

# Package ‘lute’

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**Version** 1.4.0

**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.

**License** Artistic-2.0

**Encoding** UTF-8

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

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'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'  
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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,
    returnInfo = FALSE
  )

```

## Arguments

|                                        |                                                                                                                                                           |
|----------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>bulkExpression</code>            | Bulk expression matrix.                                                                                                                                   |
| <code>bulkExpressionSet</code>         | ExpressionSet of bulk mixed signals.                                                                                                                      |
| <code>bulkExpressionIndependent</code> | Bulk expression matrix of independent samples.                                                                                                            |
| <code>referenceExpression</code>       | Signature matrix of cell type-specific signals. If not provided, can be computed from a provided ExpressionSet containing single-cell data.               |
| <code>cellScaleFactors</code>          | size factor transformations of length equal to the K cell types to deconvolve.                                                                            |
| <code>scData</code>                    | SummarizedExperiment-type object of single-cell transcriptomics data. Accepts ExpressionSet, SummarizedExperiment, and SingleCellExperiment object types. |
| <code>assayName</code>                 | Expression data type (e.g. counts, logcounts, tpm, etc.).                                                                                                 |
| <code>batchVariable</code>             | Name of variable identifying the batches in scData pData/coldata.                                                                                         |
| <code>cellTypeVariable</code>          | Name of cell type labels variable in scData pData/coldata.                                                                                                |
| <code>useOverlap</code>                | Whether to deconvolve samples overlapping bulk and sc esets (logical, FALSE).                                                                             |
| <code>returnInfo</code>                | 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"]],

```



```
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 [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)
```

---

|                   |                   |
|-------------------|-------------------|
| <i>eset_to_se</i> | <i>eset_to_se</i> |
|-------------------|-------------------|

---

**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 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 `scrn::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 `scrn::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        |
| <i>getDeconvolutionExampleDataSCDC</i> |

---

**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()
```

---

|                                   |                             |
|-----------------------------------|-----------------------------|
| <code>get_eset_from_matrix</code> | <i>get_eset_from_matrix</i> |
|-----------------------------------|-----------------------------|

---

**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**

|                                       |                                                                                                                                                                                                                                                                    |
|---------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>singleCellExperiment</code>     | Object of type <code>SingleCellExperiment</code> . Optional (see argument <code>z</code> ).                                                                                                                                                                        |
| <code>referenceExpression</code>      | Signature matrix of cell type-specific signals. Optional (see argument <code>singleCellExperiment</code> ).                                                                                                                                                        |
| <code>bulkExpression</code>           | Bulk mixed signals matrix of samples, which can be matched to single-cell samples. Optional (see argument <code>y.se</code> ).                                                                                                                                     |
| <code>bulkSummarizedExperiment</code> | <code>SummarizedExperiment</code> or similar data type containing the bulk signals matrix in its assays (e.g. accessible with <code>assays(y.se)[[assayName]]</code> using the provided <code>assayName</code> argument). Optional (see argument <code>y</code> ). |
| <code>cellScaleFactors</code>         | Cell size factor transformations of length equal to the <code>K</code> cell types to deconvolve. Optional, if not provided, uses equal weights for types.                                                                                                          |
| <code>returnInfo</code>               | Whether to return metadata and original method outputs with predicted proportions.                                                                                                                                                                                 |
| <code>markersPerType</code>           | Number of top markers to get per cell type.                                                                                                                                                                                                                        |
| <code>assayName</code>                | Name of expression matrix in <code>singleCellExperiment</code> , and optionally <code>y.se</code> , assays. Optional (e.g. "counts"; see arguments <code>singleCellExperiment</code> , <code>y.se</code> ).                                                        |
| <code>cellTypeVariable</code>         | Name of cell type variable in <code>singleCellExperiment</code> coldata.                                                                                                                                                                                           |
| <code>typemarkerAlgorithm</code>      | Which type-specific marker selection algorithm to use. If <code>NULL</code> , skips type marker analyses.                                                                                                                                                          |
| <code>deconvolutionAlgorithm</code>   | Where deconvolution algorithm to use. If <code>NULL</code> , skips deconvolution.                                                                                                                                                                                  |
| <code>verbose</code>                  | 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 | <i>Make new object of class nnlsParam</i> |
|-----------|-------------------------------------------|

---

**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**

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

---

### 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 | <i>rmse</i> |
|------|-------------|

---

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**

|                           |                        |
|---------------------------|------------------------|
| <code>firstVector</code>  | First numeric vector.  |
| <code>secondVector</code> | 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**

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

**Value**

ExpressionSet.

**Examples**

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

---

|           |                                                                        |
|-----------|------------------------------------------------------------------------|
| sce_to_se | <i>sce_to_se</i> 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 | <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

*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                                                     |
| <i>Show generic behavior for object of class <a href="#">typemarkersParam</a></i> |

---

**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 | <i>typemarkers</i> |
|-------------|--------------------|

---

**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()
```

---

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 | <i>z_matrix_from_sce</i> |
|-------------------|--------------------------|

---

**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 <a href="#">SingleCellExperiment</a> .                                          |
| 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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