deconvolution(param)

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

`nnlsParam-class` *nnlsParam-class*

Description

Uses nnls::nnls().

Details

Main constructor for class nnlsParam.

Value

New object.

See Also

deconParam

Examples

```
exampleList <- getDeconvolutionExampleData()
param <- nnlsParam(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

listPred	List of cell type proportions predictions.
columnLabels	Vector of cell type labels (e.g. "type1", "type2", etc.).
rowLabels	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

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

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 lambda 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.
`lambdaMean`	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".

`lambdaMeanNegative`
: 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".

`method`
: Type of randomization method to use. Accepts either "poisson" for poisson distribution (see ‘?rpois‘ for details), or "nbinom" for the negative binomial (a.k.a. gamm poisson) distribution (see ‘?rnbinom‘ for details).

`gammaSize`
: The gamma distribution magnitude for "positive" markers. This is applied when the "nbinom" method is used.

`gammaSizeNegative`
: 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 lgv 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	Numnber of cells to randomize.
numberTypes	Number of cell types to annotate.
fractionTypes	Vector of fractions by type.
dispersion	Disperison 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 *rmseTest*

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 *sce_to_eset Convert SingleCellExperiment to ExpressionSet.*

Description

sce_to_eset Convert SingleCellExperiment to ExpressionSet.

Usage

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

Arguments

singleCellExperiment	Object of type SingleCellExperiment (see ?SingleCellExperiment).
assayName	Name of assay to store in new eset.

Value

ExpressionSet.

Examples

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

sce_to_se *sce_to_se Convert SingleCellExperiment to SummarizedExperiment.*

Description

sce_to_se Convert SingleCellExperiment to SummarizedExperiment.

Usage

```
sce_to_se(singleCellExperiment)
```

Arguments

singleCellExperiment	Object of type SingleCellExperiment (see ?SingleCellExperiment).

Value

SummarizedExperiment.

Examples

```
sce <- randomSingleCellExperiment()
sce_to_se(sce)
```

se_to_eset *se_to_eset*

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 *se_to_sce*

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,nnlsParam-method` *Show generic behavior for object of class nnlsParam*

Description

Show generic behavior for object of class nnlsParam

Usage

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

Arguments

`object`	Object of class nnlsParam (see `?nnlsParam`).

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 *Make new object of class typemarkersParam*

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 meanratiosParam.

Value

New object of class typemarkersParam.

Examples

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

typemarkersParam-class *typemarkersParam-class*

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()
```

ypb_from_sce *ypb_from_sce*

Description

Get pseudobulk from a SingleCellExperiment object.

Usage

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

Arguments

singleCellExperiment	An object of type SingleCellExperiment.
assayName	Name of expression matrix in singleCellExperiment assays.
cellTypeVariable	Variable name for cell type labels in singleCellExperiment coldata.
sampleIdVariable	Variable name for sample/group ID labels in singleCellExperiment coldata.
cellScaleFactors	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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