

# Package ‘SpatialDDLs’

May 7, 2023

**Type** Package

**Title** Deconvolution of Spatial Transcriptomics Data Based on Neural Networks

**Version** 0.1.0

**Maintainer** Diego Mañanes <dmananesc@cnic.es>

## Description

Deconvolution of spatial transcriptomics data using deconvolution models based on deep neural networks and single-cell RNA-seq data. These models are able to make accurate estimates of the cell composition of spots in spatial transcriptomics datasets from the same context using the advances provided by deep learning and the meaningful information provided by single-cell RNA-Seq data. See Torroja and Sanchez-Cabo (2019) <[doi:10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978)> to get an overview of the method, but its application to spatial transcriptomics data will be available soon.

**License** GPL-3

**URL** <https://diegommcc.github.io/SpatialDDLs/>,  
<https://github.com/diegommcc/SpatialDDLs>

**BugReports** <https://github.com/diegommcc/SpatialDDLs/issues>

**Encoding** UTF-8

**Depends** R (>= 4.0.0)

**Imports** rlang, grr, Matrix, methods, tidyr, SpatialExperiment, SingleCellExperiment, SummarizedExperiment, zinbwave, stats, pbapply, S4Vectors, dplyr, tools, reshape2, gtools, reticulate, keras, tensorflow, ggplot2, ggpubr, RColorBrewer, grDevices

**Suggests** knitr, rmarkdown, BiocParallel, rhdf5, DelayedArray, DelayedMatrixStats, HDF5Array, testthat

**SystemRequirements** Python (>= 2.7.0), TensorFlow  
(<https://www.tensorflow.org/>)

**RoxygenNote** 7.1.2

**Collate** 'AllClasses.R' 'AllGenerics.R' 'SpatialDDLs.R' 'dnnModel.R'  
'evalMetrics.R' 'loadData.R' 'plotSpatialCoor.R'  
'simMixedSpots.R' 'simSingleCell.R' 'utils.R'

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Diego Mañanes [aut, cre] (<<https://orcid.org/0000-0001-7247-6794>>),  
 Carlos Torroja [aut] (<<https://orcid.org/0000-0001-8914-3400>>),  
 Fatima Sanchez-Cabo [aut] (<<https://orcid.org/0000-0003-1881-1664>>)

**Repository** CRAN

**Date/Publication** 2023-05-07 10:20:06 UTC

## R topics documented:

barErrorPlot . . . . .	3
barPlotCellTypes . . . . .	5
blandAltmanLehPlot . . . . .	6
calculateEvalMetrics . . . . .	8
cell.names . . . . .	9
cell.types . . . . .	10
corrExpPredPlot . . . . .	10
createSpatialDDLSubject . . . . .	13
deconv.spots . . . . .	17
DeconvDLModel-class . . . . .	17
deconvSpatialDDL . . . . .	18
distErrorPlot . . . . .	21
estimateZinbwaveParams . . . . .	23
features . . . . .	26
genMixedCellProp . . . . .	26
getProbMatrix . . . . .	29
installTFpython . . . . .	30
loadSTProfiles . . . . .	31
loadTrainedModelFromH5 . . . . .	33
method . . . . .	33
mixed.profiles . . . . .	34
model . . . . .	34
plots . . . . .	35
plotSpatialProp . . . . .	35
plotSpatialPropAll . . . . .	36
plotTrainingHistory . . . . .	37
preparingToSave . . . . .	38
prob.cell.types . . . . .	39
prob.matrix . . . . .	39
project . . . . .	40
PropCellTypes-class . . . . .	40
saveRDS . . . . .	41
saveTrainedModelAsH5 . . . . .	42
set . . . . .	43
set.list . . . . .	43
showProbPlot . . . . .	44

simMixedProfiles . . . . .	45
simSCProfiles . . . . .	48
single.cell.real . . . . .	51
single.cell.simul . . . . .	52
spatial.experiments . . . . .	52
SpatialDDLS-class . . . . .	53
SpatialDDLS-Rpackage . . . . .	54
test.deconv.metrics . . . . .	54
test.metrics . . . . .	55
test.pred . . . . .	55
trainDeconvModel . . . . .	56
trained.model . . . . .	59
training.history . . . . .	60
zinb.params . . . . .	60
ZinbParametersModel-class . . . . .	61
zinbwave.model . . . . .	61

## Index 62

---

barErrorPlot	<i>Generate bar error plots</i>
--------------	---------------------------------

---

### Description

Generate bar error plots by cell type (CellType) or by number of different cell types (nCellTypes) on test mixed transcriptional profiles.

### Usage

```
barErrorPlot(
  object,
  error = "MSE",
  by = "CellType",
  dispersion = "se",
  filter.sc = TRUE,
  title = NULL,
  angle = NULL,
  theme = NULL
)
```

### Arguments

object	<a href="#">SpatialDDLS</a> object with trained.model slot containing metrics in the test.deconv.metrics slot of a <a href="#">DeconvDLModel</a> object.
error	'MAE' or 'MSE'.
by	Variable used to show errors. Available options are: 'nCellTypes', 'CellType'.
dispersion	Standard error ('se') or standard deviation ('sd'). The former by default.

<code>filter.sc</code>	Boolean indicating whether single-cell profiles are filtered out and only correlation of results associated with mixed transcriptional profiles are shown (TRUE by default).
<code>title</code>	Title of the plot.
<code>angle</code>	Angle of ticks.
<code>theme</code>	<b>ggplot2</b> theme.

**Value**

A ggplot object.

**See Also**

[calculateEvalMetrics](#) [corrExpPredPlot](#) [distErrorPlot](#) [blandAltmanLehPlot](#)

**Examples**

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 20,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(20)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(20)),
    Cell_Type = sample(x = paste0("CellType", seq(6)), size = 20,
      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
SDDLs <- createSpatialDDLsObject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 50,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs)
# training of DDLS model
SDDLs <- trainDeconvModel(
  object = SDDLs,
```

```
    batch.size = 15,
    num.epochs = 5
  )
# evaluation using test data
SDDLs <- calculateEvalMetrics(object = SDDLs)
# bar error plots
barErrorPlot(
  object = SDDLs,
  error = "MSE",
  by = "CellType"
)
barErrorPlot(
  object = SDDLs,
  error = "MAE",
  by = "nCellTypes"
)
```

---

barPlotCellTypes      *Bar plot of deconvoluted cell type proportions*

---

### Description

Bar plot of deconvoluted cell type proportions.

### Usage

```
barPlotCellTypes(
  data,
  colors = NULL,
  simplify = NULL,
  color.line = NA,
  x.label = "Spots",
  rm.x.text = FALSE,
  title = "Results of deconvolution",
  legend.title = "Cell types",
  angle = 90,
  theme = NULL,
  index.st = NULL
)
```

### Arguments

**data**                    [SpatialDDLs](#) object with the deconv. spots slot containing predicted cell type proportions.

**colors**                  Vector of colors to be used.

<code>simplify</code>	Type of simplification performed during deconvolution. It can be <code>simpli.set</code> or <code>simpli.maj</code> (NULL by default).
<code>color.line</code>	Color of the border bars.
<code>x.label</code>	Label of x-axis.
<code>rm.x.text</code>	Logical value indicating whether to remove x-axis ticks (name of samples).
<code>title</code>	Title of the plot.
<code>legend.title</code>	Title of the legend plot.
<code>angle</code>	Angle of text ticks.
<code>theme</code>	<b>ggplot2</b> theme.
<code>index.st</code>	Name or index of the element wanted to be shown in the <code>deconv.spots</code> slot.

**Value**

A ggplot object with the provided cell proportions represented as a bar plot.

**See Also**

[deconvSpatialDDLS](#)

---

<code>blandAltmanLehPlot</code>	<i>Generate Bland-Altman agreement plots between predicted and expected cell type proportions of test data</i>
---------------------------------	--

---

**Description**

Generate Bland-Altman agreement plots between predicted and expected cell type proportions from test data. The Bland-Altman agreement plots can be shown all mixed or split by cell type (`CellType`) or the number of cell types present in spots (`nCellTypes`). See the `facet.by` argument and examples for more information.

**Usage**

```
blandAltmanLehPlot(
  object,
  colors,
  color.by = "CellType",
  facet.by = NULL,
  log.2 = FALSE,
  filter.sc = TRUE,
  density = TRUE,
  color.density = "darkblue",
  size.point = 0.05,
  alpha.point = 1,
  ncol = NULL,
  nrow = NULL,
```

```

    title = NULL,
    theme = NULL,
    ...
  )

```

### Arguments

object	<a href="#">SpatialDDL</a> s object with trained.model slot containing metrics in the test.deconv.metrics slot of a <a href="#">DeconvDLModel</a> object.
colors	Vector of colors to be used.
color.by	Variable used to color data. Options are nCellTypes and CellType.
facet.by	Variable used to show the data in different panels. If NULL, the plot is not split into different panels. Options are nCellTypes (by number of different cell types) and CellType (by cell type).
log.2	Whether to show the Bland-Altman agreement plot in log2 space (FALSE by default).
filter.sc	Boolean indicating whether single-cell profiles are filtered out and only correlations of results associated with mixed spot profiles are shown (TRUE by default).
density	Boolean indicating whether density lines should be shown (TRUE by default).
color.density	Color of density lines if the density argument is TRUE.
size.point	Size of the points (0.1 by default).
alpha.point	Alpha of the points (0.1 by default).
ncol	Number of columns if facet.by is used.
nrow	Number of rows if facet.by is used.
title	Title of the plot.
theme	<b>ggplot2</b> theme.
...	Additional argument for the facet_wrap function of <b>ggplot2</b> if facet.by is not NULL.

### Value

A ggplot object.

### See Also

[calculateEvalMetrics](#) [corrExpPredPlot](#) [distErrorPlot](#) [barErrorPlot](#)

### Examples

```

set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 20,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(20)))
    )
  )
)

```

```

    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(20)),
    Cell_Type = sample(x = paste0("CellType", seq(6)), size = 20,
                      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
SDDLs <- createSpatialDDLsObject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 50,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs)
# training of DDLs model
SDDLs <- trainDeconvModel(
  object = SDDLs,
  batch.size = 15,
  num.epochs = 5
)
# evaluation using test data
SDDLs <- calculateEvalMetrics(object = SDDLs)
# Bland-Altman plot by cell type
blandAltmanLehPlot(
  object = SDDLs,
  facet.by = "CellType",
  color.by = "CellType"
)
# Bland-Altman plot of all samples mixed
blandAltmanLehPlot(
  object = SDDLs,
  facet.by = NULL,
  color.by = "CellType",
  alpha.point = 0.3,
  log2 = TRUE
)

```

**Description**

Calculate evaluation metrics of test mixed transcriptional profiles. By default, absolute error (AbsErr), proportional absolute error (ppAbsErr), squared error (SqrErr), and proportional squared error (ppSqrErr) are calculated for each test mixed profile. In addition, each of these metrics is aggregated according to three criteria: cell type (CellType), probability bins in ranges of 0.1 (pBin), and number of different cell types present in the spot (nCellTypes).

**Usage**

```
calculateEvalMetrics(object)
```

**Arguments**

object            [SpatialDDLS](#) object with a trained model in trained.model slot and the actual cell proportions of test mixed profiles in prob.cell.types slot.

**Value**

A [SpatialDDLS](#) object with is a [DeconvDLModel](#) object. The calculated metrics are stored in the test.deconv.metrics slot of the [DeconvDLModel](#) object.

**See Also**

[distErrorPlot](#) [corrExpPredPlot](#) [blandAltmanLehPlot](#) [barErrorPlot](#)

---

cell.names

*Get and set cell.names slot in a [PropCellTypes](#) object*

---

**Description**

Get and set cell.names slot in a [PropCellTypes](#) object

**Usage**

```
cell.names(object)
```

```
cell.names(object) <- value
```

**Arguments**

object            [PropCellTypes](#) object.

value            Matrix containing names of the mixed transcriptional profiles to be simulated as rows and cells to be used to simulate them as columns.

---

cell.types	<i>Get and set cell.types slot in a <a href="#">DeconvDLModel</a> object</i>
------------	--

---

**Description**

Get and set cell.types slot in a [DeconvDLModel](#) object

**Usage**

```
cell.types(object)
cell.types(object) <- value
```

**Arguments**

object	<a href="#">DeconvDLModel</a> object.
value	Vector with cell types considered by the deep neural network model.

---

corrExpPredPlot	<i>Generate correlation plots between predicted and expected cell type proportions of test data</i>
-----------------	---

---

**Description**

Generate correlation plots between predicted and expected cell type proportions of test data. Correlation plots can be shown all mixed or split by cell type (CellType) or the number of different cell types present in the spots (nCellTypes).

**Usage**

```
corrExpPredPlot(
  object,
  colors,
  facet.by = NULL,
  color.by = "CellType",
  corr = "both",
  filter.sc = TRUE,
  pos.x.label = 0.01,
  pos.y.label = 0.95,
  sep.labels = 0.15,
  size.point = 0.1,
  alpha.point = 1,
  ncol = NULL,
  nrow = NULL,
  title = NULL,
```

```

    theme = NULL,
    ...
)

```

### Arguments

object	<a href="#">SpatialDDL</a> s object with trained.model slot containing metrics in the test.deconv.metrics slot of a <a href="#">DeconvDLModel</a> object.
colors	Vector of colors to be used.
facet.by	Show data in different panels. Options are nCellTypes (number of different cell types) and CellType (cell type) (NULL by default).
color.by	Variable used to color data. Options are nCellTypes and CellType.
corr	Correlation value shown as an annotation on the plot. Available metrics are Pearson's correlation coefficient ('pearson') and concordance correlation coefficient ('ccc'). It can be 'pearson', 'ccc' or 'both' (by default).
filter.sc	Boolean indicating whether single-cell profiles are filtered out and only mixed transcriptional profile errors are shown (TRUE by default).
pos.x.label	X-axis position of correlation annotations (0.95 by default).
pos.y.label	Y-axis position of correlation annotations (0.1 by default).
sep.labels	Space separating annotations if corr is equal to 'both' (0.15 by default).
size.point	Size of points (0.1 by default).
alpha.point	Alpha of points (0.1 by default).
ncol	Number of columns if facet.by is other than NULL.
nrow	Number of rows if facet.by is different from NULL.
title	Title of the plot.
theme	<b>ggplot2</b> theme.
...	Additional arguments for the <a href="#">facet_wrap</a> function of <b>ggplot2</b> if facet.by is not NULL.

### Value

A ggplot object.

### See Also

[calculateEvalMetrics](#) [distErrorPlot](#) [blandAltmanLehPlot](#) [barErrorPlot](#)

### Examples

```

set.seed(123)
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(

```

```

    rpois(30, lambda = 5), nrow = 15, ncol = 20,
    dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(20)))
  )
),
colData = data.frame(
  Cell_ID = paste0("RHC", seq(20)),
  Cell_Type = sample(x = paste0("CellType", seq(6)), size = 20,
    replace = TRUE)
),
rowData = data.frame(
  Gene_ID = paste0("Gene", seq(15))
)
)
SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 50,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs)
# training of DDLs model
SDDLs <- trainDeconvModel(
  object = SDDLs,
  batch.size = 15,
  num.epochs = 5
)
# evaluation using test data
SDDLs <- calculateEvalMetrics(object = SDDLs)
# correlations by cell type
corrExpPredPlot(
  object = SDDLs,
  facet.by = "CellType",
  color.by = "CellType",
  corr = "both"
)
# correlations of all samples mixed
corrExpPredPlot(
  object = SDDLs,
  facet.by = NULL,
  color.by = "CellType",
  corr = "ccc",
  pos.x.label = 0.2,
  alpha.point = 0.3
)

```

---

`createSpatialDDLSubject`*Create a [SpatialDDL](#) object*

---

## Description

Create a [SpatialDDL](#) object by providing single-cell RNA-seq data. Additionally, spatial transcriptomics data contained in [SpatialDDL](#) objects can also be provided. It is recommended to provide both types of data to calculate the intersection of genes shared between both experiments.

## Usage

```
createSpatialDDLSubject(  
  sc.data,  
  sc.cell.ID.column,  
  sc.cell.type.column,  
  sc.gene.ID.column,  
  st.data,  
  st.spot.ID.column,  
  st.gene.ID.column,  
  sc.filt.genes.cluster = FALSE,  
  sc.min.mean.counts = 0,  
  sc.filt.genes.cells = TRUE,  
  sc.min.counts = 0,  
  sc.min.cells = 0,  
  st.min.counts = 0,  
  st.min.spots = 0,  
  st.n.slides = 3,  
  shared.genes = TRUE,  
  sc.name.dataset.h5 = NULL,  
  sc.file.backend = NULL,  
  sc.name.dataset.backend = NULL,  
  sc.compression.level = NULL,  
  sc.chunk.dims = NULL,  
  sc.block.processing = FALSE,  
  verbose = TRUE,  
  project = "SpatialDDL-Proj"  
)
```

## Arguments

<code>sc.data</code>	Single-cell RNA-seq profiles to be used as reference. If data are provided from files, <code>single.cell.real</code> must be a vector of three elements: single-cell counts, cells metadata and genes metadata. On the other hand, If data are provided from a <a href="#">SingleCellExperiment</a> object, single-cell counts must be present in the assay slot, cells metadata in the <code>colData</code> slot, and genes metadata in the <code>rowData</code> slot.
----------------------	---

<code>sc.cell.ID.column</code>	Name or number of the column in cells metadata corresponding to cell names in expression matrix (single-cell RNA-seq data).
<code>sc.cell.type.column</code>	Name or column number corresponding to cell types in cells metadata.
<code>sc.gene.ID.column</code>	Name or number of the column in genes metadata corresponding to the names used for features/genes (single-cell RNA-seq data).
<code>st.data</code>	Spatial transcriptomics datasets to be deconvoluted. It can be a single <a href="#">SpatialExperiment</a> object or a list of them.
<code>st.spot.ID.column</code>	Name or number of the column in spots metadata corresponding to spot names in expression matrix (spatial transcriptomics data).
<code>st.gene.ID.column</code>	Name or number of the column in the genes metadata corresponding to the names used for features/genes (spatial transcriptomics data).
<code>sc.filt.genes.cluster</code>	Whether to filter single-cell RNA-seq genes according to a minimum threshold of mean counts per cell type <code>sc.min.mean.counts</code> .
<code>sc.min.mean.counts</code>	Minimum mean counts per cluster to filter genes.
<code>sc.filt.genes.cells</code>	Whether to filter single-cell RNA-seq genes according to a minimum number of counts <code>sc.min.counts</code> in a minimum number of cells <code>sc.min.cells</code> .
<code>sc.min.counts</code>	Minimum gene counts to filter (0 by default; single-cell RNA-seq data).
<code>sc.min.cells</code>	Minimum of cells with more than <code>min.counts</code> (0 by default; single-cell RNA-seq data).
<code>st.min.counts</code>	Minimum gene counts to filter (0 by default; spatial transcriptomics data).
<code>st.min.spots</code>	Minimum of cells with more than <code>min.counts</code> (0 by default; spatial transcriptomics data).
<code>st.n.slides</code>	Minimum number of slides ( <a href="#">SpatialExperiment</a> objects) in which a gene has to be expressed in order to keep it. This parameter is applicable only when multiple <a href="#">SpatialExperiment</a> objects are provided. Genes not present in at least <code>st.n.slides</code> will be discarded. If no filtering is desired, set <code>st.n.slides = 1</code> .
<code>shared.genes</code>	If set to TRUE, only genes present in both the single-cell and spatial transcriptomics data will be retained for further processing (TRUE by default).
<code>sc.name.dataset.h5</code>	Name of the data set if HDF5 file is provided for single-cell RNA-seq data.
<code>sc.file.backend</code>	Valid file path where to store the loaded for single-cell RNA-seq data as HDF5 file. If provided, data are stored in a HDF5 file as back-end using the <b>DelayedArray</b> and <b>HDF5Array</b> packages instead of being loaded into RAM. This is suitable for situations where you have large amounts of data that cannot be stored in memory. Note that operations on these data will be performed by

	blocks (i.e subsets of determined size), which may result in longer execution times. NULL by default.
sc.name.dataset.backend	Name of the HDF5 file dataset to be used. Note that it cannot exist. If NULL (by default), a random dataset name will be generated.
sc.compression.level	The compression level used if sc.file.backend is provided. It is an integer value between 0 (no compression) and 9 (highest and slowest compression). See <a href="#">?getHDF5DumpCompressionLevel</a> from the <b>HDF5Array</b> package for more information.
sc.chunk.dims	Specifies dimensions that HDF5 chunk will have. If NULL, the default value is a vector of two items: the number of genes considered by <a href="#">SpatialDDL</a> object during the simulation, and only one sample in order to increase read times in the following steps. A larger number of columns written in each chunk may lead to longer read times.
sc.block.processing	Boolean indicating whether single-cell RNA-seq data should be treated as blocks (only if data are provided as HDF5 file). FALSE by default. Note that using this functionality is suitable for cases where it is not possible to load data into RAM and therefore execution times will be longer.
verbose	Show informative messages during the execution (TRUE by default).
project	Name of the project for <a href="#">SpatialDDL</a> object.

## Details

### Single-cell RNA-seq data

Single-cell RNA-seq data can be provided from files (formats allowed: tsv, tsv.gz, mtx (sparse matrix) and hdf5) or a [SingleCellExperiment](#) object. Data will be stored in the `single.cell.real` slot, and must consist of three pieces of information:

- Single-cell counts: genes as rows and cells as columns.
- Cells metadata: annotations (columns) for each cell (rows).
- Genes metadata: annotations (columns) for each gene (rows).

If data are provided from files, `single.cell.real` argument must be a vector of three elements ordered so that the first file corresponds to the count matrix, the second to the cells metadata, and the last to the genes metadata. On the other hand, if data are provided as a [SingleCellExperiment](#) object, it must contain single-cell counts in `assay`, cells metadata in `colData`, and genes metadata in `rowData`. Data must be provided without any transformation (e.g. log-transformation), raw counts are preferred.

### Spatial transcriptomics data

It must be a [SpatialExperiment](#) object (or a list of them if more than one slide is going to be deconvoluted) containing the same information as the single-cell RNA-seq data: the count matrix, spots metadata, and genes metadata. Please, make sure the gene identifiers used the spatial and single-cell transcriptomics data are consistent.

**Value**

A `SpatialDDL` object with the single-cell RNA-seq data provided loaded into the `single.cell.real` slot as a `SingleCellExperiment` object. If spatial transcriptomics data are provided, they will be loaded into the `spatial.experiments` slot.

**See Also**

[estimateZinbwaveParams](#) [genMixedCellProp](#)

**Examples**

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(100, lambda = 5), nrow = 40, ncol = 30,
      dimnames = list(paste0("Gene", seq(40)), paste0("RHC", seq(30)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(30)),
    Cell_Type = sample(x = paste0("CellType", seq(4)), size = 30,
      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(40))
  )
)
counts <- matrix(
  rpois(30, lambda = 5), ncol = 6,
  dimnames = list(paste0("Gene", 1:5), paste0("Spot", 1:6))
)
coordinates <- matrix(
  c(1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3), ncol = 2
)
ste <- SpatialExperiment::SpatialExperiment(
  assays = list(counts = as.matrix(counts)),
  rowData = data.frame(Gene_ID = paste0("Gene", 1:5)),
  colData = data.frame(Cell_ID = paste0("Spot", 1:6)),
  spatialCoords = coordinates
)

SDDL <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  st.data = ste,
  st.spot.ID.column = "Cell_ID",
  st.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
```

---

deconv.spots	<i>Get and set deconv.spots slot in a <a href="#">SpatialDDLs</a> object</i>
--------------	--

---

### Description

Get and set deconv.spots slot in a [SpatialDDLs](#) object

### Usage

```
deconv.spots(object, index.st = NULL)
```

```
deconv.spots(object, index.st = NULL) <- value
```

### Arguments

object	<a href="#">SpatialDDLs</a> object.
index.st	Name or index of predicted cell proportions (same as for the <code>spatial.experiments</code> slot). If NULL (by default), all the results are returned.
value	List with predicted cell type proportions for the experiments stored in the <code>spatial.experiments</code> slot.

---

DeconvDLModel-class	<i>The DeconvDLModel Class</i>
---------------------	--------------------------------

---

### Description

The [DeconvDLModel](#) object stores all the information related to deep neural network models. It consists of the trained model, the training history, and the predictions on test data. After running [calculateEvalMetrics](#), it is possible to find the performance evaluation of the model on test data (see [?calculateEvalMetrics](#) for details).

### Details

The steps related to Deep Learning are carried out using the **keras** and **tensorflow** packages, which use the R6 classes system. If you want to save the [DeconvDLModel](#) object as an RDS file, **SpatialDDLs** provides a `saveRDS` generic function that transforms the R6 object containing the trained model into a native valid R object. Specifically, the model is converted into a list with the architecture of the network and the weights learned during training. That is the minimum information needed to use the model as predictor. If you want to keep the optimizer state, see [?saveTrainedModelAsH5](#). If you want to store either the [DeconvDLModel](#) or the [SpatialDDLs](#) objects on disk as RDA files, see [?preparingToSave](#).

**Slots**

`model` Trained deep neural network. This slot can contain an R6 `keras.engine.sequential.Sequential` object or a list with two elements: the architecture of the model and the resulting weights after training.

`training.history` List with the evolution of the selected metrics during training.

`test.metrics` Performance of the model on test data.

`test.pred` Predicted cell type proportions on test data.

`cell.types` Vector with cell types considered by the model.

`features` Vector with features (genes) considered by the model. These features will be used for subsequent predictions.

`test.deconv.metrics` Performance of the model on test data by cell type. This slot is generated by the `calculateEvalMetrics` function (see [?calculateEvalMetrics](#) for more details).

---

deconvSpatialDDLs      *Deconvolute spatial transcriptomics data*

---

**Description**

Deconvolute spatial transcriptomics data using the trained model contained in the `SpatialDDLs` object.

**Usage**

```
deconvSpatialDDLs(
  object,
  index.st,
  normalize = TRUE,
  scaling = "rescale",
  simplify.set = NULL,
  simplify.majority = NULL,
  use.generator = FALSE,
  batch.size = 64,
  verbose = TRUE
)
```

**Arguments**

<code>object</code>	<code>SpatialDDLs</code> object with <code>trained.model</code> and <code>spatial.experiments</code> slots.
<code>index.st</code>	Name or index of the dataset/slide stored in the <code>SpatialDDLs</code> object ( <code>spatial.experiments</code> slot) to be deconvolute. If missing, all datasets will be deconvoluted.
<code>normalize</code>	Normalize data before deconvolution (TRUE by default).
<code>scaling</code>	How to scale data before training. It may be: "standardize" (values are centered around the mean with a unit standard deviation) or "rescale" (values are shifted and rescaled so that they end up ranging between 0 and 1). If <code>normalize = FALSE</code> , data are not scaled.

<code>simplify.set</code>	List specifying which cell types should be compressed into a new label with the name of the list item. See examples for details. If provided, results are stored in a list with 'raw' and 'simpli.set' elements.
<code>simplify.majority</code>	List specifying which cell types should be compressed into the cell type with the highest proportion in each spot. Unlike <code>simplify.set</code> , no new labels are created. If provided, results are stored in a list with 'raw' and 'simpli.majority' elements.
<code>use.generator</code>	Boolean indicating whether to use generators for prediction (FALSE by default).
<code>batch.size</code>	Number of samples per batch. Only when <code>use.generator = TRUE</code> .
<code>verbose</code>	Show informative messages during the execution.

### Details

This function requires a [SpatialDDLs](#) object with a trained deep neural network model (`trained.model` slot), and the spatial transcriptomics datasets to be deconvoluted in the `spatial.experiments` slot. See [?createSpatialDDLSubject](#) or [?loadSTProfiles](#) for more details.

### Value

[SpatialDDLs](#) object with a `deconv.spots` slot. The output is a data frame with spot ( $i$ ) as rows and cell types ( $j$ ) as columns. Each entry represents the predicted proportion of  $j$  cell type in  $i$  spot. If `simplify.set` and/or `simplify.majority` are provided, the `deconv.spots` slot will contain a list with raw and simplified results.

### See Also

[trainDeconvModel SpatialDDLs](#)

### Examples

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 20,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(20)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(20)),
    Cell_Type = sample(x = paste0("CellType", seq(6)), size = 20,
      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
SDDLs <- createSpatialDDLSubject(
```

```

sc.data = sce,
sc.cell.ID.column = "Cell_ID",
sc.gene.ID.column = "Gene_ID",
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 50,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs)
# training of SDDLs model
SDDLs <- trainDeconvModel(
  object = SDDLs,
  batch.size = 15,
  num.epochs = 5
)
# simulating mixed profiles
ngenes <- sample(3:40, size = 1)
ncells <- sample(3:40, size = 1)
counts <- matrix(
  rpois(ngenes * ncells, lambda = 5), ncol = ncells,
  dimnames = list(paste0("Gene", seq(ngenes)), paste0("Spot", seq(ncells)))
)
coordinates <- matrix(
  rep(c(1, 2), ncells), ncol = 2
)
st <- SpatialExperiment::SpatialExperiment(
  assays = list(counts = as.matrix(counts)),
  rowData = data.frame(Gene_ID = paste0("Gene", seq(ngenes))),
  colData = data.frame(Cell_ID = paste0("Spot", seq(ncells))),
  spatialCoords = coordinates
)
SDDLs <- loadSTProfiles(
  object = SDDLs,
  st.data = st,
  st.spot.ID.column = "Cell_ID",
  st.gene.ID.column = "Gene_ID"
)
# simplify arguments
simplify <- list(CellGroup1 = c("CellType1", "CellType2", "CellType4"),
  CellGroup2 = c("CellType3", "CellType5"))
SDDLs <- deconvSpatialDDLs(
  object = SDDLs,
  index.st = 1,
  simplify.set = simplify,
  simplify.majority = simplify
)

```

---

distErrorPlot	<i>Generate box or violin plots showing error distribution</i>
---------------	--

---

### Description

Generate box or violin plots to show how errors are distributed. Errors can be shown all mixed or split by cell type (`CellType`) or number of cell types present in the spots (`nCellTypes`). See the `facet.by` argument and examples for more details.

### Usage

```
distErrorPlot(
  object,
  error,
  colors,
  x.by = "pBin",
  facet.by = NULL,
  color.by = "nCellTypes",
  filter.sc = TRUE,
  error.label = FALSE,
  pos.x.label = 4.6,
  pos.y.label = NULL,
  size.point = 0.1,
  alpha.point = 1,
  type = "violinplot",
  ylimit = NULL,
  nrow = NULL,
  ncol = NULL,
  title = NULL,
  theme = NULL,
  ...
)
```

### Arguments

object	<code>SpatialDDL</code> s object with <code>trained.model</code> slot containing metrics in the <code>test.deconv.metrics</code> slot of a <code>DeconvDLModel</code> object.
error	Error to be represented. Available errors are: absolute error ( <code>'AbsErr'</code> ), proportional absolute error ( <code>'ppAbsErr'</code> ), squared error ( <code>'SqrErr'</code> ), and proportional squared error ( <code>'ppSqrErr'</code> ).
colors	Vector of colors to be used.
x.by	Variable used for the X-axis. When <code>facet.by</code> is not <code>NULL</code> , the best choice is <code>pBin</code> (probability bins). Options: <code>nCellTypes</code> (number of different cell types), <code>CellType</code> (cell type), and <code>pBin</code> .
facet.by	Show data in different panels. Options are <code>nCellTypes</code> (number of different cell types) and <code>CellType</code> (cell type) ( <code>NULL</code> by default).

<code>color.by</code>	Variable used to color data. Options are <code>nCellTypes</code> and <code>CellType</code> .
<code>filter.sc</code>	Boolean indicating whether single-cell profiles are filtered out and only mixed transcriptional profile errors are shown (TRUE by default).
<code>error.label</code>	Boolean indicating whether to show the average error as a plot annotation (FALSE by default).
<code>pos.x.label</code>	X-axis position of error annotations.
<code>pos.y.label</code>	Y-axis position of error annotations.
<code>size.point</code>	Size of points (0.1 by default).
<code>alpha.point</code>	Alpha of points (0.1 by default).
<code>type</code>	Type of plot: 'boxplot' or 'violinplot' (the latter by default).
<code>ylim</code>	Upper limit in Y-axis if it is required (NULL by default).
<code>nrow</code>	Number of rows if <code>facet.by</code> is not NULL.
<code>ncol</code>	Number of columns if <code>facet.by</code> is not NULL.
<code>title</code>	Title of the plot.
<code>theme</code>	<b>ggplot2</b> theme.
<code>...</code>	Additional arguments for the <code>facet_wrap</code> function of <b>ggplot2</b> if <code>facet.by</code> is not NULL.

**Value**

A ggplot object.

**See Also**

[calculateEvalMetrics](#) [corrExpPredPlot](#) [blandAltmanLehPlot](#) [barErrorPlot](#)

**Examples**

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 20,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(20)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(20)),
    Cell_Type = sample(
      x = paste0("CellType", seq(6)), size = 20, replace = TRUE
    )
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
```

```

SDDLs <- createSpatialDDLsObject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 50,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs)
# training of DDLs model
SDDLs <- trainDeconvModel(
  object = SDDLs,
  batch.size = 15,
  num.epochs = 5
)
# evaluation using test data
SDDLs <- calculateEvalMetrics(object = SDDLs)
# representation, for more examples, see the vignettes
distErrorPlot(
  object = SDDLs,
  error = "AbsErr",
  facet.by = "CellType",
  color.by = "nCellTypes",
  error.label = TRUE
)
distErrorPlot(
  object = SDDLs,
  error = "AbsErr",
  x.by = "CellType",
  facet.by = NULL,
  color.by = "CellType",
  error.label = TRUE
)

```

---

estimateZinbwaveParams

*Estimate parameters of the ZINB-WaVE model to simulate new single-cell RNA-Seq expression profiles*

---

## Description

Estimate the parameters of the ZINB-WaVE model using a real single-cell RNA-Seq data set as reference to simulate new single-cell profiles and increase the signal of underrepresented cell types. This step is only needed if the size of the single-cell RNA-seq dataset is too small or there are

underrepresented cell types. After this step, the `simSCProfiles` function will use the estimated parameters to simulate new single-cell profiles. See `?simSCProfiles` for more information.

### Usage

```
estimateZinbwaveParams(
  object,
  cell.type.column,
  cell.ID.column,
  gene.ID.column,
  cell.cov.columns,
  gene.cov.columns,
  subset.cells = NULL,
  proportional = TRUE,
  set.type = "All",
  threads = 1,
  verbose = TRUE
)
```

### Arguments

<code>object</code>	<code>SpatialDDL</code> object with a <code>single.cell.real</code> slot.
<code>cell.type.column</code>	Name or column number corresponding to the cell type of each cell in cells metadata.
<code>cell.ID.column</code>	Name or column number corresponding to the cell names of expression matrix in cells metadata.
<code>gene.ID.column</code>	Name or column number corresponding to the notation used for features/genes in genes metadata.
<code>cell.cov.columns</code>	Name or column number(s) in cells metadata to be used as covariates during model fitting (if no covariates are used, set to empty or <code>NULL</code> ).
<code>gene.cov.columns</code>	Name or column number(s) in genes metadata that will be used as covariates during model fitting (if no covariates are used, set to empty or <code>NULL</code> ).
<code>subset.cells</code>	Number of cells to fit the ZINB-WaVE model. Useful when the original data set is too large to fit the model. Set a value according to the original data set and the resources available on your computer. If <code>NULL</code> (by default), all cells will be used. Must be an integer greater than or equal to the number of cell types considered and less than or equal to the total number of cells.
<code>proportional</code>	If <code>TRUE</code> , the original cell type proportions in the subset of cells generated by <code>subset.cells</code> will not be altered as far as possible. If <code>FALSE</code> , all cell types will have the same number of cells as far as possible ( <code>TRUE</code> by default).
<code>set.type</code>	Cell type(s) to evaluate ('All' by default). It is recommended fitting the model to all cell types rather than using only a subset of them to capture the total variability present in the original experiment even if only a subset of cell types is simulated.

threads	Number of threads used for estimation (1 by default). To set up the parallel environment, the <b>BiocParallel</b> package must be installed.
verbose	Show informative messages during the execution (TRUE by default).

## Details

ZINB-WaVE is a flexible model for zero-inflated count data. This function carries out the model fit to real single-cell data modeling  $Y_{ij}$  (the count of feature  $j$  for sample  $i$ ) as a random variable following a zero-inflated negative binomial (ZINB) distribution. The estimated parameters will be used for the simulation of new single-cell expression profiles by sampling a negative binomial distribution and inserting dropouts from a binomial distribution. To do so, **SpatialDDLS** uses the `zinbFit` function from the **zinbwave** package (Risso et al., 2018). For more details about the model, see Risso et al., 2018.

## Value

A **SpatialDDLS** object with `zinb.params` slot containing a `ZinbParametersModel` object. This object contains a slot with the estimated ZINB-WaVE parameters from the real single-cell RNA-Seq data.

## References

- Risso, D., Perraudeau, F., Gribkova, S. et al. (2018). A general and flexible method for signal extraction from single-cell RNA-seq data. *Nat Commun* 9, 284. doi: [doi: 10.1038/s41467017-025545](https://doi.org/10.1038/s41467017-025545).
- Torroja, C. and Sánchez-Cabo, F. (2019). digitalDLSorter: A Deep Learning algorithm to quantify immune cell populations based on scRNA-Seq data. *Frontiers in Genetics* 10, 978. doi: [doi: 10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978).

## See Also

[simSCProfiles](#)

## Examples

```
set.seed(123) # reproducibility
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 10,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(10)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(10)),
    Cell_Type = sample(x = paste0("CellType", seq(2)), size = 10,
                      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
```

```

)
)
SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
SDDLs <- estimateZinbwaveParams(
  object = SDDLs,
  cell.type.column = "Cell_Type",
  cell.ID.column = "Cell_ID",
  gene.ID.column = "Gene_ID",
  subset.cells = 2,
  verbose = TRUE
)

```

---

features	<i>Get and set features slot in a <a href="#">DeconvDLModel</a> object</i>
----------	--

---

### Description

Get and set features slot in a [DeconvDLModel](#) object

### Usage

```
features(object)
```

```
features(object) <- value
```

### Arguments

object	<a href="#">DeconvDLModel</a> object.
value	Vector with features (genes) considered by the deep neural network model.

---

genMixedCellProp	<i>Generate training and test cell type composition matrices</i>
------------------	--

---

### Description

Generate training and test cell type composition matrices for the simulation of mixed transcriptional profiles with known cell composition using single-cell expression profiles. The resulting [PropCellTypes](#) object will contain all the information needed to simulate new mixed transcriptional profiles. Note this function does not simulate the mixed profiles, this task is performed by the [simMixedProfiles](#) or [trainDeconvModel](#) functions (see Documentation).

**Usage**

```
genMixedCellProp(
  object,
  cell.ID.column,
  cell.type.column,
  num.sim.spots,
  n.cells = 100,
  train.freq.cells = 2/3,
  train.freq.spots = 2/3,
  proportion.method = c(0.6, 0.2, 0.2),
  prob.sparity = 0.8,
  min.zero.prop = NULL,
  balanced.type.cells = TRUE,
  verbose = TRUE
)
```

**Arguments**

object	<a href="#">SpatialDDL</a> S object with single.cell.real slot and, optionally, with single.cell.simul slot.
cell.ID.column	Name or column number corresponding to cell names in cells metadata.
cell.type.column	Name or column number corresponding to cell types in cells metadata.
num.sim.spots	Number of mixed profiles to be simulated. It is recommended to adjust this number according to the number of available single-cell profiles.
n.cells	Specifies the number of cells to be randomly selected and combined to generate the simulated mixed profiles. By default, it is set to 100. It controls the level of noise present in the simulated data, as it determines how many single-cell profiles will be combined to produce each spot.
train.freq.cells	Proportion of cells used to simulate training mixed transcriptional profiles (2/3 by default).
train.freq.spots	Proportion of mixed transcriptional profiles to be used for training, relative to the total number of simulated spots (num.sim.spots). The default value is 2/3.
proportion.method	Vector with three elements that controls the proportion of simulated proportions generated by each method: random sampling of a Dirichlet distribution, "pure" spots (1 cell type), and spots with a specified number of different cell types (determined by min.zero.prop), respectively. By default, 60% of the simulated proportions will follow a Dirichlet distribution, 20% will consist of only one cell type, and 20% will have a specified number of different cell types.
prob.sparity	It only affects the proportions generated by the first method (Dirichlet distribution). It determines the probability of having missing cell types in each simulated spot, as opposed to a mixture of all cell types. A higher value for this parameter will result in more sparse simulated samples.

<code>min.zero.prop</code>	This parameter controls the minimum number of cell types that will be absent in each simulated spot. If NULL (by default), this value will be half of the total number of different cell types, but increasing it will result in more spots composed of fewer cell types. This helps to create more sparse proportions and cover a wider range of situations during model training.
<code>balanced.type.cells</code>	Boolean indicating whether training and test cells will be split in a balanced way considering cell types (TRUE by default).
<code>verbose</code>	Show informative messages during the execution (TRUE by default).

## Details

First, the single-cell profiles are randomly divided into two subsets, with 2/3 of the data for training and 1/3 for testing. The default setting for this ratio can be changed using the `train.freq.cells` parameter. Next, a total of `num.sim.spots` mixed proportions are simulated using a Dirichlet distribution. This simulation takes into account the probability of missing cell types in each spot, which can be adjusted using the `prob.sparity` parameter. For each mixed sample, `n.cells` single-cell profiles are randomly selected and combined to generate the simulated mixed sample. In addition to the Dirichlet-based proportions, pure spots (containing only one cell type) and spots containing a specified number of different cell types (determined by the `min.zero.prop` parameter) are also generated in order to cover situations with only a few cell types present. The proportion of simulated spots generated by each method can be controlled using the `proportion.method` parameter. To visualize the distribution of cell type proportions generated by each method, the [showProbPlot](#) function can be used.

## Value

A [SpatialDDL](#)s object with `prob.cell.types` slot containing a list with two [PropCellTypes](#) objects (training and test). For more information about the structure of this class, see [?PropCellTypes](#).

## See Also

[simMixedProfiles PropCellTypes](#)

## Examples

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(100, lambda = 5), nrow = 40, ncol = 30,
      dimnames = list(paste0("Gene", seq(40)), paste0("RHC", seq(30)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(30)),
    Cell_Type = sample(x = paste0("CellType", seq(4)), size = 30,
                      replace = TRUE)
  ),
  rowData = data.frame(
```

```
    Gene_ID = paste0("Gene", seq(40))
  )
)

SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 10,
  verbose = TRUE
)
```

---

getProbMatrix

*Getter function for the cell composition matrix*

---

### Description

Getter function for the cell composition matrix. This function allows to access to the cell composition matrix of simulated mixed transcriptional profiles.

### Usage

```
getProbMatrix(object, type.data)
```

### Arguments

object	<a href="#">SpatialDDLs</a> object with prob.cell.types slot.
type.data	Subset of data to return: train or test.

### Value

Cell type proportion matrix.

### See Also

[genMixedCellProp](#)

---

installTFpython	<i>Install Python dependencies for SpatialDDLs</i>
-----------------	--

---

### Description

This function facilitates the installation of the required Python dependencies for the SpatialDDLs package. It requires a Python interpreter with the TensorFlow Python library and its dependencies. It utilizes the reticulate package and the installer of the tensorflow R package to perform the installation. Conda environments will be used with the new environment being named SpatialDDLs-env. This function is intended to simplify the installation process for SpatialDDLs by automatically installing Miniconda and creating a new environment named SpatialDDLs-env. For users who wish to use a different Python or conda environment, see the tensorflow::use\_condaenv function and the package vignettes for more information.

### Usage

```
installTFpython(conda = "auto", install.conda = FALSE, miniconda.path = NULL)
```

### Arguments

conda	Path to a conda executable. Using "auto" (by default) allows <b>reticulate</b> to automatically find an appropriate conda binary.
install.conda	Boolean indicating if installing miniconda automatically by using <b>reticulate</b> . If TRUE, conda argument is ignored. FALSE by default.
miniconda.path	If install.conda is TRUE, you can set the path where miniconda will be installed. If NULL, conda will find automatically the proper place.

### Value

No return value, called for side effects: installation of conda environment with a Python interpreter and Tensorflow

### Examples

```
## Not run:
notesInstallation <- installTFpython(
  method = "auto", conda = "auto", install.conda = TRUE
)

## End(Not run)
```

---

loadSTProfiles	<i>Loads spatial transcriptomics data into a SpatialDDLS object</i>
----------------	---

---

### Description

This function loads a [SpatialExperiment](#) object (or a list with several [SpatialExperiment](#) objects) into a [SpatialDDLS](#) object.

### Usage

```
loadSTProfiles(
  object,
  st.data,
  st.spot.ID.column,
  st.gene.ID.column,
  st.min.counts = 0,
  st.min.spots = 0,
  st.n.slides = 3,
  verbose = TRUE
)
```

### Arguments

object	A <a href="#">SpatialDDLS</a> object.
st.data	A <a href="#">SpatialExperiment</a> object (or a list with several <a href="#">SpatialExperiment</a> objects) to be deconvoluted.
st.spot.ID.column	Name or number of the column in spots metadata corresponding to spot names in the expression matrix.
st.gene.ID.column	Name or number of the column in genes metadata corresponding to names used for features/genes.
st.min.counts	Minimum gene counts to filter (0 by default).
st.min.spots	Minimum of spots with more than min.counts (0 by default).
st.n.slides	Minimum number of slides ( <a href="#">SpatialExperiment</a> objects) in which a gene has to be expressed in order to keep it. This parameter is applicable only when multiple <a href="#">SpatialExperiment</a> objects are provided. Genes not present in at least st.n.slides will be discarded. If no filtering is desired, set st.n.slides = 1.
verbose	Show informative messages during execution (TRUE by default).

### Details

It is recommended to perform this step when creating the [SpatialDDLS](#) object using the [createSpatialDDLSubject](#) function in order to only keep genes shared between the spatial transcriptomics and the single-cell transcriptomics data used as reference. In addition, please, make sure the gene identifiers used the spatial and single-cell transcriptomics data are consistent.

**Value**

A [SpatialDDL](#)S object with the provided spatial transcriptomics data loaded into the `spatial.experiments` slot.

**See Also**

[createSpatialDDLSubject](#) [trainDeconvModel](#)

**Examples**

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(100, lambda = 5), nrow = 40, ncol = 30,
      dimnames = list(paste0("Gene", seq(40)), paste0("RHC", seq(30)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(30)),
    Cell_Type = sample(x = paste0("CellType", seq(4)), size = 30,
      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(40))
  )
)
SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID"
)

## simulating a SpatialExperiment object
counts <- matrix(rpois(30, lambda = 5), ncol = 6)
rownames(counts) <- paste0("Gene", 1:5)
colnames(counts) <- paste0("Spot", 1:6)
coordinates <- matrix(
  c(1, 2, 3, 1, 2, 3, 1, 2, 3, 1, 2, 3), ncol = 2
)
ste <- SpatialExperiment::SpatialExperiment(
  assays = list(counts = as.matrix(counts)),
  rowData = data.frame(Gene_ID = paste0("Gene", 1:5)),
  colData = data.frame(Cell_ID = paste0("Spot", 1:6)),
  spatialCoords = coordinates
)

## previous SpatialDDLs object
SDDLs <- loadSTProfiles(
  object = SDDLs,
  st.data = ste,
```

```

    st.spot.ID.column = "Cell_ID",
    st.gene.ID.column = "Gene_ID",
  )

```

---

loadTrainedModelFromH5

*Load from an HDF5 file a trained deep neural network model into a [SpatialDDL](#) object*

---

### Description

Load from an HDF5 file a trained deep neural network model into a [SpatialDDL](#) object. Note that HDF5 file must be a valid trained model (**keras** object).

### Usage

```
loadTrainedModelFromH5(object, file.path, reset.slot = FALSE)
```

### Arguments

object	<a href="#">SpatialDDL</a> object with trained.model slot.
file.path	Valid file path where the model are stored.
reset.slot	Deletes trained.slot if it already exists. A new <a href="#">DeconvDLModel</a> object will be formed, but will not contain other slots (FALSE by default).

### Value

[SpatialDDL](#) object with trained.model slot with the new **keras** DNN model incorporated.

### See Also

[trainDeconvModel](#) [saveTrainedModelAsH5](#)

---

method	<i>Get and set method slot in a <a href="#">PropCellTypes</a> object</i>
--------	--

---

### Description

Get and set method slot in a [PropCellTypes](#) object

### Usage

```
method(object)
```

```
method(object) <- value
```

**Arguments**

object	<a href="#">PropCellTypes</a> object.
value	Vector containing the method by which cell type proportions were generated.

---

mixed.profiles	<i>Get and set mixed.profiles slot in a <a href="#">SpatialDDLS</a> object</i>
----------------	--

---

**Description**

Get and set mixed.profiles slot in a [SpatialDDLS](#) object

**Usage**

```
mixed.profiles(object, type.data = "both")
mixed.profiles(object, type.data = "both") <- value
```

**Arguments**

object	<a href="#">SpatialDDLS</a> object.
type.data	Type of data to return. It can be 'both' (default), 'train', or 'test'.
value	List with two <a href="#">SummarizedExperiment</a> objects, train and test, each one containing simulated mixed transcriptional profiles.

---

model	<i>Get and set model slot in a <a href="#">DeconvDLModel</a> object</i>
-------	---

---

**Description**

Get and set model slot in a [DeconvDLModel](#) object

**Usage**

```
model(object)
model(object) <- value
```

**Arguments**

object	<a href="#">DeconvDLModel</a> object.
value	keras.engine.sequential.Sequential object with a trained deep neural network model.

---

plots	<i>Get and set plots slot in a <a href="#">PropCellTypes</a> object</i>
-------	---

---

**Description**

Get and set plots slot in a [PropCellTypes](#) object

**Usage**

```
plots(object)
plots(object) <- value
```

**Arguments**

object	<a href="#">PropCellTypes</a> object.
value	List of lists with plots showing the distribution of cell proportions generated by each method.

---

plotSpatialProp	<i>Plot predicted proportions for a specific cell type using spatial coordinates of spots</i>
-----------------	---

---

**Description**

Color spots on the spatial coordinates according to the predicted proportions of a particular cell type. Color scale is adapted depending on the range of predicted proportions.

**Usage**

```
plotSpatialProp(
  object,
  index.st,
  cell.type,
  colors = "blues",
  set = "raw",
  limits = NULL,
  size.point = 1,
  title = NULL,
  theme = NULL
)
```

**Arguments**

object	A <a href="#">SpatialDDLS</a> object.
index.st	Index of the spatial transcriptomics data to be plotted. It can be either a position or a name if a named list was provided.
cell.type	Cell type predicted proportions to color spots by.
colors	Color scale to be used. It can be "blues" or "spectral" (the former by default).
set	If results were simplified (see <a href="#">?deconvSpatialDDLS</a> for details), what results to plot (raw by default).
limits	A vector of two elements indicating wanted limits for color scale. If NULL (by default), color scale is adjusted to max and min predicted proportions.
size.point	Size of points (0.1 by default).
title	Title of plot.
theme	<b>ggplot2</b> theme.

**Value**

A ggplot object.

**See Also**

[plotSpatialPropAll](#) [deconvSpatialDDLS](#) [trainDeconvModel](#)

---

plotSpatialPropAll	<i>Plot predicted proportions for all cell types using spatial coordinates of spots</i>
--------------------	---

---

**Description**

Color spots on the spatial coordinates plot according to their predicted cell type proportions. All cell types are represented together using the same color scale from 0 to 1.

**Usage**

```
plotSpatialPropAll(
  object,
  index.st,
  colors = "blues",
  set = "raw",
  size.point = 0.1,
  title = NULL,
  nrow = NULL,
  ncol = NULL,
  theme = NULL
)
```

**Arguments**

object	A <a href="#">SpatialDDLS</a> object.
index.st	Index of the spatial transcriptomics data to be plotted. It can be either a position or a name if a named list was provided.
colors	Color scale to be used. It can be "blues" or "spectral" (the former by default).
set	If results were simplified (see <a href="#">?deconvSpatialDDLS</a> for details), what results to plot (raw by default).
size.point	Size of points (0.1 by default).
title	Title of plot.
nrow	Number of rows in the split plot.
ncol	Number of columns in the split plot.
theme	<b>ggplot2</b> theme.

**Value**

A ggplot object.

**See Also**

[plotSpatialProp](#) [deconvSpatialDDLS](#) [trainDeconvModel](#)

---

plotTrainingHistory	<i>Plot training history of a trained SpatialDDLS deep neural network model</i>
---------------------	---

---

**Description**

Plot training history of a trained SpatialDDLS deep neural network model.

**Usage**

```
plotTrainingHistory(
  object,
  title = "History of metrics during training",
  metrics = NULL
)
```

**Arguments**

object	<a href="#">SpatialDDLS</a> object with a trained.model slot.
title	Title of plot.
metrics	Metrics to be plotted. If NULL (by default), all metrics available in the <a href="#">DeconvDLModel</a> object will be plotted.

**Value**

A ggplot object with the progression of the selected metrics during training.

**See Also**

[trainDeconvModel](#)

---

preparingToSave

*Prepare [SpatialDDLS](#) object to be saved as an RDA file*

---

**Description**

This function prepares a [SpatialDDLS](#) object to be saved as an RDA file when contains a [DeconvDLModel](#) object with a trained DNN model.

**Usage**

```
preparingToSave(object)
```

**Arguments**

**object** [SpatialDDLS](#) object with a trained.data slot containing a [DeconvDLModel](#) object with a trained DNN model.

**Details**

Since **keras** models cannot be saved natively as R objects, this function saves the structure of the model as a JSON-like character object and its weights as a list. This allows for the retrieval of the model and making predictions. It is important to note that the state of the optimizer is not saved, only the model's architecture and weights. To save the entire model, please see the [saveTrainedModelAsH5](#) and [loadTrainedModelFromH5](#) functions.

It is also possible to save a [SpatialDDLS](#) object as an RDS file with the `saveRDS` function without any preparation.

**Value**

A [SpatialDDLS](#) or [DeconvDLModel](#) object with its trained keras model transformed from a `keras.engine.sequential.Sequential` class into a list with its architecture as a JSON-like character object, and its weights as a list.

**See Also**

[saveRDS](#) [saveTrainedModelAsH5](#)

---

prob.cell.types	<i>Get and set prob.cell.types slot in a <a href="#">SpatialDDL</a> object</i>
-----------------	--

---

**Description**

Get and set prob.cell.types slot in a [SpatialDDL](#) object

**Usage**

```
prob.cell.types(object, type.data = "both")
```

```
prob.cell.types(object, type.data = "both") <- value
```

**Arguments**

object	<a href="#">SpatialDDL</a> object.
type.data	Type of data to return. It can be 'both' (default), 'train', or 'test'.
value	List with two <a href="#">PropCellTypes</a> objects corresponding to train and test data.

---

prob.matrix	<i>Get and set prob.matrix slot in a <a href="#">PropCellTypes</a> object</i>
-------------	---

---

**Description**

Get and set prob.matrix slot in a [PropCellTypes](#) object

**Usage**

```
prob.matrix(object)
```

```
prob.matrix(object) <- value
```

**Arguments**

object	<a href="#">PropCellTypes</a> object.
value	Matrix with cell types as columns and samples as rows.

---

project	<i>Get and set project slot in a <a href="#">SpatialDDL</a> object</i>
---------	--

---

**Description**

Get and set project slot in a [SpatialDDL](#) object

**Usage**

```
project(object)
```

```
project(object) <- value
```

**Arguments**

object	<a href="#">SpatialDDL</a> object.
value	Character indicating the name of the project.

---

PropCellTypes-class	<i>The PropCellTypes Class</i>
---------------------	--------------------------------

---

**Description**

The [PropCellTypes](#) class is a data storage class which contains information related to the cell type composition matrices used to simulate mixed transcriptional profiles. This matrix is stored in the `prob.matrix` slot while the rest contains additional information generated during the process and required in subsequent steps.

**Details**

See [?genMixedCellProp](#) function for information about how cell type composition matrices are generated. Plots about the cell type proportion distributions can be accessed using the [showProbPlot](#) function (see [?showProbPlot](#) for more details).

**Slots**

`prob.matrix` Matrix of cell type proportions to simulate mixed transcriptional profiles.

`cell.names` Matrix containing the name of cells to be used to generate the simulated mixed transcriptional profiles.

`set.list` List of cells ordered according to the cell type they belong to.

`set` Vector containing cell names present in the object.

`method` Vector containing the method by which cell type proportions were generated.

`plots` Plots showing the distribution of the cell type proportions. See [?showProbPlot](#) for more details.

`type.data` Character indicating the type of data contained: train or test.

---

`saveRDS`*Save SpatialDDLs objects as RDS files*

---

## Description

Save [SpatialDDLs](#) and [DeconvDLModel](#) objects as RDS files. **keras** models cannot be stored natively as R objects (e.g. RData or RDS files). By saving the architecture as a JSON-like character object and the weights as a list, it is possible to retrieve the model and make new predictions. If the `trained.model` slot is empty, the function will behave as normal. **Note:** with this option, the state of optimizer is not saved, only the model's architecture and weights. It is possible to save the entire model as an HDF5 file with the [saveTrainedModelAsH5](#) function and load it into a [SpatialDDLs](#) object with the [loadTrainedModelFromH5](#) function. See documentation for details.

## Usage

```
saveRDS(  
  object,  
  file,  
  ascii = FALSE,  
  version = NULL,  
  compress = TRUE,  
  refhook = NULL  
)  
  
## S4 method for signature 'DeconvDLModel'  
saveRDS(  
  object,  
  file,  
  ascii = FALSE,  
  version = NULL,  
  compress = TRUE,  
  refhook = NULL  
)  
  
## S4 method for signature 'SpatialDDLs'  
saveRDS(  
  object,  
  file,  
  ascii = FALSE,  
  version = NULL,  
  compress = TRUE,  
  refhook = NULL  
)
```

## Arguments

`object` [SpatialDDLs](#) or [DeconvDLModel](#) object to be saved

file	File path where the object will be saved
ascii	a logical. If TRUE or NA, an ASCII representation is written; otherwise (default), a binary one is used. See the comments in the help for <a href="#">save</a> .
version	the workspace format version to use. NULL specifies the current default version (3). The only other supported value is 2, the default from R 1.4.0 to R 3.5.0.
compress	a logical specifying whether saving to a named file is to use "gzip" compression, or one of "gzip", "bzip2" or "xz" to indicate the type of compression to be used. Ignored if file is a connection.
refhook	a hook function for handling reference objects.

**Value**

No return value, saves a [SpatialDDL](#)s object as an RDS file on disk.

**See Also**

[SpatialDDL](#)s [saveTrainedModelAsH5](#)

---

saveTrainedModelAsH5 *Save a trained [SpatialDDL](#)s deep neural network model to disk as an HDF5 file*

---

**Description**

Save a trained [SpatialDDL](#)s deep neural network model to disk as an HDF5 file. Note that this function does not save the [DeconvDLModel](#) object, only the trained **keras** model. This is the alternative to the [saveRDS](#) and [preparingToSave](#) functions if you want to keep the state of the optimizer.

**Usage**

```
saveTrainedModelAsH5(object, file.path, overwrite = FALSE)
```

**Arguments**

object	<a href="#">SpatialDDL</a> s object with trained.model slot.
file.path	Valid file path where to save the model to.
overwrite	Overwrite file if it already exists.

**Value**

No return value, saves a **keras** DNN trained model as HDF5 file on disk.

**See Also**

[trainDeconvModel](#) [loadTrainedModelFromH5](#)

---

set	<i>Get and set set slot in a <a href="#">PropCellTypes</a> object</i>
-----	---

---

**Description**

Get and set set slot in a [PropCellTypes](#) object

**Usage**

```
set(object)
```

```
set(object) <- value
```

**Arguments**

object            [PropCellTypes](#) object.

value            A vector containing the names of cells that are present in the object.

---

set.list	<i>Get and set set.list slot in a <a href="#">PropCellTypes</a> object</i>
----------	--

---

**Description**

Get and set set.list slot in a [PropCellTypes](#) object

**Usage**

```
set.list(object)
```

```
set.list(object) <- value
```

**Arguments**

object            [PropCellTypes](#) object.

value            List of cells sorted by their corresponding cell type.

---

showProbPlot	<i>Show distribution plots of the cell proportions generated by <a href="#">genMixedCellProp</a></i>
--------------	--

---

### Description

Show distribution plots of the cell proportions generated by the [genMixedCellProp](#) function.

### Usage

```
showProbPlot(object, type.data, set, type.plot = "boxplot")
```

### Arguments

object	<a href="#">SpatialDDLS</a> object with prob.cell.types slot with plot slot.
type.data	Subset of data to show: train or test.
set	Integer determining which of the 6 different subsets to display.
type.plot	Character determining which type of visualization to display. It can be 'boxplot', 'violinplot', 'linesplot' or 'ncelltypes'. See Description for more information.

### Details

These frequencies will determine the proportion of different cell types used during the simulation of mixed transcriptional profiles. Proportions generated by each method (see [?genMixedCellProp](#)) can be visualized in three ways: box plots, violin plots, and lines plots. You can also plot the probabilities based on the number of different cell types present in the samples by setting `type.plot = 'nCellTypes'`.

### Value

A ggplot object.

### See Also

[genMixedCellProp](#)

### Examples

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(100, lambda = 5), nrow = 40, ncol = 30,
      dimnames = list(paste0("Gene", seq(40)), paste0("RHC", seq(30)))
    )
  ),
  colData = data.frame(
```

```

    Cell_ID = paste0("RHC", seq(30)),
    Cell_Type = sample(x = paste0("CellType", seq(4)), size = 30,
                      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(40))
  )
)

SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 10,
  verbose = TRUE
)
showProbPlot(
  SDDLs,
  type.data = "train",
  set = 1,
  type.plot = "boxplot"
)

```

---

simMixedProfiles

*Simulate training and test mixed spot profiles*


---

## Description

Simulate training and test mixed spot transcriptional profiles using cell composition matrices generated by the [genMixedCellProp](#) function.

## Usage

```

simMixedProfiles(
  object,
  type.data = "both",
  mixing.function = "AddRowCount",
  file.backend = NULL,
  compression.level = NULL,
  block.processing = FALSE,
  block.size = 1000,
  chunk.dims = NULL,

```

```

    threads = 1,
    verbose = TRUE
)

```

## Arguments

object	<a href="#">SpatialDDL</a> S object with <code>single.cell.real/single.cell.simul</code> , and <code>prob.cell.types</code> slots.
type.data	Type of data to generate: 'train', 'test' or 'both' (the last by default).
mixing.function	Function used to build mixed transcriptional profiles. It may be: <ul style="list-style-type: none"> <li>• "AddRowCount": single-cell profiles (raw counts) are added up across cells. Then, log-CPMs are calculated (by default).</li> <li>• "MeanCPM": single-cell profiles (raw counts) are transformed into CPMs and cross-cell averages are calculated. Then, <math>\log_2(\text{CPM} + 1)</math> is calculated.</li> <li>• "AddCPM": single-cell profiles (raw counts) are transformed into CPMs and are added up across cells. Then, log-CPMs are calculated.</li> </ul>
file.backend	Valid file path to store simulated mixed expression profiles as an HDF5 file (NULL by default). If provided, data are stored in HDF5 files used as back-end by using the <b>DelayedArray</b> , <b>HDF5Array</b> and <b>rhdf5</b> packages instead of loading all data into RAM. Note that operations on this matrix will be performed in blocks (i.e subsets of determined size) which may result in longer execution times.
compression.level	The compression level used if <code>file.backend</code> is provided. It is an integer value between 0 (no compression) and 9 (highest and slowest compression). See <a href="#">?getHDF5DumpCompressionLevel</a> from the <b>HDF5Array</b> package for more information.
block.processing	Boolean indicating whether data should be simulated in blocks (only if <code>file.backend</code> is used, FALSE by default). This functionality is suitable for cases where it is not possible to load all data into memory, and it leads to longer execution times.
block.size	Only if <code>block.processing = TRUE</code> . Number of mixed expression profiles that will be simulated in each iteration. Larger numbers result in higher memory usage but shorter execution times. Set accordingly to available computational resources (1000 by default).
chunk.dims	Specifies the dimensions that HDF5 chunk will have. If NULL, the default value is a vector of two items: the number of genes considered by <a href="#">SpatialDDL</a> S object during the simulation, and a single sample to reduce read times in the following steps. A larger number of columns written in each chunk can lead to longer read times.
threads	Number of threads used during simulation (1 by default).
verbose	Show informative messages during the execution (TRUE by default).

## Details

Mixed profiles are generated under the assumption that the expression level of a particular gene in a given spot is the sum of the expression levels of the cell types that make it up weighted by their proportions. In practice, as described in Torroja and Sanchez-Cabo, 2019, these profiles are generated by summing gene expression levels of a determined number of cells specified by a known cell composition matrix. The number of simulated spots and cells used to simulate each spot are determined by the `genMixedCellProp` function. This step can be avoided by using the `on.the.fly` argument in the `trainDeconvModel` function.

**SpatialDDLs** allows to use HDF5 files as back-end to store simulated data using the **DelayedArray** and **HDF5Array** packages. This functionality allows to work without keeping the data loaded into RAM, which could be useful during some computationally heavy steps such as neural network training on RAM-limited machines. You must provide a valid file path in the `file.backend` argument to store the resulting file with the `.h5` extension. This option slows down execution times, as subsequent transformations of the data will be done in blocks. Note that if you use the `file.backend` argument with `block.processing = FALSE`, all mixed profiles will be simulated in one step and, thus, loaded into RAM. Then, the matrix will be written to an HDF5 file. To avoid the RAM collapse, these profiles can be simulated and written to HDF5 files in blocks of `block.size` size by setting `block.processing = TRUE`. We recommend this option accordingly to the computational resources available and the number of simulated spots to be generated, but, in most of the cases, it is not necessary.

## Value

A `SpatialDDLs` object with `mixed.profiles` slot containing a list with one or two entries (depending on selected `type.data` argument): `'train'` and `'test'`. Each entry consists of a `SummarizedExperiment` object with the simulated mixed slot profiles.

## References

- Fischer B, Smith M and Pau, G (2020). `rhdf5`: R Interface to HDF5. R package version 2.34.0.
- Pagès H, Hickey P and Lun A (2020). `DelayedArray`: A unified framework for working transparently with on-disk and in-memory array-like datasets. R package version 0.16.0.
- Pagès H (2020). `HDF5Array`: HDF5 backend for `DelayedArray` objects. R package version 1.18.0.

## See Also

[genMixedCellProp](#) [PropCellTypes](#) [trainDeconvModel](#)

## Examples

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(100, lambda = 5), nrow = 40, ncol = 30,
      dimnames = list(paste0("Gene", seq(40)), paste0("RHC", seq(30)))
    )
  ),
  colData = data.frame(
```

```

    Cell_ID = paste0("RHC", seq(30)),
    Cell_Type = sample(x = paste0("CellType", seq(4)), size = 30,
                      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(40))
  )
)

SDDLs <- createSpatialDDLSubject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
SDDLs <- genMixedCellProp(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  num.sim.spots = 10,
  verbose = TRUE
)
SDDLs <- simMixedProfiles(SDDLs, verbose = TRUE)

```

---

simSCProfiles

*Simulate new single-cell RNA-Seq expression profiles using the ZINB-WaVE model parameters*

---

## Description

Simulate single-cell expression profiles by randomly sampling from a negative binomial distribution and inserting dropouts by sampling from a binomial distribution using the ZINB-WaVE parameters estimated by the [estimateZinbwaveParams](#) function.

## Usage

```

simSCProfiles(
  object,
  cell.ID.column,
  cell.type.column,
  n.cells,
  suffix.names = "_Simul",
  cell.types = NULL,
  file.backend = NULL,
  name.dataset.backend = NULL,
  compression.level = NULL,
  block.processing = FALSE,
  block.size = 1000,

```

```

    chunk.dims = NULL,
    verbose = TRUE
)

```

## Arguments

<code>object</code>	<code>SpatialDDLs</code> object with <code>single.cell.real</code> and <code>zinb.params</code> slots.
<code>cell.ID.column</code>	Name or column number corresponding to the cell names of expression matrix in cells metadata.
<code>cell.type.column</code>	Name or column number corresponding to the cell type of each cell in cells metadata.
<code>n.cells</code>	Number of simulated cells generated per cell type (i.e. if you have 10 different cell types in your dataset, if <code>n.cells = 100</code> , then 1000 cell profiles will be simulated).
<code>suffix.names</code>	Suffix used on simulated cells. This suffix must be unique in the simulated cells, so make sure that this suffix does not appear in the real cell names.
<code>cell.types</code>	Vector indicating the cell types to simulate. If <code>NULL</code> (by default), <code>n.cells</code> single-cell profiles for all cell types will be simulated.
<code>file.backend</code>	Valid file path to store the simulated single-cell expression profiles as an HDF5 file ( <code>NULL</code> by default). If provided, the data are stored in HDF5 files used as back-end by using the <b>DelayedArray</b> , <b>HDF5Array</b> and <b>rhdf5</b> packages instead of loading all data into RAM memory. This is suitable for situations where you have large amounts of data that cannot be loaded into memory. Note that operations on this data will be performed in blocks (i.e subsets of determined size) which may result in longer execution times.
<code>name.dataset.backend</code>	Name of the dataset in HDF5 file to be used. Note that it cannot exist. If <code>NULL</code> (by default), a random dataset name will be used.
<code>compression.level</code>	The compression level used if <code>file.backend</code> is provided. It is an integer value between 0 (no compression) and 9 (highest and slowest compression). See <a href="#">?getHDF5DumpCompressionLevel</a> from the <b>HDF5Array</b> package for more information.
<code>block.processing</code>	Boolean indicating whether the data should be simulated in blocks (only if <code>file.backend</code> is used, <code>FALSE</code> by default). This functionality is suitable for cases where it is not possible to load all data into memory and it leads to larger execution times.
<code>block.size</code>	Only if <code>block.processing = TRUE</code> . Number of single-cell expression profiles that will be simulated in each iteration during the process. Larger numbers result in higher memory usage but shorter execution times. Set according to available computational resources (1000 by default). Note that it cannot be greater than the total number of simulated cells.
<code>chunk.dims</code>	Specifies the dimensions that HDF5 chunk will have. If <code>NULL</code> , the default value is a vector of two items: the number of genes considered by the ZINB-WaVE

model during the simulation and a single sample in order to reduce read times in the following steps. A larger number of columns written in each chunk can lead to longer read times in subsequent steps. Note that it cannot be greater than the dimensions of the simulated matrix.

verbose Show informative messages during the execution (TRUE by default).

## Details

Before this step, see [?estimateZinbwaveParams](#). As described in Torroja and Sanchez-Cabo, 2019, this function simulates a given number of transcriptional profiles for each cell type provided by randomly sampling from a negative binomial distribution with  $\mu$  and  $\theta$  estimated parameters and inserting dropouts by sampling from a binomial distribution with probability  $\pi$ . All parameters are estimated from single-cell real data using the [estimateZinbwaveParams](#) function. It uses the ZINB-WaVE model (Risso et al., 2018). For more details about the model, see [?estimateZinbwaveParams](#) and Risso et al., 2018.

The `file.backend` argument allows to create a HDF5 file with simulated single-cell profiles to be used as back-end to work with data stored on disk instead of loaded into RAM. If the `file.backend` argument is used with `block.processing = FALSE`, all the single-cell profiles will be simulated in one step and, therefore, loaded into in RAM memory. Then, data will be written in HDF5 file. To avoid to collapse RAM memory if too many single-cell profiles are goin to be simulated, single-cell profiles can be simulated and written to HDF5 files in blocks of `block.size` size by setting `block.processing = TRUE`.

## Value

A [SpatialDDLs](#) object with `single.cell.simul` slot containing a [SingleCellExperiment](#) object with the simulated single-cell expression profiles.

## References

- Risso, D., Perraudeau, F., Gribkova, S. et al. (2018). A general and flexible method for signal extraction from single-cell RNA-seq data. *Nat Commun* 9, 284. doi: [10.1038/s41467017-025545](https://doi.org/10.1038/s41467017-025545).
- Torroja, C. and Sánchez-Cabo, F. (2019). digitalDLsorter: A Deep Learning algorithm to quantify immune cell populations based on scRNA-Seq data. *Frontiers in Genetics* 10, 978. doi: [10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978).

## See Also

[estimateZinbwaveParams](#)

## Examples

```
set.seed(123) # reproducibility
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 10,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(10)))
    )
  )
)
```

```
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(10)),
    Cell_Type = sample(x = paste0("CellType", seq(2)), size = 10,
                      replace = TRUE)
  ),
  rowData = data.frame(
    Gene_ID = paste0("Gene", seq(15))
  )
)
SDDLs <- createSpatialDDLsObject(
  sc.data = sce,
  sc.cell.ID.column = "Cell_ID",
  sc.gene.ID.column = "Gene_ID",
  project = "Simul_example"
)
SDDLs <- estimateZinbwaveParams(
  object = SDDLs,
  cell.type.column = "Cell_Type",
  cell.ID.column = "Cell_ID",
  gene.ID.column = "Gene_ID",
  subset.cells = 2,
  verbose = TRUE
)
SDDLs <- simSCProfiles(
  object = SDDLs,
  cell.ID.column = "Cell_ID",
  cell.type.column = "Cell_Type",
  n.cells = 2,
  verbose = TRUE
)
```

---

single.cell.real

*Get and set single.cell.real slot in a [SpatialDDLs](#) object*

---

### **Description**

Get and set single.cell.real slot in a [SpatialDDLs](#) object

### **Usage**

```
single.cell.real(object)
```

```
single.cell.real(object) <- value
```

**Arguments**

object            [SpatialDDL](#)S object.  
value            [SingleCellExperiment](#) object with real single-cell profiles.

---

`single.cell.simul`      *Get and set `single.cell.simul` slot in a [SpatialDDL](#)S object*

---

**Description**

Get and set `single.cell.simul` slot in a [SpatialDDL](#)S object

**Usage**

```
single.cell.simul(object)

single.cell.simul(object) <- value
```

**Arguments**

object            [SpatialDDL](#)S object.  
value            [SingleCellExperiment](#) object with simulated single-cell profiles.

---

`spatial.experiments`    *Get and set `spatial.experiments` slot in a [SpatialDDL](#)S object*

---

**Description**

Get and set `spatial.experiments` slot in a [SpatialDDL](#)S object

**Usage**

```
spatial.experiments(object, index.st = NULL)

spatial.experiments(object, index.st = NULL) <- value
```

**Arguments**

object            [SpatialDDL](#)S object.  
index.st          Index of the spatial transcriptomics data within the list. It can be either an position or a name if a named list was provided. If NULL (by default), all data contained in the `spatial.experiments` slot are returned.  
value            List in which each element is a [SpatialExperiment](#) object. It can be a named list.

---

SpatialDDLS-class      *The SpatialDDLS Class*

---

## Description

The `SpatialDDL` object is the core of the **SpatialDDLS** package. This object stores different intermediate data needed for the construction of new deconvolution models, the spatial transcriptomics profiles to be deconvoluted, and the predicted cell type proportions.

## Details

This object uses other classes to store different types of data generated during the workflow:

- `SingleCellExperiment` class for single-cell RNA-Seq data storage, using sparse matrix from the **Matrix** package (`dgMatrix` class) or `HDF5Array` class in case of using HDF5 files as back-end (see below for more information).
- `SpatialExperiment` class for spatial transcriptomics data storage.
- `ZinbModel` class with estimated parameters for the simulation of new single-cell profiles.
- `SummarizedExperiment` class for simulated mixed transcriptional profiles storage.
- `PropCellTypes` class for compositional cell type matrices. See `?PropCellTypes` for details.
- `DeconvDLModel` class to store the information related to deep neural network models. See `?DeconvDLModel` for details.

In order to provide a way to work with large amounts of data on RAM-constrained machines, we provide the possibility to use HDF5 files as back-end to store count matrices of both real and simulated single-cell profiles by using the `HDF5Array` and `DelayedArray` classes from the homonymous packages.

## Slots

`single.cell.real` Real single-cell data stored in a `SingleCellExperiment` object. The count matrix is stored either as `dgMatrix` or `HDF5Array` objects.

`spatial.experiments` List of `SpatialExperiment` objects to be deconvoluted.

`zinb.params` `ZinbModel` object with estimated parameters for the simulation of new single-cell expression profiles.

`single.cell.simul` Simulated single-cell expression profiles using the ZINB-WaVE model.

`prob.cell.types` `PropCellTypes` class with cell composition matrices built for the simulation of mixed transcriptional profiles with known cell composition.

`mixed.profiles` List of simulated train and test mixed transcriptional profiles. Each entry is a `SummarizedExperiment` object. Count matrices can be stored as `HDF5Array` objects using HDF5 files as back-end in case of RAM limitations.

`trained.model` `DeconvDLModel` object with information related to the trained model. See `?DeconvDLModel` for more details.

deconv.spots Deconvolution results. It consists of a list where each element corresponds to the results for each `SpatialExperiment` object contained in the `spatial.experiments` slot.

project Name of the project.

version Version of **SpatialDDL**S this object was built under.

---

SpatialDDL-S-Rpackage *SpatialDDL: an R package to deconvolute spatial transcriptomics data using deep neural networks*

---

### Description

**SpatialDDL**S is an R package that provides a neural network-based solution for cell type deconvolution from spatial transcriptomics data. The package takes advantage of single-cell RNA sequencing (scRNA-seq) data to simulate mixed transcriptional profiles with known cell composition and train fully-connected neural networks to predict the cell type composition of spatial transcriptomics spots. The resulting trained models can be applied to new spatial transcriptomics data to predict cell type proportions, allowing for more accurate cell type identification and characterization of spatially-resolved transcriptomic data. Overall, **SpatialDDL**S is a powerful tool for cell type deconvolution in spatial transcriptomics data, providing a reliable, fast and flexible solution for researchers in the field. See Torroja and Sanchez-Cabo (2019) (doi: [10.3389/fgene.2019.00978](https://doi.org/10.3389/fgene.2019.00978)), and some examples (<https://diegomcc.github.io/SpatialDDL/>) for more details.

---

test.deconv.metrics *Get and set test.deconv.metrics slot in a `DeconvDLModel` object*

---

### Description

Get and set `test.deconv.metrics` slot in a `DeconvDLModel` object

### Usage

```
test.deconv.metrics(object, metrics = "All")

test.deconv.metrics(object, metrics = "All") <- value
```

### Arguments

object	<code>DeconvDLModel</code> object.
metrics	Metrics to show ('All' by default)
value	List with evaluation metrics to assess the performance of the model on each sample of test data.

---

test.metrics	<i>Get and set test.metrics slot in a <a href="#">DeconvDLModel</a> object</i>
--------------	--

---

**Description**

Get and set test.metrics slot in a [DeconvDLModel](#) object

**Usage**

```
test.metrics(object)
test.metrics(object) <- value
```

**Arguments**

object	<a href="#">DeconvDLModel</a> object.
value	List with evaluation metrics after prediction on test data.

---

test.pred	<i>Get and set test.pred slot in a <a href="#">DeconvDLModel</a> object</i>
-----------	---

---

**Description**

Get and set test.pred slot in a [DeconvDLModel](#) object

**Usage**

```
test.pred(object)
test.pred(object) <- value
```

**Arguments**

object	<a href="#">DeconvDLModel</a> object.
value	Matrix object with prediction results on test data.

---

trainDeconvModel	<i>Train deconvolution model for spatial transcriptomics data</i>
------------------	---

---

## Description

Train a deep neural network model using training data from the [SpatialDDLs](#) object. In addition, the trained model is evaluated using test data, and prediction results are obtained to determine its performance (see [?calculateEvalMetrics](#)).

## Usage

```
trainDeconvModel(
  object,
  type.data.train = "mixed",
  type.data.test = "mixed",
  batch.size = 64,
  num.epochs = 10,
  num.hidden.layers = 2,
  num.units = c(200, 200),
  activation.fun = "sigmoid",
  dropout.rate = 0.25,
  loss = "kullback_leibler_divergence",
  metrics = c("accuracy", "mean_absolute_error", "categorical_accuracy"),
  scaling = "rescale",
  norm.batch.layers = FALSE,
  custom.model = NULL,
  shuffle = FALSE,
  sc.downsampling = NULL,
  use.generator = FALSE,
  on.the.fly = FALSE,
  agg.function = "MeanCPM",
  threads = 1,
  view.metrics.plot = TRUE,
  verbose = TRUE
)
```

## Arguments

object	<a href="#">SpatialDDLs</a> object with <code>single.cell.real/single.cell.simul</code> , <code>prob.cell.types</code> , and <code>mixed.profiles</code> slots (the last only if <code>on.the.fly = FALSE</code> ).
type.data.train	Type of profiles used for training. It can be 'both', 'single-cell' or 'mixed' ('mixed' by default).
type.data.test	Type of profiles used for evaluation. It can be 'both', 'single-cell' or 'mixed' ('mixed' by default).
batch.size	Number of samples per gradient update (64 by default).

num.epochs	Number of epochs to train the model (10 by default).
num.hidden.layers	Number of hidden layers of the neural network (2 by default). This number must be equal to the length of num.units argument.
num.units	Vector indicating the number of neurons per hidden layer (c(200, 200) by default). The length of this vector must be equal to num.hidden.layers argument.
activation.fun	Activation function ('sigmoid' by default). See the <a href="#">keras documentation</a> to know available activation functions.
dropout.rate	Float between 0 and 1 indicating the fraction of the input neurons to be dropped in layer dropouts (0.25 by default). By default, <b>SpatialDDLs</b> implements 1 dropout layer per hidden layer.
loss	Character indicating loss function selected for model training ('kullback_leibler_divergence' by default). See the <a href="#">keras documentation</a> to know available loss functions.
metrics	Vector of metrics used to assess model performance during training and evaluation (c("accuracy", "mean_absolute_error", "categorical_accuracy") by default). See the <a href="#">keras documentation</a> to know available performance metrics.
scaling	How to scale data before training. It may be: "standardize" (values are centered around the mean with a unit standard deviation) or "rescale" (values are shifted and rescaled so that they end up ranging between 0 and 1, by default).
norm.batch.layers	Whether to include batch normalization layers between each hidden dense layer (FALSE by default).
custom.model	It allows to use a custom neural network. It must be a keras.engine.sequential.Sequential object in which the number of input neurons is equal to the number of considered features/genes, and the number of output neurons is equal to the number of cell types considered (NULL by default). If provided, the arguments related to the neural network architecture will be ignored.
shuffle	Boolean indicating whether data will be shuffled (TRUE by default).
sc.downsampling	It is only used if type.data.train is equal to 'both' or 'single-cell'. It allows to set a maximum number of single-cell profiles from a specific cell type used for training to avoid an unbalanced representation of cell types (NULL by default).
use.generator	Boolean indicating whether to use generators during training and test. Generators are automatically used when on.the.fly = TRUE or HDF5 files are used, but it can be activated by the user on demand (FALSE by default).
on.the.fly	Boolean indicating whether simulated data will be generated 'on the fly' during training (FALSE by default).
agg.function	Function used to build mixed transcriptional profiles. It may be: <ul style="list-style-type: none"> <li>"AddRowCount" (by default): single-cell profiles (raw counts) are added up across cells. Then, log-CPMs are calculated.</li> <li>"MeanCPM": single-cell profiles (raw counts) are transformed into CPMs and cross-cell averages are calculated. Then, <math>\log_2(\text{CPM} + 1)</math> is calculated.</li> </ul>

- "AddCPM": single-cell profiles (raw counts) are transformed into CPMs and are added up across cells. Then, log-CPMs are calculated.

threads	Number of threads used during simulation of mixed transcriptional profiles if <code>on.the.fly = TRUE</code> (1 by default).
view.metrics.plot	Boolean indicating whether to show plots of loss and evaluation metrics during training (TRUE by default). <b>keras</b> for R allows to see model progression during training if you are working in RStudio.
verbose	Boolean indicating whether to display model progression during training and model architecture information (TRUE by default).

## Details

### Simulation of mixed transcriptional profiles 'on the fly'

`trainDeconvModel` can avoid storing simulated mixed spot profiles by using the `on.the.fly` argument. This functionality aims at reducing the the `simMixedProfiles` function's memory usage: simulated profiles are built in each batch during training/evaluation.

### Neural network architecture

It is possible to change the model's architecture: number of hidden layers, number of neurons for each hidden layer, dropout rate, activation function, and loss function. For more customized models, it is possible to provide a pre-built model through the `custom.model` argument (a `keras.engine.sequential.Sequential` object) where it is necessary that the number of input neurons is equal to the number of considered features/genes, and the number of output neurons is equal to the number of considered cell types.

## Value

A `SpatialDDLs` object with `trained.model` slot containing a `DeconvDLModel` object. For more information about the structure of this class, see `?DeconvDLModel`.

## See Also

[plotTrainingHistory deconvSpatialDDLs](#)

## Examples

```
set.seed(123)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(
    counts = matrix(
      rpois(30, lambda = 5), nrow = 15, ncol = 10,
      dimnames = list(paste0("Gene", seq(15)), paste0("RHC", seq(10)))
    )
  ),
  colData = data.frame(
    Cell_ID = paste0("RHC", seq(10)),
    Cell_Type = sample(x = paste0("CellType", seq(2)), size = 10,
                      replace = TRUE)
  ),
)
```

```
    rowData = data.frame(
      Gene_ID = paste0("Gene", seq(15))
    )
  )
  SDDLs <- createSpatialDDLSubject(
    sc.data = sce,
    sc.cell.ID.column = "Cell_ID",
    sc.gene.ID.column = "Gene_ID",
  )
  SDDLs <- genMixedCellProp(
    object = SDDLs,
    cell.ID.column = "Cell_ID",
    cell.type.column = "Cell_Type",
    num.sim.spots = 50,
    verbose = TRUE
  )
  SDDLs <- simMixedProfiles(SDDLs)
  SDDLs <- trainDeconvModel(
    object = SDDLs,
    on.the.fly = TRUE,
    batch.size = 12,
    num.epochs = 5
  )
)
```

---

trained.model

Get and set trained.model slot in a [SpatialDDLs](#) object

---

## Description

Get and set trained.model slot in a [SpatialDDLs](#) object

## Usage

```
trained.model(object)
```

```
trained.model(object) <- value
```

## Arguments

object            [SpatialDDLs](#) object.

value            [DeconvDLModel](#) object.

---

training.history	<i>Get and set training.history slot in a <a href="#">DeconvDLModel</a> object</i>
------------------	--

---

**Description**

Get and set training.history slot in a [DeconvDLModel](#) object

**Usage**

```
training.history(object)

training.history(object) <- value
```

**Arguments**

object	<a href="#">DeconvDLModel</a> object.
value	keras_training_history object with the training history of the deep neural network model.

---

zinb.params	<i>Get and set zinb.params slot in a <a href="#">SpatialDDLS</a> object</i>
-------------	---

---

**Description**

Get and set zinb.params slot in a [SpatialDDLS](#) object

**Usage**

```
zinb.params(object)

zinb.params(object) <- value
```

**Arguments**

object	<a href="#">SpatialDDLS</a> object.
value	<a href="#">ZinbParametersModel</a> object with a valid <a href="#">ZinbModel</a> object.

---

ZinbParametersModel-class

*The Class ZinbParametersModel*

---

### Description

The ZinbParametersModel class is a wrapper class for the [ZinbModel](#) class from the **zinbwave** package.

### Details

This wrapper class contains the `zinbwave.model` slot, which holds a valid [ZinbModel](#) object.

### Slots

`zinbwave.model` A valid [ZinbModel](#) object.

### References

Risso, D., Perraudeau, F., Gribkova, S. et al. (2018). A general and flexible method for signal extraction from single-cell RNA-seq data. Nat Commun 9, 284. doi: [doi: 10.1038/s41467017-025545](https://doi.org/10.1038/s41467017-025545).

---

`zinbwave.model`

*Get and set `zinbwave.model` slot in a [ZinbParametersModel](#) object*

---

### Description

Get and set `zinbwave.model` slot in a [ZinbParametersModel](#) object

### Usage

```
zinbwave.model(object)
```

```
zinbwave.model(object) <- value
```

### Arguments

`object` [ZinbParametersModel](#) object.

`value` [ZinbModel](#) object with the estimated parameters to simulate new single-cell profiles.

# Index

barErrorPlot, [3](#), [7](#), [9](#), [11](#), [22](#)  
barPlotCellTypes, [5](#)  
blandAltmanLehPlot, [4](#), [6](#), [9](#), [11](#), [22](#)

calculateEvalMetrics, [4](#), [7](#), [8](#), [11](#), [17](#), [18](#),  
[22](#), [56](#)  
cell.names, [9](#)  
cell.names, PropCellTypes-method  
(cell.names), [9](#)  
cell.names<- (cell.names), [9](#)  
cell.names<- , PropCellTypes-method  
(cell.names), [9](#)  
cell.types, [10](#)  
cell.types, DeconvDLModel-method  
(cell.types), [10](#)  
cell.types<- (cell.types), [10](#)  
cell.types<- , DeconvDLModel-method  
(cell.types), [10](#)  
corrExpPredPlot, [4](#), [7](#), [9](#), [10](#), [22](#)  
createSpatialDDLSubject, [13](#), [19](#), [31](#), [32](#)

deconv.spots, [17](#)  
deconv.spots, SpatialDDLs-method  
(deconv.spots), [17](#)  
deconv.spots<- (deconv.spots), [17](#)  
deconv.spots<- , SpatialDDLs-method  
(deconv.spots), [17](#)  
DeconvDLModel, [3](#), [7](#), [9–11](#), [17](#), [21](#), [26](#), [33](#), [34](#),  
[37](#), [38](#), [41](#), [42](#), [53–55](#), [58–60](#)  
DeconvDLModel (DeconvDLModel-class), [17](#)  
DeconvDLModel-class, [17](#)  
deconvSpatialDDLs, [6](#), [18](#), [36](#), [37](#), [58](#)  
dgCMatrix, [53](#)  
distErrorPlot, [4](#), [7](#), [9](#), [11](#), [21](#)

estimateZinbwaveParams, [16](#), [23](#), [48](#), [50](#)

facet\_wrap, [11](#), [22](#)  
features, [26](#)  
features, DeconvDLModel-method  
(features), [26](#)  
features<- (features), [26](#)  
features<- , DeconvDLModel-method  
(features), [26](#)

genMixedCellProp, [16](#), [26](#), [29](#), [40](#), [44](#), [45](#), [47](#)  
getHDF5DumpCompressionLevel, [15](#), [46](#), [49](#)  
getProbMatrix, [29](#)

installTFpython, [30](#)

loadSTProfiles, [19](#), [31](#)  
loadTrainedModelFromH5, [33](#), [38](#), [41](#), [42](#)

method, [33](#)  
method, PropCellTypes-method (method), [33](#)  
method<- (method), [33](#)  
method<- , PropCellTypes-method (method),  
[33](#)  
mixed.profiles, [34](#)  
mixed.profiles, SpatialDDLs-method  
(mixed.profiles), [34](#)  
mixed.profiles<- (mixed.profiles), [34](#)  
mixed.profiles<- , SpatialDDLs-method  
(mixed.profiles), [34](#)  
model, [34](#)  
model, DeconvDLModel-method (model), [34](#)  
model<- (model), [34](#)  
model<- , DeconvDLModel-method (model), [34](#)

plots, [35](#)  
plots, PropCellTypes-method (plots), [35](#)  
plots<- (plots), [35](#)  
plots<- , PropCellTypes-method (plots), [35](#)  
plotSpatialProp, [35](#), [37](#)  
plotSpatialPropAll, [36](#), [36](#)  
plotTrainingHistory, [37](#), [58](#)  
preparingToSave, [17](#), [38](#), [42](#)  
prob.cell.types, [39](#)  
prob.cell.types, SpatialDDLs-method  
(prob.cell.types), [39](#)  
prob.cell.types<- (prob.cell.types), [39](#)

- prob.cell.types<- ,SpatialDDLs-method  
(prob.cell.types), 39
- prob.matrix, 39
- prob.matrix,PropCellTypes-method  
(prob.matrix), 39
- prob.matrix<- (prob.matrix), 39
- prob.matrix<- ,PropCellTypes-method  
(prob.matrix), 39
- project, 40
- project,SpatialDDLs-method (project), 40
- project<- (project), 40
- project<- ,SpatialDDLs-method (project),  
40
- PropCellTypes, 9, 26, 28, 33–35, 39, 40, 43,  
47, 53
- PropCellTypes (PropCellTypes-class), 40
- PropCellTypes-class, 40
  
- save, 42
- saveRDS, 38, 41, 42
- saveRDS,DeconvDLModel-method (saveRDS),  
41
- saveRDS,saveRDS-method (saveRDS), 41
- saveRDS,SpatialDDLs-method (saveRDS), 41
- saveTrainedModelAsH5, 17, 33, 38, 41, 42, 42
- set, 43
- set,PropCellTypes-method (set), 43
- set.list, 43
- set.list,PropCellTypes-method  
(set.list), 43
- set.list<- (set.list), 43
- set.list<- ,PropCellTypes-method  
(set.list), 43
- set<- (set), 43
- set<- ,PropCellTypes-method (set), 43
- showProbPlot, 28, 40, 44
- simMixedProfiles, 26, 28, 45
- simSCProfiles, 24, 25, 48
- single.cell.real, 51
- single.cell.real,SpatialDDLs-method  
(single.cell.real), 51
- single.cell.real<- (single.cell.real),  
51
- single.cell.real<- ,SpatialDDLs-method  
(single.cell.real), 51
- single.cell.simul, 52
- single.cell.simul,SpatialDDLs-method  
(single.cell.simul), 52
  
- single.cell.simul<-  
(single.cell.simul), 52
- single.cell.simul<- ,SpatialDDLs-method  
(single.cell.simul), 52
- SingleCellExperiment, 13, 15, 16, 50, 52, 53
- spatial.experiments, 52
- spatial.experiments,SpatialDDLs-method  
(spatial.experiments), 52
- spatial.experiments<-  
(spatial.experiments), 52
- spatial.experiments<- ,SpatialDDLs-method  
(spatial.experiments), 52
- SpatialDDLs, 3, 5, 7, 9, 11, 13, 15–19, 21, 24,  
25, 27–29, 31–34, 36–42, 44, 46, 47,  
49–53, 56, 58–60
- SpatialDDLs (SpatialDDLs-class), 53
- SpatialDDLs-class, 53
- SpatialDDLs-Rpackage, 54
- SpatialExperiment, 14, 15, 31, 52–54
- SummarizedExperiment, 34, 47, 53
  
- test.deconv.metrics, 54
- test.deconv.metrics,DeconvDLModel-method  
(test.deconv.metrics), 54
- test.deconv.metrics<-  
(test.deconv.metrics), 54
- test.deconv.metrics<- ,DeconvDLModel-method  
(test.deconv.metrics), 54
- test.metrics, 55
- test.metrics,DeconvDLModel-method  
(test.metrics), 55
- test.metrics<- (test.metrics), 55
- test.metrics<- ,DeconvDLModel-method  
(test.metrics), 55
- test.pred, 55
- test.pred,DeconvDLModel-method  
(test.pred), 55
- test.pred<- (test.pred), 55
- test.pred<- ,DeconvDLModel-method  
(test.pred), 55
- trainDeconvModel, 19, 26, 32, 33, 36–38, 42,  
47, 56
- trained.model, 19, 59
- trained.model,SpatialDDLs-method  
(trained.model), 59
- trained.model<- (trained.model), 59
- trained.model<- ,SpatialDDLs-method  
(trained.model), 59
- training.history, 60

training.history,DeconvDLModel-method  
    (training.history), [60](#)  
training.history<- (training.history),  
    [60](#)  
training.history<- ,DeconvDLModel-method  
    (training.history), [60](#)

zinb.params, [60](#)  
zinb.params,SpatialDDLs-method  
    (zinb.params), [60](#)  
zinb.params<- (zinb.params), [60](#)  
zinb.params<- ,SpatialDDLs-method  
    (zinb.params), [60](#)  
zinbFit, [25](#)  
ZinbModel, [53](#), [60](#), [61](#)  
ZinbParametersModel, [25](#), [60](#), [61](#)  
ZinbParametersModel  
    (ZinbParametersModel-class), [61](#)  
ZinbParametersModel-class, [61](#)  
zinbwave.model, [61](#)  
zinbwave.model,ZinbParametersModel-method  
    (zinbwave.model), [61](#)  
zinbwave.model<- (zinbwave.model), [61](#)  
zinbwave.model<- ,ZinbParametersModel-method  
    (zinbwave.model), [61](#)