

# Package ‘singleCellTK’

May 15, 2022

**Type** Package

**Title** Comprehensive and Interactive Analysis of Single Cell RNA-Seq Data

**Version** 2.7.0

**Depends** R (>= 4.0), SummarizedExperiment, SingleCellExperiment, DelayedArray, Biobase

**Description** The Single Cell Toolkit (SCTK) in the singleCellTK package provides an interface to popular tools for importing, quality control, analysis, and visualization of single cell RNA-seq data. SCTK allows users to seamlessly integrate tools from various packages at different stages of the analysis workflow. A general “a la carte” workflow gives users the ability access to multiple methods for data importing, calculation of general QC metrics, doublet detection, ambient RNA estimation and removal, filtering, normalization, batch correction or integration, dimensionality reduction, 2-D embedding, clustering, marker detection, differential expression, cell type labeling, pathway analysis, and data exporting. Curated workflows can be used to run Seurat and Celda. Streamlined quality control can be performed on the command line using the SCTK-QC pipeline. Users can analyze their data using commands in the R console or by using an interactive Shiny Graphical User Interface (GUI). Specific analyses or entire workflows can be summarized and shared with comprehensive HTML reports generated by Rmarkdown. Additional documentation and vignettes can be found at [camplab.net/sctk](http://camplab.net/sctk).

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** SingleCell, GeneExpression, DifferentialExpression, Alignment, Clustering, ImmunoOncology, BatchEffect, Normalization, QualityControl, DataImport, GUI

**LazyData** FALSE

**Imports** ape, batchelor, BiocParallel, celldex, colourpicker, colorspace, cowplot, cluster, ComplexHeatmap, data.table, DelayedMatrixStats, DESeq2, dplyr, DT, ExperimentHub, fields, ggplot2, ggplotify, ggrepel, ggtree, gridExtra, GSVA (>= 1.26.0), GSVAdata, igraph, KernSmooth, limma, MAST, Matrix, matrixStats, methods, msigdb, multtest, plotly, plyr, ROCR, Rtsne, S4Vectors, scater, scMerge (>= 1.2.0), scan, Seurat (>=

3.1.3), shiny, shinyjs, SingleR, SoupX, sva, reshape2, shinyalert, circlize, enrichR, celda, shinycssloaders, DropletUtils, scds ( $\geq 1.2.0$ ), reticulate ( $\geq 1.14$ ), tools, tximport, fishpond, withr, GSEABase, R.utils, zinbwave, scRNAseq ( $\geq 2.0.2$ ), TENxPBMCDData, yaml, rmarkdown, magrittr, scDbfFinder, metap, VAM ( $\geq 0.5.3$ ), tibble, rlang, TSCAN, TrajectoryUtils, generics, scuttle, utils, stats

### **RoxygenNote** 7.1.2

**Suggests** testthat, Rsubread, BiocStyle, knitr, lintr, spelling, org.Mm.eg.db, stringr, kableExtra, shinythemes, shinyBS, shinyjqui, shinyWidgets, shinyFiles, BiocGenerics, RColorBrewer, fastmap ( $\geq 1.1.0$ )

**VignetteBuilder** knitr

**URL** <https://www.camplab.net/sctk/>

**BugReports** <https://github.com/compbiomed/singleCellTK/issues>

**Language** en-US

**git\_url** <https://git.bioconductor.org/packages/singleCellTK>

**git\_branch** master

**git\_last\_commit** 289be130

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-05-15

**Author** Yichen Wang [aut, cre] (<<https://orcid.org/0000-0003-4347-5199>>), Irzam Sarfraz [aut] (<<https://orcid.org/0000-0001-8121-792X>>), Rui Hong [aut], Yusuke Koga [aut], Salam Alabdullatif [aut], David Jenkins [aut] (<<https://orcid.org/0000-0002-7451-4288>>), Vidya Akavoor [aut], Xinyun Cao [aut], Shruthi Bandyadka [aut], Anastasia Leshchuk [aut], Tyler Faits [aut], Mohammed Muzamil Khan [aut], Zhe Wang [aut], W. Evan Johnson [aut] (<<https://orcid.org/0000-0002-6247-6595>>), Joshua David Campbell [aut]

**Maintainer** Yichen Wang <wangych@bu.edu>

## **R topics documented:**

.addSeuratToMetaDataSCE . . . . .	7
.checkDiffExpResultExists . . . . .	8
.computeSignificantPC . . . . .	9

.extractSCEAnnotation . . . . .	9
.formatDEAList . . . . .	10
.getComponentNames . . . . .	11
.ggBar . . . . .	12
.ggDensity . . . . .	13
.ggScatter . . . . .	14
.ggViolin . . . . .	16
.sce2adata . . . . .	18
.seuratGetVariableFeatures . . . . .	19
.seuratInvalidate . . . . .	20
.updateAssaySCE . . . . .	21
calcEffectSizes . . . . .	21
combineSCE . . . . .	22
computeHeatmap . . . . .	23
computeZScore . . . . .	24
constructSCE . . . . .	25
convertSCEToSeurat . . . . .	25
convertSeuratToSCE . . . . .	26
dataAnnotationColor . . . . .	27
dedupRowNames . . . . .	28
detectCellOutlier . . . . .	29
diffAbundanceFET . . . . .	30
discreteColorPalette . . . . .	31
distinctColors . . . . .	32
downSampleCells . . . . .	32
downSampleDepth . . . . .	34
expData . . . . .	35
expData,ANY,character-method . . . . .	36
expData<- . . . . .	36
expData<-,ANY,character,CharacterOrNullOrMissing,logical-method . . . . .	37
expDataNames . . . . .	38
expDataNames,ANY-method . . . . .	38
expDeleteDataTag . . . . .	39
exportSCE . . . . .	40
exportSCEtoAnnData . . . . .	41
exportSCEtoFlatFile . . . . .	42
exportSCEtoSeurat . . . . .	43
expSetDataTag . . . . .	44
expTaggedData . . . . .	44
featureIndex . . . . .	45
findMarkerDiffExp . . . . .	47
findMarkerTopTable . . . . .	48
generateHTANMeta . . . . .	49
generateMeta . . . . .	50
generateSimulatedData . . . . .	51
getBiomarker . . . . .	51
getDEGTopTable . . . . .	52
getDiffAbundanceResults . . . . .	54

getEnrichRResult<-	55
getGenesetNamesFromCollection	56
getMSigDBTable	56
getPathwayResultNames	57
getSampleSummaryStatsTable	57
getSceParams	58
getSeuratVariableFeatures	59
getSoupX<-	59
getTopHVG	60
getTSCANResults	62
getTSNE	62
getUMAP	64
importAlevin	65
importAnnData	66
importBUStools	68
importCellRanger	69
importCellRangerV2Sample	73
importCellRangerV3Sample	74
importDropEst	75
importExampleData	76
importFromFiles	77
importGeneSetsFromCollection	79
importGeneSetsFromGMT	80
importGeneSetsFromList	82
importGeneSetsFromMSigDB	83
importMitoGeneSet	85
importMultipleSources	86
importOptimus	87
importSEQC	88
importSTARsolo	90
iterateSimulations	92
listSampleSummaryStatsTables	93
mergeSCEColData	94
MitoGenes	95
mouseBrainSubsetSCE	95
msigdb_table	96
plotBarcodeRankDropsResults	96
plotBarcodeRankScatter	97
plotBatchCorrCompare	99
plotBatchVariance	100
plotBcdeResults	101
plotClusterAbundance	104
plotClusterPseudo	105
plotCxdsResults	106
plotDecontXResults	108
plotDEGHeatmap	111
plotDEGRegression	113
plotDEGViolin	115

plotDEGVolcano . . . . .	116
plotDimRed . . . . .	117
plotDoubletFinderResults . . . . .	118
plotEmptyDropsResults . . . . .	120
plotEmptyDropsScatter . . . . .	122
plotMarkerDiffExp . . . . .	124
plotMASTThresholdGenes . . . . .	127
plotPathway . . . . .	128
plotPCA . . . . .	129
plotRunPerCellQCResults . . . . .	130
plotScDbfFinderResults . . . . .	132
plotScdsHybridResults . . . . .	135
plotSCEBarAssayData . . . . .	138
plotSCEBarColData . . . . .	139
plotSCEBatchFeatureMean . . . . .	141
plotSCEDensity . . . . .	142
plotSCEDensityAssayData . . . . .	143
plotSCEDensityColData . . . . .	145
plotSCEDimReduceColData . . . . .	147
plotSCEDimReduceFeatures . . . . .	149
plotSCEHeatmap . . . . .	152
plotSCEScatter . . . . .	155
plotSCEViolin . . . . .	158
plotSCEViolinAssayData . . . . .	160
plotSCEViolinColData . . . . .	163
plotScrubletResults . . . . .	165
plotSeuratElbow . . . . .	168
plotSeuratGenes . . . . .	169
plotSeuratHeatmap . . . . .	170
plotSeuratHVG . . . . .	170
plotSeuratJackStraw . . . . .	171
plotSeuratReduction . . . . .	172
plotSoupXResults . . . . .	173
plotTopHVG . . . . .	175
plotTSCANDEgenes . . . . .	176
plotTSCANPseudotimeGenes . . . . .	177
plotTSCANPseudotimeHeatmap . . . . .	178
plotTSCANResults . . . . .	179
plotTSNE . . . . .	180
plotUMAP . . . . .	181
qcInputProcess . . . . .	182
readSingleCellMatrix . . . . .	183
reportCellQC . . . . .	184
reportClusterAbundance . . . . .	185
reportDiffAbundanceFET . . . . .	186
reportDiffExp . . . . .	187
reportDropletQC . . . . .	187
reportFindMarker . . . . .	188

reportQCTool . . . . .	189
reportSeurat . . . . .	190
reportSeuratClustering . . . . .	192
reportSeuratDimRed . . . . .	194
reportSeuratFeatureSelection . . . . .	195
reportSeuratMarkerSelection . . . . .	196
reportSeuratNormalization . . . . .	198
reportSeuratResults . . . . .	199
reportSeuratRun . . . . .	200
reportSeuratScaling . . . . .	203
retrieveSCEIndex . . . . .	204
runBarcodeRankDrops . . . . .	205
runBBKNN . . . . .	206
runBcbs . . . . .	207
runCellQC . . . . .	208
runComBatSeq . . . . .	210
runCxls . . . . .	211
runCxlsBcbsHybrid . . . . .	212
runDEAnalysis . . . . .	214
runDecontX . . . . .	218
runDimReduce . . . . .	220
runDoubletFinder . . . . .	222
runDropletQC . . . . .	223
runEmptyDrops . . . . .	224
runEnrichR . . . . .	225
runFastMNN . . . . .	226
runFeatureSelection . . . . .	227
runGSVA . . . . .	228
runKMeans . . . . .	229
runLimmaBC . . . . .	230
runMNNCorrect . . . . .	231
runNormalization . . . . .	232
runPerCellQC . . . . .	234
runSCANORAMA . . . . .	237
runScDblFinder . . . . .	238
runSCMerge . . . . .	239
runScranSNN . . . . .	240
runScrublet . . . . .	242
runSeuratFindClusters . . . . .	244
runSeuratFindHVG . . . . .	246
runSeuratFindMarkers . . . . .	247
runSeuratHeatmap . . . . .	248
runSeuratICA . . . . .	249
runSeuratIntegration . . . . .	250
runSeuratJackStraw . . . . .	251
runSeuratNormalizeData . . . . .	252
runSeuratPCA . . . . .	253
runSeuratScaleData . . . . .	254

runSeuratSCTransform . . . . . 255

runSeuratTSNE . . . . . 256

runSeuratUMAP . . . . . 257

runSingleR . . . . . 258

runSoupX . . . . . 259

runTSCAN . . . . . 262

runTSCANClusterDEAnalysis . . . . . 263

runTSCANDEG . . . . . 264

runVAM . . . . . 265

runZINBWave . . . . . 266

sampleSummaryStats . . . . . 268

scaterCPM . . . . . 269

scaterlogNormCounts . . . . . 269

scaterPCA . . . . . 270

sce . . . . . 271

sceBatches . . . . . 272

scrnModelGeneVar . . . . . 272

sctkListGeneSetCollections . . . . . 273

sctkPythonInstallConda . . . . . 274

sctkPythonInstallVirtualEnv . . . . . 275

SEG . . . . . 276

selectSCTKConda . . . . . 277

selectSCTKVirtualEnvironment . . . . . 278

setRowNames . . . . . 279

setSampleSummaryStatsTable<- . . . . . 279

setSCTKDisplayRow . . . . . 280

simpleLog . . . . . 281

singleCellTK . . . . . 281

subDiffEx . . . . . 282

subsetSCECols . . . . . 283

subsetSCERows . . . . . 284

summarizeSCE . . . . . 286

trimCounts . . . . . 287

**Index** **288**

---

.addSeuratToMetaDataSCE

*.addSeuratToMetaDataSCE Adds the input seurat object to the meta-  
data slot of the input sce object (after removing the data matrices)*

---

**Description**

.addSeuratToMetaDataSCE Adds the input seurat object to the metadata slot of the input sce object (after removing the data matrices)

**Usage**

```
.addSeuratToMetaDataSCE(inSCE, seuratObject)
```

**Arguments**

inSCE	(sce) object to which seurat object should be added in the metadata slot (copy to)
seuratObject	seurat object which should be added to the metadata slot of sce object (copy from)

**Value**

Updated SingleCellExperiment object which now contains the seurat object in its metadata slot (excluding data matrices)

---

```
.checkDiffExpResultExists
```

*Check if the specified MAST result in SingleCellExperiment object is complete. But does not guarantee the biological correctness.*

---

**Description**

Check if the specified MAST result in SingleCellExperiment object is complete. But does not guarantee the biological correctness.

**Usage**

```
.checkDiffExpResultExists(inSCE, useResult, labelBy = NULL)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. a differential expression analysis function has to be run in advance.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
labelBy	A single character for a column of rowData(inSCE) as where to search for the labeling text. Default NULL.

**Value**

Stop point if found



---

`.computeSignificantPC` *.computeSignificantPC* Computes the significant principal components from an input sce object (must contain pca slot) using stdev

---

### Description

`.computeSignificantPC` Computes the significant principal components from an input sce object (must contain pca slot) using stdev

### Usage

```
.computeSignificantPC(inSCE)
```

### Arguments

inSCE (sce) object with pca computed

### Value

A numerical value indicating how many number of components are considered significant

---

`.extractSCEAnnotation` *Extract columns from row/colData and transfer to factors*

---

### Description

Extract columns from row/colData and transfer to factors

### Usage

```
.extractSCEAnnotation(inSCE, axis = NULL, columns = NULL, index = NULL)
```

### Arguments

inSCE [SingleCellExperiment](#) inherited object.  
axis Choose from "col" or "row".  
columns character vector. The columns needed to be extracted. If NULL, will return an empty data.frame with matched row names. Default NULL.  
index Valid index to subset the col/row.

### Value

A data.frame object.

---

.formatDEAList	<i>Helper function for differential expression analysis methods that accepts multiple ways of conditional subsetting and returns stable index format. Meanwhile it does all the input checkings.</i>
----------------	--

---

## Description

Helper function for differential expression analysis methods that accepts multiple ways of conditional subsetting and returns stable index format. Meanwhile it does all the input checkings.

## Usage

```
.formatDEAList(
  inSCE,
  useAssay,
  useReducedDim,
  index1 = NULL,
  index2 = NULL,
  class = NULL,
  classGroup1 = NULL,
  classGroup2 = NULL,
  groupName1,
  groupName2,
  analysisName,
  covariates = NULL,
  overwrite = FALSE
)
```

## Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	character. A string specifying which assay to use. Required.
useReducedDim	character. A string specifying which reducedDim to use for DE analysis. Usually a pathway analysis result matrix. Set useAssay to NULL when using. Required.
index1	Any type of indices that can subset a <a href="#">SingleCellExperiment</a> inherited object by cells. Specifies which cells are of interests. Default NULL.
index2	Any type of indices that can subset a <a href="#">SingleCellExperiment</a> inherited object by cells. specifies the control group against those specified by index1. If NULL when using index specification, index1 cells will be compared with all other cells. Default NULL.
class	A vector/factor with ncol(inSCE) elements, or a character scalar that specifies a column name of colData(inSCE). Default NULL.
classGroup1	a vector specifying which "levels" given in class are of interests. Default NULL.

<code>classGroup2</code>	a vector specifying which "levels" given in <code>class</code> is the control group against those specified by <code>classGroup1</code> . If NULL when using annotation specification, <code>classGroup1</code> cells will be compared with all other cells.
<code>groupName1</code>	A character scalar naming the group of interests. Required.
<code>groupName2</code>	A character scalar naming the control group. Required.
<code>analysisName</code>	A character scalar naming the DEG analysis. Required
<code>covariates</code>	A character vector of additional covariates used in linear regression methods such as Limma and DESeq2. Default NULL
<code>overwrite</code>	A logical scalar. Whether to overwrite result if exists. Default FALSE.

**Value**

A list object with part of formatted DE analysis information

**Author(s)**

Yichen Wang

---

`.getComponentNames` *.getComponentNames* Creates a list of PC/IC components to populate the picker for PC/IC heatmap generation

---

**Description**

`.getComponentNames` Creates a list of PC/IC components to populate the picker for PC/IC heatmap generation

**Usage**

```
.getComponentNames(maxComponents, component = c("PC", "IC"))
```

**Arguments**

`maxComponents` Number of components to return for the picker  
`component` Which component to use. Choices are PC or IC.

**Value**

List of component names (appended with PC or IC)

---

 .ggBar

*Bar plot plotting tool.*


---

### Description

Visualizes specified values via a violin plot.

### Usage

```
.ggBar(
  y,
  groupBy = NULL,
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
  axisLabelSize = 10,
  dotSize = 0.5,
  transparency = 1,
  defaultTheme = TRUE,
  gridLine = FALSE,
  summary = NULL,
  title = NULL,
  titleSize = 15
)
```

### Arguments

y	Numeric values to be plotted on y-axis.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.

**Value**

a ggplot of the reduced dimensions.

---

.ggDensity	<i>Density plot plotting tool.</i>
------------	------------------------------------

---

**Description**

Visualizes values stored in the specified slot of a SingleCellExperiment object via a density plot.

**Usage**

```
.ggDensity(  
  value,  
  groupBy = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  baseSize = 12,  
  axisSize = NULL,  
  axisLabelSize = NULL,  
  defaultTheme = TRUE,  
  title = NULL,  
  titleSize = NULL,  
  combinePlot = "none",  
  cutoff = NULL  
)
```

**Arguments**

- value            Numeric value that will be plotted via density plot.
- groupBy        Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
- xlab            Character vector. Label for x-axis. Default NULL.
- ylab            Character vector. Label for y-axis. Default NULL.
- baseSize        The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize.
- axisSize        Size of x/y-axis ticks. Default NULL.
- axisLabelSize   Size of x/y-axis labels. Default NULL.
- defaultTheme   Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
- title           Title of plot. Default NULL.
- titleSize       Size of title of plot. Default 15.

combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
cutoff	Numeric value. The plot will be annotated with a vertical line if set. Default NULL.

**Value**

density plot, in .ggplot.

---

*.ggScatter*

*Plot results of reduced dimensions data.*

---

**Description**

Plot results of reduced dimensions data and colors the plots by the input vector.

**Usage**

```
.ggScatter(
  inSCE,
  reducedDimName,
  sample = NULL,
  colorBy = NULL,
  groupBy = NULL,
  shape = NULL,
  conditionClass = NULL,
  labelClusters = FALSE,
  clusterLabelSize = 3.5,
  xlab = NULL,
  ylab = NULL,
  baseSize = 12,
  axisSize = NULL,
  axisLabelSize = NULL,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
  binLabel = NULL,
  dotSize = 0.5,
  transparency = 1,
  colorScale = NULL,
  colorLow = "white",
  colorMid = "gray",
  colorHigh = "blue",
  defaultTheme = TRUE,
  title = NULL,
  titleSize = NULL,
```

```
    legendTitle = NULL,  
    legendTitleSize = NULL,  
    legendSize = NULL,  
    combinePlot = "none",  
    plotLabels = NULL  
  )
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
sample	Character vector. Indicates which sample each cell belongs to.
colorBy	If provided, colors dots in the scatterplot based on value.
groupBy	If provided, facet wrap the scatterplot based on value.
shape	If provided, add shapes based on the value.
conditionClass	class of the annotation data used in colorBy. Options are NULL, "factor" or "numeric". If NULL, class will default to the original class. Default NULL.
labelClusters	Logical. Whether the cluster labels are plotted. Default FALSE.
clusterLabelSize	Numeric. Determines the size of cluster label when 'labelClusters' is set to TRUE. Default 3.5.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
axisSize	Size of x/y-axis ticks. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
colorScale	Vector. Needs to be same length as the number of unique levels of 'colorBy'. Will be used only if conditionClass = "factor" or "character". Default NULL.

colorLow	Character. A color available from 'colors()'. The color will be used to signify the lowest values on the scale. Default 'white'. Will be used only if conditionClass = "numeric".
colorMid	Character. A color available from 'colors()'. The color will be used to signify the midpoint on the scale. Default 'gray'. Will be used only if conditionClass = "numeric".
colorHigh	Character. A color available from 'colors()'. The color will be used to signify the highest values on the scale. Default 'blue'. Will be used only if conditionClass = "numeric".
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
legendTitle	title of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
legendSize	size of legend. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the reduced dimensions.

---

`.ggViolin`

*Violin plot plotting tool.*

---

**Description**

Visualizes specified values via a violin plot.

**Usage**

```
.ggViolin(
  y,
  groupBy = NULL,
  violin = TRUE,
  boxplot = TRUE,
  dots = TRUE,
  plotOrder = NULL,
  xlab = NULL,
  ylab = NULL,
```



```
baseSize = 12,  
axisSize = NULL,  
axisLabelSize = NULL,  
dotSize = 0.5,  
transparency = 1,  
defaultTheme = TRUE,  
gridLine = FALSE,  
summary = NULL,  
summaryTextSize = 3,  
combinePlot = "none",  
title = NULL,  
titleSize = NULL,  
hcutoff = NULL,  
hcolor = "red",  
hsize = 1,  
hlinetype = 1,  
vcutoff = NULL,  
vcolor = "red",  
vsize = 1,  
vlinetype = 1  
)
```

### Arguments

y	Numeric values to be plotted on y-axis.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
plotOrder	Character vector. If set, reorders the violin plots in the order of the character vector when 'groupBy' is set. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize.
axisSize	Size of x/y-axis ticks. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.

summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
hcutoff	Adds a horizontal line with the y-intercept at given value. Default NULL.
hcolor	Character. A color available from 'colors()'. Controls the color of the horizontal cutoff line, if drawn. Default 'black'.
hsize	Size of horizontal line, if drawn. Default 0.5.
hlinetype	Type of horizontal line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
vcutoff	Adds a vertical line with the x-intercept at given value. Default NULL.
vcolor	Character. A color available from 'colors()'. Controls the color of the vertical cutoff line, if drawn. Default 'black'.
vsize	Size of vertical line, if drawn. Default 0.5.
vlinetype	Type of vertical line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.

**Value**

a ggplot of the reduced dimensions.

---

.sce2adata	<i>Coverts SingleCellExperiment object from R to anndata.AnnData object in Python</i>
------------	---

---

**Description**

The AnnData object here can be saved to .h5ad file and read into Python interactive console. Mostly used senario is when you want to apply reticulated Python function, which only works with an anndata.AnnData object.

**Usage**

```
.sce2adata(SCE, useAssay = "counts")
```

### Arguments

SCE	A SingleCellExperiment object.
useAssay	Character, default "counts". The name of assay of interests that will be set as the primary matrix of the output AnnData. Available options can be listed by 'assayNames(SCE)'. The primary matrix will be saved in 'adata\$X', Other assays will be stored in 'adata\$obsm' together with the low-dimension representations (for now).

### Value

A Python anndata.AnnData object

---

.seuratGetVariableFeatures  
*.seuratGetVariableFeatures Retrieves the requested number of variable feature names*

---

### Description

.seuratGetVariableFeatures Retrieves the requested number of variable feature names

### Usage

```
.seuratGetVariableFeatures(inSCE, numberOfFeatures)
```

### Arguments

inSCE	(sce) object from which to extract the variable feature names
numberOfFeatures	numerical value indicating how many feature names should be retrieved (default is 100)

### Value

list() of variable feature names

---

<code>.seuratInvalidate</code>	<i>.seuratInvalidate Removes seurat data from the input SingleCellExperiment object specified by the task in the Seurat workflow.</i>
--------------------------------	---

---

### Description

`.seuratInvalidate` Removes seurat data from the input `SingleCellExperiment` object specified by the task in the Seurat workflow.

### Usage

```
.seuratInvalidate(  
  inSCE,  
  scaleData = TRUE,  
  varFeatures = TRUE,  
  PCA = TRUE,  
  ICA = TRUE,  
  tSNE = TRUE,  
  UMAP = TRUE,  
  clusters = TRUE  
)
```

### Arguments

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object to remove Seurat data from.
<code>scaleData</code>	Remove scaled data from seurat. Default TRUE.
<code>varFeatures</code>	Remove variable features from seurat. Default TRUE.
<code>PCA</code>	Remove PCA from seurat. Default TRUE.
<code>ICA</code>	Remove ICA from seurat. Default TRUE.
<code>tSNE</code>	Remove tSNE from seurat. Default TRUE.
<code>UMAP</code>	Remove UMAP from seurat. Default TRUE.
<code>clusters</code>	Remove clusters from seurat. Default TRUE.

### Value

Updated `SingleCellExperiment` object containing the Seurat object in the metadata slot with the data removed

---

.updateAssaySCE	<i>.updateAssaySCE Update/Modify/Add an assay in the provided SingleCellExperiment object from a Seurat object</i>
-----------------	--

---

### Description

.updateAssaySCE Update/Modify/Add an assay in the provided SingleCellExperiment object from a Seurat object

### Usage

```
.updateAssaySCE(  
  inSCE,  
  seuratObject,  
  assaySlotSCE,  
  seuratDataSlot = "counts",  
  seuratAssaySlot = "RNA"  
)
```

### Arguments

inSCE	Input SingleCellExperiment object
seuratObject	Input Seurat object
assaySlotSCE	Selected assay to update in the input SingleCellExperiment object
seuratDataSlot	Selected data slot from the Seurat object. Default "counts".
seuratAssaySlot	Selected assay from Seurat object. Default "RNA".

### Value

A [SingleCellExperiment](#) object with data from Seurat object appended to the [assay](#) slot.

---

calcEffectSizes	<i>Finds the effect sizes for all genes in the original dataset, regardless of significance.</i>
-----------------	--

---

### Description

Finds the effect sizes for all genes in the original dataset, regardless of significance.

### Usage

```
calcEffectSizes(countMatrix, condition)
```

**Arguments**

countMatrix	Matrix. A simulated counts matrix, sans labels.
condition	Factor. The condition labels for the simulated cells. If more than 2 conditions are given, the first will be compared to all others by default.

**Value**

A vector of cohen's d effect sizes for each gene.

**Examples**

```
data("mouseBrainSubsetSCE")
res <- calcEffectSizes(assay(mouseBrainSubsetSCE, "counts"),
                      condition = colData(mouseBrainSubsetSCE)$level1class)
```

---

combineSCE	<i>Combine a list of SingleCellExperiment objects as one SingleCellExperiment object</i>
------------	--

---

**Description**

Combine a list of SingleCellExperiment objects as one SingleCellExperiment object

**Usage**

```
combineSCE(sceList, by.r = NULL, by.c = NULL, combined = TRUE)
```

**Arguments**

sceList	A list contains <a href="#">SingleCellExperiment</a> objects. Currently, combineSCE function only support combining SCE objects with assay in dgCMatrx format. It does not support combining SCE with assay in delayedArray format.
by.r	Specifications of the columns used for merging rowData. If set as NULL, the rownames of rowData tables will be used to merging rowData. Default is NULL.
by.c	Specifications of the columns used for merging colData. If set as NULL, the rownames of colData tables will be used to merging colData. Default is NULL.
combined	logical; if TRUE, it will combine the list of SingleCellExperiment objects and return a SingleCellExperiment. If FALSE, it will return a list of SingleCellExperiment whose rowData, colData, assay and reducedDim data slot are compatible within SCE objects in the list. Default is TRUE.

**Value**

A [SingleCellExperiment](#) object which combines all objects in sceList. The colData is merged.

**Examples**

```
data(scExample, package = "singleCellTK")
combinedsce <- combineSCE(list(sce,sce), by.r = NULL, by.c = NULL, combined = TRUE)
```

---

computeHeatmap	<i>computeHeatmap</i> The <i>computeHeatmap</i> method computes the heatmap visualization for a set of features against a set of dimensionality reduction components. This method uses the heatmap computation algorithm code from Seurat but plots the heatmap using ComplexHeatmap and cowplot libraries.
----------------	---

---

**Description**

computeHeatmap The computeHeatmap method computes the heatmap visualization for a set of features against a set of dimensionality reduction components. This method uses the heatmap computation algorithm code from Seurat but plots the heatmap using ComplexHeatmap and cowplot libraries.

**Usage**

```
computeHeatmap(
  inSCE,
  useAssay,
  dims = 10,
  nfeatures = 30,
  cells = NULL,
  reduction = "pca",
  disp.min = -2.5,
  disp.max = 2.5,
  balanced = TRUE,
  nCol = NULL,
  externalReduction = NULL
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	The assay to use for heatmap computation.
dims	Specify the number of dimensions to use for heatmap. Default 10.
nfeatures	Specify the number of features to use for heatmap. Default is 30.
cells	Specify the samples/cells to use for heatmap computation. Default is NULL which will utilize all samples in the assay.
reduction	Specify the reduction slot in the input object. Default is "pca".
disp.min	Specify the minimum dispersion value to use for floor clipping of assay values. Default is -2.5.

disp.max	Specify the maximum dispersion value to use for ceiling clipping of assay values. Default is 2.5.
balanced	Specify if the number of up-regulated and down-regulated features should be balanced. Default is TRUE.
nCol	Specify the number of columns in the output plot. Default is NULL which will auto-compute the number of columns.
externalReduction	Specify an external reduction if not present in the input object. This external reduction should be created using CreateDimReducObject function.

**Value**

Heatmap plot object.

---

computeZScore	<i>Compute Z-Score</i>
---------------	------------------------

---

**Description**

Computes Z-Score from an input count matrix using the formula  $((x - \text{mean}(x)) / \text{sd}(x))$  for each gene across all cells. The input count matrix can either be a base matrix, dgCMatrix or a DelayedMatrix. Computations are performed using DelayedMatrixStats package to efficiently compute the Z-Score matrix.

**Usage**

```
computeZScore(counts)
```

**Arguments**

counts            matrix (base matrix, dgCMatrix or DelayedMatrix)

**Value**

z-score computed counts matrix (DelayedMatrix)

**Examples**

```
data(sce_chc1, package = "scds")
assay(sce_chc1, "countsZScore") <- computeZScore(assay(sce_chc1, "counts"))
```



---

constructSCE	<i>Create SingleCellExperiment object from csv or txt input</i>
--------------	---

---

**Description**

Create SingleCellExperiment object from csv or txt input

**Usage**

```
constructSCE(data, samplename)
```

**Arguments**

data	A <a href="#">data.table</a> object containing the count matrix.
samplename	The sample name of the data.

**Value**

A [SingleCellExperiment](#) object containing the count matrix.

---

convertSCEToSeurat	<i>convertSCEToSeurat Converts sce object to seurat while retaining all assays and metadata</i>
--------------------	---

---

**Description**

convertSCEToSeurat Converts sce object to seurat while retaining all assays and metadata

**Usage**

```
convertSCEToSeurat(  
  inSCE,  
  countsAssay = NULL,  
  normAssay = NULL,  
  scaledAssay = NULL,  
  copyColData = FALSE,  
  copyReducedDim = FALSE,  
  copyDecontX = FALSE,  
  pcaReducedDim = NULL,  
  icaReducedDim = NULL,  
  tsneReducedDim = NULL,  
  umapReducedDim = NULL  
)
```

**Arguments**

inSCE	A SingleCellExperiment object to convert to a Seurat object.
countsAssay	Which assay to use from sce object for raw counts. Default NULL.
normAssay	Which assay to use from sce object for normalized data. Default NULL.
scaledAssay	Which assay to use from sce object for scaled data. Default NULL.
copyColData	Boolean. Whether copy 'colData' of SCE object to the 'meta.data' of Seurat object. Default FALSE.
copyReducedDim	Boolean. Whether copy 'reducedDims' of the SCE object to the 'reductions' of Seurat object. Default FALSE.
copyDecontX	Boolean. Whether copy 'decontXcounts' assay of the SCE object to the 'assays' of Seurat object. Default TRUE.
pcaReducedDim	Specify a character value indicating the name of the reducedDim to store as default pca computation in the output seurat object. Default is NULL which will not store any reducedDim as the default pca. This will only work when copyReducedDim parameter is set to TRUE.
icaReducedDim	Specify a character value indicating the name of the reducedDim to store as default ica computation in the output seurat object. Default is NULL which will not store any reducedDim as the default ica. This will only work when copyReducedDim parameter is set to TRUE.
tsneReducedDim	Specify a character value indicating the name of the reducedDim to store as default tsne computation in the output seurat object. Default is NULL which will not store any reducedDim as the default tsne. This will only work when copyReducedDim parameter is set to TRUE.
umapReducedDim	Specify a character value indicating the name of the reducedDim to store as default umap computation in the output seurat object. Default is NULL which will not store any reducedDim as the default umap. This will only work when copyReducedDim parameter is set to TRUE.

**Value**

Updated seurat object that contains all data from the input sce object

**Examples**

```
data(scExample, package = "singleCellTK")
seurat <- convertSCEToSeurat(sce)
```

---

convertSeuratToSCE      *convertSeuratToSCE Converts the input seurat object to a sce object*

---

**Description**

convertSeuratToSCE Converts the input seurat object to a sce object

**Usage**

```
convertSeuratToSCE(
  seuratObject,
  normAssayName = "seuratNormData",
  scaledAssayName = "seuratScaledData"
)
```

**Arguments**

seuratObject    Input Seurat object

normAssayName    Name of assay to store the normalized data. Default "seuratNormData".

scaledAssayName    Name of assay to store the scaled data. Default "seuratScaledData".

**Value**

SingleCellExperiment output object

**Examples**

```
data(scExample, package = "singleCellTK")
seurat <- convertSCEToSeurat(sce)
sce <- convertSeuratToSCE(seurat)
```

---

dataAnnotationColor    *Generate distinct colors for all categorical col/rowData entries. Character columns will be considered as well as all-integer columns. Any column with all-distinct values will be excluded.*

---

**Description**

Generate distinct colors for all categorical col/rowData entries. Character columns will be considered as well as all-integer columns. Any column with all-distinct values will be excluded.

**Usage**

```
dataAnnotationColor(inSCE, axis = NULL, colorGen = distinctColors)
```

**Arguments**

inSCE                [SingleCellExperiment](#) inherited object.

axis                 Choose from "col" or "row".

colorGen             A function that generates color code vector by giving an integer for the number of colors. Alternatively, [rainbow](#). Default [distinctColors](#).

**Value**

A list object containing distinct colors mapped to all possible categorical entries in `rowData(inSCE)` or `colData(inSCE)`.

**Author(s)**

Yichen Wang

---

dedupRowNames	<i>Deduplicate the rownames of a matrix or SingleCellExperiment object. Adds '-1', '-2', ... '-i' to multiple duplicated rownames, and in place replace the unique rownames, store unique rownames in rowData, or return the unique rownames as character vector.</i>
---------------	---

---

**Description**

Deduplicate the rownames of a matrix or SingleCellExperiment object. Adds '-1', '-2', ... '-i' to multiple duplicated rownames, and in place replace the unique rownames, store unique rownames in `rowData`, or return the unique rownames as character vector.

**Usage**

```
dedupRowNames(x, as.rowData = FALSE, return.list = FALSE)
```

**Arguments**

<code>x</code>	A matrix like or <code>/linkS4classSingleCellExperiment</code> object, on which we can apply <code>rownames()</code> to and has duplicated rownames.
<code>as.rowData</code>	Only applicable when <code>x</code> is a <code>/linkS4classSingleCellExperiment</code> object. When set to <code>TRUE</code> , will insert a new column called <code>"rownames.uniq"</code> to <code>rowData(x)</code> , with the deduplicated rownames.
<code>return.list</code>	When set to <code>TRUE</code> , will return a character vector of the deduplicated rownames.

**Value**

By default, a matrix or `/linkS4classSingleCellExperiment` object with rownames deduplicated. When `x` is a `/linkS4classSingleCellExperiment` and `as.rowData` is set to `TRUE`, will return `x` with `rowData` updated. When `return.list` is set to `TRUE`, will return a character vector with the deduplicated rownames.

**Examples**

```
data("scExample", package = "singleCellTK")
sce <- dedupRowNames(sce)
```

---

detectCellOutlier      *Detecting outliers within the SingleCellExperiment object.*

---

### Description

A wrapper function for [isOutlier](#). Identify outliers from numeric vectors stored in the SingleCellExperiment object.

### Usage

```
detectCellOutlier(  
  inSCE,  
  slotName,  
  itemName,  
  sample = NULL,  
  nmads = 3,  
  type = "both",  
  overwrite = TRUE  
)
```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
slotName	Desired slot of SingleCellExperiment used for plotting. Possible options: "assays", "colData", "metadata", "reducedDims". Required.
itemName	Desired vector within the slot used for plotting. Required.
sample	A single character specifying a name that can be found in colData(inSCE) to directly use the cell annotation; or a character vector with as many elements as cells to indicate which sample each cell belongs to. Default NULL. <a href="#">decontX</a> will be run on cells from each sample separately.
nmads	Integer. Number of median absolute deviation. Parameter may be adjusted for more lenient or stringent outlier cutoff. Default 3.
type	Character. Type/direction of outlier detection; whether the lower/higher outliers should be detected, or both. Options are "both", "lower", "higher".
overwrite	Boolean. If TRUE, and this function has previously generated an outlier decision on the same itemName, the outlier decision will be overwritten. Default TRUE.

### Value

A [SingleCellExperiment](#) object with " " added to the [colData](#) slot. Additionally, the decontaminated counts will be added as an assay called 'decontXCounts'.

## Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- runDecontX(sce[,sample(ncol(sce),20)])
sce <- detectCellOutlier(sce, slotName = "colData", sample = sce$sample,
  nmads = 4, itemName = "decontX_contamination", type = "both")
```

---

diffAbundanceFET	<i>Calculate Differential Abundance with FET</i>
------------------	--

---

## Description

Calculate Differential Abundance with FET

## Usage

```
diffAbundanceFET(inSCE, cluster, variable, control, case, analysisName)
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
cluster	A single character, specifying the name to store the cluster label in <a href="#">colData</a> .
variable	A single character, specifying the name to store the phenotype labels in <a href="#">colData</a> .
control	character. Specifying one or more categories that can be found in the vector specified by <a href="#">variable</a> .
case	character. Specifying one or more categories that can be found in the vector specified by <a href="#">variable</a> .
analysisName	A single character. Will be used for naming the result table, which will be saved in metadata slot.

## Details

This function will calculate the cell counting and fraction by dividing all cells to groups specified by the arguments, together with statistical summary by performing Fisher Exact Tests (FET).

## Value

The original [SingleCellExperiment](#) object with `metadata(inSCE)` updated with a list `diffAbundanceFET`, containing a new `data.frame` for the analysis result, named by `analysisName`. The `data.frame` contains columns for number and fraction of cells that belong to different cases, as well as "Odds\_Ratio", "PValue" and "FDR".

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- diffAbundanceFET(inSCE = mouseBrainSubsetSCE,
                                       cluster = "tissue",
                                       variable = "level1class",
                                       case = "oligodendrocytes",
                                       control = "microglia",
                                       analysisName = "diffAbundFET")
```

---

discreteColorPalette *Generate given number of color codes*

---

**Description**

Three different generation methods are wrapped, including `distinctColors`, `[randomcoloR](SCTK_PerformingQC_Cell_V` and the ggplot default color generation.

**Usage**

```
discreteColorPalette(
  n,
  palette = c("random", "ggplot", "celda"),
  seed = 12345,
  ...
)
```

**Arguments**

<code>n</code>	An integer, the number of color codes to generate.
<code>palette</code>	A single character string. Select the method, available options are "ggplot", "celda" and "random". Default "random".
<code>seed</code>	An integer. Set the seed for random process that happens only in "random" generation. Default 12345.
<code>...</code>	Other arguments that are passed to the internal function, according to the method selected.

**Value**

A character vector of n hex color codes.

**Examples**

```
discreteColorPalette(n = 3)
```

---

distinctColors	<i>Generate a distinct palette for coloring different clusters</i>
----------------	--

---

**Description**

Generate a distinct palette for coloring different clusters

**Usage**

```
distinctColors(
  n,
  hues = c("red", "cyan", "orange", "blue", "yellow", "purple", "green", "magenta"),
  saturation.range = c(0.7, 1),
  value.range = c(0.7, 1)
)
```

**Arguments**

n	Integer; Number of colors to generate
hues	Character vector of R colors available from the colors() function. These will be used as the base colors for the clustering scheme. Different saturations and values (i.e. darkness) will be generated for each hue.
saturation.range	Numeric vector of length 2 with values between 0 and 1. Default: c(0.25, 1)
value.range	Numeric vector of length 2 with values between 0 and 1. Default: c(0.5, 1)

**Value**

A vector of distinct colors that have been converted to HEX from HSV.

**Examples**

```
distinctColors(10)
```

---

downSampleCells	<i>Estimate numbers of detected genes, significantly differentially expressed genes, and median significant effect size</i>
-----------------	---

---

**Description**

Estimate numbers of detected genes, significantly differentially expressed genes, and median significant effect size



**Usage**

```
downSampleCells(
  originalData,
  useAssay = "counts",
  minCountDetec = 10,
  minCellsDetec = 3,
  minCellnum = 10,
  maxCellnum = 1000,
  realLabels,
  depthResolution = 10,
  iterations = 10,
  totalReads = 1e+06
)
```

**Arguments**

originalData	The <a href="#">SingleCellExperiment</a> object storing all assay data from the shiny app.
useAssay	Character. The name of the assay to be used for subsampling.
minCountDetec	Numeric. The minimum number of reads found for a gene to be considered detected.
minCellsDetec	Numeric. The minimum number of cells a gene must have at least 1 read in for it to be considered detected.
minCellnum	Numeric. The minimum number of virtual cells to include in the smallest simulated dataset.
maxCellnum	Numeric. The maximum number of virtual cells to include in the largest simulated dataset.
realLabels	Character. The name of the condition of interest. Must match a name from sample data. If only two factors present in the corresponding colData, will default to t-test. If multiple factors, will default to ANOVA.
depthResolution	Numeric. How many different read depth should the script simulate? Will simulate a number of experimental designs ranging from 10 reads to maxReadDepth, with logarithmic spacing.
iterations	Numeric. How many times should each experimental design be simulated?
totalReads	Numeric. How many aligned reads to put in each simulated dataset.

**Value**

A 3-dimensional array, with dimensions = c(iterations, depthResolution, 3). [,1] contains the number of detected genes in each simulated dataset, [,2] contains the number of significantly differentially expressed genes in each simulation, and [,3] contains the median significant effect size in each simulation. If no genes are significantly differentially expressed, the median effect size defaults to infinity.

**Examples**

```
data("mouseBrainSubsetSCE")
subset <- mouseBrainSubsetSCE[seq(100),]
res <- downSampleCells(subset,
                        realLabels = "level1class",
                        iterations=2)
```

---

downSampleDepth	<i>Estimate numbers of detected genes, significantly differentially expressed genes, and median significant effect size</i>
-----------------	---

---

**Description**

Estimate numbers of detected genes, significantly differentially expressed genes, and median significant effect size

**Usage**

```
downSampleDepth(
  originalData,
  useAssay = "counts",
  minCount = 10,
  minCells = 3,
  maxDepth = 1e+07,
  realLabels,
  depthResolution = 10,
  iterations = 10
)
```

**Arguments**

originalData	<a href="#">SingleCellExperiment</a> object storing all assay data from the shiny app.
useAssay	Character. The name of the assay to be used for subsampling.
minCount	Numeric. The minimum number of reads found for a gene to be considered detected.
minCells	Numeric. The minimum number of cells a gene must have at least 1 read in for it to be considered detected.
maxDepth	Numeric. The highest number of total reads to be simulated.
realLabels	Character. The name of the condition of interest. Must match a name from sample data.
depthResolution	Numeric. How many different read depth should the script simulate? Will simulate a number of experimental designs ranging from 10 reads to maxReadDepth, with logarithmic spacing.
iterations	Numeric. How many times should each experimental design be simulated?

**Value**

A 3-dimensional array, with dimensions = c(iterations, depthResolution, 3). [,1] contains the number of detected genes in each simulated dataset, [,2] contains the number of significantly differentially expressed genes in each simulation, and [,3] contains the mediansignificant effect size in each simulation. If no genes are significantly differentially expressed, the median effect size defaults to infinity.

**Examples**

```
data("mouseBrainSubsetSCE")
subset <- mouseBrainSubsetSCE[seq(1000),]
res <- downSampleDepth(subset,
                       realLabels = "level1class",
                       iterations=2)
```

---

expData	<i>expData</i> Get data item from an input SingleCellExperiment object. The data item can be an assay, altExp (subset) or a reducedDim, which is retrieved based on the name of the data item.
---------	--

---

**Description**

expData Get data item from an input SingleCellExperiment object. The data item can be an assay, altExp (subset) or a reducedDim, which is retrieved based on the name of the data item.

**Usage**

```
expData(inSCE, assayName)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
assayName	Specify the name of the data item to retrieve.

**Value**

Specified data item.

**Examples**

```
data(scExample, package = "singleCellTK")
mat <- expData(sce, "counts")
```

---

expData,ANY,character-method

*expData* Get data item from an input SingleCellExperiment object. The data item can be an assay, altExp (subset) or a reducedDim, which is retrieved based on the name of the data item.

---

### Description

expData Get data item from an input SingleCellExperiment object. The data item can be an assay, altExp (subset) or a reducedDim, which is retrieved based on the name of the data item.

### Usage

```
## S4 method for signature 'ANY,character'
expData(inSCE, assayName)
```

### Arguments

inSCE            Input SingleCellExperiment object.  
 assayName        Specify the name of the data item to retrieve.

### Value

Specified data item.

### Examples

```
data(scExample, package = "singleCellTK")
mat <- expData(sce, "counts")
```

---

expData<-

*expData* Store data items using tags to identify the type of data item stored. To be used as a replacement for assay<- setter function but with additional parameter to set a tag to a data item.

---

### Description

expData Store data items using tags to identify the type of data item stored. To be used as a replacement for assay<- setter function but with additional parameter to set a tag to a data item.

### Usage

```
expData(inSCE, assayName, tag = NULL, altExp = FALSE) <- value
```

**Arguments**

inSCE	Input SingleCellExperiment object.
assayName	Specify the name of the input assay.
tag	Specify the tag to store against the input assay. Default is NULL, which will set the tag to "uncategorized".
altExp	A logical value indicating if the input assay is a altExp or a subset assay.
value	An input matrix-like value to store in the SCE object.

**Value**

A SingleCellExperiment object containing the newly stored data.

**Examples**

```
data(scExample, package = "singleCellTK")
mat <- expData(sce, "counts")
expData(sce, "counts", tag = "raw") <- mat
```

---

expData<-,ANY,character,CharacterOrNullOrMissing,logical-method

*expData Store data items using tags to identify the type of data item stored. To be used as a replacement for assay<- setter function but with additional parameter to set a tag to a data item.*

---

**Description**

expData Store data items using tags to identify the type of data item stored. To be used as a replacement for assay<- setter function but with additional parameter to set a tag to a data item.

**Usage**

```
## S4 replacement method for signature 'ANY,character,CharacterOrNullOrMissing,logical'
expData(inSCE, assayName, tag = NULL, altExp = FALSE) <- value
```

**Arguments**

inSCE	Input SingleCellExperiment object.
assayName	Specify the name of the input assay.
tag	Specify the tag to store against the input assay. Default is NULL, which will set the tag to "uncategorized".
altExp	A logical value indicating if the input assay is a altExp or a subset assay.
value	An input matrix-like value to store in the SCE object.

**Value**

A SingleCellExperiment object containing the newly stored data.

**Examples**

```
data(scExample, package = "singleCellTK")
mat <- expData(sce, "counts")
expData(sce, "counts", tag = "raw") <- mat
```

---

expDataNames	<i>expDataNames</i> Get names of all the data items in the input SingleCellExperiment object including assays, altExps and reducedDims.
--------------	---

---

**Description**

expDataNames Get names of all the data items in the input SingleCellExperiment object including assays, altExps and reducedDims.

**Usage**

```
expDataNames(inSCE)
```

**Arguments**

inSCE            Input SingleCellExperiment object.

**Value**

A combined vector of assayNames, altExpNames and reducedDimNames.

**Examples**

```
data(scExample, package = "singleCellTK")
expDataNames(sce)
```

---

expDataNames,ANY-method	<i>expDataNames</i> Get names of all the data items in the input SingleCellExperiment object including assays, altExps and reducedDims.
-------------------------	---

---

**Description**

expDataNames Get names of all the data items in the input SingleCellExperiment object including assays, altExps and reducedDims.

**Usage**

```
## S4 method for signature 'ANY'
expDataNames(inSCE)
```

**Arguments**

inSCE            Input SingleCellExperiment object.

**Value**

A combined vector of assayNames, altExpNames and reducedDimNames.

**Examples**

```
data(scExample, package = "singleCellTK")
expDataNames(sce)
```

---

expDeleteDataTag	<i>expDeleteDataTag Remove tag against an input data from the stored tag information in the metadata of the input object.</i>
------------------	---

---

**Description**

expDeleteDataTag Remove tag against an input data from the stored tag information in the metadata of the input object.

**Usage**

```
expDeleteDataTag(inSCE, assay)
```

**Arguments**

inSCE            Input SingleCellExperiment object.  
assay            Name of the assay or the data item against which a tag should be removed.

**Value**

The input SingleCellExperiment object with tag information removed from the metadata slot.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- expSetDataTag(sce, "raw", "counts")
sce <- expDeleteDataTag(sce, "counts")
```

---

`exportSCE`*Export data in SingleCellExperiment object*

---

## Description

Export data in SingleCellExperiment object

## Usage

```
exportSCE(  
  inSCE,  
  samplename = "sample",  
  directory = "./",  
  type = "Cells",  
  format = c("SCE", "AnnData", "FlatFile", "HTAN", "Seurat")  
)
```

## Arguments

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object that contains the data. QC metrics are stored in <code>colData</code> of the <code>singleCellExperiment</code> object.
<code>samplename</code>	Sample name. This will be used as name of subdirectories and the prefix of flat file output. Default is 'sample'.
<code>directory</code>	Output directory. Default is './'.
<code>type</code>	Type of data. The type of data stored in <code>SingleCellExperiment</code> object. It can be 'Droplets'(raw droplets matrix) or 'Cells' (cells matrix).
<code>format</code>	The format of output. It currently supports flat files, rds files and python h5 files. It can output multiple formats. Default: <code>c("SCE", "AnnData", "FlatFile", "HTAN")</code> .

## Value

Generates a file containing data from `inSCE`, in specified format.

## Examples

```
data(scExample)  
## Not run:  
exportSCE(sce, format = "SCE")  
  
## End(Not run)
```



---

exportSCEtoAnnData      *Export a [SingleCellExperiment](#) R object as Python `annData` object*

---

### Description

Writes all assays, colData, rowData, reducedDims, and altExps objects in a [SingleCellExperiment](#) to a Python `annData` object in the `.h5ad` format. All parameters of `AnnData.write_h5ad` function ([https://icb-anndata.readthedocs-hosted.com/en/stable/anndata.AnnData.write\\_h5ad.html](https://icb-anndata.readthedocs-hosted.com/en/stable/anndata.AnnData.write_h5ad.html)) are available as parameters to this export function and set to defaults. Defaults can be overridden at function call.

### Usage

```
exportSCEtoAnnData(
  sce,
  useAssay = "counts",
  outputDir = "./",
  prefix = "sample",
  overwrite = TRUE,
  compression = c("gzip", "lzf", "None"),
  compressionOpts = NULL,
  forceDense = FALSE
)
```

### Arguments

<code>sce</code>	<a href="#">SingleCellExperiment</a> R object to be exported.
<code>useAssay</code>	Character. The name of assay of interests that will be set as the primary matrix of the output <code>AnnData</code> . Default "counts".
<code>outputDir</code>	Path to the directory where <code>.h5ad</code> outputs will be written. Default is the current working directory.
<code>prefix</code>	Prefix to use for the name of the output file. Default "sample".
<code>overwrite</code>	Boolean. Default TRUE.
<code>compression</code>	If output file compression is required, this variable accepts 'gzip', 'lzf' or "None" as inputs. Default "gzip".
<code>compressionOpts</code>	Integer. Sets the compression level
<code>forceDense</code>	Default False Write sparse data as a dense matrix. Refer <code>anndata.write_h5ad</code> documentation for details. Default NULL.

### Value

Generates a Python `annData` object containing data from `inSCE`.

**Examples**

```
data(sce_chcl, package = "scds")
## Not run:
exportSCEtoAnnData(sce=sce_chcl, compression="gzip")

## End(Not run)
```

---

exportSCEtoFlatFile    *Export a [SingleCellExperiment](#) object to flat text files*

---

**Description**

Writes all assays, colData, rowData, reducedDims, and altExps objects in a [SingleCellExperiment](#) to text files. The items in the 'metadata' slot remain stored in list and are saved in an RDS file.

**Usage**

```
exportSCEtoFlatFile(
  sce,
  outputDir = "./",
  overwrite = TRUE,
  gzipped = TRUE,
  prefix = "SCE"
)
```

**Arguments**

sce	<a href="#">SingleCellExperiment</a> object to be exported.
outputDir	Name of the directory to store the exported file(s).
overwrite	Boolean. Whether to overwrite the output files. Default TRUE.
gzipped	Boolean. TRUE if the output files are to be gzip compressed. FALSE otherwise. Default TRUE.
prefix	Prefix of file names.

**Value**

Generates text files containing data from inSCE.

**Examples**

```
data(sce_chcl, package = "scds")
## Not run:
exportSCEtoFlatFile(sce_chcl, "sce_chcl")

## End(Not run)
```

---

exportSCEToSeurat	<i>Export data in Seurat object</i>
-------------------	-------------------------------------

---

## Description

Export data in Seurat object

## Usage

```
exportSCEToSeurat(  
  inSCE,  
  prefix = "sample",  
  outputDir = "./",  
  overwrite = TRUE,  
  copyColData = TRUE,  
  copyReducedDim = TRUE,  
  copyDecontX = TRUE  
)
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object that contains the data. QC metrics are stored in colData of the singleCellExperiment object.
prefix	Prefix to use for the name of the output file. Default "sample".
outputDir	Path to the directory where outputs will be written. Default is the current working directory.
overwrite	Boolean. Whether overwrite the output if it already exists in the outputDir. Default TRUE.
copyColData	Boolean. Whether copy 'colData' of SCE object to the 'meta.data' of Seurat object. Default TRUE.
copyReducedDim	Boolean. Whether copy 'reducedDims' of the SCE object to the 'reductions' of Seurat object. Default TRUE.
copyDecontX	Boolean. Whether copy 'decontXcounts' assay of the SCE object to the 'assays' of Seurat object. Default TRUE.

## Value

Generates a Seurat object containing data from inSCE.

---

expSetDataTag	<i>expSetDataTag</i> Set tag to an assay or a data item in the input SCE object.
---------------	--

---

**Description**

expSetDataTag Set tag to an assay or a data item in the input SCE object.

**Usage**

```
expSetDataTag(inSCE, assayType, assays)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
assayType	Specify a character(1) value as a tag that should be set against a data item.
assays	Specify name(s) character() of data item(s) against which the tag should be set.

**Value**

The input SingleCellExperiment object with tag information stored in the metadata slot.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- expSetDataTag(sce, "raw", "counts")
```

---

expTaggedData	<i>expTaggedData</i> Returns a list of names of data items from the input SingleCellExperiment object based upon the input parameters.
---------------	--

---

**Description**

expTaggedData Returns a list of names of data items from the input SingleCellExperiment object based upon the input parameters.

**Usage**

```
expTaggedData(
  inSCE,
  tags = NULL,
  redDims = FALSE,
  recommended = NULL,
  showTags = TRUE
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
tags	A character() value indicating if the data items should be returned separated by the specified tags. Default is NULL indicating that returned names of the data items are simply returned as a list with default tag as "uncategorized".
redDims	A logical value indicating if reducedDims should be returned as well separated with 'redDims' tag.
recommended	A character() vector indicating the tags that should be displayed as recommended. Default is NULL.
showTags	A logical value indicating if the tags should be shown. If FALSE, output is just a simple list, not separated by tags.

**Value**

A list of names of data items specified by the other parameters.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- expSetDataTag(sce, "raw", "counts")
tags <- expTaggedData(sce)
```

---

featureIndex	<i>Retrieve row index for a set of features</i>
--------------	---

---

**Description**

This will return indices of features among the rownames or rowData of a data.frame, matrix, or a [SummarizedExperiment](#) object including a [SingleCellExperiment](#). Partial matching (i.e. grepping) can be used by setting exactMatch = FALSE.

**Usage**

```
featureIndex(
  features,
  inSCE,
  by = "rownames",
  exactMatch = TRUE,
  removeNA = FALSE,
  errorOnNoMatch = TRUE,
  warningOnPartialMatch = TRUE
)
```

**Arguments**

features	Character vector of feature names to find in the rows of inSCE.
inSCE	A data.frame, matrix, or <a href="#">SingleCellExperiment</a> object to search.
by	Character. Where to search for features in inSCE. If set to "rownames" then the features will be searched for among rownames(inSCE). If inSCE inherits from class <a href="#">SummarizedExperiment</a> , then by can be one of the fields in the row annotation data.frame (i.e. one of colnames(rowData(inSCE))).
exactMatch	Boolean. Whether to only identify exact matches or to identify partial matches using <a href="#">grep</a> .
removeNA	Boolean. If set to FALSE, features not found in inSCE will be given NA and the returned vector will be the same length as features. If set to TRUE, then the NA values will be removed from the returned vector. Default FALSE.
errorOnNoMatch	Boolean. If TRUE, an error will be given if no matches are found. If FALSE, an empty vector will be returned if removeNA is set to TRUE or a vector of NA if removeNA is set to FALSE. Default TRUE.
warningOnPartialMatch	Boolean. If TRUE, a warning will be given if some of the entries in features were not found in inSCE. The warning will list the features not found. Default TRUE.

**Value**

A vector of row indices for the matching features in inSCE.

**Author(s)**

Yusuke Koga, Joshua D. Campbell

**See Also**

[retrieveFeatureInfo](#) from package 'scater' and [link{regex}](#) for how to use regular expressions when exactMatch = FALSE.

**Examples**

```
data(scExample)
ix <- featureIndex(features = c("MT-CYB", "MT-ND2"),
                   inSCE = sce,
                   by = "feature_name")
```

---

findMarkerDiffExp	<i>Find the marker gene set for each cluster With an input SingleCellExperiment object and specifying the clustering labels, this function iteratively call the differential expression analysis on each cluster against all the others.</i>
-------------------	--

---

## Description

Find the marker gene set for each cluster With an input SingleCellExperiment object and specifying the clustering labels, this function iteratively call the differential expression analysis on each cluster against all the others.

## Usage

```
findMarkerDiffExp(
  inSCE,
  useAssay = "logcounts",
  method = c("wilcox", "MAST", "DESeq2", "Limma", "ANOVA"),
  cluster = "cluster",
  covariates = NULL,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.6,
  maxCtrlExprPerc = 0.4,
  minMeanExpr = 0.5
)
```

## Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useAssay	character. A string specifying which assay to use for the MAST calculations. Default "logcounts".
method	A single character for specific differential expression analysis method. Choose from 'wilcox', 'MAST', 'DESeq2', 'Limma', and 'ANOVA'. Default "wilcox".
cluster	One single character to specify a column in colData(inSCE) for the clustering label. Alternatively, a vector or a factor is also acceptable. Default "cluster".
covariates	A character vector of additional covariates to use when building the model. All covariates must exist in names(colData(inSCE)). Not applicable when method is "MAST" method. Default NULL.
log2fcThreshold	Only out put DEGs with the absolute values of log2FC larger than this value. Default NULL
fdrThreshold	Only out put DEGs with FDR value smaller than this value. Default 1
minClustExprPerc	A numeric scalar. The minimum cutoff of the percentage of cells in the cluster of interests that expressed the marker gene. Default 0.7.

maxCtrlExprPerc	A numeric scalar. The maximum cutoff of the percentage of cells out of the cluster (control group) that expressed the marker gene. Default 0.4.
minMeanExpr	A numeric scalar. The minimum cutoff of the mean expression value of the marker in the cluster of interests. Default 1.

**Value**

The input [SingleCellExperiment](#) object with `metadata(inSCE)$findMarker` updated with a `data.table` of the up-regulated DEGs for each cluster.

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- findMarkerDiffExp(mouseBrainSubsetSCE,
                                         useAssay = "logcounts",
                                         cluster = "level1class")
```

---

findMarkerTopTable      *Fetch the table of top markers that pass the filtering*

---

**Description**

Fetch the table of top markers that pass the filtering

**Usage**

```
findMarkerTopTable(
  inSCE,
  log2fcThreshold = 1,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.7,
  maxCtrlExprPerc = 0.4,
  minMeanExpr = 1,
  topN = 10
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
log2fcThreshold	Only use DEGs with the absolute values of log2FC larger than this value. Default 1
fdrThreshold	Only use DEGs with FDR value smaller than this value. Default 0.05
minClustExprPerc	A numeric scalar. The minimum cutoff of the percentage of cells in the cluster of interests that expressed the marker gene. Default 0.7.



maxCtrlExprPerc	A numeric scalar. The maximum cutoff of the percentage of cells out of the cluster (control group) that expressed the marker gene. Default 0.4.
minMeanExpr	A numeric scalar. The minimum cutoff of the mean expression value of the marker in the cluster of interests. Default 1.
topN	An integer. Only to fetch this number of top markers for each cluster in maximum, in terms of log2FC value. Use NULL to cancel the top N subscription. Default 10.

### Details

Users have to run `findMarkerDiffExp()` prior to using this function to extract a top marker table.

### Value

An organized data.frame object, with the top marker gene information.

### Examples

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- findMarkerDiffExp(mouseBrainSubsetSCE,
                                         useAssay = "logcounts",
                                         cluster = "level1class")
findMarkerTopTable(mouseBrainSubsetSCE)
```

---

generateHTANMeta

*Generate HTAN manifest file for droplet and cell count data*

---

### Description

Generate HTAN manifest file for droplet and cell count data

### Usage

```
generateHTANMeta(
  dropletSCE = NULL,
  cellSCE = NULL,
  samplename,
  htan_biospecimen_id,
  dir,
  dataType = c("Droplet", "Cell", "Both")
)
```

**Arguments**

dropletSCE	A <a href="#">SingleCellExperiment</a> object containing droplet count matrix data
cellSCE	A <a href="#">SingleCellExperiment</a> object containing cell count matrix data
samplename	The sample name of the <a href="#">SingleCellExperiment</a> objects
htan_biospecimen_id	The HTAN biospecimen id of the sample in <a href="#">SingleCellExperiment</a> object
dir	The output directory of the SCTK QC pipeline.
dataType	Type of the input data. It can be one of "Droplet", "Cell" or "Both".

**Value**

A [SingleCellExperiment](#) object which combines all objects in sceList. The colData is merged.

---

generateMeta	<i>Generate HTAN manifest file for droplet and cell count data</i>
--------------	--

---

**Description**

Generate HTAN manifest file for droplet and cell count data

**Usage**

```
generateMeta(
  dropletSCE = NULL,
  cellSCE = NULL,
  samplename,
  dir,
  HTAN = TRUE,
  dataType = c("Droplet", "Cell", "Both")
)
```

**Arguments**

dropletSCE	A <a href="#">SingleCellExperiment</a> object containing droplet count matrix data
cellSCE	A <a href="#">SingleCellExperiment</a> object containing cell count matrix data
samplename	The sample name of the <a href="#">SingleCellExperiment</a> objects
dir	The output directory of the SCTK QC pipeline.
HTAN	Whether generates manifest file including HTAN specific ID (HTAN Biospecimen ID, HTAN parent file ID and HTAN patient ID). Default is TRUE.
dataType	Type of the input data. It can be one of "Droplet", "Cell" or "Both".

**Value**

A [SingleCellExperiment](#) object which combines all objects in sceList. The colData is merged.

---

generateSimulatedData *Generates a single simulated dataset, bootstrapping from the input counts matrix.*

---

### Description

Generates a single simulated dataset, bootstrapping from the input counts matrix.

### Usage

```
generateSimulatedData(totalReads, cells, originalData, realLabels)
```

### Arguments

totalReads	Numeric. The total number of reads in the simulated dataset, to be split between all simulated cells.
cells	Numeric. The number of virtual cells to simulate.
originalData	Matrix. The original raw read count matrix. When used within the Shiny app, this will be assay(SCEsetObject, "counts").
realLabels	Factor. The condition labels for differential expression. If only two factors present, will default to t-test. If multiple factors, will default to ANOVA.

### Value

A simulated counts matrix, the first row of which contains the 'true' labels for each virtual cell.

### Examples

```
data("mouseBrainSubsetSCE")
res <- generateSimulatedData(
  totalReads = 1000, cells=10,
  originalData = assay(mouseBrainSubsetSCE, "counts"),
  realLabels = colData(mouseBrainSubsetSCE)[, "level1class"])
```

---

getBiomarker *Given a list of genes and a SingleCellExperiment object, return the binary or continuous expression of the genes.*

---

### Description

Given a list of genes and a SingleCellExperiment object, return the binary or continuous expression of the genes.

**Usage**

```
getBiomarker(
  inSCE,
  gene,
  binary = "Binary",
  useAssay = "counts",
  featureLocation = NULL,
  featureDisplay = NULL
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
gene	gene list
binary	"Binary" for binary expression or "Continuous" for a gradient. Default: "Binary"
useAssay	Indicates which assay to use. The default is "counts".
featureLocation	Indicates which column name of rowData to query gene.
featureDisplay	Indicates which column name of rowData to use to display feature for visualization.

**Value**

getBiomarker(): A data.frame of expression values

**Examples**

```
data("mouseBrainSubsetSCE")
getBiomarker(mouseBrainSubsetSCE, gene="C1qa")
```

---

getDEGTopTable

*Get Top Table of a DEG analysis*

---

**Description**

Users have to run `runDEAnalysis()` first, any of the wrapped functions of this generic function. Users can set further filters on the result. A `data.frame` object, with variables of `Gene`, `Log2_FC`, `Pvalue`, and `FDR`, will be returned.

**Usage**

```

getDEGTopTable(
  inSCE,
  useResult,
  labelBy = NULL,
  onlyPos = FALSE,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL
)

```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object, with of the singleCellTK DEG method performed in advance.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
labelBy	A single character for a column of rowData(inSCE) as where to search for the labeling text. Default NULL for the "rownames".
onlyPos	logical. Whether to only fetch DEG with positive log2_FC value. Default FALSE.
log2fcThreshold	numeric. Only fetch DEGs with the absolute values of log2FC larger than this value. Default 0.25.
fdrThreshold	numeric. Only fetch DEGs with FDR value smaller than this value. Default 0.05.
minGroup1MeanExp	numeric. Only fetch DEGs with mean expression in group1 greater then this value. Default NULL.
maxGroup2MeanExp	numeric. Only fetch DEGs with mean expression in group2 less then this value. Default NULL.
minGroup1ExprPerc	numeric. Only fetch DEGs expressed in greater then this fraction of cells in group1. Default NULL.
maxGroup2ExprPerc	numeric. Only fetch DEGs expressed in less then this fraction of cells in group2. Default NULL.

**Value**

A data.frame object of the top DEGs, with variables of Gene, Log2\_FC, Pvalue, and FDR.



```

                                control = "microglia",
                                analysisName = "diffAbund")
result <- getDiffAbundanceResults(mouseBrainSubsetSCE, "diffAbund")

```

---

getEnrichRResult<-      *Get or Set EnrichR Result*

---

## Description

Get or Set EnrichR Result

## Usage

```

getEnrichRResult(inSCE, analysisName) <- value

getEnrichRResult(inSCE, analysisName)

## S4 method for signature 'SingleCellExperiment'
getEnrichRResult(inSCE, analysisName)

## S4 replacement method for signature 'SingleCellExperiment'
getEnrichRResult(inSCE, analysisName) <- value

```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
analysisName	A string that identifies each specific analysis
value	The EnrichR result table

## Value

For getter method, a data.frame of the EnrichR result; For setter method, inSCE with EnrichR results updated.

## See Also

[runEnrichR](#)

## Examples

```

data("mouseBrainSubsetSCE")
if (Biobase::testBioCConnection()) {
  mouseBrainSubsetSCE <- runEnrichR(mouseBrainSubsetSCE, features = "Cmtm5",
                                   db = "GO_Cellular_Component_2017",
                                   analysisName = "analysis1")
  result <- getEnrichRResult(mouseBrainSubsetSCE, "analysis1")
}

```

---

getGenesetNamesFromCollection  
*List geneset names from geneSetCollection*

---

**Description**

List geneset names from geneSetCollection

**Usage**

```
getGenesetNamesFromCollection(inSCE, geneSetCollectionName)
```

**Arguments**

inSCE            Input [SingleCellExperiment](#) object.  
geneSetCollectionName  
                  The name of an imported geneSetCollection.

**Value**

A character vector of available genesets from the collection.

---

getMSigDBTable            *Shows MSigDB categories*

---

**Description**

Returns a data.frame that shows MSigDB categories and subcategories as well as descriptions for each. The entries in the ID column in this table can be used as input for [importGeneSetsFromMSigDB](#).

**Usage**

```
getMSigDBTable()
```

**Value**

data.frame, containing MSigDB categories

**Author(s)**

Joshua D. Campbell

**See Also**

[importGeneSetsFromMSigDB](#) for importing MSigDB gene sets.



### Examples

```
getMSigDBTable()
```

---

```
getPathwayResultNames
```

*List pathway analysis result names*

---

### Description

List pathway analysis result names

### Usage

```
getPathwayResultNames(inSCE, stopIfNone = FALSE)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
stopIfNone	Whether to stop and raise an error if no results found. If FALSE, will return an empty character vector.

### Details

Pathway analysis results will be stored as matrices in reducedDims slot of inSCE. This function lists the result names stored in metadata slot when analysis is performed.

### Value

A character vector of valid pathway analysis result names.

---

```
getSampleSummaryStatsTable
```

*Stores and returns table of SCTK QC outputs to metadata.*

---

### Description

Stores and returns table of QC metrics generated from QC algorithms within the metadata slot of the SingleCellExperiment object.

### Usage

```
getSampleSummaryStatsTable(inSCE, statsName, ...)
```

```
## S4 method for signature 'SingleCellExperiment'  
getSampleSummaryStatsTable(inSCE, statsName, ...)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved <a href="#">assay</a> data and/or <a href="#">colData</a> data. Required.
statsName	A character value indicating the slot that stores the stats table within the meta-data of the <a href="#">SingleCellExperiment</a> object. Required.
...	Other arguments passed to the function.

**Value**

A matrix/array object. Contains a summary table for QC statistics generated from [SingleCellTK](#).

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- sampleSummaryStats(sce, simple = TRUE, statsName = "qc_table")
getSampleSummaryStatsTable(sce, statsName = "qc_table")
```

---

getSceParams

*Extract QC parameters from the SingleCellExperiment object*

---

**Description**

Extract QC parameters from the [SingleCellExperiment](#) object

**Usage**

```
getSceParams(
  inSCE,
  skip = c("scrublet", "runDecontX", "runBarcodeRanksMetaOutput"),
  ignore = c("algorithms", "estimates", "contamination", "z", "sample", "rank",
    "BPPARAM", "batch", "geneSetCollection", "barcodeArgs"),
  directory = "./",
  samplename = "",
  writeYAML = TRUE
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object.
skip	Skip extracting the parameters of the provided QC functions.
ignore	Skip extracting the content within QC functions.
directory	The output directory of the <a href="#">SCTK_runQC.R</a> pipeline.
samplename	The sample name of the <a href="#">SingleCellExperiment</a> objects.
writeYAML	Whether output yaml file to store parameters. Default if TRUE. If FALSE, return character object.

**Value**

If writeYAML TRUE, a yaml object will be generated. If FALSE, character object.

---

```
getSeuratVariableFeatures
  Get variable feature names after running runSeuratFindHVG function
```

---

**Description**

Get variable feature names after running runSeuratFindHVG function

**Usage**

```
getSeuratVariableFeatures(inSCE)
```

**Arguments**

inSCE            Input SingleCellExperiment object.

**Value**

A list of variable feature names.

---

```
getSoupX<-            Get or Set SoupX Result
```

---

**Description**

S4 method for getting and setting SoupX results that cannot be appended to either rowData(inSCE) or colData(inSCE).

S4 method for getting and setting SoupX results that cannot be appended to either rowData(inSCE) or colData(inSCE).

**Usage**

```
getSoupX(inSCE, sampleID, background = FALSE) <- value
```

```
getSoupX(inSCE, sampleID = NULL, background = FALSE)
```

```
## S4 method for signature 'SingleCellExperiment'
getSoupX(inSCE, sampleID = NULL, background = FALSE)
```

```
## S4 replacement method for signature 'SingleCellExperiment'
getSoupX(inSCE, sampleID, background = FALSE) <- value
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object. For getter method, <a href="#">runSoupX</a> must have been already applied.
sampleID	Character vector. For getter method, the samples that should be included in the returned list. Leave this NULL for all samples. Default NULL. For setter method, only one sample allowed.
background	Logical. Whether background was applied when running <a href="#">runSoupX</a> . Default FALSE.
value	Dedicated list object of SoupX results.

**Value**

For getter method, a list with SoupX results for specified samples. For setter method, inSCE with SoupX results updated.

For getter method, a list with SoupX results for specified samples. For setter method, inSCE with SoupX results updated.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
# SoupX does not work for toy example,
# can be tested with `sce <- importExampleData("pbmc3k")`
sce <- runSoupX(sce, sample = "sample")
soupXResults <- getSoupX(sce)

## End(Not run)
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
# SoupX does not work for toy example,
# can be tested with `sce <- importExampleData("pbmc3k")`
sce <- runSoupX(sce, sample = "sample")
soupXResults <- getSoupX(sce)

## End(Not run)
```

**getTopHVG**


---

*getTopHVG* Extracts the top variable genes from an input *SingleCellExperiment* object. Note that the variability metrics must be computed using the `runFeatureSelection` method before extracting the feature names of the top variable features. If `altExp` parameter is a character value, this function will return the input *SingleCellExperiment* object with the subset containing only the top variable features stored as an `altExp` slot in returned object. However, if this parameter is set to NULL, only the names of the top variable features will be returned as a character vector.

---

**Description**

getTopHVG Extracts the top variable genes from an input `SingleCellExperiment` object. Note that the variability metrics must be computed using the `'runFeatureSelection'` method before extracting the feature names of the top variable features. If `'altExp'` parameter is a character value, this function will return the input `SingleCellExperiment` object with the subset containing only the top variable features stored as an `altExp` slot in returned object. However, if this parameter is set to `NULL`, only the names of the top variable features will be returned as a character vector.

**Usage**

```
getTopHVG(inSCE, method, n = 2000, altExp = NULL)
```

**Arguments**

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object
<code>method</code>	Specify which method to use for variable gene extraction from either Seurat "vst", "mean.var.plot", "dispersion" or Scran "modelGeneVar".
<code>n</code>	Specify the number of top variable genes to extract.
<code>altExp</code>	A character value that specifies the name of the <code>altExp</code> slot that should be created to store the subset <code>SingleCellExperiment</code> object containing only the top <code>'n'</code> variable features. Default value is <code>NULL</code> , which will not store the subset <code>SingleCellExperiment</code> object and instead will only return the names of the top <code>'n'</code> variable features.

**Value**

A character vector of the top variable feature names or the input `SingleCellExperiment` object with subset of variable features stored as an `altExp` in the object.

**Author(s)**

Irzam Sarfraz

**Examples**

```
data(sce_chcl, package = "scds")
sce_chcl <- scranModelGeneVar(sce_chcl, "counts")
# return top 10 variable genes
topGenes <- getTopHVG(sce_chcl, "modelGeneVar", 10)
```

---

getTSCANResults	<i>getTSCANResults accessor function</i>
-----------------	--

---

### Description

getTSCANResults accessor function

### Usage

```
getTSCANResults(x, analysisName = NULL, pathName = NULL)

## S4 method for signature 'SingleCellExperiment'
getTSCANResults(x, analysisName = NULL, pathName = NULL)

getTSCANResults(x, analysisName, pathName = NULL) <- value

## S4 replacement method for signature 'SingleCellExperiment'
getTSCANResults(x, analysisName, pathName = NULL) <- value

listTSCANResults(x)

## S4 method for signature 'SingleCellExperiment'
listTSCANResults(x)
```

### Arguments

x	Input <a href="#">SingleCellExperiment</a> object.
analysisName	Algorithm name implemented
pathName	Sub folder name within the analysisName
value	Value to be stored within the pathName or analysisName

### Value

Get or set TSCAN results

---

getTSNE	<i>Run t-SNE dimensionality reduction method on a SingleCellExperiment Object</i>
---------	---

---

### Description

Run t-SNE dimensionality reduction method on a SingleCellExperiment Object

**Usage**

```
getTSNE(
  inSCE,
  useAssay = "logcounts",
  useAltExp = NULL,
  useReducedDim = NULL,
  reducedDimName = "TSNE",
  nIterations = 1000,
  perplexity = 30,
  run_pca = TRUE,
  ntop = NULL,
  seed = NULL
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useAssay	Assay to use for tSNE computation. If useAltExp is specified, useAssay has to exist in assays(altExp(inSCE, useAltExp)). Default "logcounts"
useAltExp	The subset to use for tSNE computation, usually for the selected.variable features. Default NULL.
useReducedDim	The low dimension representation to use for UMAP computation. Default NULL.
reducedDimName	a name to store the results of the dimension reductions. Default "TSNE".
nIterations	maximum iterations. Default 1000.
perplexity	perplexity parameter. Default 30.
run_pca	run tSNE on PCA components? Default TRUE.
ntop	Number of top features to use as a further variable feature selection. Default NULL.
seed	Random seed for reproducibility of tSNE results. Default NULL will use global seed in use by the R environment.

**Value**

A [SingleCellExperiment](#) object with tSNE computation updated in reducedDim(inSCE, reducedDimName).

**Examples**

```
data("mouseBrainSubsetSCE")
#add a CPM assay
assay(mouseBrainSubsetSCE, "cpm") <- apply(
  assay(mouseBrainSubsetSCE, "counts"), 2, function(x) {
    x / (sum(x) / 1000000)
  })
mouseBrainSubsetSCE <- getTSNE(mouseBrainSubsetSCE, useAssay = "cpm",
  reducedDimName = "TSNE_cpm",
  perplexity = NULL)
```

---

getUMAP	<i>Uniform Manifold Approximation and Projection(UMAP) algorithm for dimension reduction.</i>
---------	---

---

### Description

Uniform Manifold Approximation and Projection(UMAP) algorithm for dimension reduction.

### Usage

```
getUMAP(
  inSCE,
  useAssay = "counts",
  useAltExp = NULL,
  useReducedDim = NULL,
  sample = NULL,
  reducedDimName = "UMAP",
  logNorm = TRUE,
  nNeighbors = 30,
  nIterations = 200,
  alpha = 1,
  minDist = 0.01,
  spread = 1,
  pca = TRUE,
  initialDims = 25,
  nTop = 2000,
  seed = NULL
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useAssay	Assay to use for UMAP computation. If useAltExp is specified, useAssay has to exist in <code>assays(altExp(inSCE, useAltExp))</code> . Default "counts".
useAltExp	The subset to use for UMAP computation, usually for the selected.variable features. Default NULL.
useReducedDim	The low dimension representation to use for UMAP computation. Default NULL.
sample	Character vector. Indicates which sample each cell belongs to. If given a single character, will take the annotation from <code>colData</code> . Default NULL.
reducedDimName	A name to store the results of the dimension reduction coordinates obtained from this method. Default "UMAP".
logNorm	Whether the counts will need to be log-normalized prior to generating the UMAP via <code>logNormCounts</code> . Will not normalize when using useReducedDim. Default TRUE.



nNeighbors	The size of local neighborhood used for manifold approximation. Larger values result in more global views of the manifold, while smaller values result in more local data being preserved. Default 30. See ‘?scater::calculateUMAP’ for more information.
nIterations	The number of iterations performed during layout optimization. Default is 200.
alpha	The initial value of "learning rate" of layout optimization. Default is 1.
minDist	The effective minimum distance between embedded points. Smaller values will result in a more clustered/clumped embedding where nearby points on the manifold are drawn closer together, while larger values will result on a more even dispersal of points. Default 0.01. See ‘?scater::calculateUMAP’ for more information.
spread	The effective scale of embedded points. In combination with minDist, this determines how clustered/clumped the embedded points are. Default 1. See ‘?scater::calculateUMAP’ for more information.
pca	Logical. Whether to perform dimension reduction with PCA before UMAP. Will not perform PCA if using useReducedDim. Default TRUE
initialDims	Number of dimensions from PCA to use as input in UMAP. Default 25.
nTop	Number of features with the highest variances to use for dimensionality reduction. Default 2000.
seed	Random seed for reproducibility of UMAP results. Default NULL will use global seed in use by the R environment.

**Value**

A [SingleCellExperiment](#) object with UMAP computation updated in `reducedDim(inSCE, reducedDimName)`.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE = sce, useAssay = "counts", reducedDimName = "UMAP")
```

---

importAlevin

*Construct SCE object from Salmon-Alevin output*


---

**Description**

Construct SCE object from Salmon-Alevin output

**Usage**

```
importAlevin(
  alevinDir = NULL,
  sampleName = "sample",
  delayedArray = FALSE,
  class = c("Matrix", "matrix"),
  rowNamesDedup = TRUE
)
```

**Arguments**

alevinDir	Character. The output directory of salmon-Alevin pipeline. It should contain subfolder named 'alevin', which contains the count data which is stored in 'quants_mat.gz'. Default NULL.
sampleName	Character. A user-defined sample name for the sample to be imported. The 'sampleName' will be appended to the beginning of cell barcodes. Default is 'sample'.
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

**Value**

A `SingleCellExperiment` object containing the count matrix, the feature annotations, and the cell annotation (which includes QC metrics stored in 'featureDump.txt').

---

importAnnData	<i>Create a SingleCellExperiment Object from Python AnnData .h5ad files</i>
---------------	---

---

**Description**

This function reads in one or more Python AnnData files in the .h5ad format and returns a single [SingleCellExperiment](#) object containing all the AnnData samples by concatenating their counts matrices and related information slots.

**Usage**

```
importAnnData(
  sampleDirs = NULL,
  sampleNames = NULL,
  delayedArray = FALSE,
  class = c("Matrix", "matrix"),
  rowNamesDedup = TRUE
)
```

**Arguments**

sampleDirs	Folder containing the .h5ad file. Can be one of - <ul style="list-style-type: none"> <li>• Default current working directory.</li> <li>• Full path to the directory containing the .h5ad file. E.g sampleDirs = '/path/to/sample'</li> </ul>
------------	--

	<ul style="list-style-type: none"> <li>• A vector of folder paths for the samples to import. E.g. <code>sampleDirs = c('/path/to/sample1', '/path/to/sample2', '/path/to/sample3')</code> <code>importAnnData</code> will return a single SCE object containing all the samples with the sample name appended to each colname in <code>colData</code></li> </ul>
<code>sampleNames</code>	<p>The prefix/name of the <code>.h5ad</code> file without the <code>.h5ad</code> extension e.g. if <code>'sample.h5ad'</code> is the filename, pass <code>sampleNames = 'sample'</code>. Can be one of -</p> <ul style="list-style-type: none"> <li>• Default <code>sample</code>.</li> <li>• A vector of samples to import. Length of vector must be equal to length of <code>sampleDirs</code> vector E.g. <code>sampleDirs = c('sample1', 'sample2', 'sample3')</code> <code>importAnnData</code> will return a single SCE object containing all the samples with the sample name appended to each colname in <code>colData</code></li> </ul>
<code>delayedArray</code>	<p>Boolean. Whether to read the expression matrix as <code>DelayedArray</code> object. Default <code>FALSE</code>.</p>
<code>class</code>	<p>Character. The class of the expression matrix stored in the SCE object. Can be one of <code>"Matrix"</code> (as returned by <code>readMM</code> function), or <code>"matrix"</code> (as returned by <code>matrix</code> function). Default <code>"Matrix"</code>.</p>
<code>rowNamesDedup</code>	<p>Boolean. Whether to deduplicate rownames. Default <code>TRUE</code>.</p>

## Details

`importAnnData` converts scRNA-seq data in the `AnnData` format to the `SingleCellExperiment` object. The `.X` slot in `AnnData` is transposed to the features x cells format and becomes the `'counts'` matrix in the assay slot. The `.vars AnnData` slot becomes the SCE `rowData` and the `.obs AnnData` slot becomes the SCE `colData`. Multidimensional data in the `.obsm AnnData` slot is ported over to the SCE `reducedDims` slot. Additionally, unstructured data in the `.uns AnnData` slot is available through the SCE `metadata` slot. There are 2 currently known minor issues - `Anndata` python module depends on another python module `h5py` to read `hd5` format files. If there are errors reading the `.h5ad` files, such as `"ValueError: invalid shape in fixed-type tuple."` the user will need to do downgrade `h5py` by running `pip3 install --user h5py==2.9.0` Additionally there might be errors in converting some python objects in the unstructured data slots. There are no known R solutions at present. Refer <https://github.com/rstudio/reticulate/issues/209>

## Value

A `SingleCellExperiment` object.

## Examples

```
file.path <- system.file("extdata/annData_pbmc_3k", package = "singleCellTK")
## Not run:
sce <- importAnnData(sampleDirs = file.path,
                    sampleNames = 'pbmc3k_20by20')

## End(Not run)
```

---

importBUStools	<i>Construct SCE object from BUStools output</i>
----------------	--

---

## Description

Read the barcodes, features (genes), and matrix from BUStools output. Import them as one [Single-CellExperiment](#) object. Note the cells in the output files for BUStools 0.39.4 are not filtered.

## Usage

```
importBUStools(
  BUStoolsDirs,
  samples,
  matrixFileNames = "genes.mtx",
  featuresFileNames = "genes.genes.txt",
  barcodesFileNames = "genes.barcodes.txt",
  gzipped = "auto",
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

## Arguments

BUStoolsDirs	A vector of paths to BUStools output files. Each sample should have its own path. For example: <code>./genecount</code> . Must have the same length as <code>samples</code> .
samples	A vector of user-defined sample names for the samples to be imported. Must have the same length as <code>BUStoolsDirs</code> .
matrixFileNames	Filenames for the Market Exchange Format (MEX) sparse matrix files ( <code>.mtx</code> files). Must have length 1 or the same length as <code>samples</code> .
featuresFileNames	Filenames for the feature annotation files. Must have length 1 or the same length as <code>samples</code> .
barcodesFileNames	Filenames for the cell barcode list file. Must have length 1 or the same length as <code>samples</code> .
gzipped	Boolean. TRUE if the BUStools output files ( <code>barcodes.txt</code> , <code>genes.txt</code> , and <code>genes.mtx</code> ) were gzip compressed. FALSE otherwise. This is FALSE in BUStools 0.39.4. Default "auto" which automatically detects if the files are gzip compressed. Must have length 1 or the same length as <code>samples</code> .
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray-class</a> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

**Value**

A SingleCellExperiment object containing the count matrix, the gene annotation, and the cell annotation.

**Examples**

```
# Example #1
# FASTQ files were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.0
# /pbmc_1k_v3
# They were concatenated as follows:
# cat pbmc_1k_v3_S1_L001_R1_001.fastq.gz pbmc_1k_v3_S1_L002_R1_001.fastq.gz >
# pbmc_1k_v3_R1.fastq.gz
# cat pbmc_1k_v3_S1_L001_R2_001.fastq.gz pbmc_1k_v3_S1_L002_R2_001.fastq.gz >
# pbmc_1k_v3_R2.fastq.gz
# The following BUStools command generates the gene, cell, and
# matrix files

# bustools correct -w ./3M-february-2018.txt -p output.bus | \
# bustools sort -T tmp/ -t 4 -p - | \
# bustools count -o genecount/genes \
# -g ./transcripts_to_genes.txt \
# -e matrix.ec \
# -t transcripts.txt \
# --genecounts -

# The top 20 genes and the first 20 cells are included in this example.
sce <- importBUStools(
  BUStoolsDirs = system.file("extdata/BUStools_PBMC_1k_v3_20x20/genecount/",
    package = "singleCellTK"),
  samples = "PBMC_1k_v3_20x20")
```

---

importCellRanger      *Construct SCE object from Cell Ranger output*

---

**Description**

Read the filtered barcodes, features, and matrices for all samples from (preferably a single run of) Cell Ranger output. Import and combine them as one big [SingleCellExperiment](#) object.

**Usage**

```
importCellRanger(
  cellRangerDirs = NULL,
  sampleDirs = NULL,
  sampleNames = NULL,
  cellRangerOuts = NULL,
  dataType = c("filtered", "raw"),
  matrixFileNames = "matrix.mtx.gz",
```

```

featuresFileNames = "features.tsv.gz",
barcodesFileNames = "barcodes.tsv.gz",
gzipped = "auto",
class = c("Matrix", "matrix"),
delayedArray = FALSE,
rowNamesDedup = TRUE
)

importCellRangerV2(
  cellRangerDirs = NULL,
  sampleDirs = NULL,
  sampleNames = NULL,
  dataTypeV2 = c("filtered", "raw"),
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  reference = NULL,
  cellRangerOutsV2 = NULL,
  rowNamesDedup = TRUE
)

importCellRangerV3(
  cellRangerDirs = NULL,
  sampleDirs = NULL,
  sampleNames = NULL,
  dataType = c("filtered", "raw"),
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)

```

### Arguments

- cellRangerDirs** The root directories where Cell Ranger was run. These folders should contain sample specific folders. Default NULL, meaning the paths for each sample will be specified in *samples* argument.
- sampleDirs** Default NULL. Can be one of
- NULL. All samples within cellRangerDirs will be imported. The order of samples will be first determined by the order of cellRangerDirs and then by [list.dirs](#). This is only for the case where cellRangerDirs is specified.
  - A list of vectors containing the folder names for samples to import. Each vector in the list corresponds to samples from one of cellRangerDirs. These names are the same as the folder names under cellRangerDirs. This is only for the case where cellRangerDirs is specified.
  - A vector of folder paths for the samples to import. This is only for the case where cellRangerDirs is NULL.
- The cells in the final SCE object will be ordered in the same order of sampleDirs.
- sampleNames** A vector of user-defined sample names for the samples to be imported. Must have the same length as length(unlist(sampleDirs)) if sampleDirs is not

	<p>NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>. Default NULL, in which case the folder names will be used as sample names.</p>
cellRangerOuts	<p>Character vector. The intermediate paths to filtered or raw cell barcode, feature, and matrix files for each sample. <b>Supercedes</b> <code>dayaType</code>. If NULL, <code>dayaType</code> will be used to determine Cell Ranger output directory. If not NULL, <code>dayaType</code> will be ignored and <code>cellRangerOuts</code> specifies the paths. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>. Reference genome names might need to be appended for CellRanger version below 3.0.0 if reads were mapped to multiple genomes when running Cell Ranger pipeline. Probable options include "outs/filtered_feature_bc_matrix/", "outs/raw_feature_bc_matrix/", "outs/filtered_gene_bc_matrix/", "outs/raw_gene_bc_matrix/".</p>
dayaType	<p>Character. The type of data to import. Can be one of "filtered" (which is equivalent to <code>cellRangerOuts = "outs/filtered_feature_bc_matrix/"</code> or <code>cellRangerOuts = "outs/filtered_gene_bc_matrix/"</code>) or "raw" (which is equivalent to <code>cellRangerOuts = "outs/raw_feature_bc_matrix/"</code> or <code>cellRangerOuts = "outs/raw_gene_bc_matrix/"</code>). Default "filtered" which imports the counts for filtered cell barcodes only.</p>
matrixFileNames	<p>Character vector. Filenames for the Market Exchange Format (MEX) sparse matrix files (matrix.mtx or matrix.mtx.gz files). Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>.</p>
featuresFileNames	<p>Character vector. Filenames for the feature annotation files. They are usually named <i>features.tsv.gz</i> or <i>genes.tsv</i>. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>.</p>
barcodesFileNames	<p>Character vector. Filename for the cell barcode list files. They are usually named <i>barcodes.tsv.gz</i> or <i>barcodes.tsv</i>. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>.</p>
gzipped	<p>TRUE if the Cell Ranger output files (barcodes.tsv, features.tsv, and matrix.mtx) were gzip compressed. FALSE otherwise. This is true after Cell Ranger 3.0.0 update. Default "auto" which automatically detects if the files are gzip compressed. If not "auto", <code>gzipped</code> must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>.</p>
class	<p>Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".</p>

delayedArray	Boolean. Whether to read the expression matrix as <code>DelayedArray</code> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.
dataTypeV2	Character. The type of output to import for Cellranger version below 3.0.0. Whether to import the filtered or the raw data. Can be one of 'filtered' or 'raw'. Default 'filtered'. When <code>cellRangerOuts</code> is specified, <code>dataTypeV2</code> and reference will be ignored.
reference	Character vector. The reference genome names. Default NULL. If not NULL, it must give the length and order as <code>length(unlist(sampleDirs))</code> if <code>sampleDirs</code> is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code> . Only needed for Cellranger version below 3.0.0.
cellRangerOutsV2	Character vector. The intermediate paths to filtered or raw cell barcode, feature, and matrix files for each sample for Cellranger version below 3.0.0. If NULL, reference and <code>dataTypeV2</code> will be used to determine Cell Ranger output directory. If it has length 1, it assumes that all samples use the same genome reference and the function will load only filtered or raw data.

## Details

`importCellRangerV2` imports output from Cell Ranger V2. `importCellRangerV2Sample` imports output from one sample from Cell Ranger V2. `importCellRangerV3` imports output from Cell Ranger V3. `importCellRangerV3Sample` imports output from one sample from Cell Ranger V3. Some implicit assumptions which match the output structure of Cell Ranger V2 & V3 are made in these 4 functions including `cellRangerOuts`, `matrixFileName`, `featuresFileName`, `barcodesFileName`, and `gzipped`. Alternatively, user can call `importCellRanger` to explicitly specify these arguments.

## Value

A `SingleCellExperiment` object containing the combined count matrix, the feature annotations, and the cell annotation.

## Examples

```
# Example #1
# The following filtered feature, cell, and matrix files were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/
# 3.0.0/hgmm_1k_v3
# The top 10 hg19 & mm10 genes are included in this example.
# Only the first 20 cells are included.
sce <- importCellRanger(
  cellRangerDirs = system.file("extdata/", package = "singleCellTK"),
  sampleDirs = "hgmm_1k_v3_20x20",
  sampleNames = "hgmm1kv3",
  dataType = "filtered")
# The following filtered feature, cell, and matrix files were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/
# 2.1.0/pbmc4k
```



```
# Top 20 genes are kept. 20 cell barcodes are extracted.
sce <- importCellRangerV2(
  cellRangerDirs = system.file("extdata/", package = "singleCellTK"),
  sampleDirs = "pbmc_4k_v2_20x20",
  sampleNames = "pbmc4k_20",
  reference = 'GRCh38',
  dataTypeV2 = "filtered")
sce <- importCellRangerV3(
  cellRangerDirs = system.file("extdata/", package = "singleCellTK"),
  sampleDirs = "hgmm_1k_v3_20x20",
  sampleNames = "hgmm1kv3",
  dataType = "filtered")
```

---

```
importCellRangerV2Sample
```

*Construct SCE object from Cell Ranger V2 output for a single sample*

---

## Description

Read the filtered barcodes, features, and matrices for all samples from Cell Ranger V2 output. Files are assumed to be named "matrix.mtx", "genes.tsv", and "barcodes.tsv".

## Usage

```
importCellRangerV2Sample(
  dataDir = NULL,
  sampleName = NULL,
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

## Arguments

dataDir	A path to the directory containing the data files. Default "/".
sampleName	A User-defined sample name. This will be prepended to all cell barcode IDs. Default "sample".
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

## Value

A `SingleCellExperiment` object containing the count matrix, the feature annotations, and the cell annotation for the sample.

**Examples**

```
sce <- importCellRangerV2Sample(
  dataDir = system.file("extdata/pbmc_4k_v2_20x20/outs/",
    "filtered_gene_bc_matrices/GRCh38", package = "singleCellTK"),
  sampleName = "pbmc4k_20")
```

---

```
importCellRangerV3Sample
```

*Construct SCE object from Cell Ranger V3 output for a single sample*

---

**Description**

Read the filtered barcodes, features, and matrices for all samples from Cell Ranger V3 output. Files are assumed to be named "matrix.mtx.gz", "features.tsv.gz", and "barcodes.tsv.gz".

**Usage**

```
importCellRangerV3Sample(
  dataDir = "./",
  sampleName = "sample",
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

**Arguments**

dataDir	A path to the directory containing the data files. Default "./".
sampleName	A User-defined sample name. This will be prepended to all cell barcode IDs. Default "sample".
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

**Value**

A SingleCellExperiment object containing the count matrix, the feature annotations, and the cell annotation for the sample.

**Examples**

```
sce <- importCellRangerV3Sample(
  dataDir = system.file("extdata/hgmm_1k_v3_20x20/outs/",
    "filtered_feature_bc_matrix", package = "singleCellTK"),
  sampleName = "hgmm1kv3")
```

importDropEst

*Create a SingleCellExperiment Object from DropEst output*

## Description

imports the RDS file created by DropEst (<https://github.com/hms-dbmi/dropEst>) and create a SingleCellExperiment object from either the raw or filtered counts matrix. Additionally parse through the RDS to obtain appropriate feature annotations as SCE coldata, in addition to any metadata.

## Usage

```
importDropEst(
  sampleDirs = NULL,
  dataType = c("filtered", "raw"),
  rdsFileName = "cell.counts",
  sampleNames = NULL,
  delayedArray = FALSE,
  class = c("Matrix", "matrix"),
  rowNamesDedup = TRUE
)
```

## Arguments

sampleDirs	A path to the directory containing the data files. Default "/".
dataType	can be "filtered" or "raw". Default "filtered".
rdsFileName	File name prefix of the DropEst RDS output. default is "cell.counts"
sampleNames	A User-defined sample name. This will be prepended to all cell barcode IDs. Default "sample".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

## Details

importDropEst expects either raw counts matrix stored as "cm\_raw" or filtered counts matrix stored as "cm" in the DropEst rds output. ColData is obtained from the DropEst corresponding to "mean\_reads\_per\_umi", "aligned\_reads\_per\_cell", "aligned\_umis\_per\_cell", "requested\_umis\_per\_cb", "requested\_reads\_per\_umi". If using filtered counts matrix, the colData dataframe is subset to contain features from the filtered counts matrix alone. If any annotations of ("saturation\_info", "merge\_targets", "reads\_per\_umi\_per\_cell") are found in the DropEst rds, they will be added to the SCE metadata field

**Value**

A `SingleCellExperiment` object containing the count matrix, the feature annotations from `DropEst` as `ColData`, and any metadata from `DropEst`

**Examples**

```
# Example results were generated as per instructions from the developers of dropEst described in
# https://github.com/hms-dbmi/dropEst/blob/master/examples/EXAMPLES.md
sce <- importDropEst(sampleDirs = system.file("extdata/dropEst_scg71", package = "singleCellTK"),
                    sampleNames = 'scg71')
```

---

<code>importExampleData</code>	<i>Retrieve example datasets</i>
--------------------------------	----------------------------------

---

**Description**

Retrieves published example datasets stored in `SingleCellExperiment` using the `scRNAseq` and `TENxPBMCDData` packages. See 'Details' for a list of available datasets.

**Usage**

```
importExampleData(
  dataset,
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

**Arguments**

<code>dataset</code>	Character. Name of the dataset to retrieve.
<code>class</code>	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" or "matrix". "Matrix" will store the data as a sparse matrix from package <code>Matrix</code> while "matrix" will store the data in a standard matrix. Default "Matrix".
<code>delayedArray</code>	Boolean. Whether to read the expression matrix as <code>DelayedArray</code> object or not. Default FALSE.
<code>rowNamesDedup</code>	Boolean. Whether to deduplicate rownames. Default TRUE.

**Details**

See the list below for the available datasets and their descriptions.

**"fluidigm\_pollen"** Retrieved with `ReprocessedFluidigmData`. Returns a dataset of 65 human neural cells from Pollen et al. (2014), each sequenced at high and low coverage (SRA accession SRP041736).

- "**allen\_tasic**" Retrieved with [ReprocessedAllenData](#). Returns a dataset of 379 mouse brain cells from Tasic et al. (2016).
- "**pbmc3k**" Retrieved with [TENxPBMCData](#). 2,700 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.
- "**pbmc4k**" Retrieved with [TENxPBMCData](#). 4,340 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.
- "**pbmc6k**" Retrieved with [TENxPBMCData](#). 5,419 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.
- "**pbmc8k**" Retrieved with [TENxPBMCData](#). 8,381 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.
- "**pbmc33k**" Retrieved with [TENxPBMCData](#). 33,148 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.
- "**pbmc68k**" Retrieved with [TENxPBMCData](#). 68,579 peripheral blood mononuclear cells (PBMCs) from 10X Genomics.

**Value**

The specified [SingleCellExperiment](#) object.

**Author(s)**

Joshua D. Campbell, David Jenkins

**Examples**

```
sce <- importExampleData("pbmc3k")
```

---

importFromFiles	<i>Create a SingleCellExperiment object from files</i>
-----------------	--

---

**Description**

Create a SingleCellExperiment object from files

**Usage**

```
importFromFiles(  
  assayFile,  
  annotFile = NULL,  
  featureFile = NULL,  
  assayName = "counts",  
  inputDataFrames = FALSE,  
  class = c("Matrix", "matrix"),  
  delayedArray = FALSE,  
  annotFileHeader = FALSE,  
  annotFileRowName = 1,  
)
```

```

annotFileSep = "\t",
featureHeader = FALSE,
featureRowName = 1,
featureSep = "\t",
gzipped = "auto",
rowNamesDedup = TRUE
)

```

## Arguments

assayFile	The path to a file in .mtx, .txt, .csv, .tab, or .tsv format.
annotFile	The path to a text file that contains columns of annotation information for each cell in the assayFile. This file should have the same number of rows as there are columns in the assayFile. If multiple samples are represented in the dataset, this should be denoted by a column called 'sample' within the annotFile.
featureFile	The path to a text file that contains columns of annotation information for each gene in the count matrix. This file should have the same genes in the same order as assayFile. This is optional.
assayName	The name of the assay that you are uploading. The default is "counts".
inputDataFrames	If TRUE, assayFile, annotFile and featureFile should be data.frames object (or its inheritance) instead of file paths. The default is FALSE.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
annotFileHeader	Whether there's a header (colnames) in the cell annotation file. Default is FALSE.
annotFileRowName	Which column is used as the rownames for the cell annotation file. This should match to the colnames of the assayFile. Default is 1 (first column).
annotFileSep	Separator used for the cell annotation file. Default is "\t".
featureHeader	Whether there's a header (colnames) in the feature annotation file. Default is FALSE.
featureRowName	Which column is used as the rownames for the feature annotation file. This should match to the rownames of the assayFile. Default is 1. (first column).
featureSep	Separator used for the feature annotation file. Default is "\t".
gzipped	Whether the input file is gzipped. Default is "auto" and it will automatically detect whether the file is gzipped. Other options are TRUE or FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

## Details

Creates a [SingleCellExperiment](#) object from a counts file in various formats, and files of cell and feature annotation.

**Value**

a [SingleCellExperiment](#) object

---

```
importGeneSetsFromCollection
```

*Imports gene sets from a [GeneSetCollection](#) object*

---

**Description**

Converts a list of gene sets stored in a [GeneSetCollection](#) object and stores it in the metadata of the [SingleCellExperiment](#) object. These gene sets can be used in downstream quality control and analysis functions in [singleCellTK](#).

**Usage**

```
importGeneSetsFromCollection(
  inSCE,
  geneSetCollection,
  collectionName = "GeneSetCollection",
  by = "rownames"
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>geneSetCollection</code>	A <a href="#">GeneSetCollection</a> object. See <a href="#">GeneSetCollection</a> for more details.
<code>collectionName</code>	Character. Name of collection to add gene sets to. If this collection already exists in <code>inSCE</code> , then these gene sets will be added to that collection. Any gene sets within the collection with the same name will be overwritten. Default <a href="#">GeneSetCollection</a> .
<code>by</code>	Character, character vector, or NULL. Describes the location within <code>inSCE</code> where the gene identifiers in <code>geneSetCollection</code> should be mapped. If set to "rownames" then the features will be searched for among <code>rownames(inSCE)</code> . This can also be set to one of the column names of <code>rowData(inSCE)</code> in which case the gene identifiers will be mapped to that column in the <code>rowData</code> of <code>inSCE</code> . <code>by</code> can be a vector the same length as the number of gene sets in the <a href="#">GeneSetCollection</a> and the elements of the vector can point to different locations within <code>inSCE</code> . Finally, <code>by</code> can be NULL. In this case, the location of the gene identifiers in <code>inSCE</code> should be saved in the description slot for each gene set in the <a href="#">GeneSetCollection</a> . See <a href="#">featureIndex</a> for more information. Default "rownames".

**Details**

The gene identifiers in gene sets in the [GeneSetCollection](#) will be mapped to the rownames of `inSCE` using the `by` parameter and stored in a [GeneSetCollection](#) object from package [GSEABase](#). This object is stored in `metadata(inSCE)$sctk$genesets`, which can be accessed in downstream analysis functions such as [runCellQC](#).

**Value**

A [SingleCellExperiment](#) object with gene set from collectionName output stored to the [metadata](#) slot.

**Author(s)**

Joshua D. Campbell

**See Also**

[importGeneSetsFromList](#) for importing from lists, [importGeneSetsFromGMT](#) for importing from GMT files, and [importGeneSetsFromMSigDB](#) for importing MSigDB gene sets.

**Examples**

```
data(scExample)
library(GSEABase)
gs1 <- GeneSet(setName = "geneset1", geneIds = rownames(sce)[seq(10)])
gs2 <- GeneSet(setName = "geneset2", geneIds = rownames(sce)[seq(11,20)])
gsc <- GeneSetCollection(list(gs1, gs2))
sce <- importGeneSetsFromCollection(inSCE = sce,
                                   geneSetCollection = gsc,
                                   by = "rownames")
```

---

`importGeneSetsFromGMT` *Imports gene sets from a GMT file*

---

**Description**

Converts a list of gene sets stored in a GMT file into a [GeneSetCollection](#) and stores it in the metadata of the [SingleCellExperiment](#) object. These gene sets can be used in downstream quality control and analysis functions in [singleCellTK](#).

**Usage**

```
importGeneSetsFromGMT(
  inSCE,
  file,
  collectionName = "GeneSetCollection",
  by = "rownames",
  sep = "\t"
)
```



## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
file	Character. Path to GMT file. See <a href="#">getGmt</a> for more information on reading GMT files.
collectionName	Character. Name of collection to add gene sets to. If this collection already exists in inSCE, then these gene sets will be added to that collection. Any gene sets within the collection with the same name will be overwritten. Default <code>GeneSetCollection</code> .
by	Character, character vector, or NULL. Describes the location within inSCE where the gene identifiers in <code>geneSetList</code> should be mapped. If set to "rownames" then the features will be searched for among <code>rownames(inSCE)</code> . This can also be set to one of the column names of <code>rowData(inSCE)</code> in which case the gene identifiers will be mapped to that column in the <code>rowData</code> of inSCE. <code>by</code> can be a vector the same length as the number of gene sets in the GMT file and the elements of the vector can point to different locations within inSCE. Finally, <code>by</code> can be NULL. In this case, the location of the gene identifiers in inSCE should be saved in the description (2nd column) of the GMT file. See <a href="#">featureIndex</a> for more information. Default "rownames".
sep	Character. Delimiter of the GMT file. Default "\t".

## Details

The gene identifiers in gene sets in the GMT file will be mapped to the rownames of inSCE using the `by` parameter and stored in a [GeneSetCollection](#) object from package [GSEABase](#). This object is stored in `metadata(inSCE)$sctk$genesets`, which can be accessed in downstream analysis functions such as [runCellQC](#).

## Value

A [SingleCellExperiment](#) object with gene set from `collectionName` output stored to the `metadata` slot.

## Author(s)

Joshua D. Campbell

## See Also

[importGeneSetsFromList](#) for importing from lists, [importGeneSetsFromCollection](#) for importing from [GeneSetCollection](#) objects, and [importGeneSetsFromMSigDB](#) for importing MSigDB gene sets.

## Examples

```
data(scExample)

# GMT file containing gene symbols for a subset of human mitochondrial genes
gmt <- system.file("extdata/mito_subset.gmt", package = "singleCellTK")
```

```
# "feature_name" is the second column in the GMT file, so the ids will
# be mapped using this column in the 'rowData' of 'sce'. This
# could also be accomplished by setting by = "feature_name" in the
# function call.
sce <- importGeneSetsFromGMT(inSCE = sce, file = gmt, by = NULL)
```

---

```
importGeneSetsFromList
```

*Imports gene sets from a list*

---

### Description

Converts a list of gene sets into a [GeneSetCollection](#) and stores it in the metadata of the [SingleCellExperiment](#) object. These gene sets can be used in downstream quality control and analysis functions in [singleCellTK](#).

### Usage

```
importGeneSetsFromList(
  inSCE,
  geneSetList,
  collectionName = "GeneSetCollection",
  by = "rownames"
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
geneSetList	Named List. A list containing one or more gene sets. Each element of the list should be a character vector of gene identifiers. The names of the list will become the gene set names in the <a href="#">GeneSetCollection</a> object.
collectionName	Character. Name of collection to add gene sets to. If this collection already exists in inSCE, then these gene sets will be added to that collection. Any gene sets within the collection with the same name will be overwritten. Default <a href="#">GeneSetCollection</a> .
by	Character or character vector. Describes the location within inSCE where the gene identifiers in geneSetList should be mapped. If set to "rownames" then the features will be searched for among rownames(inSCE). This can also be set to one of the column names of rowData(inSCE) in which case the gene identifiers will be mapped to that column in the rowData of inSCE. Finally, by can be a vector the same length as the number of gene sets in geneSetList and the elements of the vector can point to different locations within inSCE. See <a href="#">featureIndex</a> for more information. Default "rownames".

**Details**

The gene identifiers in gene sets in `geneSetList` will be mapped to the rownames of `inSCE` using the `by` parameter and stored in a [GeneSetCollection](#) object from package [GSEABase](#). This object is stored in `metadata(inSCE)$sctk$genesets`, which can be accessed in downstream analysis functions such as [runCellQC](#).

**Value**

A [SingleCellExperiment](#) object with gene set from `collectionName` output stored to the `metadata` slot.

**Author(s)**

Joshua D. Campbell

**See Also**

[importGeneSetsFromCollection](#) for importing from [GeneSetCollection](#) objects, [importGeneSetsFromGMT](#) for importing from GMT files, and [importGeneSetsFromMSigDB](#) for importing MSigDB gene sets.

**Examples**

```
data(scExample)

# Generate gene sets from 'rownames'
gs1 <- rownames(sce)[seq(10)]
gs2 <- rownames(sce)[seq(11,20)]
gs <- list("geneset1" = gs1, "geneset2" = gs2)
sce <- importGeneSetsFromList(inSCE = sce,
                             geneSetList = gs,
                             by = "rownames")

# Generate a gene set for mitochondrial genes using
# Gene Symbols stored in 'rowData'
mito.ix <- grep("^MT-", rowData(sce)$feature_name)
mito <- list(mito = rowData(sce)$feature_name[mito.ix])
sce <- importGeneSetsFromList(inSCE = sce,
                             geneSetList = mito,
                             by = "feature_name")
```

---

```
importGeneSetsFromMSigDB
```

*Imports gene sets from MSigDB*

---

**Description**

Gets a list of MSigDB gene sets stores it in the metadata of the [SingleCellExperiment](#) object. These gene sets can be used in downstream quality control and analysis functions in [singleCellTK](#).

**Usage**

```
importGeneSetsFromMSigDB(
  inSCE,
  categoryIDs,
  species = "Homo sapiens",
  mapping = c("gene_symbol", "human_gene_symbol", "entrez_gene"),
  by = "rownames",
  verbose = TRUE
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
categoryIDs	Character vector containing the MSigDB gene set ids. The column ID in the table returned by <code>getMSigDBTable()</code> shows the list of possible gene set IDs that can be obtained.
species	Character. Species available can be found using the function <code>msigdbr_show_species</code> . Default "Homo sapiens".
mapping	Character. One of "gene_symbol", "human_gene_symbol", or "entrez_gene". Gene identifiers to be used for MSigDB gene sets. IDs denoted by the <code>by</code> parameter must be either in gene symbol or Entrez gene id format to match IDs from MSigDB.
by	Character. Describes the location within <code>inSCE</code> where the gene identifiers in the MSigDB gene sets should be mapped. If set to "rownames" then the features will be searched for among <code>rownames(inSCE)</code> . This can also be set to one of the column names of <code>rowData(inSCE)</code> in which case the gene identifiers will be mapped to that column in the <code>rowData</code> of <code>inSCE</code> . See <a href="#">featureIndex</a> for more information. Default "rownames".
verbose	Boolean. Whether to display progress. Default TRUE.

**Details**

The gene identifiers in gene sets from MSigDB will be retrieved using the `msigdbr` package. They will be mapped to the IDs in `inSCE` using the `by` parameter and stored in a [GeneSetCollection](#) object from package `GSEABase`. This object is stored in `metadata(inSCE)$sctk$genesets`, which can be accessed in downstream analysis functions such as `runCellQC`.

**Value**

A [SingleCellExperiment](#) object with gene set from `collectionName` output stored to the `metadata` slot.

**Author(s)**

Joshua D. Campbell

**See Also**

[importGeneSetsFromList](#) for importing from lists, [importGeneSetsFromGMT](#) for importing from GMT files, and [GeneSetCollection](#) objects.

**Examples**

```
data(scExample)
sce <- importGeneSetsFromMSigDB(inSCE = sce,
                                categoryIDs = "H",
                                species = "Homo sapiens",
                                mapping = "gene_symbol",
                                by = "feature_name")
```

---

importMitoGeneSet	<i>Import mitochondrial gene sets</i>
-------------------	---------------------------------------

---

**Description**

Imports mitochondrial gene sets and stores it in the metadata of the [SingleCellExperiment](#) object. These gene sets can be used in downstream quality control and analysis functions in [singleCellTK](#).

**Usage**

```
importMitoGeneSet(
  inSCE,
  reference = "human",
  id = "ensembl",
  by = "rownames",
  collectionName = "human_mito"
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
reference	Character. Species available are "human" and "mouse".
id	Types of gene id. Now it supports "symbol", "entrez", "ensembl" and "ensemblTranscriptID".
by	Character. Describes the location within inSCE where the gene identifiers in the mitochondrial gene sets should be mapped. If set to "rownames" then the features will be searched for among rownames(inSCE). This can also be set to one of the column names of rowData(inSCE) in which case the gene identifiers will be mapped to that column in the rowData of inSCE. See <a href="#">featureIndex</a> for more information. Default "rownames".
collectionName	Character. Name of collection to add gene sets to. If this collection already exists in inSCE, then these gene sets will be added to that collection. Any gene sets within the collection with the same name will be overwritten.

**Details**

The gene identifiers of mitochondrial genes will be loaded with "data(AllMito)". Currently, it supports human and mouse reference. Also, it supports entrez ID, gene symbol, ensemble ID and ensemble transcript ID. They will be mapped to the IDs in inSCE using the by parameter and stored in a [GeneSetCollection](#) object from package [GSEABase](#). This object is stored in metadata(inSCE)\$sctk\$genesets, which can be accessed in downstream analysis functions such as [runCellQC](#).

**Value**

A [SingleCellExperiment](#) object with gene set from collectionName output stored to the [metadata](#) slot.

**Author(s)**

Rui Hong

**See Also**

[importGeneSetsFromList](#) for importing from lists, [importGeneSetsFromGMT](#) for importing from GMT files, and [GeneSetCollection](#) objects.

**Examples**

```
data(scExample)
sce <- importMitoGeneSet(inSCE = sce,
                        reference = "human",
                        id = "ensembl",
                        collectionName = "human_mito",
                        by = "rownames")
```

---

`importMultipleSources` *Imports samples from different sources and compiles them into a list of SCE objects*

---

**Description**

Imports samples from different sources and compiles them into a list of SCE objects

**Usage**

```
importMultipleSources(allImportEntries, delayedArray = FALSE)
```

**Arguments**

`allImportEntries` object containing the sources and parameters of all the samples being imported (from the UI)

`delayedArray` Boolean. Whether to read the expression matrix as [DelayedArray](#) object or not. Default FALSE.

**Value**

A list of [SingleCellExperiment](#) object containing the droplet or cell data or both, depending on the dataType that users provided.

---

importOptimus	<i>Construct SCE object from Optimus output</i>
---------------	---

---

**Description**

Read the barcodes, features (genes), and matrices from Optimus outputs. Import them as one [SingleCellExperiment](#) object.

**Usage**

```
importOptimus(
  OptimusDirs,
  samples,
  matrixLocation = "call-MergeCountFiles/sparse_counts.npz",
  colIndexLocation = "call-MergeCountFiles/sparse_counts_col_index.npy",
  rowIndexLocation = "call-MergeCountFiles/sparse_counts_row_index.npy",
  cellMetricsLocation = "call-MergeCellMetrics/merged-cell-metrics.csv.gz",
  geneMetricsLocation = "call-MergeGeneMetrics/merged-gene-metrics.csv.gz",
  emptyDropsLocation = "call-RunEmptyDrops/empty_drops_result.csv",
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

**Arguments**

**OptimusDirs** A vector of root directories of Optimus output files. The paths should be something like this: /PATH/T0/bb4a2a5e-ff34-41b6-97d2-0c0c0c534530. Each entry in OptimusDirs is considered a sample and should have its own path. Must have the same length as samples.

**samples** A vector of user-defined sample names for the sample to be imported. Must have the same length as OptimusDirs.

**matrixLocation** Character. It is the intermediate path to the filtered count matrix file saved in sparse matrix format (. npz). Default call-MergeCountFiles/sparse\_counts.npz which works for optimus\_v1.4.0.

**colIndexLocation**

Character. The intermediate path to the barcode index file. Default call-MergeCountFiles/sparse\_co

**rowIndexLocation**

Character. The intermediate path to the feature (gene) index file. Default call-MergeCountFiles/spars

cellMetricsLocation	Character. It is the intermediate path to the cell metrics file (merged-cell-metrics.csv.gz). Default call-MergeCellMetrics/merged-cell-metrics.csv.gz which works for optimus_v1.4.0.
geneMetricsLocation	Character. It is the intermediate path to the feature (gene) metrics file (merged-gene-metrics.csv.gz). Default call-MergeGeneMetrics/merged-gene-metrics.csv.gz which works for optimus_v1.4.0.
emptyDropsLocation	Character. It is the intermediate path to <a href="#">emptyDrops</a> metrics file (empty_drops_result.csv). Default call-RunEmptyDrops/empty_drops_result.csv which works for optimus_v1.4.0.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

**Value**

A [SingleCellExperiment](#) object containing the count matrix, the gene annotation, and the cell annotation.

**Examples**

```
file.path <- system.file("extdata/Optimus_20x1000",
  package = "singleCellTK")
## Not run:
sce <- importOptimus(OptimusDirs = file.path,
  samples = "Optimus_20x1000")

## End(Not run)
```

---

importSEQC

---

*Construct SCE object from seqc output*


---

**Description**

Read the filtered barcodes, features, and matrices for all samples from (preferably a single run of) seqc output. Import and combine them as one big [SingleCellExperiment](#) object.



**Usage**

```
importSEQC(
  seqcDirs = NULL,
  samples = NULL,
  prefix = NULL,
  gzipped = FALSE,
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  cbNotFirstCol = TRUE,
  feNotFirstCol = TRUE,
  combinedSample = TRUE,
  rowNamesDedup = TRUE
)
```

**Arguments**

seqcDirs	A vector of paths to seqc output files. Each sample should have its own path. For example: <code>"/pbmc_1k_50x50"</code> . Must have the same length as <code>samples</code> .
samples	A vector of user-defined sample names for the samples to be imported. Must have the same length as <code>seqcDirs</code> .
prefix	A vector containing the prefix of file names within each sample directory. It cannot be null and the vector should have the same length as <code>samples</code> .
gzipped	Boolean. TRUE if the seqc output files ( <code>sparse_counts_barcode.csv</code> , <code>sparse_counts_genes.csv</code> , and <code>sparse_molecule_counts.mtx</code> ) were <code>gzip</code> compressed. FALSE otherwise. Default seqc outputs are not <code>gzip</code> ed. Default FALSE.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of <code>"Matrix"</code> (as returned by <code>readMM</code> function), or <code>"matrix"</code> (as returned by <code>matrix</code> function). Default <code>"Matrix"</code> .
delayedArray	Boolean. Whether to read the expression matrix as <code>DelayedArray</code> object or not. Default FALSE.
cbNotFirstCol	Boolean. TRUE if first column of <code>sparse_counts_barcode.csv</code> is row index and it will be removed. FALSE the first column will be kept.
feNotFirstCol	Boolean. TRUE if first column of <code>sparse_counts_genes.csv</code> is row index and it will be removed. FALSE the first column will be kept.
combinedSample	Boolean. If TRUE, <code>importSEQC</code> returns a <code>SingleCellExperiment</code> object containing the combined count matrix, feature annotations and the cell annotations. If FALSE, <code>importSEQC</code> returns a list containing multiple <code>SingleCellExperiment</code> objects. Each <code>SingleCellExperiment</code> contains count matrix, feature annotations and cell annotations for each sample.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Only applied if <code>combinedSample</code> is TRUE or only one <code>seqcDirs</code> specified. Default TRUE.

**Details**

`importSEQC` imports output from seqc. The default `sparse_counts_barcode.csv` or `sparse_counts_genes.csv` from seqc output contains two columns. The first column is row index and the second column

is cell-barcode or gene symbol. importSEQC will remove first column. Alternatively, user can call `cbNotFirstCol` or `feNotFirstCol` as `FALSE` to keep the first column of these files. When `combinedSample` is `TRUE`, importSEQC will combined count matrix with genes detected in at least one sample.

### Value

A `SingleCellExperiment` object containing the combined count matrix, the feature annotations, and the cell annotation.

### Examples

```
# Example #1
# The following filtered feature, cell, and matrix files were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/
# 3.0.0/pbmc_1k_v3
# The top 50 hg38 genes are included in this example.
# Only the top 50 cells are included.
sce <- importSEQC(
  seqcDirs = system.file("extdata/pbmc_1k_50x50", package = "singleCellTK"),
  samples = "pbmc_1k_50x50",
  prefix = "pbmc_1k",
  combinedSample = FALSE)
```

---

importSTARsolo

*Construct SCE object from STARsolo outputs*

---

### Description

Read the barcodes, features (genes), and matrices from STARsolo outputs. Import them as one [SingleCellExperiment](#) object.

### Usage

```
importSTARsolo(
  STARsoloDirs,
  samples,
  STARsoloOuts = "Gene/filtered",
  matrixFileNames = "matrix.mtx",
  featuresFileNames = "features.tsv",
  barcodesFileNames = "barcodes.tsv",
  gzipped = "auto",
  class = c("Matrix", "matrix"),
  delayedArray = FALSE,
  rowNamesDedup = TRUE
)
```

**Arguments**

STARsoloDirs	A vector of root directories of STARsolo output files. The paths should be something like this: <b>/PATH/TO/prefixSolo.out</b> . For example: ./Solo.out. Each sample should have its own path. Must have the same length as samples.
samples	A vector of user-defined sample names for the sample to be imported. Must have the same length as STARsoloDirs.
STARsoloOuts	Character vector. The intermediate paths to filtered or raw cell barcode, feature, and matrix files for each of samples. Default "Gene/filtered" which works for STAR 2.7.3a. Must have length 1 or the same length as samples.
matrixFileNames	Filenames for the Market Exchange Format (MEX) sparse matrix file (.mtx file). Must have length 1 or the same length as samples.
featuresFileNames	Filenames for the feature annotation file. Must have length 1 or the same length as samples.
barcodesFileNames	Filenames for the cell barcode list file. Must have length 1 or the same length as samples.
gzipped	Boolean. TRUE if the STARsolo output files (barcodes.tsv, features.tsv, and matrix.mtx) were gzip compressed. FALSE otherwise. This is FALSE in STAR 2.7.3a. Default "auto" which automatically detects if the files are gzip compressed. Must have length 1 or the same length as samples.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <a href="#">readMM</a> function), or "matrix" (as returned by <a href="#">matrix</a> function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default FALSE.
rowNamesDedup	Boolean. Whether to deduplicate rownames. Default TRUE.

**Value**

A SingleCellExperiment object containing the count matrix, the gene annotation, and the cell annotation.

**Examples**

```
# Example #1
# FASTQ files were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.0
# /pbmc_1k_v3
# They were concatenated as follows:
# cat pbmc_1k_v3_S1_L001_R1_001.fastq.gz pbmc_1k_v3_S1_L002_R1_001.fastq.gz >
# pbmc_1k_v3_R1.fastq.gz
# cat pbmc_1k_v3_S1_L001_R2_001.fastq.gz pbmc_1k_v3_S1_L002_R2_001.fastq.gz >
# pbmc_1k_v3_R2.fastq.gz
# The following STARsolo command generates the filtered feature, cell, and
# matrix files
```

```

# STAR \
# --genomeDir ./index \
# --readFilesIn ./pbmc_1k_v3_R2.fastq.gz \
#               ./pbmc_1k_v3_R1.fastq.gz \
# --readFilesCommand zcat \
# --outSAMtype BAM Unsorted \
# --outBAMcompression -1 \
# --soloType CB_UMI_Simple \
# --soloCBwhitelist ./737K-august-2016.txt \
# --soloUMIlen 12

# The top 20 genes and the first 20 cells are included in this example.
sce <- importSTARsolo(
  STARsoloDirs = system.file("extdata/STARsolo_PBMC_1k_v3_20x20",
    package = "singleCellTK"),
  samples = "PBMC_1k_v3_20x20")

```

---

iterateSimulations      *Returns significance data from a snapshot.*

---

## Description

Returns significance data from a snapshot.

## Usage

```

iterateSimulations(
  originalData,
  useAssay = "counts",
  realLabels,
  totalReads,
  cells,
  iterations
)

```

## Arguments

originalData	The <a href="#">SingleCellExperiment</a> object storing all assay data from the shiny app.
useAssay	Character. The name of the assay to be used for subsampling.
realLabels	Character. The name of the condition of interest. Must match a name from sample data.
totalReads	Numeric. The total number of reads in the simulated dataset, to be split between all simulated cells.
cells	Numeric. The number of virtual cells to simulate.
iterations	Numeric. How many times should each experimental design be simulated.

**Value**

A matrix of significance information from a snapshot

**Examples**

```
data("mouseBrainSubsetSCE")
res <- iterateSimulations(mouseBrainSubsetSCE, realLabels = "level1class",
                          totalReads = 1000, cells = 10, iterations = 2)
```

---

listSampleSummaryStatsTables

*Lists the table of SCTK QC outputs stored within the metadata.*

---

**Description**

Returns a character vector of the tables within the metadata slot of the SingleCellExperiment object.

**Usage**

```
listSampleSummaryStatsTables(inSCE, ...)

## S4 method for signature 'SingleCellExperiment'
listSampleSummaryStatsTables(inSCE, ...)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved table within the <a href="#">metadata</a> data. Required.
...	Other arguments passed to the function.

**Value**

A character vector. Contains a list of summary tables within the SingleCellExperiment object.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- sampleSummaryStats(sce, simple = TRUE, statsName = "qc_table")
listSampleSummaryStatsTables(sce)
```

---

mergeSCEColData	<i>Merging colData from two singleCellExperiment objects</i>
-----------------	--

---

### Description

Merges colData of the singleCellExperiment objects obtained from the same dataset which contain differing colData. (i.e. raw data and filtered data)

### Usage

```
mergeSCEColData(inSCE1, inSCE2, id1 = "column_name", id2 = "column_name")
```

### Arguments

inSCE1	Input SingleCellExperiment object. The function will output this singleCellExperiment object with a combined colData from inSCE1 and inSCE2.
inSCE2	Input SingleCellExperiment object. colData from this object will be merged with colData from inSCE1 and loaded into inSCE1.
id1	Character vector. Column in colData of inSCE1 that will be used to combine inSCE1 and inSCE2. Default "column_name"
id2	Character vector. Column in colData of inSCE2 that will be used to combine inSCE1 and inSCE2. Default "column_name"

### Value

SingleCellExperiment object containing combined colData from both singleCellExperiment for samples in inSCE1.

### Examples

```
sce1 <- importCellRanger(  
  cellRangerDirs = system.file("extdata/", package = "singleCellTK"),  
  sampleDirs = "hgmm_1k_v3_20x20",  
  sampleNames = "hgmm1kv3",  
  dataType = "filtered")  
data(scExample)  
sce2 <- sce  
sce <- mergeSCEColData(inSCE1 = sce1, inSCE2 = sce2, id1 = "column_name", id2 = "column_name")
```

---

MitoGenes	<i>List of mitochondrial genes of multiple reference</i>
-----------	--

---

**Description**

A list of gene set that contains mitochondrial genes of multiple reference (hg38, hg19, mm10 and mm9). It contains multiple types of gene identifier: gene symbol, entrez ID, ensemble ID and ensemble transcript ID. It's used for the function 'importMitoGeneSet'.

**Usage**

```
data("MitoGenes")
```

**Format**

A list

**Examples**

```
data("MitoGenes")
```

---

mouseBrainSubsetSCE	<i>Example Single Cell RNA-Seq data in SingleCellExperiment Object, GSE60361 subset</i>
---------------------	---

---

**Description**

A subset of 30 cells from a single cell RNA-Seq experiment from Zeisel, et al. Science 2015. The data was produced from cells from the mouse somatosensory cortex (S1) and hippocampus (CA1). 15 of the cells were identified as oligodendrocytes and 15 of the cell were identified as microglia.

**Usage**

```
data("mouseBrainSubsetSCE")
```

**Format**

SingleCellExperiment

**Source**

DOI: 10.1126/science.aaa1934

**Examples**

```
data("mouseBrainSubsetSCE")
```

---

msigdb_table	<i>MSigDB gene set Category table</i>
--------------	---------------------------------------

---

**Description**

A table of gene set categories that can be download from MSigDB. The categories and descriptions can be found here: <https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp>. The IDs in the first column can be used to retrieve the gene sets for these categories using the [importGeneSetsFromMSigDB](#) function.

**Usage**

```
data("msigdb_table")
```

**Format**

A data.frame.

**Examples**

```
data("msigdb_table")
```

---

plotBarcodeRankDropsResults	<i>Plots for runEmptyDrops outputs.</i>
-----------------------------	---

---

**Description**

A wrapper function which visualizes outputs from the runEmptyDrops function stored in the col-Data slot of the SingleCellExperiment object via plots.

**Usage**

```
plotBarcodeRankDropsResults(  
  inSCE,  
  sample = NULL,  
  defaultTheme = TRUE,  
  dotSize = 0.5,  
  titleSize = 18,  
  axisLabelSize = 18,  
  axisSize = 15,  
  legendSize = 15  
)
```



**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runBarcodeRankDrops</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
titleSize	Size of title of plot. Default 18.
axisLabelSize	Size of x/y-axis labels. Default 18.
axisSize	Size of x/y-axis ticks. Default 15.
legendSize	size of legend. Default 15.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- runBarcodeRankDrops(inSCE=sce)
plotBarcodeRankDropsResults(inSCE=sce)
```

---

plotBarcodeRankScatter

*Plots for runBarcodeRankDrops outputs.*

---

**Description**

A plotting function which visualizes outputs from the runBarcodeRankDrops function stored in the colData slot of the SingleCellExperiment object via scatterplot.

**Usage**

```
plotBarcodeRankScatter(
  inSCE,
  sample = NULL,
  defaultTheme = TRUE,
  dotSize = 0.5,
  title = NULL,
  titleSize = 18,
  xlab = NULL,
  ylab = NULL,
  axisSize = 12,
  axisLabelSize = 15,
  legendSize = 10,
  combinePlot = "none",
```

```

    sampleRelHeights = 1,
    sampleRelWidths = 1
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runBarcodeRankDrops</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 18.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 12.
axisLabelSize	Size of x/y-axis labels. Default 15.
legendSize	size of legend. Default 10.
combinePlot	Boolean. If multiple plots are generated (multiple samples, etc.), will combined plots using 'cowplot::plot_grid'.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default TRUE.

### Value

a ggplot object of the scatter plot.

### Examples

```

data(scExample, package="singleCellTK")
sce <- runBarcodeRankDrops(inSCE=sce)
plotBarcodeRankScatter(inSCE=sce)

```

---

plotBatchCorrCompare *Plot comparison of batch corrected result against original assay*

---

## Description

Plot comparison of batch corrected result against original assay

## Usage

```
plotBatchCorrCompare(  
  inSCE,  
  corrMat,  
  batch = NULL,  
  condition = NULL,  
  origAssay = NULL,  
  origLogged = NULL,  
  method = NULL,  
  matType = NULL  
)
```

## Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
corrMat	A single character indicating the name of the corrected matrix.
batch	A single character. The name of batch annotation column in <code>colData(inSCE)</code> .
condition	A single character. The name of an additional covariate annotation column in <code>colData(inSCE)</code> .
origAssay	A single character indicating what the original assay used for batch correction is.
origLogged	Logical scalar indicating whether <code>origAssay</code> is log-normalized.
method	A single character indicating the name of the batch correction method. Only used for the titles of plots.
matType	A single character indicating the type of the batch correction result matrix, choose from "assay", "altExp", "reducedDim".

## Details

Four plots will be combined. Two of them are violin/box-plots for percent variance explained by the batch variation, and optionally the covariate, for original and corrected. The other two are UMAPs of the original assay and the correction result matrix. If SCTK batch correction methods are performed in advance, this function will automatically detect necessary input. Otherwise, users can also customize the input. Future improvement might include solution to reduce redundant UMAP calculation.

**Value**

An object of class "gtable", combining four ggplots.

**Author(s)**

Yichen Wang

**Examples**

```
data("sceBatches")
sceBatches <- scatterlogNormCounts(sceBatches, "logcounts")
sceBatches <- runLimmaBC(sceBatches)
plotBatchCorrCompare(sceBatches, "LIMMA", condition = "cell_type")
```

---

plotBatchVariance	<i>Plot the percent of the variation that is explained by batch and condition in the data</i>
-------------------	---

---

**Description**

Visualize the percent variation in the data that is explained by batch and condition, individually, and that explained by combining both annotations. Plotting only the variation explained by batch is supported but not recommended, because this can be confounded by potential condition.

**Usage**

```
plotBatchVariance(
  inSCE,
  useAssay = NULL,
  useReddim = NULL,
  useAltExp = NULL,
  batch = "batch",
  condition = NULL,
  title = NULL
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useAssay	A single character. The name of the assay that stores the value to plot. For useReddim and useAltExp also. Default NULL.
useReddim	A single character. The name of the dimension reduced matrix that stores the value to plot. Default NULL.
useAltExp	A single character. The name of the alternative experiment that stores an assay of the value to plot. Default NULL.
batch	A single character. The name of batch annotation column in colData(inSCE). Default "batch".

condition	A single character. The name of an additional condition annotation column in <code>colData(inSCE)</code> . Default NULL.
title	A single character. The title text on the top. Default NULL.

### Details

When condition and batch both are causing some variation, if the difference between full variation and condition variation is close to batch variation, this might imply that batches are causing some effect; if the difference is much less than batch variation, then the batches are likely to be confounded by the conditions.

### Value

A ggplot object of a boxplot of variation explained by batch, condition, and batch+condition.

### Examples

```
data('sceBatches', package = 'singleCellTK')
plotBatchVariance(sceBatches,
                  useAssay="counts",
                  batch="batch",
                  condition = "cell_type")
```

---

plotBcdsResults      *Plots for runBcds outputs.*

---

### Description

A wrapper function which visualizes outputs from the `runBcds` function stored in the `colData` slot of the `SingleCellExperiment` object via various plots.

### Usage

```
plotBcdsResults(
  inSCE,
  sample = NULL,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,
  boxplot = FALSE,
  dots = TRUE,
  reducedDimName = "UMAP",
  xlab = NULL,
  ylab = NULL,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
```

```

binLabel = NULL,
defaultTheme = TRUE,
dotSize = 0.5,
summary = "median",
summaryTextSize = 3,
transparency = 1,
baseSize = 15,
titleSize = NULL,
axisLabelSize = NULL,
axisSize = NULL,
legendSize = NULL,
legendTitleSize = NULL,
relHeights = 1,
relWidths = c(1, 1, 1),
plotNCols = NULL,
plotNRows = NULL,
labelSamples = TRUE,
samplePerColumn = TRUE,
sampleRelHeights = 1,
sampleRelWidths = 1
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runBcDs</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single <code>.ggplot</code> object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.

bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 15. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNCols	Number of columns when plots are combined in a grid.
plotNRows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runBcds(sce)
plotBcdsResults(inSCE=sce, reducedDimName="UMAP")
```

---

plotClusterAbundance *Plot the differential Abundance*

---

## Description

Plot the differential Abundance

## Usage

```
plotClusterAbundance(inSCE, cluster, variable, combinePlot = c("all", "none"))
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
cluster	A single character, specifying the name to store the cluster label in <a href="#">colData</a> .
variable	A single character, specifying the name to store the phenotype labels in <a href="#">colData</a> .
combinePlot	Must be either "all" or "none". "all" will combine all plots into a single <a href="#">ggplot</a> object. Default "all".

## Details

This function will visualize the differential abundance in two given variables, by making bar plots that presents the cell counting and fraction in different cases.

## Value

When `combinePlot = "none"`, a list with 4 [ggplot](#) objects; when `combinePlot = "all"`, a single [ggplot](#) object with for subplots.

## Examples

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
plotClusterAbundance(inSCE = mouseBrainSubsetSCE,
                     cluster = "tissue",
                     variable = "level1class")
```



---

plotClusterPseudo	<i>Run plotClusterPseudo function to plot TSCAN-derived pseudotimes around cluster in the dataset.</i>
-------------------	--

---

### Description

A wrapper function which visualizes outputs from the [runTSCANClusterDEAnalysis](#) function. Each point is a cell in the cluster and is colored by its pseudotime value along the path to which it was assigned.

### Usage

```
plotClusterPseudo(inSCE, useClusters, pathIndex = NULL, useReducedDim)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useClusters	Choose the cluster containing the branch point in the data in order to recompute the pseudotimes so that the root lies at the cluster center, allowing us to detect genes that are associated with the divergence of the branches.
pathIndex	Path number for which the pseudotime values should be used. PathIndex corresponds to one path from the root node to one of the terminal nodes.
useReducedDim	Saved dimension reduction name in inSCE. Required.

### Value

A plots with the TSCAN-derived pseudotimes of all the cells along the path belonging to the cluster

### Author(s)

Nida Pervaiz

### Examples

```
data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterLogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
  useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
  reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
sce <- runTSCANClusterDEAnalysis(inSCE = sce, useClusters = 5)
plotClusterPseudo(inSCE = sce, useClusters = 5, pathIndex = NULL,
  useReducedDim = "TSNE")
```

---

plotCxlsResults      *Plots for runCxls outputs.*

---

### Description

A wrapper function which visualizes outputs from the runCxls function stored in the colData slot of the SingleCellExperiment object via various plots.

### Usage

```
plotCxlsResults(  
  inSCE,  
  sample = NULL,  
  shape = NULL,  
  groupBy = NULL,  
  combinePlot = "all",  
  violin = TRUE,  
  boxplot = FALSE,  
  dots = TRUE,  
  reducedDimName = "UMAP",  
  xlab = NULL,  
  ylab = NULL,  
  dim1 = NULL,  
  dim2 = NULL,  
  bin = NULL,  
  binLabel = NULL,  
  defaultTheme = TRUE,  
  dotSize = 0.5,  
  summary = "median",  
  summaryTextSize = 3,  
  transparency = 1,  
  baseSize = 15,  
  titleSize = NULL,  
  axisLabelSize = NULL,  
  axisSize = NULL,  
  legendSize = NULL,  
  legendTitleSize = NULL,  
  relHeights = 1,  
  relWidths = c(1, 1, 1),  
  plotNCols = NULL,  
  plotNRows = NULL,  
  labelSamples = TRUE,  
  samplePerColumn = TRUE,  
  sampleRelHeights = 1,  
  sampleRelWidths = 1  
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runCxds</a> .
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single <a href="#">.ggplot</a> object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.

legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNCols	Number of columns when plots are combined in a grid.
plotNRows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runCxls(sce)
plotCxlsResults(inSCE=sce, reducedDimName="UMAP")
```

---

plotDecontXResults      *Plots for runDecontX outputs.*

---

**Description**

A wrapper function which visualizes outputs from the runDecontX function stored in the colData slot of the SingleCellExperiment object via various plots.

**Usage**

```
plotDecontXResults(
  inSCE,
  sample = NULL,
  bgResult = FALSE,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
```

```

violin = TRUE,
boxplot = FALSE,
dots = TRUE,
reducedDimName = "UMAP",
xlab = NULL,
ylab = NULL,
dim1 = NULL,
dim2 = NULL,
bin = NULL,
binLabel = NULL,
defaultTheme = TRUE,
dotSize = 0.5,
summary = "median",
summaryTextSize = 3,
transparency = 1,
baseSize = 15,
titleSize = NULL,
axisLabelSize = NULL,
axisSize = NULL,
legendSize = NULL,
legendTitleSize = NULL,
relHeights = 1,
relWidths = c(1, 1, 1),
plotNCols = NULL,
plotNRows = NULL,
labelSamples = TRUE,
labelClusters = TRUE,
clusterLabelSize = 3.5,
samplePerColumn = TRUE,
sampleRelHeights = 1,
sampleRelWidths = 1
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runDecontX</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
bgResult	Boolean. If TRUE, will plot decontX results generated with raw/droplet matrix. Default FALSE.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single <code>.ggplot</code> object, while "sample" will output a list of plots separated by sample. Default "all".

<code>violin</code>	Boolean. If TRUE, will plot the violin plot. Default TRUE.
<code>boxplot</code>	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
<code>dots</code>	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
<code>reducedDimName</code>	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required. Default = "UMAP"
<code>xlab</code>	Character vector. Label for x-axis. Default NULL.
<code>ylab</code>	Character vector. Label for y-axis. Default NULL.
<code>dim1</code>	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
<code>dim2</code>	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
<code>bin</code>	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
<code>binLabel</code>	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
<code>defaultTheme</code>	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
<code>dotSize</code>	Size of dots. Default 0.5.
<code>summary</code>	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
<code>summaryTextSize</code>	The text size of the summary statistic displayed above the violin plot. Default 3.
<code>transparency</code>	Transparency of the dots, values will be 0-1. Default 1.
<code>baseSize</code>	The base font size for all text. Default 12. Can be overwritten by <code>titleSize</code> , <code>axisSize</code> , and <code>axisLabelSize</code> , <code>legendSize</code> , <code>legendTitleSize</code> .
<code>titleSize</code>	Size of title of plot. Default NULL.
<code>axisLabelSize</code>	Size of x/y-axis labels. Default NULL.
<code>axisSize</code>	Size of x/y-axis ticks. Default NULL.
<code>legendSize</code>	size of legend. Default NULL.
<code>legendTitleSize</code>	size of legend title. Default NULL.
<code>relHeights</code>	Relative heights of plots when <code>combine</code> is set.
<code>relWidths</code>	Relative widths of plots when <code>combine</code> is set.
<code>plotNCols</code>	Number of columns when plots are combined in a grid.
<code>plotNRows</code>	Number of rows when plots are combined in a grid.
<code>labelSamples</code>	Will label sample name in title of plot if TRUE. Default TRUE.
<code>labelClusters</code>	Logical. Whether the cluster labels are plotted. Default FALSE.
<code>clusterLabelSize</code>	Numeric. Determines the size of cluster label when 'labelClusters' is set to TRUE. Default 3.5.

samplePerColumn  
If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.

sampleRelHeights  
If there are multiple samples and combining by "all", the relative heights for each plot.

sampleRelWidths  
If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runDecontX(sce)
plotDecontXResults(inSCE=sce, reducedDimName="decontX_UMAP")
```

---

plotDEGHeatmap

*Heatmap visualization of DEG result*

---

**Description**

Heatmap visualization of DEG result

**Usage**

```
plotDEGHeatmap(
  inSCE,
  useResult,
  doLog = FALSE,
  onlyPos = FALSE,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL,
  useAssay = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  rowDataName = NULL,
```

```

colDataName = NULL,
colSplitBy = "condition",
rowSplitBy = "regulation",
title = paste0("DE Analysis: ", useResult),
...
)

```

## Arguments

**inSCE** [SingleCellExperiment](#) inherited object.

**useResult** character. A string specifying the analysisName used when running a differential expression analysis function.

**doLog** Logical scalar. Whether to do  $\log(\text{assay} + 1)$  transformation on the assay used for the analysis. Default FALSE.

**onlyPos** logical. Whether to only plot DEG with positive  $\log_2\_FC$  value. Default FALSE.

**log2fcThreshold** numeric. Only plot DEGs with the absolute values of  $\log_2FC$  larger than this value. Default 0.25.

**fdrThreshold** numeric. Only plot DEGs with FDR value smaller than this value. Default 0.05.

**minGroup1MeanExp** numeric. Only plot DEGs with mean expression in group1 greater than this value. Default NULL.

**maxGroup2MeanExp** numeric. Only plot DEGs with mean expression in group2 less than this value. Default NULL.

**minGroup1ExprPerc** numeric. Only plot DEGs expressed in greater than this fraction of cells in group1. Default NULL.

**maxGroup2ExprPerc** numeric. Only plot DEGs expressed in less than this fraction of cells in group2. Default NULL.

**useAssay** character. A string specifying an assay of expression value to plot. By default the assay used for `runMAST()` will be used. Default NULL.

**featureAnnotations** data.frame, with rownames containing all the features going to be plotted. Character columns should be factors. Default NULL.

**cellAnnotations** data.frame, with rownames containing all the cells going to be plotted. Character columns should be factors. Default NULL.

**featureAnnotationColor** A named list. Customized color settings for feature labeling. Should match the entries in the `featureAnnotations` or `rowDataName`. For each entry, there should be a list/vector of colors named with categories. Default NULL.

**cellAnnotationColor** A named list. Customized color settings for cell labeling. Should match the entries in the `cellAnnotations` or `colDataName`. For each entry, there should be a list/vector of colors named with categories. Default NULL.



rowDataName	character. The column name(s) in rowData that need to be added to the annotation. Default NULL.
colDataName	character. The column name(s) in colData that need to be added to the annotation. Default NULL.
colSplitBy	character. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either colDataName or names(cellAnnotations). Default "condition".
rowSplitBy	character. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either rowDataName or names(featureAnnotations). Default "regulation".
title	character. Main title of the heatmap. Default "DE Analysis: <useResult>".
...	Other arguments passed to <a href="#">plotSCEHeatmap</a>

### Details

A differential expression analysis function has to be run in advance so that information is stored in the metadata of the input SCE object. This function wraps [plotSCEHeatmap](#). A feature annotation basing on the log2FC level called "regulation" will be automatically added. A cell annotation basing on the condition selection while running the analysis called "condition", and the annotations used from colData(inSCE) while setting the condition and covariates will also be added.

### Value

A [ggplot](#) object

### Author(s)

Yichen Wang

### Examples

```
data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type", classGroup1 = "alpha",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
plotDEGHeatmap(sce.w, "w.aVSb")
```

---

plotDEGRegression      *Create linear regression plot to show the expression the of top DEGs*

---

### Description

Create linear regression plot to show the expression the of top DEGs

**Usage**

```
plotDEGRegression(
  inSCE,
  useResult,
  threshP = FALSE,
  labelBy = NULL,
  nrow = 6,
  ncol = 6,
  defaultTheme = TRUE,
  isLogged = TRUE,
  check_sanity = TRUE
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
threshP	logical. Whether to plot threshold values from adaptive thresholding, instead of using the assay used by when performing DE analysis. Default FALSE.
labelBy	A single character for a column of rowData(inSCE) as where to search for the labeling text. Default NULL.
nrow	Integer. Number of rows in the plot grid. Default 6.
ncol	Integer. Number of columns in the plot grid. Default 6.
defaultTheme	Logical scalar. Whether to use default SCTK theme in ggplot. Default TRUE.
isLogged	Logical scalar. Whether the assay used for the analysis is logged. If not, will do a log(assay + 1) transformation. Default TRUE.
check_sanity	Logical scalar. Whether to perform MAST's sanity check to see if the counts are logged. Default TRUE

**Details**

Any of the differential expression analysis method from SCTK should be performed prior to using this function

**Value**

A ggplot object of linear regression

**Examples**

```
data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type", classGroup1 = "alpha",
  groupName1 = "w.alpha", groupName2 = "w.beta",
  analysisName = "w.aVSb")
plotDEGRegression(sce.w, "w.aVSb")
```

---

plotDEGViolin	<i>Generate violin plot to show the expression of top DEGs</i>
---------------	--

---

### Description

Generate violin plot to show the expression of top DEGs

### Usage

```
plotDEGViolin(  
  inSCE,  
  useResult,  
  threshP = FALSE,  
  labelBy = NULL,  
  nrow = 6,  
  ncol = 6,  
  defaultTheme = TRUE,  
  isLogged = TRUE,  
  check_sanity = TRUE  
)
```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
threshP	logical. Whether to plot threshold values from adaptive thresholding, instead of using the assay used by runMAST(). Default FALSE.
labelBy	A single character for a column of rowData(inSCE) as where to search for the labeling text. Default NULL.
nrow	Integer. Number of rows in the plot grid. Default 6.
ncol	Integer. Number of columns in the plot grid. Default 6.
defaultTheme	Logical scalar. Whether to use default SCTK theme in ggplot. Default TRUE.
isLogged	Logical scalar. Whether the assay used for the analysis is logged. If not, will do a log(assay + 1) transformation. Default TRUE.
check_sanity	Logical scalar. Whether to perform MAST's sanity check to see if the counts are logged. Default TRUE

### Details

Any of the differential expression analysis method from SCTK should be performed prior to using this function

### Value

A ggplot object of violin plot

**Examples**

```

data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type", classGroup1 = "alpha",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
plotDEGViolin(sce.w, "w.aVSb")

```

---

plotDEGVolcano	<i>Generate volcano plot for DEGs</i>
----------------	---------------------------------------

---

**Description**

Generate volcano plot for DEGs

**Usage**

```

plotDEGVolcano(
  inSCE,
  useResult,
  labelTopN = 10,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05
)

```

**Arguments**

<code>inSCE</code>	<a href="#">SingleCellExperiment</a> inherited object.
<code>useResult</code>	character. A string specifying the analysisName used when running a differential expression analysis function.
<code>labelTopN</code>	Integer, label this number of top DEGs that pass the filters.
<code>log2fcThreshold</code>	numeric. Label genes with the absolute values of log2FC greater than this value as regulated. Default 0.25.
<code>fdrThreshold</code>	numeric. Label genes with FDR value less than this value as regulated. Default 0.05.

**Details**

Any of the differential expression analysis method from SCTK should be performed prior to using this function to generate volcano plots.

**Value**

A ggplot object of volcano plot

**Examples**

```

data("sceBatches")
sceBatches <- scaterlogNormCounts(sceBatches, "logcounts")
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type", classGroup1 = "alpha",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
plotDEGVolcano(sce.w, "w.aVSb")

```

---

plotDimRed	<i>Plot dimensionality reduction from computed metrics including PCA, ICA, tSNE and UMAP</i>
------------	--

---

**Description**

Plot dimensionality reduction from computed metrics including PCA, ICA, tSNE and UMAP

**Usage**

```

plotDimRed(
  inSCE,
  useReduction,
  showLegend = FALSE,
  xDim = 1,
  yDim = 2,
  xAxisLabel = NULL,
  yAxisLabel = NULL
)

```

**Arguments**

inSCE	Input SCE object
useReduction	Reduction to plot
showLegend	If legends should be plotted or not
xDim	Numeric value indicating the dimension to use for X-axis. Default is 1 (refers to PC1).
yDim	Numeric value indicating the dimension to use for Y-axis. Default is 2 (refers to PC2).
xAxisLabel	Specify the label for x-axis. Default is NULL which will specify the label as 'x'.
yAxisLabel	Specify the label for y-axis. Default is NULL which will specify the label as 'y'.

**Value**

plot object

### Examples

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
plotDimRed(mouseBrainSubsetSCE, "PCA_logcounts")
```

---

plotDoubletFinderResults

*Plots for runDoubletFinder outputs.*

---

### Description

A wrapper function which visualizes outputs from the runDoubletFinder function stored in the colData slot of the SingleCellExperiment object via various plots.

### Usage

```
plotDoubletFinderResults(  
  inSCE,  
  sample = NULL,  
  shape = NULL,  
  groupBy = NULL,  
  combinePlot = "all",  
  violin = TRUE,  
  boxplot = FALSE,  
  dots = TRUE,  
  reducedDimName = "UMAP",  
  xlab = NULL,  
  ylab = NULL,  
  dim1 = NULL,  
  dim2 = NULL,  
  bin = NULL,  
  binLabel = NULL,  
  defaultTheme = TRUE,  
  dotSize = 0.5,  
  summary = "median",  
  summaryTextSize = 3,  
  transparency = 1,  
  baseSize = 15,  
  titleSize = NULL,  
  axisLabelSize = NULL,  
  axisSize = NULL,  
  legendSize = NULL,  
  legendTitleSize = NULL,  
  relHeights = 1,  
  relWidths = c(1, 1, 1),  
  plotNcols = NULL,  
  plotNrows = NULL,  
  labelSamples = TRUE,
```

```

    samplePerColumn = TRUE,
    sampleRelHeights = 1,
    sampleRelWidths = 1
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runDoubletFinder</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.

titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNcols	Number of columns when plots are combined in a grid.
plotNrows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runDoubletFinder(sce)
plotDoubletFinderResults(inSCE=sce, reducedDimName="UMAP")
```

---

plotEmptyDropsResults *Plots for runEmptyDrops outputs.*

---

**Description**

A wrapper function which visualizes outputs from the runEmptyDrops function stored in the colData slot of the SingleCellExperiment object via plots.



**Usage**

```
plotEmptyDropsResults(
  inSCE,
  sample = NULL,
  combinePlot = "all",
  fdrCutoff = 0.01,
  defaultTheme = TRUE,
  dotSize = 0.5,
  titleSize = 18,
  axisLabelSize = 18,
  axisSize = 15,
  legendSize = 15,
  legendTitleSize = 16,
  relHeights = 1,
  relWidths = 1,
  samplePerColumn = TRUE,
  sampleRelHeights = 1,
  sampleRelWidths = 1
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runScrublet</a> . Required.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to. Default NULL.
<code>combinePlot</code>	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "all".
<code>fdrCutoff</code>	Numeric. Thresholds barcodes based on the FDR values from <code>runEmptyDrops</code> as "Empty Droplet" or "Putative Cell". Default 0.01.
<code>defaultTheme</code>	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
<code>dotSize</code>	Size of dots. Default 0.5.
<code>titleSize</code>	Size of title of plot. Default 18.
<code>axisLabelSize</code>	Size of x/y-axis labels. Default 18.
<code>axisSize</code>	Size of x/y-axis ticks. Default 15.
<code>legendSize</code>	size of legend. Default 15.
<code>legendTitleSize</code>	size of legend title. Default 16.
<code>relHeights</code>	Relative heights of plots when combine is set.
<code>relWidths</code>	Relative widths of plots when combine is set.
<code>samplePerColumn</code>	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.

sampleRelHeights  
If there are multiple samples and combining by "all", the relative heights for each plot.

sampleRelWidths  
If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- runEmptyDrops(inSCE=sce)
plotEmptyDropsResults(inSCE=sce)
```

---

plotEmptyDropsScatter *Plots for runEmptyDrops outputs.*

---

**Description**

A plotting function which visualizes outputs from the runEmptyDrops function stored in the colData slot of the SingleCellExperiment object via scatterplot.

**Usage**

```
plotEmptyDropsScatter(
  inSCE,
  sample = NULL,
  fdrCutoff = 0.01,
  defaultTheme = TRUE,
  dotSize = 0.5,
  title = NULL,
  titleSize = 18,
  xlab = NULL,
  ylab = NULL,
  axisSize = 12,
  axisLabelSize = 15,
  legendTitle = NULL,
  legendTitleSize = 12,
  legendSize = 10,
  combinePlot = "none",
  relHeights = 1,
  relWidths = 1,
  samplePerColumn = TRUE,
  sampleRelHeights = 1,
  sampleRelWidths = 1
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runEmptyDrops</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
fdrCutoff	Numeric. Thresholds barcodes based on the FDR values from <a href="#">runEmptyDrops</a> as "Empty Droplet" or "Putative Cell". Default 0.01.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 18.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 12.
axisLabelSize	Size of x/y-axis labels. Default 15.
legendTitle	Title of legend. Default NULL.
legendTitleSize	size of legend title. Default 12.
legendSize	size of legend. Default 10.
combinePlot	Boolean. If multiple plots are generated (multiple samples, etc.), will combined plots using 'cowplot::plot_grid'. Default TRUE.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

a ggplot object of the scatter plot.

**Examples**

```
data(scExample, package="singleCellTK")
sce <- runEmptyDrops(inSCE=sce)
plotEmptyDropsScatter(inSCE=sce)
```

---

plotMarkerDiffExp      *Plot a heatmap to visualize the result of [findMarkerDiffExp](#)*

---

### Description

This function will first reads the result saved in metadata slot, named by "findMarker" and generated by [findMarkerDiffExp](#). Then it do the filtering on the statistics based on the input parameters and get unique genes to plot. We choose the genes that are identified as up-regulated only. As for the genes identified as up-regulated for multiple clusters, we only keep the belonging towards the one they have the highest Log2FC value. In the heatmap, there will always be a cell annotation for the cluster labeling used when finding the markers, and a feature annotation for which cluster each gene belongs to. And by default we split the heatmap by these two annotations. Additional legends can be added and the splitting can be canceled.

This function will first reads the result saved in metadata slot, named by "findMarker" and generated by [findMarkerDiffExp](#). Then it do the filtering on the statistics based on the input parameters and get unique genes to plot. We choose the genes that are identified as up-regulated only. As for the genes identified as up-regulated for multiple clusters, we only keep the belonging towards the one they have the highest Log2FC value. In the heatmap, there will always be a cell annotation for the cluster labeling used when finding the markers, and a feature annotation for which cluster each gene belongs to. And by default we split the heatmap by these two annotations. Additional legends can be added and the splitting can be canceled.

### Usage

```
plotMarkerDiffExp(
  inSCE,
  orderBy = "size",
  log2fcThreshold = 1,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.7,
  maxCtrlExprPerc = 0.4,
  minMeanExpr = 1,
  topN = 10,
  decreasing = TRUE,
  rowDataName = NULL,
  colDataName = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  colSplitBy = ifelse(is.null(orderBy), NULL, colnames(inSCE@metadata$findMarker)[5]),
  rowSplitBy = "marker",
  rowDend = FALSE,
  colDend = FALSE,
  title = "Top Marker Heatmap",
  ...
)
```

```

)

plotMarkerDiffExp(
  inSCE,
  orderBy = "size",
  log2fcThreshold = 1,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.7,
  maxCtrlExprPerc = 0.4,
  minMeanExpr = 1,
  topN = 10,
  decreasing = TRUE,
  rowDataName = NULL,
  colDataName = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  colSplitBy = ifelse(is.null(orderBy), NULL, colnames(inSCE@metadata$findMarker)[5]),
  rowSplitBy = "marker",
  rowDend = FALSE,
  colDend = FALSE,
  title = "Top Marker Heatmap",
  ...
)

```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
orderBy	The ordering method of the clusters on the splitted heatmap. Can be chosen from "size" or "name", specified with vector of ordered unique cluster labels, or set as NULL for unsplitted heatmap. Default "size".
log2fcThreshold	Only use DEGs with the absolute values of log2FC larger than this value. Default 1
fdrThreshold	Only use DEGs with FDR value smaller than this value. Default 0.05
minClustExprPerc	A numeric scalar. The minimum cutoff of the percentage of cells in the cluster of interests that expressed the marker gene. Default 0.7.
maxCtrlExprPerc	A numeric scalar. The maximum cutoff of the percentage of cells out of the cluster (control group) that expressed the marker gene. Default 0.4.
minMeanExpr	A numeric scalar. The minimum cutoff of the mean expression value of the marker in the cluster of interests. Default 1.
topN	An integer. Only to plot this number of top markers for each cluster in maximum, in terms of log2FC value. Use NULL to cancel the top N subscription. Default 10.

decreasing	Order the cluster decreasingly. Default TRUE.
rowDataName	character. The column name(s) in rowData that need to be added to the annotation. Default NULL.
colDataName	character. The column name(s) in colData that need to be added to the annotation. Default NULL.
featureAnnotations	data.frame, with rownames containing all the features going to be plotted. Character columns should be factors. Default NULL.
cellAnnotations	data.frame, with rownames containing all the cells going to be plotted. Character columns should be factors. Default NULL.
featureAnnotationColor	A named list. Customized color settings for feature labeling. Should match the entries in the featureAnnotations or rowDataName. For each entry, there should be a list/vector of colors named with categories. Default NULL.
cellAnnotationColor	A named list. Customized color settings for cell labeling. Should match the entries in the cellAnnotations or colDataName. For each entry, there should be a list/vector of colors named with categories. Default NULL.
colSplitBy	character vector. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either colDataName or names(cellAnnotations). Default is the value of cluster in <code>findMarkerDiffExp</code> when orderBy is not NULL, or NULL otherwise.
rowSplitBy	character vector. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either rowDataName or names(featureAnnotations). Default "marker", which indicates an auto generated annotation for this plot.
rowDend	Whether to display row dendrogram. Default FALSE.
colDend	Whether to display column dendrogram. Default FALSE.
title	Text of the title, at the top of the heatmap. Default "Top Marker Heatmap".
...	Other arguments passed to <code>plotSCEHeatmap</code> .

**Value**

A [Heatmap](#) object

A [Heatmap](#) object

**Author(s)**

Yichen Wang

Yichen Wang

**Examples**

```
data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
```

```
sce.w <- findMarkerDiffExp(sce.w, method = "wilcox", cluster = "cell_type")
plotMarkerDiffExp(sce.w)
data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- findMarkerDiffExp(sce.w, method = "wilcox", cluster = "cell_type")
plotMarkerDiffExp(sce.w)
```

---

plotMASTThresholdGenes

*MAST Identify adaptive thresholds*

---

### Description

Calculate and produce a list of thresholded counts (on natural scale), thresholds, bins, densities estimated on each bin, and the original data from [thresholdSCRNACountMatrix](#)

### Usage

```
plotMASTThresholdGenes(
  inSCE,
  useAssay = "logcounts",
  doPlot = TRUE,
  isLogged = TRUE,
  check_sanity = TRUE
)
```

### Arguments

inSCE	SingleCellExperiment object
useAssay	character, default "logcounts"
doPlot	Logical scalar. Whether to directly plot in the plotting area. If FALSE, will return a graphical object which can be visualized with <code>grid.draw()</code> . Default TRUE.
isLogged	Logical scalar. Whether the assay used for the analysis is logged. If not, will do a $\log(\text{assay} + 1)$ transformation. Default TRUE.
check_sanity	Logical scalar. Whether to perform MAST's sanity check to see if the counts are logged. Default TRUE

### Value

Plot the thresholding onto the plotting region if `plot == TRUE` or a graphical object if `plot == FALSE`.

### Examples

```
data("mouseBrainSubsetSCE")
plotMASTThresholdGenes(mouseBrainSubsetSCE)
```

---

plotPathway

*Generate violin plots for pathway analysis results*


---

### Description

Generate violin plots for pathway analysis results

### Usage

```
plotPathway(
  inSCE,
  resultName,
  geneset,
  groupBy = NULL,
  boxplot = FALSE,
  violin = TRUE,
  dots = TRUE,
  summary = "median",
  axisSize = 10,
  axisLabelSize = 10,
  dotSize = 0.5,
  transparency = 1,
  defaultTheme = TRUE,
  gridLine = FALSE,
  title = geneset,
  titleSize = NULL
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object. With <code>runGSVA()</code> or <code>runVAM()</code> applied in advance.
resultName	A single character of the name of a score matrix, which should be found in <code>getPathwayResultNames(inSCE)</code> .
geneset	A single character specifying the geneset of interest. Should be found in the <code>geneSetCollection</code> used for performing the analysis.
groupBy	Either a single character specifying a column of <code>colData(inSCE)</code> or a vector of equal length as the number of cells. Default <code>NULL</code> .
boxplot	Boolean, Whether to add a boxplot. Default <code>FALSE</code> .
violin	Boolean, Whether to add a violin plot. Default <code>TRUE</code> .
dots	Boolean, If <code>TRUE</code> , will plot dots for each violin plot. Default <code>TRUE</code> .
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median", and <code>NULL</code> for not adding. Default "median".
axisSize	Size of x/y-axis ticks. Default 10.



axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
title	Title of plot. Default using geneset.
titleSize	Size of the title of the plot. Default 15.

### Details

runGSVA() or runVAM() should be applied in advance of using this function. Users can group the data by specifying groupby.

### Value

A ggplot object for the violin plot

### Examples

```
data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
gs1 <- rownames(sce)[seq(10)]
gs2 <- rownames(sce)[seq(11,20)]
gs <- list("geneset1" = gs1, "geneset2" = gs2)
sce <- importGeneSetsFromList(inSCE = sce, geneSetList = gs,
                             by = "rownames")
sce <- runVAM(inSCE = sce, geneSetCollectionName = "GeneSetCollection",
             useAssay = "logcounts")
plotPathway(sce, "VAM_GeneSetCollection_CDF", "geneset1")
```

---

plotPCA

*Plot PCA run data from its components.*

---

### Description

Plot PCA run data from its components.

### Usage

```
plotPCA(
  inSCE,
  colorBy = "No Color",
  shape = "No Shape",
  pcX = "PC1",
  pcY = "PC2",
```

```

    reducedDimName = "PCA",
    runPCA = FALSE,
    useAssay = "logcounts"
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
colorBy	The variable to color clusters by
shape	Shape of the points
pcX	User choice for the first principal component
pcY	User choice for the second principal component
reducedDimName	a name to store the results of the dimension reduction coordinates obtained from this method. This is stored in the <a href="#">SingleCellExperiment</a> object in the reduced-Dims slot. Required.
runPCA	Run PCA if the reducedDimName does not exist. the Default is FALSE.
useAssay	Indicate which assay to use. The default is "logcounts".

### Value

A PCA plot

### Examples

```

data("mouseBrainSubsetSCE")
plotPCA(mouseBrainSubsetSCE, colorBy = "level1class",
        reducedDimName = "PCA_counts")

```

---

plotRunPerCellQCResults

*Plots for runPerCellQC outputs.*

---

### Description

A wrapper function which visualizes outputs from the runPerCellQC function stored in the colData slot of the [SingleCellExperiment](#) object via various plots.

### Usage

```

plotRunPerCellQCResults(
  inSCE,
  sample = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,

```

```

    boxplot = FALSE,
    dots = TRUE,
    dotSize = 0.5,
    summary = "median",
    summaryTextSize = 3,
    baseSize = 15,
    axisSize = NULL,
    axisLabelSize = NULL,
    transparency = 1,
    defaultTheme = TRUE,
    titleSize = NULL,
    relHeights = 1,
    relWidths = 1,
    labelSamples = TRUE,
    plotNcols = NULL,
    plotNrows = NULL,
    samplePerColumn = TRUE,
    sampleRelHeights = 1,
    sampleRelWidths = 1
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from runPerCellQC. Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default FALSE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default "median".
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
baseSize	The base font size for all text. Default 15. Can be overwritten by titleSize, axisSize, and axisLabelSize.
axisSize	Size of x/y-axis ticks. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
transparency	Transparency of the dots, values will be 0-1. Default 1.

defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
titleSize	Size of title of plot. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
plotNcols	Number of columns when plots are combined in a grid.
plotNRows	Number of rows when plots are combined in a grid.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
## Not run:
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runPerCellQC(sce)
plotRunPerCellQCResults(inSCE=sce)

## End(Not run)
```

---

plotScDblFinderResults

*Plots for runScDblFinder outputs.*

---

**Description**

A wrapper function which visualizes outputs from the runScDblFinder function stored in the colData slot of the SingleCellExperiment object via various plots.

**Usage**

```

plotScDbfFinderResults(
  inSCE,
  sample = NULL,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,
  boxplot = FALSE,
  dots = TRUE,
  reducedDimName = "UMAP",
  xlab = NULL,
  ylab = NULL,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
  binLabel = NULL,
  defaultTheme = TRUE,
  dotSize = 0.5,
  summary = "median",
  summaryTextSize = 3,
  transparency = 1,
  baseSize = 15,
  titleSize = NULL,
  axisLabelSize = NULL,
  axisSize = NULL,
  legendSize = NULL,
  legendTitleSize = NULL,
  relHeights = 1,
  relWidths = c(1, 1, 1),
  plotNcols = NULL,
  plotNrows = NULL,
  labelSamples = TRUE,
  samplePerColumn = TRUE,
  sampleRelHeights = 1,
  sampleRelWidths = 1
)

```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runScDbfFinder</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.

combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNcols	Number of columns when plots are combined in a grid.
plotNrows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.

`samplePerColumn`  
If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.

`sampleRelHeights`  
If there are multiple samples and combining by "all", the relative heights for each plot.

`sampleRelWidths`  
If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runScDblFinder(sce)
plotScDblFinderResults(inSCE=sce, reducedDimName="UMAP")
```

---

`plotScdsHybridResults` *Plots for runCxdBcdsHybrid outputs.*

---

**Description**

A wrapper function which visualizes outputs from the `runCxdBcdsHybrid` function stored in the `colData` slot of the `SingleCellExperiment` object via various plots.

**Usage**

```
plotScdsHybridResults(
  inSCE,
  sample = NULL,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,
  boxplot = FALSE,
  dots = TRUE,
  reducedDimName = "UMAP",
  xlab = NULL,
  ylab = NULL,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
  binLabel = NULL,
```

```

defaultTheme = TRUE,
dotSize = 0.5,
summary = "median",
summaryTextSize = 3,
transparency = 1,
baseSize = 15,
titleSize = NULL,
axisLabelSize = NULL,
axisSize = NULL,
legendSize = NULL,
legendTitleSize = NULL,
relHeights = 1,
relWidths = c(1, 1, 1),
plotNCols = NULL,
plotNRows = NULL,
labelSamples = TRUE,
samplePerColumn = TRUE,
sampleRelHeights = 1,
sampleRelWidths = 1
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runCxdsBcHybrid</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.



bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNCols	Number of columns when plots are combined in a grid.
plotNRows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runCxlsBcxsHybrid(sce)
plotScdsHybridResults(inSCE=sce, reducedDimName="UMAP")
```

---

plotSCEBarAssayData *Bar plot of assay data.*

---

### Description

Visualizes values stored in the assay slot of a SingleCellExperiment object via a bar plot.

### Usage

```
plotSCEBarAssayData(
  inSCE,
  feature,
  sample = NULL,
  useAssay = "counts",
  featureLocation = NULL,
  featureDisplay = NULL,
  groupBy = NULL,
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
  axisLabelSize = 10,
  dotSize = 0.5,
  transparency = 1,
  defaultTheme = TRUE,
  gridLine = FALSE,
  summary = NULL,
  title = NULL,
  titleSize = NULL,
  combinePlot = TRUE
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
feature	Name of feature stored in assay of SingleCellExperiment object.
sample	Character vector. Indicates which sample each cell belongs to.
useAssay	Indicate which assay to use. Default "counts".
featureLocation	Indicates which column name of rowData to query gene.
featureDisplay	Indicates which column name of rowData to use to display feature for visualization.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.

xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
combinePlot	Boolean. If multiple plots are generated (multiple samples, etc.), will combined plots using 'cowplot::plot_grid'. Default TRUE.

**Value**

a ggplot of the barplot of assay data.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEBarAssayData(
  inSCE = mouseBrainSubsetSCE,
  feature = "ApoE", groupBy = "sex"
)
```

---

plotSCEBarColData      *Bar plot of colData.*

---

**Description**

Visualizes values stored in the colData slot of a SingleCellExperiment object via a bar plot.

**Usage**

```
plotSCEBarColData(
  inSCE,
  coldata,
  sample = NULL,
  groupBy = NULL,
  dots = TRUE,
  xlab = NULL,
```

```

ylab = NULL,
axisSize = 10,
axisLabelSize = 10,
dotSize = 0.5,
transparency = 1,
defaultTheme = TRUE,
gridLine = FALSE,
summary = NULL,
title = NULL,
titleSize = NULL,
combinePlot = TRUE
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
coldata	colData value that will be plotted.
sample	Character vector. Indicates which sample each cell belongs to.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
combinePlot	Boolean. If multiple plots are generated (multiple samples, etc.), will combined plots using 'cowplot::plot_grid'. Default TRUE.

### Value

a ggplot of the barplot of coldata.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEBarColData(
  inSCE = mouseBrainSubsetSCE,
  coldata = "age", groupBy = "sex"
)
```

---

```
plotSCEBatchFeatureMean
```

*Plot mean feature value in each batch of a SingleCellExperiment object*

---

**Description**

Plot mean feature value in each batch of a SingleCellExperiment object

**Usage**

```
plotSCEBatchFeatureMean(
  inSCE,
  useAssay = NULL,
  useReddim = NULL,
  useAltExp = NULL,
  batch = "batch",
  xlab = "batch",
  ylab = "Feature Mean",
  ...
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useAssay	A single character. The name of the assay that stores the value to plot. For useReddim and useAltExp also. Default NULL.
useReddim	A single character. The name of the dimension reduced matrix that stores the value to plot. Default NULL.
useAltExp	A single character. The name of the alternative experiment that stores an assay of the value to plot. Default NULL.
batch	A single character. The name of batch annotation column in colData(inSCE). Default "batch".
xlab	label for x-axis. Default "batch".
ylab	label for y-axis. Default "Feature Mean".
...	Additional arguments passed to <a href="#">.ggViolin</a> .

**Value**

ggplot

**Examples**

```
data('sceBatches', package = 'singleCellTK')
plotSCEBatchFeatureMean(sceBatches, useAssay = "counts")
```

---

plotSCEDensity	<i>Density plot of any data stored in the SingleCellExperiment object.</i>
----------------	--

---

**Description**

Visualizes values stored in any slot of a SingleCellExperiment object via a density plot.

**Usage**

```
plotSCEDensity(
  inSCE,
  slotName,
  itemName,
  sample = NULL,
  feature = NULL,
  dimension = NULL,
  groupBy = NULL,
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
  axisLabelSize = 10,
  defaultTheme = TRUE,
  title = NULL,
  titleSize = 18,
  cutoff = NULL,
  combinePlot = "none",
  plotLabels = NULL
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
slotName	Desired slot of SingleCellExperiment used for plotting. Possible options: "assays", "colData", "metadata", "reducedDims". Required.
itemName	Desired vector within the slot used for plotting. Required.
sample	Character vector. Indicates which sample each cell belongs to.

feature	Desired name of feature stored in assay of SingleCellExperiment object. Only used when "assays" slotName is selected. Default NULL.
dimension	Desired dimension stored in the specified reducedDims. Either an integer which indicates the column or a character vector specifies column name. By default, the 1st dimension/column will be used. Only used when "reducedDims" slotName is selected. Default NULL.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
cutoff	Numeric value. The plot will be annotated with a vertical line if set. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot object of the density plot.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEDensity(
  inSCE = mouseBrainSubsetSCE, slotName = "assays",
  itemName = "counts", feature = "ApoE", groupBy = "sex"
)
```

---

plotSCEDensityAssayData

*Density plot of assay data.*

---

**Description**

Visualizes values stored in the assay slot of a SingleCellExperiment object via a density plot.

**Usage**

```
plotSCEDensityAssayData(
  inSCE,
  feature,
  sample = NULL,
  useAssay = "counts",
  featureLocation = NULL,
  featureDisplay = NULL,
  groupBy = NULL,
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
  axisLabelSize = 10,
  defaultTheme = TRUE,
  cutoff = NULL,
  title = NULL,
  titleSize = 18,
  combinePlot = "none",
  plotLabels = NULL
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
feature	Name of feature stored in assay of SingleCellExperiment object.
sample	Character vector. Indicates which sample each cell belongs to.
useAssay	Indicate which assay to use. Default "counts".
featureLocation	Indicates which column name of rowData to query gene.
featureDisplay	Indicates which column name of rowData to use to display feature for visualization.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
cutoff	Numeric value. The plot will be annotated with a vertical line if set. Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.



combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the density plot of assay data.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEDensityAssayData(
  inSCE = mouseBrainSubsetSCE,
  feature = "ApoE"
)
```

---

plotSCEDensityColData *Density plot of colData.*

---

**Description**

Visualizes values stored in the colData slot of a SingleCellExperiment object via a density plot.

**Usage**

```
plotSCEDensityColData(
  inSCE,
  coldata,
  sample = NULL,
  groupBy = NULL,
  xlab = NULL,
  ylab = NULL,
  baseSize = 12,
  axisSize = NULL,
  axisLabelSize = NULL,
  defaultTheme = TRUE,
  title = NULL,
  titleSize = 18,
  cutoff = NULL,
  combinePlot = "none",
  plotLabels = NULL
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
<code>coldata</code>	<code>colData</code> value that will be plotted.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to.
<code>groupBy</code>	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <code>SingleCellExperiment</code> object, or can be retrieved from the <code>colData</code> slot. Default <code>NULL</code> .
<code>xlab</code>	Character vector. Label for x-axis. Default <code>NULL</code> .
<code>ylab</code>	Character vector. Label for y-axis. Default <code>NULL</code> .
<code>baseSize</code>	The base font size for all text. Default 12. Can be overwritten by <code>titleSize</code> , <code>axisSize</code> , and <code>axisLabelSize</code> , <code>legendSize</code> , <code>legendTitleSize</code> .
<code>axisSize</code>	Size of x/y-axis ticks. Default <code>NULL</code> .
<code>axisLabelSize</code>	Size of x/y-axis labels. Default <code>NULL</code> .
<code>defaultTheme</code>	Removes grid in plot and sets axis title size to 10 when <code>TRUE</code> . Default <code>TRUE</code> .
<code>title</code>	Title of plot. Default <code>NULL</code> .
<code>titleSize</code>	Size of title of plot. Default 15.
<code>cutoff</code>	Numeric value. The plot will be annotated with a vertical line if set. Default <code>NULL</code> .
<code>combinePlot</code>	Must be either "all", "sample", or "none". "all" will combine all plots into a single <code>.ggplot</code> object, while "sample" will output a list of plots separated by sample. Default "none".
<code>plotLabels</code>	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a `ggplot` of the density plot of `colData`.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEDensityColData(
  inSCE = mouseBrainSubsetSCE,
  coldata = "age", groupBy = "sex"
)
```

---

`plotSCEDimReduceColData`*Dimension reduction plot tool for colData*

---

**Description**

Plot results of reduced dimensions data and colors by annotation data stored in the colData slot.

**Usage**

```
plotSCEDimReduceColData(  
  inSCE,  
  colorBy,  
  reducedDimName,  
  sample = NULL,  
  groupBy = NULL,  
  conditionClass = NULL,  
  shape = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  baseSize = 12,  
  axisSize = NULL,  
  axisLabelSize = NULL,  
  dim1 = NULL,  
  dim2 = NULL,  
  bin = NULL,  
  binLabel = NULL,  
  dotSize = 0.5,  
  transparency = 1,  
  colorScale = NULL,  
  colorLow = "white",  
  colorMid = "gray",  
  colorHigh = "blue",  
  defaultTheme = TRUE,  
  title = NULL,  
  titleSize = 15,  
  labelClusters = TRUE,  
  clusterLabelSize = 3.5,  
  legendTitle = NULL,  
  legendTitleSize = NULL,  
  legendSize = NULL,  
  combinePlot = "none",  
  plotLabels = NULL  
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
<code>colorBy</code>	Color by a condition(any column of the annotation data). Required.
<code>reducedDimName</code>	Saved dimension reduction matrix name in the <a href="#">SingleCellExperiment</a> object. Required.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to.
<code>groupBy</code>	Group by a condition(any column of the annotation data). Default NULL.
<code>conditionClass</code>	Class of the annotation data used in <code>colorBy</code> . Options are NULL, "factor" or "numeric". If NULL, class will default to the original class. Default NULL.
<code>shape</code>	Add shapes to each condition.
<code>xlab</code>	Character vector. Label for x-axis. Default NULL.
<code>ylab</code>	Character vector. Label for y-axis. Default NULL.
<code>baseSize</code>	The base font size for all text. Default 12. Can be overwritten by <code>titleSize</code> , <code>axisSize</code> , and <code>axisLabelSize</code> , <code>legendSize</code> , <code>legendTitleSize</code> .
<code>axisSize</code>	Size of x/y-axis ticks. Default NULL.
<code>axisLabelSize</code>	Size of x/y-axis labels. Default NULL.
<code>dim1</code>	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
<code>dim2</code>	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
<code>bin</code>	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
<code>binLabel</code>	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
<code>dotSize</code>	Size of dots. Default 0.5.
<code>transparency</code>	Transparency of the dots, values will be 0-1. Default 1.
<code>colorScale</code>	Vector. Needs to be same length as the number of unique levels of <code>colorBy</code> . Will be used only if <code>conditionClass</code> = "factor" or "character". Default NULL.
<code>colorLow</code>	Character. A color available from 'colors()'. The color will be used to signify the lowest values on the scale. Default 'white'.
<code>colorMid</code>	Character. A color available from 'colors()'. The color will be used to signify the midpoint on the scale. Default 'gray'.
<code>colorHigh</code>	Character. A color available from 'colors()'. The color will be used to signify the highest values on the scale. Default 'blue'.
<code>defaultTheme</code>	adds grid to plot when TRUE. Default TRUE.
<code>title</code>	Title of plot. Default NULL.

titleSize	Size of title of plot. Default 15.
labelClusters	Logical. Whether the cluster labels are plotted.
clusterLabelSize	Numeric. Determines the size of cluster label when 'labelClusters' is set to TRUE. Default 3.5.
legendTitle	title of legend. Default NULL.
legendTitleSize	size of legend title. Default 12.
legendSize	size of legend. Default NULL. Default FALSE.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the reduced dimension plot of coldata.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEDimReduceColdData(
  inSCE = mouseBrainSubsetSCE, colorBy = "tissue",
  shape = NULL, conditionClass = "factor",
  reducedDimName = "TSNE_counts",
  xlab = "tSNE1", ylab = "tSNE2", labelClusters = TRUE
)

plotSCEDimReduceColdData(
  inSCE = mouseBrainSubsetSCE, colorBy = "age",
  shape = NULL, conditionClass = "numeric",
  reducedDimName = "TSNE_counts", bin = c(-Inf, 20, 25, +Inf),
  xlab = "tSNE1", ylab = "tSNE2", labelClusters = FALSE
)
```

---

plotSCEDimReduceFeatures

*Dimension reduction plot tool for assay data*

---

**Description**

Plot results of reduced dimensions data and colors by feature data stored in the assays slot.

**Usage**

```
plotSCEDimReduceFeatures(
  inSCE,
  feature,
  reducedDimName,
  sample = NULL,
  featureLocation = NULL,
  featureDisplay = NULL,
  shape = NULL,
  useAssay = "logcounts",
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
  axisLabelSize = 10,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
  binLabel = NULL,
  dotSize = 0.5,
  transparency = 1,
  colorLow = "white",
  colorMid = "gray",
  colorHigh = "blue",
  defaultTheme = TRUE,
  title = NULL,
  titleSize = 15,
  legendTitle = NULL,
  legendSize = 10,
  legendTitleSize = 12,
  groupBy = NULL,
  combinePlot = "none",
  plotLabels = NULL
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
feature	Name of feature stored in assay of SingleCellExperiment object.
reducedDimName	saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
sample	Character vector. Indicates which sample each cell belongs to.
featureLocation	Indicates which column name of rowData to query gene.
featureDisplay	Indicates which column name of rowData to use to display feature for visualization.
shape	add shapes to each condition. Default NULL.

useAssay	Indicate which assay to use. The default is "logcounts"
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
colorLow	Character. A color available from 'colors()'. The color will be used to signify the lowest values on the scale. Default 'white'.
colorMid	Character. A color available from 'colors()'. The color will be used to signify the midpoint on the scale. Default 'gray'.
colorHigh	Character. A color available from 'colors()'. The color will be used to signify the highest values on the scale. Default 'blue'.
defaultTheme	adds grid to plot when TRUE. Default TRUE.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
legendTitle	title of legend. Default NULL.
legendSize	size of legend. Default 10.
legendTitleSize	size of legend title. Default 12.
groupBy	Facet wrap the scatterplot based on value. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the reduced dimension plot of feature data.

**Examples**

```

data("mouseBrainSubsetSCE")
plotSCEDimReduceFeatures(
  inSCE = mouseBrainSubsetSCE, feature = "ApoE",
  shape = NULL, reducedDimName = "TSNE_counts",
  useAssay = "counts", xlab = "tSNE1", ylab = "tSNE2"
)

```

---

plotSCEHeatmap

*Plot heatmap of using data stored in SingleCellExperiment Object*


---

**Description**

Plot heatmap of using data stored in SingleCellExperiment Object

**Usage**

```

plotSCEHeatmap(
  inSCE,
  useAssay = "logcounts",
  doLog = FALSE,
  featureIndex = NULL,
  cellIndex = NULL,
  scale = TRUE,
  trim = c(-2, 2),
  featureIndexBy = "rownames",
  cellIndexBy = "rownames",
  rowDataName = NULL,
  colDataName = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  rowSplitBy = NULL,
  colSplitBy = NULL,
  rowLabel = FALSE,
  colLabel = FALSE,
  rowLabelSize = 8,
  colLabelSize = 8,
  rowDend = TRUE,
  colDend = TRUE,
  title = NULL,
  rowTitle = "Genes",
  colTitle = "Cells",
  rowGap = grid::unit(0, "mm"),
  colGap = grid::unit(0, "mm"),
  border = FALSE,

```



```

    colorScheme = NULL,
    ...
)

plotSCEDimReduceHeatmap(
  inSCE,
  useReducedDim,
  featureIndex = NULL,
  cellIndex = NULL,
  doLog = FALSE,
  scale = FALSE,
  trim = c(-2, 2),
  cellIndexBy = "rownames",
  colDataName = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  rowSplitBy = NULL,
  colSplitBy = NULL,
  rowLabel = FALSE,
  colLabel = FALSE,
  rowLabelSize = 8,
  colLabelSize = 8,
  rowDend = TRUE,
  colDend = TRUE,
  title = NULL,
  rowTitle = "Dimensions",
  colTitle = "Cells",
  rowGap = grid::unit(0, "mm"),
  colGap = grid::unit(0, "mm"),
  border = FALSE,
  colorScheme = NULL,
  ...
)

```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useAssay	character. A string indicating the assay name that provides the expression level to plot. Only for plotSCEHeatmap.
doLog	Logical scalar. Whether to do $\log(\text{assay} + 1)$ transformation on the assay indicated by useAssay. Default FALSE.
featureIndex	A vector that can subset the input SCE object by rows (features). Alternatively, it can be a vector identifying features in another feature list indicated by featureIndexBy. Default NULL.
cellIndex	A vector that can subset the input SCE object by columns (cells). Alternatively, it can be a vector identifying cells in another cell list indicated by featureIndexBy.

	Default NULL.
scale	Whether to perform z-score scaling on each row. Default TRUE.
trim	A 2-element numeric vector. Values outside of this range will be trimmed to their nearest bound. Default <code>c(-2, 2)</code>
featureIndexBy	A single character specifying a column name of <code>rowData(inSCE)</code> , or a vector of the same length as <code>nrow(inSCE)</code> , where we search for the non-rowname feature indices. Not applicable for <code>plotSCEDimReduceHeatmap</code> . Default <code>"rownames"</code> .
cellIndexBy	A single character specifying a column name of <code>colData(inSCE)</code> , or a vector of the same length as <code>ncol(inSCE)</code> , where we search for the non-rowname cell indices. Default <code>"rownames"</code> .
rowDataName	character. The column name(s) in <code>rowData</code> that need to be added to the annotation. Not applicable for <code>plotSCEDimReduceHeatmap</code> . Default NULL.
colDataName	character. The column name(s) in <code>colData</code> that need to be added to the annotation. Default NULL.
featureAnnotations	<code>data.frame</code> , with <code>rownames</code> containing all the features going to be plotted. Character columns should be factors. Default NULL.
cellAnnotations	<code>data.frame</code> , with <code>rownames</code> containing all the cells going to be plotted. Character columns should be factors. Default NULL.
featureAnnotationColor	A named list. Customized color settings for feature labeling. Should match the entries in the <code>featureAnnotations</code> or <code>rowDataName</code> . For each entry, there should be a list/vector of colors named with categories. Default NULL.
cellAnnotationColor	A named list. Customized color settings for cell labeling. Should match the entries in the <code>cellAnnotations</code> or <code>colDataName</code> . For each entry, there should be a list/vector of colors named with categories. Default NULL.
rowSplitBy	character. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either <code>rowDataName</code> or <code>names(featureAnnotations)</code> . Default NULL.
colSplitBy	character. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either <code>colDataName</code> or <code>names(cellAnnotations)</code> . Default NULL.
rowLabel	Use a logical for whether to display all the feature names, a single character to display a column of <code>rowData(inSCE)</code> annotation, a vector of the same length as <code>full/subset nrow(inSCE)</code> to display customized info. Default FALSE.
colLabel	Use a logical for whether to display all the cell names, a single character to display a column of <code>colData(inSCE)</code> annotation, a vector of the same length as <code>full/subset ncol(inSCE)</code> to display customized info. Default FALSE.
rowLabelSize	A number for the font size of feature names. Default 8
colLabelSize	A number for the font size of cell names. Default 8
rowDend	Whether to display row dendrogram. Default TRUE.
colDend	Whether to display column dendrogram. Default TRUE.

title	The main title of the whole plot. Default NULL.
rowTitle	The subtitle for the rows. Default "Genes".
colTitle	The subtitle for the columns. Default "Cells".
rowGap	A numeric value or a <a href="#">unit</a> object. For the gap size between rows of the splitted heatmap. Default <code>grid::unit(0, 'mm')</code> .
colGap	A numeric value or a <a href="#">unit</a> object. For the gap size between columns of the splitted heatmap. Default <code>grid::unit(0, 'mm')</code> .
border	A logical scalar. Whether to show the border of the heatmap or splitted heatmaps. Default TRUE.
colorScheme	function. A function that generates color code by giving a value. Can be generated by <a href="#">colorRamp2</a> . Default NULL.
...	Other arguments passed to <a href="#">Heatmap</a> .
useReducedDim	character. A string indicating the reducedDim name that provides the expression level to plot. Only for <code>plotSCEDimReduceHeatmap</code> .

**Value**

A [ggplot](#) object.

**Author(s)**

Yichen Wang

**Examples**

```
data(scExample, package = "singleCellTK")
plotSCEHeatmap(sce[1:3,1:3], useAssay = "counts")
```

---

plotSCEScatter

*Dimension reduction plot tool for all types of data*

---

**Description**

Plot results of reduced dimensions data of counts stored in any slot in the `SingleCellExperiment` object.

**Usage**

```
plotSCEScatter(
  inSCE,
  annotation,
  reducedDimName = NULL,
  slot = NULL,
  sample = NULL,
  feature = NULL,
```

```

groupBy = NULL,
shape = NULL,
conditionClass = NULL,
xlab = NULL,
ylab = NULL,
axisSize = 10,
axisLabelSize = 10,
dim1 = NULL,
dim2 = NULL,
bin = NULL,
binLabel = NULL,
dotSize = 0.5,
transparency = 1,
colorLow = "white",
colorMid = "gray",
colorHigh = "blue",
defaultTheme = TRUE,
title = NULL,
titleSize = 15,
labelClusters = TRUE,
legendTitle = NULL,
legendTitleSize = 12,
legendSize = 10,
combinePlot = "none",
plotLabels = NULL
)

```

### Arguments

inSCE	Input SingleCellExperiment object with saved dimension reduction components or a variable with saved results. Required.
annotation	Desired vector within the slot used for plotting. Default NULL.
reducedDimName	saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object.
slot	Desired slot of SingleCellExperiment used for plotting. Possible options: "assays", "colData", "metadata", "reducedDims". Default NULL.
sample	Character vector. Indicates which sample each cell belongs to.
feature	name of feature stored in assay of SingleCellExperiment object. Will be used only if "assays" slot is chosen. Default NULL.
groupBy	Group by a condition(any column of the annotation data). Default NULL.
shape	add shapes to each condition.
conditionClass	class of the annotation data used in colorBy. Options are NULL, "factor" or "numeric". If NULL, class will default to the original class. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.

axisLabelSize	Size of x/y-axis labels. Default 10.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from reducedDims, or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.
binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
colorLow	Character. A color available from 'colors()'. The color will be used to signify the lowest values on the scale. Default 'white'.
colorMid	Character. A color available from 'colors()'. The color will be used to signify the midpoint on the scale. Default 'gray'.
colorHigh	Character. A color available from 'colors()'. The color will be used to signify the highest values on the scale. Default 'blue'.
defaultTheme	adds grid to plot when TRUE. Default TRUE.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
labelClusters	Logical. Whether the cluster labels are plotted.
legendTitle	title of legend. Default NULL.
legendTitleSize	size of legend title. Default 12.
legendSize	size of legend. Default 10.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the reduced dimensions.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEScatter(
  inSCE = mouseBrainSubsetSCE, legendTitle = NULL,
  slot = "assays", annotation = "counts", feature = "ApoE",
  reducedDimName = "TSNE_counts", labelClusters = FALSE
)
```

---

plotSCEViolin      *Violin plot of any data stored in the SingleCellExperiment object.*

---

### Description

Visualizes values stored in any slot of a SingleCellExperiment object via a violin plot.

### Usage

```
plotSCEViolin(  
  inSCE,  
  slotName,  
  itemName,  
  feature = NULL,  
  sample = NULL,  
  dimension = NULL,  
  groupBy = NULL,  
  violin = TRUE,  
  boxplot = TRUE,  
  dots = TRUE,  
  plotOrder = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  axisSize = 10,  
  axisLabelSize = 10,  
  dotSize = 0.5,  
  transparency = 1,  
  defaultTheme = TRUE,  
  gridLine = FALSE,  
  summary = NULL,  
  title = NULL,  
  titleSize = NULL,  
  hcutoff = NULL,  
  hcolor = "red",  
  hsize = 1,  
  hlinetype = 1,  
  vcutoff = NULL,  
  vcolor = "red",  
  vsize = 1,  
  vlinetype = 1,  
  combinePlot = "none",  
  plotLabels = NULL  
)
```

### Arguments

`inSCE`      Input [SingleCellExperiment](#) object with saved dimension reduction components or a variable with saved results. Required.

slotName	Desired slot of SingleCellExperiment used for plotting. Possible options: "assays", "colData", "metadata", "reducedDims". Required.
itemName	Desired vector within the slot used for plotting. Required.
feature	Desired name of feature stored in assay of SingleCellExperiment object. Only used when "assays" slotName is selected. Default NULL.
sample	Character vector. Indicates which sample each cell belongs to.
dimension	Desired dimension stored in the specified reducedDims. Either an integer which indicates the column or a character vector specifies column name. By default, the 1st dimension/column will be used. Only used when "reducedDims" slotName is selected. Default NULL.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
plotOrder	Character vector. If set, reorders the violin plots in the order of the character vector when 'groupBy' is set. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.
transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
hcutoff	Adds a horizontal line with the y-intercept at given value. Default NULL.
hcolor	Character. A color available from 'colors()'. Controls the color of the horizontal cutoff line, if drawn. Default 'black'.
hsize	Size of horizontal line, if drawn. Default 0.5.
hlinetype	Type of horizontal line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
vcutoff	Adds a vertical line with the x-intercept at given value. Default NULL.
vcolor	Character. A color available from 'colors()'. Controls the color of the vertical cutoff line, if drawn. Default 'black'.

vsize	Size of vertical line, if drawn. Default 0.5.
vlinetype	Type of vertical line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the violin plot.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEViolin(
  inSCE = mouseBrainSubsetSCE, slotName = "assays",
  itemName = "counts", feature = "ApoE", groupBy = "sex"
)
```

---

plotSCEViolinAssayData

*Violin plot of assay data.*

---

**Description**

Visualizes values stored in the assay slot of a SingleCellExperiment object via a violin plot.

**Usage**

```
plotSCEViolinAssayData(
  inSCE,
  feature,
  sample = NULL,
  useAssay = "counts",
  featureLocation = NULL,
  featureDisplay = NULL,
  groupBy = NULL,
  violin = TRUE,
  boxplot = TRUE,
  dots = TRUE,
  plotOrder = NULL,
  xlab = NULL,
  ylab = NULL,
  axisSize = 10,
```



```

    axisLabelSize = 10,
    dotSize = 0.5,
    transparency = 1,
    defaultTheme = TRUE,
    gridLine = FALSE,
    summary = NULL,
    title = NULL,
    titleSize = NULL,
    hcutoff = NULL,
    hcolor = "red",
    hsize = 1,
    hlinetype = 1,
    vcutoff = NULL,
    vcolor = "red",
    vsize = 1,
    vlinetype = 1,
    combinePlot = "none",
    plotLabels = NULL
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
feature	Name of feature stored in assay of SingleCellExperiment object.
sample	Character vector. Indicates which sample each cell belongs to.
useAssay	Indicate which assay to use. Default "counts".
featureLocation	Indicates which column name of rowData to query gene.
featureDisplay	Indicates which column name of rowData to use to display feature for visualization.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
plotOrder	Character vector. If set, reorders the violin plots in the order of the character vector when 'groupBy' is set. Default NULL.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
axisSize	Size of x/y-axis ticks. Default 10.
axisLabelSize	Size of x/y-axis labels. Default 10.
dotSize	Size of dots. Default 0.5.

transparency	Transparency of the dots, values will be 0-1. Default 1.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
gridLine	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
title	Title of plot. Default NULL.
titleSize	Size of title of plot. Default 15.
hcutoff	Adds a horizontal line with the y-intercept at given value. Default NULL.
hcolor	Character. A color available from 'colors()'. Controls the color of the horizontal cutoff line, if drawn. Default 'black'.
hsize	Size of horizontal line, if drawn. Default 0.5.
hlinetype	Type of horizontal line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
vcutoff	Adds a vertical line with the x-intercept at given value. Default NULL.
vcolor	Character. A color available from 'colors()'. Controls the color of the vertical cutoff line, if drawn. Default 'black'.
vsize	Size of vertical line, if drawn. Default 0.5.
vlinetype	Type of vertical line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

### Value

a ggplot of the violin plot of assay data.

### Examples

```
data("mouseBrainSubsetSCE")
plotSCEViolinAssayData(
  inSCE = mouseBrainSubsetSCE,
  feature = "ApoE", groupBy = "sex"
)
```

---

plotSCEViolinColData *Violin plot of colData.*

---

### Description

Visualizes values stored in the colData slot of a SingleCellExperiment object via a violin plot.

### Usage

```
plotSCEViolinColData(  
  inSCE,  
  coldata,  
  sample = NULL,  
  groupBy = NULL,  
  violin = TRUE,  
  boxplot = TRUE,  
  dots = TRUE,  
  plotOrder = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  baseSize = 12,  
  axisSize = NULL,  
  axisLabelSize = NULL,  
  dotSize = 0.5,  
  transparency = 1,  
  defaultTheme = TRUE,  
  gridLine = FALSE,  
  summary = NULL,  
  summaryTextSize = 3,  
  title = NULL,  
  titleSize = NULL,  
  hcutoff = NULL,  
  hcolor = "red",  
  hsize = 1,  
  hlinetype = 1,  
  vcutoff = NULL,  
  vcolor = "red",  
  vsize = 1,  
  vlinetype = 1,  
  combinePlot = "none",  
  plotLabels = NULL  
)
```

### Arguments

**inSCE** Input [SingleCellExperiment](#) object with saved dimension reduction components or a variable with saved results. Required.

<code>coldata</code>	colData value that will be plotted.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to.
<code>groupBy</code>	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the SingleCellExperiment object, or can be retrieved from the colData slot. Default NULL.
<code>violin</code>	Boolean. If TRUE, will plot the violin plot. Default TRUE.
<code>boxplot</code>	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
<code>dots</code>	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
<code>plotOrder</code>	Character vector. If set, reorders the violin plots in the order of the character vector when 'groupBy' is set. Default NULL.
<code>xlab</code>	Character vector. Label for x-axis. Default NULL.
<code>ylab</code>	Character vector. Label for y-axis. Default NULL.
<code>baseSize</code>	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize.
<code>axisSize</code>	Size of x/y-axis ticks. Default NULL.
<code>axisLabelSize</code>	Size of x/y-axis labels. Default NULL.
<code>dotSize</code>	Size of dots. Default 0.5.
<code>transparency</code>	Transparency of the dots, values will be 0-1. Default 1.
<code>defaultTheme</code>	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
<code>gridLine</code>	Adds a horizontal grid line if TRUE. Will still be drawn even if defaultTheme is TRUE. Default FALSE.
<code>summary</code>	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
<code>summaryTextSize</code>	The text size of the summary statistic displayed above the violin plot. Default 3.
<code>title</code>	Title of plot. Default NULL.
<code>titleSize</code>	Size of title of plot. Default 15.
<code>hcutoff</code>	Adds a horizontal line with the y-intercept at given value. Default NULL.
<code>hcolor</code>	Character. A color available from 'colors()'. Controls the color of the horizontal cutoff line, if drawn. Default 'black'.
<code>hsize</code>	Size of horizontal line, if drawn. Default 0.5.
<code>hlinetype</code>	Type of horizontal line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.
<code>vcutoff</code>	Adds a vertical line with the x-intercept at given value. Default NULL.
<code>vcolor</code>	Character. A color available from 'colors()'. Controls the color of the vertical cutoff line, if drawn. Default 'black'.
<code>vsize</code>	Size of vertical line, if drawn. Default 0.5.
<code>vlinetype</code>	Type of vertical line, if drawn. can be specified with either an integer or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash). Default 1.

combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single .ggplot object, while "sample" will output a list of plots separated by sample. Default "none".
plotLabels	labels to each plot. If set to "default", will use the name of the samples as the labels. If set to "none", no label will be plotted.

**Value**

a ggplot of the violin plot of coldata.

**Examples**

```
data("mouseBrainSubsetSCE")
plotSCEViolinColData(
  inSCE = mouseBrainSubsetSCE,
  coldata = "age", groupBy = "sex"
)
```

---

plotScrubletResults     *Plots for runScrublet outputs.*

---

**Description**

A wrapper function which visualizes outputs from the runScrublet function stored in the colData slot of the SingleCellExperiment object via various plots.

**Usage**

```
plotScrubletResults(
  inSCE,
  sample = NULL,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,
  boxplot = FALSE,
  dots = TRUE,
  reducedDimName,
  xlab = NULL,
  ylab = NULL,
  dim1 = NULL,
  dim2 = NULL,
  bin = NULL,
  binLabel = NULL,
  defaultTheme = TRUE,
  dotSize = 0.5,
  summary = "median",
```

```

summaryTextSize = 3,
transparency = 1,
baseSize = 15,
titleSize = NULL,
axisLabelSize = NULL,
axisSize = NULL,
legendSize = NULL,
legendTitleSize = NULL,
relHeights = 1,
relWidths = c(1, 1, 1),
plotNCols = NULL,
plotNRows = NULL,
labelSamples = TRUE,
samplePerColumn = TRUE,
sampleRelHeights = 1,
sampleRelWidths = 1
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <a href="#">runScrublet</a> . Required.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value.
groupBy	Groupings for each numeric value. A user may input a vector equal length to the number of the samples in the <a href="#">SingleCellExperiment</a> object, or can be retrieved from the colData slot. Default NULL.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single <code>.ggplot</code> object, while "sample" will output a list of plots separated by sample. Default "all".
violin	Boolean. If TRUE, will plot the violin plot. Default TRUE.
boxplot	Boolean. If TRUE, will plot boxplots for each violin plot. Default TRUE.
dots	Boolean. If TRUE, will plot dots for each violin plot. Default TRUE.
reducedDimName	Saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	1st dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
dim2	2nd dimension to be used for plotting. Can either be a string which specifies the name of the dimension to be plotted from <code>reducedDims</code> , or a numeric value which specifies the index of the dimension to be plotted. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into the 'bin' groups. If more than one value, will bin numeric values using values as a cut point.

binLabel	Character vector. Labels for the bins created by the 'bin' parameter. Default NULL.
defaultTheme	Removes grid in plot and sets axis title size to 10 when TRUE. Default TRUE.
dotSize	Size of dots. Default 0.5.
summary	Adds a summary statistic, as well as a crossbar to the violin plot. Options are "mean" or "median". Default NULL.
summaryTextSize	The text size of the summary statistic displayed above the violin plot. Default 3.
transparency	Transparency of the dots, values will be 0-1. Default 1.
baseSize	The base font size for all text. Default 12. Can be overwritten by titleSize, axisSize, and axisLabelSize, legendSize, legendTitleSize.
titleSize	Size of title of plot. Default NULL.
axisLabelSize	Size of x/y-axis labels. Default NULL.
axisSize	Size of x/y-axis ticks. Default NULL.
legendSize	size of legend. Default NULL.
legendTitleSize	size of legend title. Default NULL.
relHeights	Relative heights of plots when combine is set.
relWidths	Relative widths of plots when combine is set.
plotNCols	Number of columns when plots are combined in a grid.
plotNRows	Number of rows when plots are combined in a grid.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
samplePerColumn	If TRUE, when there are multiple samples and combining by "all", the output .ggplot will have plots from each sample on a single column. Default TRUE.
sampleRelHeights	If there are multiple samples and combining by "all", the relative heights for each plot.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot.

**Value**

list of .ggplot objects

**Examples**

```
data(scExample, package="singleCellTK")
## Not run:
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- getUMAP(inSCE=sce, useAssay="counts", reducedDimName="UMAP")
sce <- runScrublet(sce)
plotScrubletResults(inSCE=sce, reducedDimName="UMAP")

## End(Not run)
```

---

plotSeuratElbow	<i>plotSeuratElbow</i> Computes the plot object for elbow plot from the <i>pca</i> slot in the input <i>sce</i> object
-----------------	--

---

### Description

plotSeuratElbow Computes the plot object for elbow plot from the *pca* slot in the input *sce* object

### Usage

```
plotSeuratElbow(
  inSCE,
  significantPC = NULL,
  reduction = "pca",
  ndims = 20,
  externalReduction = NULL,
  interactive = TRUE
)
```

### Arguments

<code>inSCE</code>	( <i>sce</i> ) object from which to compute the elbow plot ( <i>pca</i> should be computed)
<code>significantPC</code>	Number of significant principal components to plot. This is used to alter the color of the points for the corresponding PCs. If <code>NULL</code> , all points will be the same color. Default <code>NULL</code> .
<code>reduction</code>	Reduction to use for elbow plot generation. Either <code>"pca"</code> or <code>"ica"</code> . Default <code>"pca"</code> .
<code>ndims</code>	Number of components to use. Default 20.
<code>externalReduction</code>	Pass <code>DimReduc</code> object if PCA/ICA computed through other libraries. Default <code>NULL</code> .
<code>interactive</code>	Logical value indicating if the returned object should be an interactive plotly object if <code>TRUE</code> or a <code>ggplot</code> object if set to <code>FALSE</code> . Default is <code>TRUE</code> .

### Value

plot object

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
```



```
plotSeuratElbow(sce)

## End(Not run)
```

---

plotSeuratGenes      *Compute and plot visualizations for marker genes*

---

## Description

Compute and plot visualizations for marker genes

## Usage

```
plotSeuratGenes(
  inSCE,
  scaledAssayName = "seuratScaledData",
  plotType,
  features,
  groupVariable,
  splitBy = NULL,
  cols = c("lightgrey", "blue"),
  ncol = 1,
  combine = FALSE
)
```

## Arguments

inSCE	Input SingleCellExperiment object.
scaledAssayName	Specify the name of the scaled assay stored in the input object.
plotType	Specify the type of the plot to compute. Options are limited to "ridge", "violin", "feature", "dot" and "heatmap".
features	Specify the features to compute the plot against.
groupVariable	Specify the column name from the colData slot that should be used as grouping variable.
splitBy	Specify the column name from the colData slot that should be used to split samples. Default is NULL.
cols	Specify two colors to form a gradient between. Default is c("lightgrey", "blue").
ncol	Visualizations will be adjusted in "ncol" number of columns. Default is 1.
combine	A logical value that indicates if the plots should be combined together into a single plot if TRUE, else if FALSE returns separate ggplot objects for each feature. Only works when plotType parameter is "feature", "violin" or "ridge". For "heatmap" and "dot", plots for all features are always combined into a single plot. Default FALSE.

**Value**

Plot object

---

plotSeuratHeatmap	<i>plotSeuratHeatmap</i> Modifies the heatmap plot object so it contains specified number of heatmaps in a single plot
-------------------	--

---

**Description**

plotSeuratHeatmap Modifies the heatmap plot object so it contains specified number of heatmaps in a single plot

**Usage**

```
plotSeuratHeatmap(plotObject, dims, ncol, labels)
```

**Arguments**

plotObject	plot object computed from runSeuratHeatmap() function
dims	numerical value of how many heatmaps to draw (default is 0)
ncol	numerical value indicating that in how many columns should the heatmaps be distributed (default is 2)
labels	list() of labels to draw on heatmaps

**Value**

modified plot object

---

plotSeuratHVG	<i>plotSeuratHVG</i> Plot highly variable genes from input sce object (must have highly variable genes computations stored)
---------------	---

---

**Description**

plotSeuratHVG Plot highly variable genes from input sce object (must have highly variable genes computations stored)

**Usage**

```
plotSeuratHVG(inSCE, labelPoints = 0)
```

**Arguments**

inSCE	(sce) object that contains the highly variable genes computations
labelPoints	Numeric value indicating the number of top genes that should be labeled. Default is 0, which will not label any point.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
plotSeuratHVG(sce)

## End(Not run)
```

---

plotSeuratJackStraw    *plotSeuratJackStraw Computes the plot object for jackstraw plot from the pca slot in the input sce object*

---

**Description**

plotSeuratJackStraw Computes the plot object for jackstraw plot from the pca slot in the input sce object

**Usage**

```
plotSeuratJackStraw(
  inSCE,
  dims = NULL,
  xmax = 0.1,
  ymax = 0.3,
  externalReduction = NULL
)
```

**Arguments**

inSCE	(sce) object from which to compute the jackstraw plot (pca should be computed)
dims	Number of components to plot in Jackstraw. If NULL, then all components are plotted Default NULL.
xmax	X-axis maximum on each QQ plot. Default 0.1.
ymax	Y-axis maximum on each QQ plot. Default 0.3.
externalReduction	Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.

**Value**

plot object

**Examples**

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
sce <- runSeuratJackStraw(sce, useAssay = "counts")
plotSeuratJackStraw(sce)

## End(Not run)

```

---

plotSeuratReduction *plotSeuratReduction Plots the selected dimensionality reduction method*

---

**Description**

plotSeuratReduction Plots the selected dimensionality reduction method

**Usage**

```

plotSeuratReduction(
  inSCE,
  useReduction = c("pca", "ica", "tsne", "umap"),
  showLegend = FALSE,
  groupBy = NULL,
  splitBy = NULL
)

```

**Arguments**

inSCE	(sce) object which has the selected dimensionality reduction algorithm already computed and stored
useReduction	Dimensionality reduction to plot. One of "pca", "ica", "tsne", or "umap". Default "umap".
showLegend	Select if legends and labels should be shown on the output plot or not. Either "TRUE" or "FALSE". Default FALSE.
groupBy	Specify a colData column name that be used for grouping. Default is NULL.
splitBy	Specify a colData column name that be used for splitting the output plot. Default is NULL.

**Value**

plot object

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
plotSeuratReduction(sce, useReductionPlot = "pca")
## End(Not run)
```

---

plotSoupXResults      *Plot SoupX Result*

---

## Description

This function will generate a combination of plots basing on the correction done by SoupX. For each sample, there will be a UMAP with cluster labeling, followed by a number of UMAPs showing the change in selected top markers. The cluster labeling is what should be used for SoupX to estimate the contamination. The Soup Fraction is calculated by subtracting the gene expression value of the output corrected matrix from that of the original input matrix, and then divided by the input.

## Usage

```
plotSoupXResults(
  inSCE,
  sample = NULL,
  background = FALSE,
  reducedDimName = NULL,
  plotNCols = 3,
  plotNRows = 2,
  baseSize = 8,
  combinePlot = c("all", "sample", "none"),
  xlab = NULL,
  ylab = NULL,
  dim1 = NULL,
  dim2 = NULL,
  labelClusters = FALSE,
  clusterLabelSize = 3.5,
  defaultTheme = TRUE,
  dotSize = 0.5,
  transparency = 1,
  titleSize = NULL,
  axisLabelSize = NULL,
  axisSize = NULL,
  legendSize = NULL,
  legendTitleSize = NULL
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object. With <a href="#">runSoupX</a> already applied.
sample	Character vector. Indicates which sample each cell belongs to. Default NULL.
background	Logical. Whether background was applied when running <a href="#">runSoupX</a> . Default FALSE.
reducedDimName	Character. The embedding to use for plotting. Leave it NULL for using the sample-specific UMAPs generated when running <a href="#">runSoupX</a> . Default NULL.
plotNCols	Integer. Number of columns for the plot grid per sample. Will determine the number of top markers to show together with plotNRows. Default 3.
plotNRows	Integer. Number of rows for the plot grid per sample. Will determine the number of top markers to show together with plotNCols. Default 2.
baseSize	Numeric. The base font size for all text. Default 12. Can be overwritten by <code>titleSize</code> , <code>axisSize</code> , and <code>axisLabelSize</code> , <code>legendSize</code> , <code>legendTitleSize</code> . Default 8.
combinePlot	Must be either "all", "sample", or "none". "all" will combine all plots into a single <code>ggplot</code> object, while "sample" will output a list of plots separated by sample. Default "all".
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
dim1	See <a href="#">plotSCEDimReduceColData</a> . Default NULL.
dim2	See <a href="#">plotSCEDimReduceColData</a> . Default NULL.
labelClusters	Logical. Whether the cluster labels are plotted. Default FALSE.
clusterLabelSize	Numeric. Determines the size of cluster label when <code>labelClusters</code> is set to TRUE. Default 3.5.
defaultTheme	Logical. Adds grid to plot when TRUE. Default TRUE.
dotSize	Numeric. Size of dots. Default 0.5.
transparency	Numeric. Transparency of the dots, values will be from 0 to 1. Default 1.
titleSize	Numeric. Size of title of plot. Default 15.
axisLabelSize	Numeric. Size of x/y-axis labels. Default NULL.
axisSize	Numeric. Size of x/y-axis ticks. Default NULL.
legendSize	Numeric. Size of legend. Default NULL.
legendTitleSize	Numeric. Size of legend title. Default NULL.

**Value**

`ggplot` object of the combination of UMAPs. See description.

**Examples**

```

data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
# SoupX does not work for toy example,
# can be tested with `sce <- importExampleData("pbmc3k")`
sce <- runSoupX(sce, sample = "sample")
plotSoupXResults(sce)

## End(Not run)

```

---

plotTopHVG

*Plot highly variable genes*


---

**Description**

Plot highly variable genes

**Usage**

```

plotTopHVG(
  inSCE,
  method = c("vst", "mean.var.plot", "dispersion", "modelGeneVar"),
  hvgList = NULL,
  n = NULL,
  labelsCount = NULL
)

```

**Arguments**

inSCE	Input SingleCellExperiment object containing the computations.
method	Select either "vst", "mean.var.plot", "dispersion" or "modelGeneVar".
hvgList	Character vector indicating the labels of highly variable genes.
n	Specify the number of top genes to highlight in red. If hvgList parameter is not provided, this parameter can be used simply to specify the number of top genes to highlight in red.
labelsCount	Specify the number of data points/genes to label. By default, all top genes will be labeled.

**Value**

plot object

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- scranModelGeneVar(mouseBrainSubsetSCE, "logcounts")
plotTopHVG(mouseBrainSubsetSCE, method = "modelGeneVar",
           n = 1000, labelsCount = 0)
```

---

plotTSCANDEgenes	<i>Run plotTSCANDEgenes function to plot cells colored by the expression of a gene of interest</i>
------------------	--

---

**Description**

A wrapper function which plots all the cells in the cluster containing the branch point of the MST in the dataset. Each point is a cell colored by the expression of a gene of interest and the relevant edges of the MST are overlaid on top.

**Usage**

```
plotTSCANDEgenes(inSCE, geneSymbol, useClusters = NULL, useReducedDim)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
geneSymbol	Choose the gene of interest from the DE genes in order to know the level of expression of gene in clusters.
useClusters	Choose the cluster containing the branch point in the data in order to recompute the pseudotimes so that the root lies at the cluster center, allowing us to detect genes that are associated with the divergence of the branches.
useReducedDim	Saved dimension reduction name in inSCE. Required.

**Value**

A plots with the cells colored by the expression of a gene of interest.

**Author(s)**

Nida Pervaiz

**Examples**

```
data("scExample", package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterLogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                  useAssay = "logcounts", reducedDimName = "PCA")
```



```
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
                   reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
sce <- runTSCANClusterDEAnalysis(inSCE = sce, useClusters = 5)
plotTSCANDEGenes(inSCE = sce, geneSymbol = "CD74", useReducedDim = "TSNE")
```

---

plotTSCANPseudotimeGenes

*Run plotTSCANPseudotimeGenes function to plot genes with significant changes*

---

## Description

A wrapper function which visualizes outputs from the [runTSCANDEG](#) function. Plots the genes that increase or decrease in expression with increasing pseudotime along the path in the MST.

## Usage

```
plotTSCANPseudotimeGenes(
  inSCE,
  pathIndex,
  direction = c("increasing", "decreasing"),
  n = 10
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path number for which the pseudotime values should be used. PathIndex corresponds to one path from the root node to one of the terminal nodes.
direction	Which direction to use. Choices are increasing or decreasing.
n	An integer. Only to plot this number of top genes that are increasing/decreasing in expression with increasing pseudotime along the path in the MST. Default 10.

## Value

A plot with the top genes that increase/decrease in expression with increasing pseudotime along the path in the MST

## Author(s)

Nida Pervaiz

**Examples**

```

data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterLogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                  useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
                  reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
plotTSCANPseudotimeGenes(inSCE = sce, pathIndex = 4,
                        direction = "increasing")

```

---

plotTSCANPseudotimeHeatmap

*Run plotTSCANPseudotimeHeatmap function to plot heatmap for top genes*

---

**Description**

A wrapper function which visualizes outputs from the [runTSCANDEG](#) function. Plots the top genes that increase in expression with increasing pseudotime along the path in the MST

**Usage**

```
plotTSCANPseudotimeHeatmap(inSCE, pathIndex, topN = 50)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path number for which the pseudotime values should be used. PathIndex corresponds to one path from the root node to one of the terminal nodes.
topN	An integer. Only to plot this number of top genes along the path in the MST, in terms of log2FC value. Use NULL to cancel the top N subscription. Default 50.

**Value**

A plot with the top genes that increase in expression with increasing pseudotime along the path in the MST.

**Author(s)**

Nida Pervaiz

**Examples**

```

data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                   useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
                   reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
plotTSCANPseudotimeHeatmap(inSCE = sce, pathIndex = 4, topN = 5)

```

---

plotTSCANResults

*Plot MST pseudotime values for cells*


---

**Description**

A wrapper function which visualizes outputs from the [runTSCAN](#) function. Plots the pseudotime ordering of the cells by projecting them onto the MST

**Usage**

```
plotTSCANResults(inSCE, useReducedDim)
```

**Arguments**

`inSCE`            Input [SingleCellExperiment](#) object.  
`useReducedDim`   Saved dimension reduction name in `inSCE` object. Required.

**Value**

A plot with the pseudotime ordering of the cells by projecting them onto the MST.

**Author(s)**

Nida Pervaiz

**Examples**

```

data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                   useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",

```

```

        reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
plotTSCANResults(inSCE = sce, useReducedDim = "TSNE")

```

---

plotTSNE	<i>Plot t-SNE plot on dimensionality reduction data run from t-SNE method.</i>
----------	--

---

### Description

Plot t-SNE plot on dimensionality reduction data run from t-SNE method.

### Usage

```

plotTSNE(
  inSCE,
  colorBy = "No Color",
  shape = "No Shape",
  reducedDimName = "TSNE",
  runTSNE = FALSE,
  useAssay = "logcounts"
)

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
colorBy	color by condition.
shape	add shape to each distinct label.
reducedDimName	a name to store the results of the dimension reduction coordinates obtained from this method. This is stored in the SingleCellExperiment object in the reduced-Dims slot. Required.
runTSNE	Run t-SNE if the reducedDimName does not exist. the Default is FALSE.
useAssay	Indicate which assay to use. The default is "logcounts".

### Value

A t-SNE plot

### Examples

```

data("mouseBrainSubsetSCE")
plotTSNE(mouseBrainSubsetSCE, colorBy = "level1class",
         reducedDimName = "TSNE_counts")

```

---

plotUMAP	<i>Plot UMAP results either on already run results or run first and then plot.</i>
----------	--

---

## Description

Plot UMAP results either on already run results or run first and then plot.

## Usage

```
plotUMAP(  
  inSCE,  
  colorBy = "No Color",  
  shape = "No Shape",  
  reducedDimName = "UMAP",  
  runUMAP = FALSE,  
  useAssay = "logcounts"  
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components. Required
colorBy	color by a condition(any column of the annotation data).
shape	add shapes to each condition.
reducedDimName	saved dimension reduction name in the <a href="#">SingleCellExperiment</a> object. Required.
runUMAP	If the dimension reduction components are already available set this to FALSE, otherwise set to TRUE. Default is False.
useAssay	Indicate which assay to use. The default is "logcounts"

## Value

a UMAP plot of the reduced dimensions.

## Examples

```
data(scExample, package = "singleCellTK")  
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")  
sce <- getUMAP(inSCE = sce, useAssay = "counts", reducedDimName = "UMAP")  
plotUMAP(sce, shape = "No Shape", reducedDimName = "UMAP",  
         runUMAP = TRUE, useAssay = "counts")
```

---

qcInputProcess	<i>Create SingleCellExperiment object from command line input arguments</i>
----------------	---

---

### Description

Create SingleCellExperiment object from command line input arguments

### Usage

```
qcInputProcess(
  preproc,
  samplename,
  path,
  raw,
  fil,
  ref,
  rawFile,
  filFile,
  dataType
)
```

### Arguments

preproc	Method used to preprocess the data. It's one of the path provided in <code>-preproc</code> argument.
samplename	The sample name of the data. It's one of the path provided in <code>-sample</code> argument.
path	Base path of the dataset. It's one of the path provided in <code>-bash_path</code> argument.
raw	The directory contains droplet matrix, gene and cell barcodes information. It's one of the path provided in <code>-raw_data_path</code> argument.
fil	The directory contains cell matrix, gene and cell barcodes information. It's one of the path provided in <code>-cell_data_path</code> argument.
ref	The name of reference used by cellranger. Only need for CellrangerV2 data.
rawFile	The full path of the RDS file or Matrix file of the raw gene count matrix. It's one of the path provided in <code>-raw_data</code> argument.
filFile	The full path of the RDS file or Matrix file of the cell count matrix. It's one of the path provided in <code>-cell_data</code> argument.
dataType	Type of the input. It can be "Both", "Droplet" or "Cell". It's one of the path provided in <code>-genome</code> argument.

### Value

A list of [SingleCellExperiment](#) object containing the droplet or cell data or both, depending on the dataType that users provided.

---

readSingleCellMatrix *Read single cell expression matrix*

---

## Description

Automatically detect the format of the input file and read the file.

## Usage

```
readSingleCellMatrix(  
  file,  
  class = c("Matrix", "matrix"),  
  delayedArray = TRUE,  
  colIndexLocation = NULL,  
  rowIndexLocation = NULL  
)
```

## Arguments

file	Path to input file. Supported file endings include .mtx, .txt, .csv, .tab, .tsv, .npz, and their corresponding gzip, bzip2, or xz compressed extensions (*.gz, *.bz2, or *.xz).
class	Character. Class of matrix. One of "Matrix" or "matrix". Specifying "Matrix" will convert to a sparse format which should be used for datasets with large numbers of cells. Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as <a href="#">DelayedArray</a> object or not. Default TRUE.
colIndexLocation	Character. For Optimus output, the path to the barcode index .npy file. Used only if file has .npz extension. Default NULL.
rowIndexLocation	Character. For Optimus output, The path to the feature (gene) index .npy file. Used only if file has .npz extension. Default NULL.

## Value

A [DelayedArray](#) object or matrix.

## Examples

```
mat <- readSingleCellMatrix(system.file("extdata/hgmm_1k_v3_20x20/outs/",  
  "filtered_feature_bc_matrix/matrix.mtx.gz", package = "singleCellTK"))
```

---

reportCellQC	<i>Get runCellQC .html report</i>
--------------	-----------------------------------

---

### Description

A function to generate .html Rmarkdown report containing the visualizations of the runCellQC function output

### Usage

```
reportCellQC(  
  inSCE,  
  output_file = NULL,  
  output_dir = NULL,  
  subTitle = NULL,  
  studyDesign = NULL,  
  useReducedDim = NULL  
)
```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object containing the filtered count matrix with the output from runCellQC function
output_file	Character. The name of the generated file. If NULL/default then the output file name will be based on the name of the Rmarkdown template.
output_dir	Character. The name of the output directory to save the rendered file. If NULL/default the file is stored to the current working directory
subTitle	subtitle of the QC HTML report. Default is NULL.
studyDesign	Character. The description of the data set and experiment design. It would be shown at the top of QC HTML report. Default is NULL.
useReducedDim	Character. The name of the saved dimension reduction slot including cells from all samples in then <a href="#">SingleCellExperiment</a> object, Default is NULL

### Value

.html file

### Examples

```
data(scExample, package = "singleCellTK")  
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")  
## Not run:  
sce <- runCellQC(sce)  
reportCellQC(inSCE = sce)  
  
## End(Not run)
```



---

`reportClusterAbundance`*Get plotClusterAbundance .html report*

---

## Description

A function to generate .html Rmarkdown report containing the visualizations of the plotClusterAbundance function output

## Usage

```
reportClusterAbundance(  
  inSCE,  
  cluster,  
  variable,  
  output_dir = ".",  
  output_file = "plotClusterAbundance_Report",  
  pdf = FALSE,  
  showSession = TRUE  
)
```

## Arguments

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>cluster</code>	A single character, specifying the name to store the cluster label in <a href="#">colData</a> .
<code>variable</code>	A single character, specifying the name to store the phenotype labels in <a href="#">colData</a> .
<code>output_dir</code>	name of the output directory to save the rendered file. If NULL the file is stored to the current working directory. Default NULL.
<code>output_file</code>	name of the generated file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
<code>pdf</code>	A logical value indicating if a pdf should also be generated for each figure in the report. Default is TRUE.
<code>showSession</code>	A logical value indicating if session information should be displayed or not. Default is TRUE.

## Value

An HTML file of the report will be generated at the path specified in the arguments.

---

 reportDiffAbundanceFET

*Get diffAbundanceFET .html report*


---

### Description

A function to generate .html Rmarkdown report containing the visualizations of the diffAbundanceFET function output

### Usage

```
reportDiffAbundanceFET(
  inSCE,
  cluster,
  variable,
  control,
  case,
  analysisName,
  output_dir = ".",
  output_file = "DifferentialAbundanceFET_Report",
  pdf = FALSE,
  showSession = TRUE
)
```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
cluster	A single character, specifying the name to store the cluster label in <a href="#">colData</a> .
variable	A single character, specifying the name to store the phenotype labels in <a href="#">colData</a> .
control	character. Specifying one or more categories that can be found in the vector specified by <code>variable</code> .
case	character. Specifying one or more categories that can be found in the vector specified by <code>variable</code> .
analysisName	A single character. Will be used for naming the result table, which will be saved in metadata slot.
output_dir	name of the output directory to save the rendered file. If NULL the file is stored to the current working directory. Default NULL.
output_file	name of the generated file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is TRUE.
showSession	A logical value indicating if session information should be displayed or not. Default is TRUE.

**Value**

An HTML file of the report will be generated at the path specified in the arguments.

---

reportDiffExp	<i>Get runDEAnalysis .html report</i>
---------------	---------------------------------------

---

**Description**

A function to generate .html Rmarkdown report containing the visualizations of the `runDEAnalysis` function output

**Usage**

```
reportDiffExp(inSCE, study, output_file = NULL, output_dir = NULL)
```

**Arguments**

inSCE	A <code>SingleCellExperiment</code> object containing the output from <code>runDEAnalysis</code> function
study	The specific analysis to visualize, used as <code>analysisName</code> argument when running differential expression.
output_file	name of the generated file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
output_dir	name of the output directory to save the rendered file. If NULL the file is stored to the current working directory. Default NULL.

**Value**

Saves the HTML report in the specified output directory.

---

reportDropletQC	<i>Get runDropletQC .html report</i>
-----------------	--------------------------------------

---

**Description**

A function to generate .html Rmarkdown report containing the visualizations of the `runDropletQC` function output

**Usage**

```
reportDropletQC(
  inSCE,
  output_file = NULL,
  output_dir = NULL,
  subTitle = NULL,
  studyDesign = NULL
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object containing the full droplet count matrix with the output from runDropletQC function
output_file	name of the generated file. If NULL/default then the output file name will be based on the name of the Rmarkdown template
output_dir	name of the output directory to save the rendered file. If NULL/default the file is stored to the current working directory
subTitle	subtitle of the QC HTML report. Default is NULL.
studyDesign	description of the data set and experiment design. It would be shown at the top of QC HTML report. Default is NULL.

**Value**

.html file

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runDropletQC(sce)
reportDropletQC(inSCE = sce)

## End(Not run)
```

---

reportFindMarker	<i>Get findMarkerDiffExp .html report</i>
------------------	---

---

**Description**

A function to generate .html Rmarkdown report containing the visualizations of the [findMarkerDiffExp](#) function output

**Usage**

```
reportFindMarker(inSCE, output_file = NULL, output_dir = NULL)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object containing the output from <a href="#">findMarkerDiffExp</a> function
output_file	name of the generated file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
output_dir	name of the output directory to save the rendered file. If NULL the file is stored to the current working directory. Default NULL.

**Value**

An HTML file of the report will be generated at the path specified in the arguments.

---

reportQCTool	<i>Get .html report of the output of the selected QC algorithm</i>
--------------	--

---

## Description

A function to generate .html Rmarkdown report for the specified QC algorithm output

## Usage

```
reportQCTool(
  inSCE,
  algorithm = c("BarcodeRankDrops", "EmptyDrops", "QCMetrics", "Scrublet",
    "ScDblFinder", "Cxds", "Bcbs", "CxdsBcbsHybrid", "DoubletFinder", "DecontX", "SoupX"),
  output_file = NULL,
  output_dir = NULL
)
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object containing the count matrix (full droplets or filtered matrix, depends on the selected QC algorithm) with the output from at least one of these functions: runQCMetrics, runScrublet, runScDblFinder, runCxds, runBcbs, runCxdsBcbsHybrid, runDecontX, runBarcodeRankDrops, runEmptyDrops
algorithm	Character. Specifies which QC algorithm report to generate. Available options are "BarcodeRankDrops", "EmptyDrops", "QCMetrics", "Scrublet", "ScDblFinder", "Cxds", "Bcbs", "CxdsBcbsHybrid", "DoubletFinder", "DecontX" and "SoupX".
output_file	name of the generated file. If NULL/default then the output file name will be based on the name of the selected QC algorithm name .
output_dir	name of the output directory to save the rendered file. If NULL/default the file is stored to the current working directory

## Value

.html file

## Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
sce <- runDecontX(sce)
sce <- getUMAP(sce)
reportQCTool(inSCE = sce, algorithm = "DecontX")

## End(Not run)
```

---

reportSeurat	<i>Generates an HTML report for the complete Seurat workflow and returns the SCE object with the results computed and stored inside the object.</i>
--------------	---

---

### Description

Generates an HTML report for the complete Seurat workflow and returns the SCE object with the results computed and stored inside the object.

### Usage

```
reportSeurat(  
  inSCE,  
  biological.group = NULL,  
  phenotype.groups = NULL,  
  selected.markers = NULL,  
  clustering.resolution = 0.8,  
  variable.features = 2000,  
  pc.count = 50,  
  outputFile = NULL,  
  outputDir = NULL,  
  subtitle = NULL,  
  authors = NULL,  
  showSession = FALSE,  
  pdf = FALSE,  
  runHVG = TRUE,  
  plotHVG = TRUE,  
  runDimRed = TRUE,  
  plotJackStraw = FALSE,  
  plotElbowPlot = TRUE,  
  plotHeatmaps = TRUE,  
  runClustering = TRUE,  
  plotTSNE = TRUE,  
  plotUMAP = TRUE,  
  minResolution = 0.3,  
  maxResolution = 1.5,  
  runMSClusters = TRUE,  
  runMSBioGroup = TRUE,  
  forceRun = FALSE  
)
```

### Arguments

inSCE            Input [SingleCellExperiment](#) object.

<code>biological.group</code>	A character value that specifies the name of the <code>colData()</code> column to use as the main biological group in the Seurat report for marker selection and grouping.
<code>phenotype.groups</code>	A character vector that specifies the names of the <code>colData()</code> columns to use for differential expression in addition to the <code>biological.group</code> parameter.
<code>selected.markers</code>	A character vector containing the user-specified gene symbols or feature names of marker genes that be used to generate gene plots in addition to the gene markers computed from differential expression.
<code>clustering.resolution</code>	A numeric value indicating the user-specified final resolution to use with clustering. Default is 0.8.
<code>variable.features</code>	A numeric value indicating the number of top variable features to identify. Default 2000.
<code>pc.count</code>	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.
<code>outputFile</code>	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
<code>outputDir</code>	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
<code>subtitle</code>	A character value specifying the subtitle to use in the report. Default NULL.
<code>authors</code>	A character value specifying the names of the authors to use in the report. Default NULL.
<code>showSession</code>	A logical value indicating if session information should be displayed or not. Default is FALSE.
<code>pdf</code>	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
<code>runHVG</code>	A logical value indicating if the feature selection computation should be run or not. Default is TRUE.
<code>plotHVG</code>	A logical value indicating if the plot for the top most variable genes should be visualized in a mean-to-variance plot. Default is TRUE.
<code>runDimRed</code>	A logical value indicating if PCA should be computed. Default is TRUE.
<code>plotJackStraw</code>	A logical value indicating if JackStraw plot be visualized for the principal components. Default is FALSE.
<code>plotElbowPlot</code>	A logical value indicating if the ElbowPlot be visualized for the principal components. Default is TRUE.
<code>plotHeatmaps</code>	A logical value indicating if heatmaps should be plotted for the principal components. Default is TRUE.
<code>runClustering</code>	A logical value indicating if clustering section should be run in the report. Default is TRUE.
<code>plotTSNE</code>	A logical value indicating if TSNE plots should be visualized for clustering results. Default is TRUE.

plotUMAP	A logical value indicating if the UMAP plots should be visualized for the clustering results. Default is TRUE.
minResolution	A numeric value indicating the minimum resolution to use for clustering. Default is 0.3.
maxResolution	A numeric value indicating the maximum resolution to use for clustering. Default is 1.5.
runMSClusters	A logical value indicating if marker selection should be run between clusters. Default is TRUE.
runMSBioGroup	A logical value indicating if marker selection should be run between the <code>biological.group</code> parameter. Default is TRUE.
forceRun	A logical value indicating if all algorithms should be re-run regardless if they have been computed previously in the input object. Default is FALSE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratClustering

*Generates an HTML report for Seurat Clustering and returns the SCE object with the results computed and stored inside the object.*

---

**Description**

Generates an HTML report for Seurat Clustering and returns the SCE object with the results computed and stored inside the object.

**Usage**

```
reportSeuratClustering(
  inSCE,
  biological.group = NULL,
  phenotype.groups = NULL,
  runClustering = TRUE,
  plotTSNE = TRUE,
  plotUMAP = TRUE,
  minResolution = 0.3,
  maxResolution = 1.5,
  numClusters = 10,
  significant_PC = 10,
  outputFile = NULL,
  outputDir = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = FALSE
)
```



**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
biological.group	A character value that specifies the name of the colData() column to use as the main biological group in the Seurat report for marker selection and grouping.
phenotype.groups	A character vector that specifies the names of the colData() columns to use for differential expression in addition to the biological.group parameter.
runClustering	A logical value indicating if Clustering should be run or not in the report. Default is TRUE. If FALSE, parameters plotTSNE and plotUMAP are also set to FALSE.
plotTSNE	A logical value indicating if TSNE plots should be visualized in the clustering section of the report. Default is TRUE.
plotUMAP	A logical value indicating if UMAP plots should be visualized in the clustering section of the report. Default is TRUE.
minResolution	A numeric value indicating the minimum resolution to use for clustering. Default 0.3.
maxResolution	A numeric value indicating the maximum resolution to use for clustering. Default 1.5.
numClusters	temp (to remove)
significant_PC	temp (change to pc.use)
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratDimRed	<i>Generates an HTML report for Seurat Dimensionality Reduction and returns the SCE object with the results computed and stored inside the object.</i>
--------------------	--

---

### Description

Generates an HTML report for Seurat Dimensionality Reduction and returns the SCE object with the results computed and stored inside the object.

### Usage

```
reportSeuratDimRed(
  inSCE,
  pc.count = 50,
  runDimRed = TRUE,
  plotJackStraw = FALSE,
  plotElbowPlot = TRUE,
  plotHeatmaps = TRUE,
  outputFile = NULL,
  outputDir = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = FALSE
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pc.count	A numeric value indicating the number of principal components to compute. Default is 50.
runDimRed	A logical value indicating if dimensionality reduction should be computed. Default TRUE.
plotJackStraw	A logical value indicating if JackStraw plot should be visualized. Default FALSE.
plotElbowPlot	A logical value indicating if ElbowPlot should be visualized. Default TRUE.
plotHeatmaps	A logical value indicating if heatmaps should be visualized. Default TRUE.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.

showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

```
reportSeuratFeatureSelection
```

*Generates an HTML report for Seurat Feature Selection and returns the SCE object with the results computed and stored inside the object.*

---

**Description**

Generates an HTML report for Seurat Feature Selection and returns the SCE object with the results computed and stored inside the object.

**Usage**

```
reportSeuratFeatureSelection(
  inSCE,
  variable.features = 2000,
  runHVG = TRUE,
  plotHVG = TRUE,
  outputFile = NULL,
  outputDir = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = FALSE
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
variable.features	A numeric value indicating the number of top variable features to identify. Default 2000.
runHVG	A logical value indicating if the feature selection algorithm should be run or not. Default TRUE.

plotHVG	A logical value indicating if the mean-to-variance plot of the top variable feature should be visualized or not. Default TRUE.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratMarkerSelection

*Generates an HTML report for Seurat Results (including Clustering & Marker Selection) and returns the SCE object with the results computed and stored inside the object.*

---

**Description**

Generates an HTML report for Seurat Results (including Clustering & Marker Selection) and returns the SCE object with the results computed and stored inside the object.

**Usage**

```
reportSeuratMarkerSelection(
  inSCE,
  biological.group = NULL,
  phenotype.groups = NULL,
  selected.markers = NULL,
  runMarkerSelection = TRUE,
  plotMarkerSelection = TRUE,
  countFeatures = 10,
  outputFile = NULL,
  outputDir = NULL,
  subtitle = NULL,
```

```

  authors = NULL,
  showSession = FALSE,
  pdf = FALSE
)

```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
biological.group	A character value that specifies the name of the colData() column to use as the main biological group in the Seurat report for marker selection and grouping.
phenotype.groups	A character vector that specifies the names of the colData() columns to use for differential expression in addition to the biological.group parameter.
selected.markers	A character vector containing the user-specified gene symbols or feature names of marker genes that be used to generate gene plots in addition to the gene markers computed from differential expression.
runMarkerSelection	A logical value indicating if the marker selection computation should be run or not. Default TRUE.
plotMarkerSelection	A logical value indicating if the gene marker plots should be visualized or not. Default TRUE.
countFeatures	A numeric value indicating the number of top features to visualize in each group. Default 10.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.

## Value

A [SingleCellExperiment](#) object with computations stored.

---

```
reportSeuratNormalization
```

*Generates an HTML report for Seurat Normalization and returns the SCE object with the results computed and stored inside the object.*

---

### Description

Generates an HTML report for Seurat Normalization and returns the SCE object with the results computed and stored inside the object.

### Usage

```
reportSeuratNormalization(
  inSCE,
  outputFile = NULL,
  outputDir = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = FALSE
)
```

### Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object previously passed through <code>reportSeuratRun()</code> .
<code>outputFile</code>	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
<code>outputDir</code>	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
<code>subtitle</code>	A character value specifying the subtitle to use in the report. Default NULL.
<code>authors</code>	A character value specifying the names of the authors to use in the report. Default NULL.
<code>showSession</code>	A logical value indicating if session information should be displayed or not. Default is FALSE.
<code>pdf</code>	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
<code>forceRun</code>	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

### Value

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratResults	<i>Generates an HTML report for Seurat Results (including Clustering &amp; Marker Selection) and returns the SCE object with the results computed and stored inside the object.</i>
---------------------	---

---

## Description

Generates an HTML report for Seurat Results (including Clustering & Marker Selection) and returns the SCE object with the results computed and stored inside the object.

## Usage

```
reportSeuratResults(  
  inSCE,  
  biological.group = NULL,  
  phenotype.groups = NULL,  
  selected.markers = NULL,  
  clustering.resolution = 0.8,  
  pc.count = 50,  
  plotTSNE = TRUE,  
  plotUMAP = TRUE,  
  runClustering = TRUE,  
  runMSClusters = TRUE,  
  runMSBioGroup = TRUE,  
  outputFile = NULL,  
  outputDir = NULL,  
  subtitle = NULL,  
  authors = NULL,  
  showSession = FALSE,  
  pdf = FALSE,  
  forceRun = FALSE  
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object previously passed through <code>reportSeuratRun()</code> .
biological.group	A character value that specifies the name of the <code>colData()</code> column to use as the main biological group in the Seurat report for marker selection and grouping.
phenotype.groups	A character vector that specifies the names of the <code>colData()</code> columns to use for differential expression in addition to the <code>biological.group</code> parameter.
selected.markers	A character vector containing the user-specified gene symbols or feature names of marker genes that be used to generate gene plots in addition to the gene markers computed from differential expression.

clustering.resolution	A numeric value indicating the user-specified final resolution to use with clustering. Default is 0.8.
pc.count	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.
plotTSNE	A logical value indicating if TSNE plots should be visualized in the clustering section of the report. Default is TRUE.
plotUMAP	A logical value indicating if UMAP plots should be visualized in the clustering section of the report. Default is TRUE.
runClustering	A logical value indicating if Clustering should be run or not in the report. Default is TRUE. If FALSE, parameters plotTSNE and plotUMAP are also set to FALSE.
runMSClusters	A logical value indicating if the marker selection section for identifying marker genes between clusters should be run and visualized in the report. Default TRUE.
runMSBioGroup	A logical value indicating if the marker selection section for identifying marker genes between the biological.group parameter should be run and visualized in the report. Default TRUE.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratRun	<i>Generates an HTML report for Seurat Run (including Normalization, Feature Selection, Dimensionality Reduction &amp; Clustering) and returns the SCE object with the results computed and stored inside the object.</i>
-----------------	---

---



## Description

Generates an HTML report for Seurat Run (including Normalization, Feature Selection, Dimensionality Reduction & Clustering) and returns the SCE object with the results computed and stored inside the object.

## Usage

```
reportSeuratRun(  
  inSCE,  
  biological.group = NULL,  
  phenotype.groups = NULL,  
  variable.features = 2000,  
  pc.count = 50,  
  runHVG = TRUE,  
  plotHVG = TRUE,  
  runDimRed = TRUE,  
  plotJackStraw = FALSE,  
  plotElbowPlot = TRUE,  
  plotHeatmaps = TRUE,  
  runClustering = TRUE,  
  plotTSNE = TRUE,  
  plotUMAP = TRUE,  
  minResolution = 0.3,  
  maxResolution = 1.5,  
  outputFile = NULL,  
  outputDir = NULL,  
  subtitle = NULL,  
  authors = NULL,  
  showSession = FALSE,  
  pdf = FALSE,  
  forceRun = FALSE  
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
biological.group	A character value that specifies the name of the colData() column to use as the main biological group in the Seurat report for tSNE & UMAP visualization.
phenotype.groups	A character value that specifies the name of the colData() column to use as additional phenotype variables in the Seurat report for tSNE & UMAP visualization.
variable.features	A numeric value indicating the number of top variable genes to identify in the report. Default is 2000.
pc.count	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.

runHVG	A logical value indicating if feature selection should be run in the report. Default TRUE.
plotHVG	A logical value indicating if the top variable genes should be visualized through a mean-to-variance plot. Default is TRUE.
runDimRed	A logical value indicating if PCA should be computed in the report. Default is TRUE.
plotJackStraw	A logical value indicating if the JackStraw plot should be visualized for the principal components. Default is FALSE.
plotElbowPlot	A logical value indicating if the ElbowPlot should be visualized for the principal components. Default is FALSE.
plotHeatmaps	A logical value indicating if the Heatmaps should be visualized for the principal components. Default is FALSE.
runClustering	A logical value indicating if Clustering should be run over multiple resolutions as defined by the minResolution and maxResolution parameters. Default is TRUE.
plotTSNE	A logical value indicating if TSNE plot should be visualized for clusters. Default is TRUE.
plotUMAP	A logical value indicating if UMAP plot should be visualized for clusters. Default is TRUE.
minResolution	A numeric value indicating the minimum resolution to use for clustering. Default 0.3.
maxResolution	A numeric value indicating the maximum resolution to use for clustering. Default 1.5.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

### Value

A `SingleCellExperiment` object with computations stored.

---

reportSeuratScaling *Generates an HTML report for Seurat Scaling and returns the SCE object with the results computed and stored inside the object.*

---

### Description

Generates an HTML report for Seurat Scaling and returns the SCE object with the results computed and stored inside the object.

### Usage

```
reportSeuratScaling(  
  inSCE,  
  outputFile = NULL,  
  outputDir = NULL,  
  subtitle = NULL,  
  authors = NULL,  
  showSession = FALSE,  
  pdf = FALSE,  
  forceRun = FALSE  
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
outputFile	Specify the name of the generated output HTML file. If NULL then the output file name will be based on the name of the Rmarkdown template. Default NULL.
outputDir	Specify the name of the output directory to save the rendered HTML file. If NULL the file is stored to the current working directory. Default NULL.
subtitle	A character value specifying the subtitle to use in the report. Default NULL.
authors	A character value specifying the names of the authors to use in the report. Default NULL.
showSession	A logical value indicating if session information should be displayed or not. Default is FALSE.
pdf	A logical value indicating if a pdf should also be generated for each figure in the report. Default is FALSE.
forceRun	A logical value indicating if all computations previously computed should be re-calculated regardless if these computations are available in the input object. Default is FALSE.

### Value

A [SingleCellExperiment](#) object with computations stored.

---

retrieveSCEIndex	<i>Retrieve cell/feature index by giving identifiers saved in col/rowData</i>
------------------	---

---

### Description

Originally written in [retrieveFeatureIndex](#). Modified for also retrieving cell indices and only working for [SingleCellExperiment](#) object. This will return indices of features among the `rowData/colData`. Partial matching (i.e. grepping) can be used.

### Usage

```
retrieveSCEIndex(  
  inSCE,  
  IDs,  
  axis,  
  by = NULL,  
  exactMatch = TRUE,  
  firstMatch = TRUE  
)
```

### Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object. Required
<code>IDs</code>	Character vector of identifiers for features or cells to find in <code>rowData</code> or <code>colData</code> of <code>inSCE</code>
<code>axis</code>	A character scalar to specify whether to search for features or cells. Use "row", "feature" or "gene" for features; "col" or "cell" for cells.
<code>by</code>	Character. In which column to search for features/cells in <code>rowData/colData</code> . Default NULL for search the <code>rownames/colnames</code>
<code>exactMatch</code>	A logical scalar. Whether to only identify exact matches or to identify partial matches using <a href="#">grep</a> . Default TRUE
<code>firstMatch</code>	A logical scalar. Whether to only identify the first matches or to return all plausible matches. Default TRUE

### Value

A unique, non-NA numeric vector of indices for the matching features/cells in `inSCE`.

### Author(s)

Yusuke Koga, Joshua Campbell

### Examples

```
data(scExample, package = "singleCellTK")  
retrieveSCEIndex(inSCE = sce, IDs = "ENSG00000205542",  
  axis = "row")
```

---

runBarcodeRankDrops    *Identify empty droplets using [barcodeRanks](#).*

---

## Description

Run [barcodeRanks](#) on a count matrix provided in a [SingleCellExperiment](#) object. Distinguish between droplets containing cells and ambient RNA in a droplet-based single-cell RNA sequencing experiment.

## Usage

```
runBarcodeRankDrops(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  lower = 100,
  fitBounds = NULL,
  df = 20
)
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object. Must contain a raw counts matrix before empty droplets have been removed.
sample	Character vector. Indicates which sample each cell belongs to <a href="#">emptyDrops</a> will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
useAssay	A string specifying which assay in the SCE to use.
lower	See <a href="#">emptyDrops</a> for more information. Default 100.
fitBounds	See <a href="#">emptyDrops</a> for more information. Default NULL.
df	See <a href="#">emptyDrops</a> for more information. Default 20.

## Value

A [SingleCellExperiment](#) object with the [barcodeRanks](#) output table appended to the `colData` slot. The columns include `dropletUtils_BarcodeRank_Knee` and `dropletUtils_BarcodeRank_Knee` Please refer to the documentation of [barcodeRanks](#) for details.

## Examples

```
# The following unfiltered PBMC_1k_v3 data were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.0
# /pbmc_1k_v3
# Only the top 10 cells with most counts and the last 10 cells with non-zero
# counts are included in this example.
# This example only serves as an proof of concept and a tutorial on how to
```

```
# run the function. The results should not be
# used for drawing scientific conclusions.
data(scExample, package = "singleCellTK")
sce <- runBarcodeRankDrops(inSCE = sce)
```

---

runBBKNN	<i>Apply BBKNN batch effect correction method to SingleCellExperiment object</i>
----------	--

---

## Description

BBKNN, an extremely fast graph-based data integration algorithm. It modifies the neighbourhood construction step to produce a graph that is balanced across all batches of the data.

## Usage

```
runBBKNN(
  inSCE,
  useAssay = "logcounts",
  batch = "batch",
  reducedDimName = "BBKNN",
  nComponents = 50L
)
```

## Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".
reducedDimName	A single character. The name for the corrected low-dimensional representation. Will be saved to <code>reducedDim(inSCE)</code> . Default "BBKNN".
nComponents	An integer. Number of principle components or the dimensionality, adopted in the pre-PCA-computation step, the BBKNN step (for how many PCs the algorithm takes into account), and the final UMAP combination step where the value represent the dimensionality of the updated reducedDim. Default 50L.

## Value

The input [SingleCellExperiment](#) object with `reducedDim(inSCE, reducedDimName)` updated.

## References

Krzysztof Polanski et al., 2020

## Examples

```
## Not run:
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sceBatches.small <- sample(sceBatches, 20)
sceCorr <- runBBKNN(sceBatches.small, useAssay = "logcounts",
                    nComponents = 10)

## End(Not run)
```

---

runBcDs

*Find doublets/multiplets using [bcDs](#).*

---

## Description

A wrapper function for [bcDs](#). Annotate doublets/multiplets using a binary classification approach to discriminate artificial doublets from original data. Generate a doublet score for each cell. Infer doublets if `estNdbl` is TRUE.

## Usage

```
runBcDs(
  inSCE,
  sample = NULL,
  seed = 12345,
  ntop = 500,
  srat = 1,
  verb = FALSE,
  retRes = FALSE,
  nmax = "tune",
  varImp = FALSE,
  estNdbl = FALSE,
  useAssay = "counts"
)
```

## Arguments

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object. Needs counts in assays slot.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to. <a href="#">bcDs</a> will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
<code>seed</code>	Seed for the random number generator. Default 12345.
<code>ntop</code>	See <a href="#">bcDs</a> for more information. Default 500.
<code>srat</code>	See <a href="#">bcDs</a> for more information. Default 1.
<code>verb</code>	See <a href="#">bcDs</a> for more information. Default FALSE.

retRes	See <a href="#">bcds</a> for more information. Default FALSE.
nmax	See <a href="#">bcds</a> for more information. Default "tune".
varImp	See <a href="#">bcds</a> for more information. Default FALSE.
estNdbl	See <a href="#">bcds</a> for more information. Default FALSE.
useAssay	A string specifying which assay in the SCE to use.

### Value

A [SingleCellExperiment](#) object with [bcds](#) output appended to the [colData](#) slot. The columns include *bcds\_score* and optionally *bcds\_call*. Please refer to the documentation of [bcds](#) for details.

### Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runBcds(sce)
```

---

runCellQC

*Perform comprehensive single cell QC*

---

### Description

A wrapper function to run several QC algorithms on a [SingleCellExperiment](#) object containing cells after empty droplets have been removed.

### Usage

```
runCellQC(
  inSCE,
  algorithms = c("QCMetrics", "scDblFinder", "cxds", "bcds", "cxds_bcds_hybrid",
    "decontX", "decontX_bg", "soupX", "soupX_bg"),
  sample = NULL,
  collectionName = NULL,
  geneSetList = NULL,
  geneSetListLocation = "rownames",
  geneSetCollection = NULL,
  mitoRef = NULL,
  mitoIDType = NULL,
  mitoPrefix = NULL,
  mitoID = NULL,
  mitoGeneLocation = NULL,
  useAssay = "counts",
  background = NULL,
  bgAssayName = NULL,
  bgBatch = NULL,
  seed = 12345,
  paramsList = NULL
)
```



**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object.
algorithms	Character vector. Specify which QC algorithms to run. Available options are "QCMetrics", "scrublet", "doubletFinder", "scDbfFinder", "cxds", "bcds", "cxds_bcds_hybrid", "decontX" and "soupX".
sample	Character vector. Indicates which sample each cell belongs to. Algorithms will be run on cells from each sample separately.
collectionName	Character. Name of a <a href="#">GeneSetCollection</a> obtained by using one of the import-GeneSet* functions. Default NULL.
geneSetList	See runPerCellQC. Default NULL.
geneSetListLocation	See runPerCellQC. Default NULL.
geneSetCollection	See runPerCellQC. Default NULL.
mitoRef, mitoIDType, mitoPrefix, mitoID, mitoGeneLocation	Arguments used to import mitochondrial genes and quantify their expression. Please see <a href="#">runPerCellQC</a> for detailed information.
useAssay	A string specifying which assay contains the count matrix for cells.
background	A <a href="#">SingleCellExperiment</a> with the matrix located in the assay slot under bgAssayName. It should have the same structure as inSCE except it contains the matrix of empty droplets instead of cells. When supplied, empirical distribution of transcripts from these empty droplets will be used as the contamination distribution. It is only used in algorithms "decontX" and "soupX". Default NULL.
bgAssayName	Character. Name of the assay to use if background is a <a href="#">SingleCellExperiment</a> . If NULL, the function will use the same value as useAssay. It is only used in algorithms "decontX" and "soupX". Default is NULL.
bgBatch	Batch labels for background. If background is a <a href="#">SingleCellExperiment</a> object, this can be a single character specifying a name that can be found in colData(background) to directly use the barcode annotation. Its unique values should be the same as those in sample, such that each batch of cells have their corresponding batch of empty droplets as background, pointed by this parameter. It is only used in algorithms "decontX" and "soupX". Default to NULL.
seed	Seed for the random number generator. Default 12345.
paramsList	A list containing parameters for QC functions. Default NULL.

**Value**

[SingleCellExperiment](#) object containing the outputs of the specified algorithms in the [colData](#) of inSCE.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
```

```
sce <- runCellQC(sce)

## End(Not run)
```

---

runComBatSeq	<i>Apply ComBat-Seq batch effect correction method to SingleCellExperiment object</i>
--------------	---

---

### Description

The ComBat-Seq batch adjustment approach assumes that batch effects represent non-biological but systematic shifts in the mean or variability of genomic features for all samples within a processing batch. It uses either parametric or non-parametric empirical Bayes frameworks for adjusting data for batch effects.

### Usage

```
runComBatSeq(
  inSCE,
  useAssay = "counts",
  batch = "batch",
  covariates = NULL,
  bioCond = NULL,
  useSVA = FALSE,
  assayName = "ComBatSeq",
  shrink = FALSE,
  shrinkDisp = FALSE,
  nGene = NULL
)
```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "counts".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".
covariates	A character vector indicating the fields in <a href="#">colData</a> that annotates other covariates, such as the cell types. Default NULL.
bioCond	A single character indicating a field in <a href="#">colData</a> that annotates the biological conditions. Default NULL.
useSVA	A logical scalar. Whether to estimate surrogate variables and use them as an empirical control. Default FALSE.
assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "ComBat".

shrink	A logical scalar. Whether to apply shrinkage on parameter estimation. Default FALSE.
shrinkDisp	A logical scalar. Whether to apply shrinkage on dispersion. Default FALSE.
nGene	An integer. Number of random genes to use in empirical Bayes estimation, only useful when shrink is set to TRUE. Default NULL.

### Details

For the parameters `covariates` and `useSVA`, when the cell type information is known, it is recommended to specify the cell type annotation to the argument `covariates`; if the cell types are unknown but expected to be balanced, it is recommended to run with default settings, yet informative `covariates` could still be useful. If the cell types are unknown and are expected to be unbalanced, it is recommended to set `useSVA` to TRUE.

### Value

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

### Examples

```
data('sceBatches', package = 'singleCellTK')
sceBatches <- sample(sceBatches, 40)
# Cell type known
sceBatches <- runComBatSeq(sceBatches, "counts", "batch",
                          covariates = "cell_type",
                          assayName = "ComBat_cell_seq")
# Cell type unknown but balanced
#sceBatches <- runComBatSeq(sceBatches, "counts", "batch",
#                           assayName = "ComBat_seq")
# Cell type unknown and unbalanced
#sceBatches <- runComBatSeq(sceBatches, "counts", "batch",
#                           useSVA = TRUE,
#                           assayName = "ComBat_sva_seq")
```

---

runCxls

*Find doublets/multiplets using [cxds](#).*

---

### Description

A wrapper function for [cxds](#). Annotate doublets/multiplets using co-expression based approach. Generate a doublet score for each cell. Infer doublets if `estNdbl` is TRUE.

### Usage

```
runCxls(
  inSCE,
  sample = NULL,
  seed = 12345,
```

```

ntop = 500,
binThresh = 0,
verb = FALSE,
retRes = FALSE,
estNdbl = FALSE,
useAssay = "counts"
)

```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object. Needs counts in assays slot.
sample	Character vector. Indicates which sample each cell belongs to. <a href="#">cxls</a> will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
seed	Seed for the random number generator. Default 12345.
ntop	See <a href="#">cxls</a> for more information. Default 500.
binThresh	See <a href="#">cxls</a> for more information. Default 0.
verb	See <a href="#">cxls</a> for more information. Default FALSE.
retRes	See <a href="#">cxls</a> for more information. Default FALSE.
estNdbl	See <a href="#">cxls</a> for more information. Default FALSE.
useAssay	A string specifying which assay in the SCE to use.

### Value

A [SingleCellExperiment](#) object with [cxls](#) output appended to the `colData` slot. The columns include `cxls_score` and optionally `cxls_call`. Please refer to the documentation of [cxls](#) for details.

### Examples

```

data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- runCxls(sce)

```

---

runCxlsBcdsHybrid      *Find doublets/multiplets using [cxls\\_bcds\\_hybrid](#).*

---

### Description

A wrapper function for [cxls\\_bcds\\_hybrid](#). Annotate doublets/multiplets using a binary classification approach to discriminate artificial doublets from original data. Generate a doublet score for each cell. Infer doublets if `estNdbl` is TRUE.

**Usage**

```
runCxdsBcdsHybrid(
  inSCE,
  sample = NULL,
  seed = 12345,
  nTop = 500,
  cxdsArgs = list(),
  bcdsArgs = list(),
  verb = FALSE,
  estNdbl = FALSE,
  force = FALSE,
  useAssay = "counts"
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object. Needs counts in assays slot.
sample	Character vector. Indicates which sample each cell belongs to. <a href="#">cxds_bcds_hybrid</a> will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
seed	Seed for the random number generator. Default 12345.
nTop	The number of top variable genes to consider. Used in both <code>cxds</code> and <code>bcds</code> . Default 500.
cxdsArgs	See <a href="#">cxds_bcds_hybrid</a> for more information. Default NULL.
bcdsArgs	See <a href="#">cxds_bcds_hybrid</a> for more information. Default NULL.
verb	See <a href="#">cxds_bcds_hybrid</a> for more information. Default FALSE.
estNdbl	See <a href="#">cxds_bcds_hybrid</a> for more information. Default FALSE.
force	See <a href="#">cxds_bcds_hybrid</a> for more information. Default FALSE.
useAssay	A string specifying which assay in the SCE to use.

**Value**

A [SingleCellExperiment](#) object with [cxds\\_bcds\\_hybrid](#) output appended to the `colData` slot. The columns include `hybrid_score` and optionally `hybrid_call`. Please refer to the documentation of [cxds\\_bcds\\_hybrid](#) for details.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- runCxdsBcdsHybrid(sce)
```

---

runDEAnalysis	<i>Perform differential expression analysis on SCE object</i>
---------------	---

---

**Description**

Perform differential expression analysis on SCE object

**Usage**

```
runDEAnalysis(method = c("wilcox", "MAST", "DESeq2", "Limma", "ANOVA"), ...)
```

```
runDESeq2(  
  inSCE,  
  useAssay = "counts",  
  useReducedDim = NULL,  
  index1 = NULL,  
  index2 = NULL,  
  class = NULL,  
  classGroup1 = NULL,  
  classGroup2 = NULL,  
  analysisName,  
  groupName1,  
  groupName2,  
  covariates = NULL,  
  fullReduced = TRUE,  
  onlyPos = FALSE,  
  log2fcThreshold = NULL,  
  fdrThreshold = NULL,  
  minGroup1MeanExp = NULL,  
  maxGroup2MeanExp = NULL,  
  minGroup1ExprPerc = NULL,  
  maxGroup2ExprPerc = NULL,  
  overwrite = FALSE  
)
```

```
runLimmaDE(  
  inSCE,  
  useAssay = "logcounts",  
  useReducedDim = NULL,  
  index1 = NULL,  
  index2 = NULL,  
  class = NULL,  
  classGroup1 = NULL,  
  classGroup2 = NULL,  
  analysisName,  
  groupName1,  
  groupName2,
```

```
    covariates = NULL,  
    onlyPos = FALSE,  
    log2fcThreshold = NULL,  
    fdrThreshold = NULL,  
    minGroup1MeanExp = NULL,  
    maxGroup2MeanExp = NULL,  
    minGroup1ExprPerc = NULL,  
    maxGroup2ExprPerc = NULL,  
    overwrite = FALSE  
  )
```

```
runANOVA(  
  inSCE,  
  useAssay = "logcounts",  
  useReducedDim = NULL,  
  index1 = NULL,  
  index2 = NULL,  
  class = NULL,  
  classGroup1 = NULL,  
  classGroup2 = NULL,  
  analysisName,  
  groupName1,  
  groupName2,  
  covariates = NULL,  
  onlyPos = FALSE,  
  log2fcThreshold = NULL,  
  fdrThreshold = NULL,  
  minGroup1MeanExp = NULL,  
  maxGroup2MeanExp = NULL,  
  minGroup1ExprPerc = NULL,  
  maxGroup2ExprPerc = NULL,  
  overwrite = FALSE  
)
```

```
runMAST(  
  inSCE,  
  useAssay = "logcounts",  
  useReducedDim = NULL,  
  index1 = NULL,  
  index2 = NULL,  
  class = NULL,  
  classGroup1 = NULL,  
  classGroup2 = NULL,  
  analysisName,  
  groupName1,  
  groupName2,  
  covariates = NULL,  
  onlyPos = FALSE,
```

```

log2fcThreshold = NULL,
fdrThreshold = NULL,
minGroup1MeanExp = NULL,
maxGroup2MeanExp = NULL,
minGroup1ExprPerc = NULL,
maxGroup2ExprPerc = NULL,
overwrite = FALSE,
check_sanity = TRUE
)

runWilcox(
  inSCE,
  useAssay = "logcounts",
  useReducedDim = NULL,
  index1 = NULL,
  index2 = NULL,
  class = NULL,
  classGroup1 = NULL,
  classGroup2 = NULL,
  analysisName,
  groupName1,
  groupName2,
  covariates = NULL,
  onlyPos = FALSE,
  log2fcThreshold = NULL,
  fdrThreshold = NULL,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL,
  overwrite = FALSE
)

```

## Arguments

method	Character. Specify which method to use when using <code>runDEAnalysis()</code> . Choose from "wilcox", "MAST", "DESeq2", "Limma", "ANOVA". Default "wilcox".
...	Arguments to pass to specific methods when using the generic <code>runDEAnalysis()</code> .
inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useAssay	character. A string specifying which assay to use for the DE regression. Default "counts" for DESeq2, "logcounts" for other methods.
useReducedDim	character. A string specifying which reducedDim to use for DE analysis. Usually a pathway analysis result matrix. Set useAssay to NULL when using. Default NULL.
index1	Any type of indices that can subset a <a href="#">SingleCellExperiment</a> inherited object by cells. Specifies which cells are of interests. Default NULL.



index2	Any type of indices that can subset a <a href="#">SingleCellExperiment</a> inherited object by cells. specifies the control group against those specified by index1. If NULL when using index specification, index1 cells will be compared with all other cells. Default NULL.
class	A vector/factor with ncol(inSCE) elements, or a character scalar that specifies a column name of colData(inSCE). Default NULL.
classGroup1	a vector specifying which "levels" given in class are of interests. Default NULL.
classGroup2	a vector specifying which "levels" given in class is the control group against those specified by classGroup1. If NULL when using annotation specification, classGroup1 cells will be compared with all other cells.
analysisName	A character scalar naming the DEG analysis. Required
groupName1	A character scalar naming the group of interests. Required.
groupName2	A character scalar naming the control group. Required.
covariates	A character vector of additional covariates to use when building the model. All covariates must exist in names(colData(inSCE)). Default NULL.
fullReduced	Logical, DESeq2 only argument. Whether to apply LRT (Likelihood ratio test) with a 'full' model. Default TRUE.
onlyPos	Whether to only output DEG with positive log2_FC value. Default FALSE.
log2fcThreshold	Only out put DEGs with the absolute values of log2FC greater than this value. Default NULL.
fdrThreshold	Only out put DEGs with FDR value less than this value. Default NULL.
minGroup1MeanExp	Only out put DEGs with mean expression in group1 greater then this value. Default NULL.
maxGroup2MeanExp	Only out put DEGs with mean expression in group2 less then this value. Default NULL.
minGroup1ExprPerc	Only out put DEGs expressed in greater then this fraction of cells in group1. Default NULL.
maxGroup2ExprPerc	Only out put DEGs expressed in less then this fraction of cells in group2. Default NULL.
overwrite	A logical scalar. Whether to overwrite result if exists. Default FALSE.
check_sanity	Logical, MAST only argument. Whether to perform MAST's sanity check to see if the counts are logged. Default TRUE.

## Details

SCTK provides Limma, MAST, DESeq2, ANOVA and Wilcoxon test for differential expression analysis, where DESeq2 expects non-negative integer assay input while others expect logcounts.

Condition specification allows two methods: 1. Index level selection. Arguments index1 and index2 will be used. 2. Annotation level selection. Arguments class, classGroup1 and classGroup2 will be used.

**Value**

The input [SingleCellExperiment](#) object with `metadata(inSCE)$diffExp` updated with the results: a list named by `analysisName`, with `$groupNames` containing the naming of the two conditions, `$useAssay` and `$useReducedDim` storing the matrix name that was used for calculation, `$select` storing the cell selection indices (logical) for each condition, `$result` storing a `data.frame` of the DEGs summary, and `$method` storing the character method name used.

**See Also**

See [plotDEGHeatmap](#), [plotDEGRegression](#), [plotDEGViolin](#) and [plotDEGVolcano](#) for visualization method after running DE analysis.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
sce <- runDEAnalysis(method = "Limma", inSCE = sce, groupName1 = "group1",
  groupName2 = "group2", index1 = seq(20), index2 = seq(21,40),
  analysisName = "Limma")
```

---

`runDecontX`*Detecting contamination with DecontX.*

---

**Description**

A wrapper function for [decontX](#). Identify potential contamination from experimental factors such as ambient RNA.

**Usage**

```
runDecontX(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  background = NULL,
  bgAssayName = NULL,
  bgBatch = NULL,
  z = NULL,
  maxIter = 500,
  delta = c(10, 10),
  estimateDelta = TRUE,
  convergence = 0.001,
  iterLogLik = 10,
  varGenes = 5000,
  dbscanEps = 1,
```

```

    seed = 12345,
    logfile = NULL,
    verbose = TRUE
)

```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
sample	A single character specifying a name that can be found in <code>colData(inSCE)</code> to directly use the cell annotation; or a character vector with as many elements as cells to indicate which sample each cell belongs to. Default NULL. <a href="#">decontX</a> will be run on cells from each sample separately.
useAssay	A string specifying which assay in the SCE to use. Default 'counts'.
background	A <a href="#">SingleCellExperiment</a> with the matrix located in the assay slot under <code>bgAssayName</code> . It should have the same structure as <code>inSCE</code> except it contains the matrix of empty droplets instead of cells. When supplied, empirical distribution of transcripts from these empty droplets will be used as the contamination distribution. Default NULL.
bgAssayName	Character. Name of the assay to use if background is a <a href="#">SingleCellExperiment</a> . If NULL, the function will use the same value as <code>useAssay</code> . Default is NULL.
bgBatch	Batch labels for background. If background is a <a href="#">SingleCellExperiment</a> object, this can be a single character specifying a name that can be found in <code>colData(background)</code> to directly use the barcode annotation; or a numeric / character vector that has as many elements as barcodes to indicate which sample each barcode belongs to. Its unique values should be the same as those in <code>sample</code> , such that each batch of cells have their corresponding batch of empty droplets as background, pointed by this parameter. Default to NULL.
z	Numeric or character vector. Cell cluster labels. If NULL, PCA will be used to reduce the dimensionality of the dataset initially, 'umap' from the 'uwot' package will be used to further reduce the dataset to 2 dimensions and the 'dbSCAN' function from the 'dbSCAN' package will be used to identify clusters of broad cell types. Default NULL.
maxIter	Integer. Maximum iterations of the EM algorithm. Default 500.
delta	Numeric Vector of length 2. Concentration parameters for the Dirichlet prior for the contamination in each cell. The first element is the prior for the native counts while the second element is the prior for the contamination counts. These essentially act as pseudocounts for the native and contamination in each cell. If <code>estimateDelta = TRUE</code> , this is only used to produce a random sample of proportions for an initial value of contamination in each cell. Then <code>fit_dirichlet</code> is used to update delta in each iteration. If <code>estimateDelta = FALSE</code> , then delta is fixed with these values for the entire inference procedure. Fixing delta and setting a high number in the second element will force <code>decontX</code> to be more aggressive and estimate higher levels of contamination at the expense of potentially removing native expression. Default <code>c(10, 10)</code> .
estimateDelta	Boolean. Whether to update delta at each iteration.

convergence	Numeric. The EM algorithm will be stopped if the maximum difference in the contamination estimates between the previous and current iterations is less than this. Default 0.001.
iterLogLik	Integer. Calculate log likelihood every <code>iterLogLik</code> iteration. Default 10.
varGenes	Integer. The number of variable genes to use in dimensionality reduction before clustering. Variability is calculated using <code>modelGeneVar</code> function from the 'scran' package. Used only when <code>z</code> is not provided. Default 5000.
dbscanEps	Numeric. The clustering resolution parameter used in 'dbscan' to estimate broad cell clusters. Used only when <code>z</code> is not provided. Default 1.
seed	Integer. Passed to <code>with_seed</code> . For reproducibility, a default value of 12345 is used. If NULL, no calls to <code>with_seed</code> are made.
logfile	Character. Messages will be redirected to a file named 'logfile'. If NULL, messages will be printed to stdout. Default NULL.
verbose	Logical. Whether to print log messages. Default TRUE.

### Value

A `SingleCellExperiment` object with 'decontX\_Contamination' and 'decontX\_Clusters' added to the `colData` slot. Additionally, the decontaminated counts will be added as an assay called 'decontXCounts'.

### Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- runDecontX(sce[, sample(ncol(sce), 20)])
```

---

runDimReduce

*Generic Wrapper function for running dimensionality reduction*

---

### Description

Generic Wrapper function for running dimensionality reduction

### Usage

```
runDimReduce(
  inSCE,
  method = c("scaterPCA", "seuratPCA", "seuratICA", "rTSNE", "seuratTSNE",
    "scaterUMAP", "seuratUMAP"),
  useAssay = NULL,
  useReducedDim = NULL,
  useAltExp = NULL,
  reducedDimName,
  nComponents = 20,
  seed = NULL,
  ...
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
method	One from "scaterPCA", "seuratPCA", "seuratICA", "rTSNE", "seuratTSNE", "scaterUMAP" and "seuratUMAP".
useAssay	Assay to use for computation. If useAltExp is specified, useAssay has to exist in assays(altExp(inSCE, useAltExp)). Default "counts".
useReducedDim	The low dimension representation to use for embedding computation. Default NULL.
useAltExp	The subset to use for computation, usually for the selected variable features. Default NULL.
reducedDimName	The name of the result matrix. Required.
nComponents	Specify the number of dimensions to compute with the selected method in case of PCA/ICA and the number of components to use in the case of TSNE/UMAP methods.
seed	Random seed for reproducibility of results. Default NULL will use global seed in use by the R environment.
...	The other arguments for running a specific algorithm. Please refer to the one you use.

**Details**

Wrapper function to run one of the available dimensionality reduction algorithms integrated within SCTK from [scaterPCA](#), [runSeuratPCA](#), [runSeuratICA](#), [getTSNE](#), [runSeuratTSNE](#), [getUMAP](#) and [runSeuratUMAP](#). Users can use an assay by specifying useAssay, use the assay in an altExp by specifying both useAltExp and useAssay, or use a low-dimensionality representation by specifying useReducedDim.

**Value**

The input [SingleCellExperiment](#) object with reducedDim updated with the result.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runNormalization(sce, useAssay = "counts",
                       outAssayName = "logcounts_scaled",
                       normalizationMethod = "logNormCounts",
                       scale = TRUE)
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                   useAssay = "logcounts_scaled",
                   reducedDimName = "PCA")
```

---

runDoubletFinder      *Generates a doublet score for each cell via doubletFinder*

---

### Description

Uses doubletFinder to determine cells within the dataset suspected to be doublets.

### Usage

```
runDoubletFinder(
  inSCE,
  useAssay = "counts",
  sample = NULL,
  seed = 12345,
  seuratNfeatures = 2000,
  seuratPcs = seq(15),
  seuratRes = 1.5,
  formationRate = 0.075,
  nCores = NULL,
  verbose = FALSE
)
```

### Arguments

inSCE	Input SingleCellExperiment object. Must contain a counts matrix
useAssay	Indicate which assay to use. Default "counts".
sample	Numeric vector. Each cell will be assigned a sample number.
seed	Seed for the random number generator. Default 12345.
seuratNfeatures	Integer. Number of highly variable genes to use. Default 2000.
seuratPcs	Numeric vector. The PCs used in seurat function to determine number of clusters. Default 1:15.
seuratRes	Numeric vector. The resolution parameter used in seurat, which adjusts the number of clusters determined via the algorithm. Default 1.5.
formationRate	Doublet formation rate used within algorithm. Default 0.075.
nCores	Number of cores used for running the function.
verbose	Boolean. Whether to print messages from Seurat and DoubletFinder. Default FALSE.

### Value

SingleCellExperiment object containing the 'doublet\_finder\_doublet\_score'.

## Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
sce <- runDoubletFinder(sce)
```

---

runDropletQC

*Perform comprehensive droplet QC*

---

## Description

A wrapper function to run several QC algorithms for determining empty droplets in single cell RNA-seq data

## Usage

```
runDropletQC(
  inSCE,
  algorithms = c("QCMetrics", "emptyDrops", "barcodeRanks"),
  sample = NULL,
  useAssay = "counts",
  paramsList = NULL
)
```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object containing the full droplet count matrix
algorithms	Character vector. Specify which QC algorithms to run. Available options are "emptyDrops" and "barcodeRanks".
sample	Character vector. Indicates which sample each cell belongs to. Algorithms will be run on cells from each sample separately.
useAssay	A string specifying which assay contains the count matrix for droplets.
paramsList	A list containing parameters for QC functions. Default NULL.

## Value

SingleCellExperiment object containing the outputs of the specified algorithms in the `colData` of `inSCE`.

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runDropletQC(sce)

## End(Not run)
```

---

runEmptyDrops

*Identify empty droplets using [emptyDrops](#).*


---

## Description

Run [emptyDrops](#) on the count matrix in the provided [SingleCellExperiment](#) object. Distinguish between droplets containing cells and ambient RNA in a droplet-based single-cell RNA sequencing experiment.

## Usage

```
runEmptyDrops(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  lower = 100,
  niters = 10000,
  testAmbient = FALSE,
  ignore = NULL,
  alpha = NULL,
  retain = NULL,
  barcodeArgs = list(),
  BPPARAM = BiocParallel::SerialParam()
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object. Must contain a raw counts matrix before empty droplets have been removed.
sample	Character vector. Indicates which sample each cell belongs to. <a href="#">emptyDrops</a> will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
useAssay	A string specifying which assay in the SCE to use.
lower	See <a href="#">emptyDrops</a> for more information.
niters	See <a href="#">emptyDrops</a> for more information.
testAmbient	See <a href="#">emptyDrops</a> for more information.
ignore	See <a href="#">emptyDrops</a> for more information.
alpha	See <a href="#">emptyDrops</a> for more information.
retain	See <a href="#">emptyDrops</a> for more information.
barcodeArgs	See <a href="#">emptyDrops</a> for more information.
BPPARAM	See <a href="#">emptyDrops</a> for more information.



**Value**

A [SingleCellExperiment](#) object with the [emptyDrops](#) output table appended to the [colData](#) slot. The columns include *emptyDrops\_total*, *emptyDrops\_logprob*, *emptyDrops\_pvalue*, *emptyDrops\_limited*, *emptyDrops\_fdr*. Please refer to the documentation of [emptyDrops](#) for details.

**Examples**

```
# The following unfiltered PBMC_1k_v3 data were downloaded from
# https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.0
# /pbmc_1k_v3
# Only the top 10 cells with most counts and the last 10 cells with non-zero
# counts are included in this example.
# This example only serves as an proof of concept and a tutorial on how to
# run the function. The results should not be
# used for drawing scientific conclusions.
data(scExample, package = "singleCellTK")
sce <- runEmptyDrops(inSCE = sce)
```

---

runEnrichR

*Run EnrichR on SCE object*


---

**Description**

Run EnrichR on SCE object

**Usage**

```
runEnrichR(
  inSCE,
  features,
  analysisName,
  db = NULL,
  by = "rownames",
  featureName = NULL
)
```

**Arguments**

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>features</code>	Character vector, selected genes for enrichment analysis.
<code>analysisName</code>	A string that identifies each specific analysis.
<code>db</code>	Character vector. Selected database name(s) from the <a href="#">enrichR</a> database list. If <code>NULL</code> then <a href="#">EnrichR</a> will be run on all the available databases on the <a href="#">enrichR</a> database. See details. Default <code>NULL</code> .
<code>by</code>	Character. From where should we find the features? <code>"rownames"</code> for from <code>rownames(inSCE)</code> , otherwise, from a column of feature metadata ( <code>rowData(inSCE)[[by]]</code> ). See details. Default <code>"rownames"</code> .

**featureName** Character. Indicates the actual feature identifiers to be passed to EnrichR. Can be "rownames", a column in feature metadata (`rowData(inSCE)[[featureName]]`), or a character vector with its length equals to `nrow(inSCE)`. See details. Default "rownames".

### Details

EnrichR works by querying the specified features to its online databases, thus it requires the Internet connection.

Available db options could be shown by running `enrichR::listEnrichrDbs()$libraryName`

This function checks for the existence of features in the SCE object. When features do not have a match in `rownames(inSCE)`, users may try to specify by to pass the check.

EnrichR expects gene symbols/names as the input (i.e. Ensembl ID might not work). When specified features are not qualified for this, users may try to specify `featureName` to change the identifier type to pass to EnrichR.

### Value

Updates `inSCE` metadata with a data.frame of enrichment terms overlapping in the respective databases along with p-values, z-scores etc.

### See Also

[getEnrichRResult](#)

### Examples

```
data("mouseBrainSubsetSCE")
if (Biobase::testBioCConnection()) {
  mouseBrainSubsetSCE <- runEnrichR(mouseBrainSubsetSCE, features = "Cmtm5",
                                   db = "GO_Cellular_Component_2017",
                                   analysisName = "analysis1")
}
```

---

runFastMNN

*Apply a fast version of the mutual nearest neighbors (MNN) batch effect correction method to SingleCellExperiment object*

---

### Description

fastMNN is a variant of the classic MNN method, modified for speed and more robust performance. For introduction of MNN, see [runMNNCorrect](#).

**Usage**

```
runFastMNN(
  inSCE,
  useAssay = "logcounts",
  reducedDimName = "fastMNN",
  batch = "batch",
  pcInput = FALSE
)
```

**Arguments**

inSCE	inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts". Alternatively, see pcInput parameter.
reducedDimName	A single character. The name for the corrected low-dimensional representation. Will be saved to reducedDim(inSCE). Default "fastMNN".
batch	A single character indicating a field in <code>colData</code> that annotates the batches. Default "batch".
pcInput	A logical scalar. Whether to use a low-dimension matrix for batch effect correction. If TRUE, useAssay will be searched from reducedDimNames(inSCE). Default FALSE.

**Value**

The input `SingleCellExperiment` object with `reducedDim(inSCE, reducedDimName)` updated.

**References**

Lun ATL, et al., 2016

**Examples**

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sceCorr <- runFastMNN(sceBatches, useAssay = 'logcounts', pcInput = FALSE)
```

---

runFeatureSelection	<i>Wrapper function to run all of the feature selection methods integrated within the singleCellTK package including three methods from Seurat ('vst', 'mean.var.plot' or 'dispersion') and the Scran 'modelGeneVar' method.</i>
---------------------	--

---

**Description**

Wrapper function to run all of the feature selection methods integrated within the singleCellTK package including three methods from Seurat ('vst', 'mean.var.plot' or 'dispersion') and the Scran 'modelGeneVar' method.

**Usage**

```
runFeatureSelection(
  inSCE,
  useAssay,
  hvgMethod = c("vst", "mean.var.plot", "dispersion", "modelGeneVar")
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	Specify the name of the assay that should be used. A normalized assay is recommended for use with this function.
hvgMethod	Specify the method to use for variable gene selection. Options include "vst", "mean.var.plot" or "dispersion" from Seurat and "modelGeneVar" from Scran.

**Value**

A SingleCellExperiment object that contains the computed statistics in the rowData slot of the output object. This function does not return the names of the variable features but only computes the statistics that are stored in the rowData slot of the. To get the names of the variable features getTopHVG function should be used after computing these statistics.

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runFeatureSelection(mouseBrainSubsetSCE,
                                           "logcounts",
                                           "modelGeneVar")
```

---

runGSVA

*Run GSVA analysis on a [SingleCellExperiment](#) object*


---

**Description**

Run GSVA analysis on a [SingleCellExperiment](#) object

**Usage**

```
runGSVA(
  inSCE,
  useAssay = "logcounts",
  resultNamePrefix = NULL,
  geneSetCollectionName,
  ...
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useAssay</code>	Indicate which assay to use. The default is "logcounts"
<code>resultNamePrefix</code>	Character. Prefix to the name the GSVA results which will be stored in the <code>reducedDim</code> slot of <code>inSCE</code> . The names of the output matrix will be <code>resultNamePrefix_Scores</code> . If this parameter is set to <code>NULL</code> , then "GSVA_geneSetCollectionName_" will be used. Default <code>NULL</code> .
<code>geneSetCollectionName</code>	Character. The name of the gene set collection to use. parameter.
<code>...</code>	Parameters to pass to <code>gsva()</code>

**Value**

A [SingleCellExperiment](#) object with pathway activity scores from GSVA stored in `reducedDim` as `GSVA_geneSetCollectionName_Scores`.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
gs1 <- rownames(sce)[seq(10)]
gs2 <- rownames(sce)[seq(11,20)]
gs <- list("geneset1" = gs1, "geneset2" = gs2)

sce <- importGeneSetsFromList(inSCE = sce, geneSetList = gs,
                             by = "rownames")
sce <- runGSVA(inSCE = sce, geneSetCollectionName = "GeneSetCollection", useAssay = "logcounts")
```

---

runKMeans

*Get clustering with KMeans*


---

**Description**

Perform KMeans clustering on a [SingleCellExperiment](#) object, with `kmeans`.

**Usage**

```
runKMeans(
  inSCE,
  useReducedDim = "PCA",
  clusterName = "KMeans_cluster",
  nCenters,
  nIter = 10,
```

```

nStart = 1,
seed = 12345,
algorithm = c("Hartigan-Wong", "Lloyd", "MacQueen")
)

```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
useReducedDim	A single character, specifying which low-dimension representation to perform the clustering algorithm on. Default "PCA".
clusterName	A single character, specifying the name to store the cluster label in <a href="#">colData</a> . Default "scransNN_cluster".
nCenters	An integer, the number of centroids (clusters).
nIter	An integer, the maximum number of iterations allowed. Default 10.
nStart	An integer, the number of random sets to choose. Default 1.
seed	An integer. The seed for the random number generator. Default 12345.
algorithm	A single character. Choose from "Hartigan-Wong", "Lloyd", "MacQueen". May be abbreviated. Default "Hartigan-Wong".

### Value

The input [SingleCellExperiment](#) object with factor cluster labeling updated in `colData(inSCE)[[clusterName]]`.

### Examples

```

data("mouseBrainSubsetSCE")
mouseBrainSubsetSCE <- runKMeans(mouseBrainSubsetSCE,
                                useReducedDim = "PCA_logcounts",
                                nCenters = 2)

```

---

runLimmaBC	<i>Apply Limma's batch effect correction method to SingleCellExperiment object</i>
------------	--

---

### Description

Limma's batch effect removal function fits a linear model to the data, then removes the component due to the batch effects.

### Usage

```
runLimmaBC(inSCE, useAssay = "logcounts", assayName = "LIMMA", batch = "batch")
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "LIMMA".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".

**Value**

The input [SingleCellExperiment](#) object with assay(inSCE, assayName) updated.

**References**

Gordon K Smyth, et al., 2003

**Examples**

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sceCorr <- runLimmaBC(sceBatches)
```

---

runMNNCorrect	<i>Apply the mutual nearest neighbors (MNN) batch effect correction method to SingleCellExperiment object</i>
---------------	---

---

**Description**

MNN is designed for batch correction of single-cell RNA-seq data where the batches are partially confounded with biological conditions of interest. It does so by identifying pairs of MNN in the high-dimensional log-expression space. For each MNN pair, a pairwise correction vector is computed by applying a Gaussian smoothing kernel with bandwidth 'sigma'.

**Usage**

```
runMNNCorrect(  
  inSCE,  
  useAssay = "logcounts",  
  batch = "batch",  
  assayName = "MNN",  
  k = 20L,  
  sigma = 0.1  
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".
assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "MNN".
k	An integer. Specifies the number of nearest neighbours to consider when defining MNN pairs. This should be interpreted as the minimum frequency of each cell type or state in each batch. Larger values will improve the precision of the correction by increasing the number of MNN pairs, at the cost of reducing accuracy by allowing MNN pairs to form between cells of different type. Default 20L.
sigma	A Numeric scalar. Specifies how much information is shared between MNN pairs when computing the batch effect. Larger values will share more information, approaching a global correction for all cells in the same batch. Smaller values allow the correction to vary across cell types, which may be more accurate but comes at the cost of precision. Default 0.1.

**Value**

The input [SingleCellExperiment](#) object with assay(inSCE, assayName) updated.

**References**

Lun ATL, et al., 2016 & 2018

**Examples**

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sceCorr <- runMNNCorrect(sceBatches)
```

---

runNormalization

*Wrapper function to run any of the integrated normalization/transformation methods in the singleCellTK. The available methods include 'LogNormalize', 'CLR', 'RC' and 'SCTransform' from Seurat, 'logNormCounts' and 'CPM' from Scater. Additionally, users can 'scale' using Z.Score, 'transform' using log, log1p and sqrt, add 'pseudocounts' and trim the final matrices between a range of values.*

---



## Description

Wrapper function to run any of the integrated normalization/transformation methods in the single-CellTK. The available methods include 'LogNormalize', 'CLR', 'RC' and 'SCTransform' from Seurat, 'logNormCounts' and 'CPM' from Scater. Additionally, users can 'scale' using Z.Score, 'transform' using log, log1p and sqrt, add 'pseudocounts' and trim the final matrices between a range of values.

## Usage

```
runNormalization(
  inSCE,
  useAssay = "counts",
  outAssayName = "customNormalizedAssay",
  normalizationMethod = NULL,
  scale = FALSE,
  seuratScaleFactor = 10000,
  transformation = NULL,
  pseudocountsBeforeNorm = NULL,
  pseudocountsBeforeTransform = NULL,
  trim = NULL,
  verbose = TRUE
)
```

## Arguments

inSCE	Input SingleCellExperiment object.
useAssay	Specify the name of the assay that should be used.
outAssayName	Specify the name of the new output assay.
normalizationMethod	Specify a normalization method from 'LogNormalize', 'CLR', 'RC' and 'SCTransform' from Seurat or 'logNormCounts' and 'CPM' from scater packages. Default NULL is set which will not run any normalization method.
scale	Logical value indicating if the data should be scaled using Z.Score. Default FALSE.
seuratScaleFactor	Specify the 'scaleFactor' argument if a Seurat normalization method is selected. Default is 10000. This parameter will not be used if methods other than seurat are selected.
transformation	Specify the transformation options to run on the selected assay. Options include 'log2' (base 2 log transformation), 'log1p' (natural log + 1 transformation) and 'sqrt' (square root). Default value is NULL, which will not run any transformation.
pseudocountsBeforeNorm	Specify a numeric pseudo value that should be added to the assay before normalization is performed. Default is NULL, which will not add any value.

pseudocountsBeforeTransform	Specify a numeric pseudo value that should be added to the assay before transformation is run. Default is NULL, which will not add any value.
trim	Specify a vector of two numeric values that should be used as the upper and lower trim values to trim the assay between these two values. For example, <code>c(10, -10)</code> will trim the values between 10 and -10. Default is NULL, which will not trim the data assay.
verbose	Logical value indicating if progress messages should be displayed to the user. Default is TRUE.

**Value**

Output SCE object with new normalized/transformed assay stored.

**Examples**

```
data(sce_chcl, package = "scds")
sce_chcl <- runNormalization(
  inSCE = sce_chcl,
  normalizationMethod = "LogNormalize",
  useAssay = "counts",
  outAssayName = "logcounts")
```

---

runPerCellQC

*Wrapper for calculating QC metrics with scater.*


---

**Description**

A wrapper function for [addPerCellQC](#). Calculate general quality control metrics for each cell in the count matrix.

**Usage**

```
runPerCellQC(
  inSCE,
  useAssay = "counts",
  collectionName = NULL,
  geneSetList = NULL,
  geneSetListLocation = "rownames",
  geneSetCollection = NULL,
  mitoRef = NULL,
  mitoIDType = NULL,
  mitoPrefix = NULL,
  mitoID = NULL,
  mitoGeneLocation = NULL,
  percent_top = c(50, 100, 200, 500),
  use_altexps = FALSE,
```

```

    flatten = TRUE,
    detectionLimit = 0,
    BPPARAM = BiocParallel::SerialParam()
  )

```

## Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useAssay</code>	A string specifying which assay in the SCE to use. Default "counts".
<code>collectionName</code>	Character. Name of a <a href="#">GeneSetCollection</a> obtained by using one of the <a href="#">importGeneSet*</a> functions. Default NULL.
<code>geneSetList</code>	List of gene sets to be quantified. The genes in the assays will be matched to the genes in the list based on <code>geneSetListLocation</code> . Default NULL.
<code>geneSetListLocation</code>	Character or numeric vector. If set to 'rownames', then the genes in 'geneSetList' will be looked up in <code>rownames(inSCE)</code> . If another character is supplied, then genes will be looked up in the column names of <code>rowData(inSCE)</code> . A character vector with the same length as <code>geneSetList</code> can be supplied if the IDs for different gene sets are found in different places, including a mixture of 'rownames' and <code>rowData(inSCE)</code> . An integer or integer vector can be supplied to denote the column index in <code>rowData(inSCE)</code> . Default 'rownames'.
<code>geneSetCollection</code>	Class of <a href="#">GeneSetCollection</a> from package <a href="#">GSEABase</a> . The location of the gene IDs in <code>inSCE</code> should be in the description slot of each gene set and should follow the same notation as <code>geneSetListLocation</code> . The function <a href="#">getGmt</a> can be used to read in gene sets from a GMT file. If reading a GMT file, the second column for each gene set should be the description denoting the location of the gene IDs in <code>inSCE</code> . These gene sets will be included with those from <code>geneSetList</code> if both parameters are provided.
<code>mitoRef</code>	Character. The species used to extract mitochondrial genes ID from build-in mitochondrial geneset in <a href="#">SCTK</a> . Available species options are "human" and "mouse". Default is NULL.
<code>mitoIDType</code>	Character. Types of mitochondrial gene id. Now it supports "symbol", "entrez", "ensembl" and "ensemblTranscriptID". It is used with <code>mitoRef</code> to extract mitochondrial genes from build-in mitochondrial geneset in <a href="#">SCTK</a> . Default NULL.
<code>mitoPrefix</code>	Character. The prefix used to get mitochondrial gene from either <code>rownames(inSCE)</code> or columns of <code>rowData(inSCE)</code> specified by <code>mitoGeneLocation</code> . This parameter is usually used to extract mito genes from gene symbol. For example, <code>mitoPrefix = "^MT-"</code> can be used to detect mito gene symbols like "MT-ND4".
<code>mitoID</code>	Character. A vector of mitochondrial genes to be quantified.
<code>mitoGeneLocation</code>	Character. Describes the location within <code>inSCE</code> where the gene identifiers in the mitochondrial gene sets should be mapped. If set to "rownames" then the features will be searched for among <code>rownames(inSCE)</code> . This can also be set to one of the column names of <code>rowData(inSCE)</code> in which case the gene identifiers will be mapped to that column in the <code>rowData</code> of <code>inSCE</code> . See <a href="#">featureIndex</a> for more information. Default NULL.

percent_top	An integer vector. Each element is treated as a number of top genes to compute the percentage of library size occupied by the most highly expressed genes in each cell.
use_altexps	Logical scalar indicating whether QC statistics should be computed for alternative Experiments in x. If TRUE, statistics are computed for all alternative experiments. Alternatively, an integer or character vector specifying the alternative Experiments to use to compute QC statistics. Alternatively NULL, in which case alternative experiments are not used.
flatten	Logical scalar indicating whether the nested <a href="#">DataFrame-class</a> in the output should be flattened.
detectionLimit	A numeric scalar specifying the lower detection limit for expression.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying whether the QC calculations should be parallelized.

## Details

This function allows multiple ways to import mitochondrial genes and quantify their expression.

- Using `mitoRef`, `mitoIDType` and `mitoGeneLocation` parameters will load the build-in mitochondrial geneset in SCTK package.
- Using `mitoPrefix` and `mitoGeneLocation` parameters will extract mitochondrial genes from either `rownames(inSCE)` or columns of `rowData(inSCE)` specified by parameter `mitoGeneLocation`
- Using `mitoID` and `mitoGeneLocation` parameters will quantify the expression of mitochondrial genes stored in `mitoID`.

`mitoGeneLocation` is required if you use any methods mentioned above to quantify mitochondrial gene expression. Please make sure `mitoGeneLocation` is pointing to the location within `inSCE` object that stores the correct mitochondrial genes ID.

## Value

A [SingleCellExperiment](#) object with cell QC metrics added to the `colData` slot. If `geneSetList` or `geneSetCollection` are provided, then the `rownames` for each gene set will be saved in `metadata(inSCE)$scater$addPerC`

## Examples

```
data(scExample, package = "singleCellTK")
mito.ix = grep("^MT-", rowData(sce)$feature_name)
geneSet <- list("Mito"=rownames(sce)[mito.ix])
sce <- runPerCellQC(sce, geneSetList = geneSet)
```

---

runSCANORAMA	<i>Apply the mutual nearest neighbors (MNN) batch effect correction method to SingleCellExperiment object</i>
--------------	---

---

### Description

SCANORAMA is analogous to computer vision algorithms for panorama stitching that identify images with overlapping content and merge these into a larger panorama.

### Usage

```
runSCANORAMA(  
  inSCE,  
  useAssay = "logcounts",  
  batch = "batch",  
  SIGMA = 15,  
  ALPHA = 0.1,  
  KNN = 20L,  
  assayName = "SCANORAMA"  
)
```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Scanorama requires a transformed normalized expression assay. Default "logcounts".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".
SIGMA	A numeric scalar. Algorithmic parameter, correction smoothing parameter on Gaussian kernel. Default 15.
ALPHA	A numeric scalar. Algorithmic parameter, alignment score minimum cutoff. Default 0.1.
KNN	An integer. Algorithmic parameter, number of nearest neighbors to use for matching. Default 20L.
assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "SCANORAMA".

### Value

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

### References

Brian Hie et al, 2019

## Examples

```
## Not run:
data('sceBatches', package = 'singleCellTK')
sceBatches <- scaterlogNormCounts(sceBatches)
sceCorr <- runSCANORAMA(sceBatches, "ScaterLogNormCounts")

## End(Not run)
```

---

runScDbfFinder	<i>Detect doublet cells using <a href="#">scDbfFinder</a>.</i>
----------------	--

---

## Description

A wrapper function for [scDbfFinder](#). Identify potential doublet cells based on simulations of putative doublet expression profiles. Generate a doublet score for each cell.

## Usage

```
runScDbfFinder(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  nNeighbors = 50,
  simDoublets = max(10000, ncol(inSCE)),
  seed = 12345,
  BPPARAM = BiocParallel::SerialParam()
)
```

## Arguments

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>sample</code>	Character vector. Indicates which sample each cell belongs to. <a href="#">scDbfFinder</a> will be run on cells from each sample separately.
<code>useAssay</code>	A string specifying which assay in the SCE to use.
<code>nNeighbors</code>	Number of nearest neighbors used to calculate density for doublet detection. Default 50.
<code>simDoublets</code>	Number of simulated doublets created for doublet detection. Default 10000.
<code>seed</code>	Seed for the random number generator. Default 12345.
<code>BPPARAM</code>	A <a href="#">BiocParallelParam</a> object specifying whether the neighbour searches should be parallelized.

## Details

This function is a wrapper function for [scDbfFinder](#). `runScDbfFinder` runs [scDbfFinder](#) for each sample within `inSCE` iteratively. The resulting doublet scores for all cells will be appended to the `colData` of `inSCE`.

**Value**

A [SingleCellExperiment](#) object with the scDbfFinder QC outputs added to the `colData` slot.

**References**

Lun ATL (2018). Detecting doublet cells with scran. [https://l1la.github.io/SingleCellThoughts/software/doublet\\_detection/bycell.html](https://l1la.github.io/SingleCellThoughts/software/doublet_detection/bycell.html)

**See Also**

[scDbfFinder](#)

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runScDbfFinder(sce)
```

---

runSCMerge	<i>Apply scMerge batch effect correction method to SingleCellExperiment object</i>
------------	--

---

**Description**

The scMerge method leverages factor analysis, stably expressed genes (SEGs) and (pseudo-) replicates to remove unwanted variations and merge multiple scRNA-Seq data.

**Usage**

```
runSCMerge(
  inSCE,
  useAssay = "logcounts",
  batch = "batch",
  assayName = "scMerge",
  seg = NULL,
  kmeansK = NULL,
  cellType = "cell_type",
  nCores = 1L
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
batch	A single character indicating a field in <code>colData</code> that annotates the batches. Default "batch".

assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "scMerge".
seg	A vector of gene names or indices that specifies SEG (Stably Expressed Genes) set as negative control. Pre-defined dataset with human and mouse SEG lists is available to user by running <code>data('SEG')</code> . Default NULL, and this value will be auto-detected by default with <a href="#">scSEGIndex</a> .
kmeansK	An integer vector. Indicating the kmeans' K-value for each batch (i.e. how many subclusters in each batch should exist), in order to construct pseudo-replicates. The length of <code>codekmeansK</code> needs to be the same as the number of batches. Default NULL, and this value will be auto-detected by default, depending on <code>cellType</code> .
cellType	A single character. A string indicating a field in <code>colData(inSCE)</code> that defines different cell types. Default 'cell_type'.
nCores	An integer. The number of cores of processors to allocate for the task. Default 1L.

**Value**

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

**References**

Hoa, et al., 2020

**Examples**

```
data('sceBatches', package = 'singleCellTK')
## Not run:
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
sceCorr <- runSCMerge(sceBatches)

## End(Not run)
```

---

runScranSNN

*Get clustering with SNN graph*


---

**Description**

Perform SNN graph clustering on a [SingleCellExperiment](#) object, with graph construction by [buildSNNGraph](#) and graph clustering by "igraph" package.



**Usage**

```
runScranSNN(
  inSCE,
  useAssay = NULL,
  useReducedDim = NULL,
  useAltExp = NULL,
  altExpAssay = "counts",
  altExpRedDim = NULL,
  clusterName = "scransnn_cluster",
  k = 10,
  nComp = 50,
  weightType = c("rank", "number", "jaccard"),
  algorithm = c("walktrap", "louvain", "infomap", "fastGreedy", "labelProp",
    "leadingEigen")
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object.
useAssay	A single character, specifying which <a href="#">assay</a> to perform the clustering algorithm on. Default NULL.
useReducedDim	A single character, specifying which low-dimension representation ( <a href="#">reducedDim</a> ) to perform the clustering algorithm on. Default NULL.
useAltExp	A single character, specifying the assay which <a href="#">altExp</a> to perform the clustering algorithm on. Default NULL.
altExpAssay	A single character, specifying which <a href="#">assay</a> in the chosen <a href="#">altExp</a> to work on. Only used when useAltExp is set. Default "counts".
altExpRedDim	A single character, specifying which <a href="#">reducedDim</a> within the <a href="#">altExp</a> specified by useAltExp to use. Only used when useAltExp is set. Default NULL.
clusterName	A single character, specifying the name to store the cluster label in <a href="#">colData</a> . Default "scransnn_cluster".
k	An integer, the number of nearest neighbors used to construct the graph. Smaller value indicates higher resolution and larger number of clusters. Default 10.
nComp	An integer, the number of components to use when useAssay or useAltExp is specified. WON'T work with useReducedDim. Default 50.
weightType	A single character, that specifies the edge weighing scheme when constructing the Shared Nearest-Neighbor (SNN) graph. Choose from "rank", "number", "jaccard". Default "rank".
algorithm	A single character, that specifies the community detection algorithm to work on the SNN graph. Choose from "walktrap", "louvain", "infomap", "fastGreedy", "labelProp", "leadingEigen". Default "walktrap".

**Value**

The input [SingleCellExperiment](#) object with factor cluster labeling updated in `colData(inSCE)[[clusterName]]`.

## References

Aaron Lun and et. al., 2016

## Examples

```
data("mouseBrainSubsetSCE")
mouseBrainSubsetSCE <- runScranSNN(mouseBrainSubsetSCE,
                                   useReducedDim = "PCA_logcounts")
```

---

runScrublet	<i>Find doublets using scrublet.</i>
-------------	--------------------------------------

---

## Description

A wrapper function that calls `scrub_doublets` from python module `scrublet`. Simulates doublets from the observed data and uses a k-nearest-neighbor classifier to calculate a continuous `scrublet_score` (between 0 and 1) for each transcriptome. The score is automatically thresholded to generate `scrublet_call`, a boolean array that is TRUE for predicted doublets and FALSE otherwise.

## Usage

```
runScrublet(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  simDoubletRatio = 2,
  nNeighbors = NULL,
  minDist = NULL,
  expectedDoubletRate = 0.1,
  stdevDoubletRate = 0.02,
  syntheticDoubletUmiSubsampling = 1,
  useApproxNeighbors = TRUE,
  distanceMetric = "euclidean",
  getDoubletNeighborParents = FALSE,
  minCounts = 3,
  minCells = 3L,
  minGeneVariabilityPctl = 85,
  logTransform = FALSE,
  meanCenter = TRUE,
  normalizeVariance = TRUE,
  nPrinComps = 30L,
  tsneAngle = NULL,
  tsnePerplexity = NULL,
  verbose = TRUE,
  seed = 12345
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object. Needs counts in assays slot.
sample	Character vector. Indicates which sample each cell belongs to. Scrublet will be run on cells from each sample separately. If NULL, then all cells will be processed together. Default NULL.
useAssay	A string specifying which assay in the SCE to use. Default 'counts'.
simDoubletRatio	Numeric. Number of doublets to simulate relative to the number of observed transcriptomes. Default 2.0.
nNeighbors	Integer. Number of neighbors used to construct the KNN graph of observed transcriptomes and simulated doublets. If NULL, this is set to $\text{round}(0.5 * \sqrt{n\_cells})$ . Default NULL.
minDist	Float Determines how tightly UMAP packs points together. If NULL, this is set to 0.1. Default NULL.
expectedDoubletRate	The estimated doublet rate for the experiment. Default 0.1.
stdevDoubletRate	Uncertainty in the expected doublet rate. Default 0.02.
syntheticDoubletUmiSubsampling	Numeric. Rate for sampling UMIs when creating synthetic doublets. If 1.0, each doublet is created by simply adding the UMIs from two randomly sampled observed transcriptomes. For values less than 1, the UMI counts are added and then randomly sampled at the specified rate. Default: 1.0.
useApproxNeighbors	Boolean. Use approximate nearest neighbor method (annoy) for the KNN classifier. Default TRUE.
distanceMetric	Character. Distance metric used when finding nearest neighbors. For list of valid values, see the documentation for annoy (if useApproxNeighbors is TRUE) or sklearn.neighbors.NearestNeighbors (if useApproxNeighbors is FALSE). Default "euclidean".
getDoubletNeighborParents	Boolean. If TRUE, return the parent transcriptomes that generated the doublet neighbors of each observed transcriptome. This information can be used to infer the cell states that generated a given doublet state. Default FALSE.
minCounts	Numeric. Used for gene filtering prior to PCA. Genes expressed at fewer than minCounts in fewer than minCells (see below) are excluded. Default 3.
minCells	Integer. Used for gene filtering prior to PCA. Genes expressed at fewer than minCounts (see above) in fewer than minCells are excluded. Default 3.
minGeneVariabilityPctl	Numeric. Used for gene filtering prior to PCA. Keep the most highly variable genes (in the top minGeneVariabilityPctl percentile), as measured by the <i>v</i> -statistic (Klein <i>et al.</i> , Cell 2015). Default 85.
logTransform	Boolean. If TRUE, log-transform the counts matrix ( $\log_{10}(1+TPM)$ ). sklearn.decomposition.TruncatedSVD will be used for dimensionality reduction, unless meanCenter is TRUE. Default FALSE.

meanCenter	If TRUE, center the data such that each gene has a mean of 0. <code>sklearn.decomposition.PCA</code> will be used for dimensionality reduction. Default TRUE.
normalizeVariance	Boolean. If TRUE, normalize the data such that each gene has a variance of 1. <code>sklearn.decomposition.TruncatedSVD</code> will be used for dimensionality reduction, unless meanCenter is TRUE. Default TRUE.
nPrinComps	Integer. Number of principal components used to embed the transcriptomes prior to k-nearest-neighbor graph construction. Default 30.
tsneAngle	Float. Determines angular size of a distant node as measured from a point in the t-SNE plot. If default, it is set to 0.5 Default NULL.
tsnePerplexity	Integer. The number of nearest neighbors that is used in other manifold learning algorithms. If default, it is set to 30. Default NULL.
verbose	Boolean. If TRUE, print progress updates. Default TRUE.
seed	Seed for the random number generator. Default 12345.

**Value**

A [SingleCellExperiment](#) object with `scrub_doublets` output appended to the `colData` slot. The columns include `scrublet_score` and `scrublet_call`.

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runScrublet(sce)

## End(Not run)
```

---

`runSeuratFindClusters` *runSeuratFindClusters* Computes the clusters from the input `sce` object and stores them back in `sce` object

---

**Description**

`runSeuratFindClusters` Computes the clusters from the input `sce` object and stores them back in `sce` object

**Usage**

```
runSeuratFindClusters(
  inSCE,
  useAssay = "seuratScaledData",
  useReduction = c("pca", "ica"),
  dims = 10,
  algorithm = c("louvain", "multilevel", "SLM"),
```

```

    groupSingletons = TRUE,
    resolution = 0.8,
    externalReduction = NULL,
    verbose = TRUE
  )

```

### Arguments

inSCE	(sce) object from which clusters should be computed and stored in
useAssay	Assay containing scaled counts to use for clustering.
useReduction	Reduction method to use for computing clusters. One of "pca" or "ica". Default "pca".
dims	numeric value of how many components to use for computing clusters. Default 10.
algorithm	selected algorithm to compute clusters. One of "louvain", "multilevel", or "SLM". Use louvain for "original Louvain algorithm" and multilevel for "Louvain algorithm with multilevel refinement". Default louvain.
groupSingletons	boolean if singletons should be grouped together or not. Default TRUE.
resolution	Set the resolution parameter to find larger (value above 1) or smaller (value below 1) number of communities. Default 0.8.
externalReduction	Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

### Value

Updated sce object which now contains the computed clusters

### Examples

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
sce <- runSeuratFindClusters(sce, useAssay = "counts")

## End(Not run)

```

---

runSeuratFindHVG	<i>runSeuratFindHVG Find highly variable genes and store in the input sce object</i>
------------------	--

---

### Description

runSeuratFindHVG Find highly variable genes and store in the input sce object

### Usage

```
runSeuratFindHVG(
  inSCE,
  useAssay = "counts",
  hvgMethod = "vst",
  hvgNumber = 2000,
  altExp = FALSE,
  verbose = TRUE
)
```

### Arguments

inSCE	(sce) object to compute highly variable genes from and to store back to it
useAssay	Specify the name of the assay to use for computation of variable genes. It is recommended to use a raw counts assay with the 'vst' method and normalized assay with all other methods. Default is "counts".
hvgMethod	selected method to use for computation of highly variable genes. One of 'vst', 'dispersion', or 'mean.var.plot'. Default method is 'vst' which uses the raw counts. All other methods use normalized counts.
hvgNumber	numeric value of how many genes to select as highly variable. Default 2000
altExp	Logical value indicating if the input object is an altExperiment. Default FALSE.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

### Value

Updated SingleCellExperiment object with highly variable genes computation stored

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")

## End(Not run)
```

---

runSeuratFindMarkers *runSeuratFindMarkers*

---

## Description

runSeuratFindMarkers

## Usage

```
runSeuratFindMarkers(  
  inSCE,  
  cells1 = NULL,  
  cells2 = NULL,  
  group1 = NULL,  
  group2 = NULL,  
  allGroup = NULL,  
  conserved = FALSE,  
  test = "wilcox",  
  onlyPos = FALSE,  
  minPCT = 0.1,  
  threshUse = 0.25,  
  verbose = TRUE  
)
```

## Arguments

inSCE	Input SingleCellExperiment object.
cells1	A list of sample names included in group1.
cells2	A list of sample names included in group2.
group1	Name of group1.
group2	Name of group2.
allGroup	Name of all groups.
conserved	Logical value indicating if markers conserved between two groups should be identified. Default is FALSE.
test	Test to use for DE. Default "wilcox".
onlyPos	Logical value indicating if only positive markers should be returned.
minPCT	Numeric value indicating the minimum fraction of min.pct cells in which genes are detected. Default is 0.1.
threshUse	Numeric value indicating the logFC threshold value on which on average, at least X-fold difference (log-scale) between the two groups of cells exists. Default is 0.25.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

**Value**

A `SingleCellExperiment` object that contains marker genes populated in a `data.frame` stored inside metadata slot.

---

runSeuratHeatmap	<i>runSeuratHeatmap Computes the heatmap plot object from the pca slot in the input sce object</i>
------------------	--

---

**Description**

runSeuratHeatmap Computes the heatmap plot object from the pca slot in the input sce object

**Usage**

```
runSeuratHeatmap(
  inSCE,
  useAssay,
  useReduction = c("pca", "ica"),
  dims = NULL,
  nfeatures = 30,
  cells = NULL,
  ncol = NULL,
  balanced = TRUE,
  fast = TRUE,
  combine = TRUE,
  raster = TRUE,
  externalReduction = NULL
)
```

**Arguments**

inSCE	(sce) object from which to compute heatmap (pca should be computed)
useAssay	Assay containing scaled counts to use in heatmap.
useReduction	Reduction method to use for computing clusters. One of "pca" or "ica". Default "pca".
dims	Number of components to generate heatmap plot objects. If NULL, a heatmap will be generated for all components. Default NULL.
nfeatures	Number of features to include in the heatmap. Default 30.
cells	Numeric value indicating the number of top cells to plot. Default is NULL which indicates all cells.
ncol	Numeric value indicating the number of columns to use for plot. Default is NULL which will automatically compute accordingly.
balanced	Plot equal number of genes with positive and negative scores. Default is TRUE.
fast	See <a href="#">DimHeatmap</a> for more information. Default TRUE.



combine See [DimHeatmap](#) for more information. Default TRUE.

raster See [DimHeatmap](#) for more information. Default TRUE.

externalReduction Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.

## Value

plot object

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
heatmap <- runSeuratHeatmap(sce, useAssay = "counts")
plotSeuratHeatmap(heatmap)

## End(Not run)
```

---

runSeuratICA	<i>runSeuratICA Computes ICA on the input sce object and stores the calculated independent components within the sce object</i>
--------------	---

---

## Description

runSeuratICA Computes ICA on the input sce object and stores the calculated independent components within the sce object

## Usage

```
runSeuratICA(
  inSCE,
  useAssay,
  reducedDimName = "seuratICA",
  features = NULL,
  nics = 20,
  seed = NULL
)
```

**Arguments**

inSCE	(sce) object on which to compute ICA
useAssay	Assay containing scaled counts to use in ICA.
reducedDimName	Name of new reducedDims object containing Seurat ICA Default seuratICA.
features	Specify the feature names or rownames which should be used for computation of ICA. Default is NULL which will use the previously stored variable features.
nics	Number of independent components to compute. Default 20.
seed	Random seed for reproducibility of results. Default NULL will use global seed in use by the R environment.

**Value**

Updated SingleCellExperiment object which now contains the computed independent components

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratICA(sce, useAssay = "counts")

## End(Not run)
```

---

runSeuratIntegration *runSeuratIntegration* A wrapper function to Seurat Batch-Correction/Integration workflow.

---

**Description**

runSeuratIntegration A wrapper function to Seurat Batch-Correction/Integration workflow.

**Usage**

```
runSeuratIntegration(
  inSCE,
  useAssay = "counts",
  batch,
  newAssayName = "SeuratIntegratedAssay",
  kAnchor,
  kFilter,
  kWeight,
  ndims = 10
)
```

**Arguments**

inSCE	Input SingleCellExperiment object that contains the assay to batch-correct.
useAssay	Assay to batch-correct.
batch	Batch variable from colData slot of SingleCellExperiment object.
newAssayName	Assay name for the batch-corrected output assay.
kAnchor	Number of neighbours to use for finding the anchors in the <a href="#">FindIntegrationAnchors</a> function.
kFilter	Number of neighbours to use for filtering the anchors in the <a href="#">FindIntegrationAnchors</a> function.
kWeight	Number of neighbours to use when weighing the anchors in the <a href="#">IntegrateData</a> function.
ndims	Number of dimensions to use. Default 10.

**Value**

A SingleCellExperiment object that contains the batch-corrected assay inside the altExp slot of the object

---

runSeuratJackStraw	<i>runSeuratJackStraw Compute jackstraw plot and store the computations in the input sce object</i>
--------------------	---

---

**Description**

runSeuratJackStraw Compute jackstraw plot and store the computations in the input sce object

**Usage**

```
runSeuratJackStraw(
  inSCE,
  useAssay,
  dims = NULL,
  numReplicate = 100,
  propFreq = 0.025,
  externalReduction = NULL
)
```

**Arguments**

inSCE	(sce) object on which to compute and store jackstraw plot
useAssay	Assay containing scaled counts to use in JackStraw calculation.
dims	Number of components to test in Jackstraw. If NULL, then all components are used. Default NULL.

numReplicate	Numeric value indicating the number of replicate samplings to perform. Default value is 100.
propFreq	Numeric value indicating the proportion of data to randomly permute for each replicate. Default value is 0.025.
externalReduction	Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.

### Value

Updated SingleCellExperiment object with jackstraw computations stored in it

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
sce <- runSeuratJackStraw(sce, useAssay = "counts")

## End(Not run)
```

---

runSeuratNormalizeData

*runSeuratNormalizeData Wrapper for NormalizeData() function from seurat library Normalizes the sce object according to the input parameters*

---

### Description

runSeuratNormalizeData Wrapper for NormalizeData() function from seurat library Normalizes the sce object according to the input parameters

### Usage

```
runSeuratNormalizeData(
  inSCE,
  useAssay,
  normAssayName = "seuratNormData",
  normalizationMethod = "LogNormalize",
  scaleFactor = 10000,
  verbose = TRUE
)
```

**Arguments**

`inSCE` (sce) object to normalize

`useAssay` Assay containing raw counts to use for normalization.

`normAssayName` Name of new assay containing normalized data. Default `seuratNormData`.

`normalizationMethod` selected normalization method. Default `"LogNormalize"`.

`scaleFactor` numeric value that represents the scaling factor. Default `10000`.

`verbose` Logical value indicating if informative messages should be displayed. Default is `TRUE`.

**Value**

Normalized `SingleCellExperiment` object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")

## End(Not run)
```

---

<code>runSeuratPCA</code>	<i>runSeuratPCA Computes PCA on the input sce object and stores the calculated principal components within the sce object</i>
---------------------------	---

---

**Description**

`runSeuratPCA` Computes PCA on the input sce object and stores the calculated principal components within the sce object

**Usage**

```
runSeuratPCA(  
  inSCE,  
  useAssay = "seuratScaledData",  
  reducedDimName = "seuratPCA",  
  nPCs = 20,  
  features = NULL,  
  seed = NULL,  
  verbose = TRUE  
)
```

**Arguments**

inSCE	(sce) object on which to compute PCA
useAssay	Assay containing scaled counts to use in PCA.
reducedDimName	Name of new reducedDims object containing Seurat PCA. Default seuratPCA.
nPCs	numeric value of how many components to compute. Default 20.
features	Specify the feature names or rownames which should be used for computation of PCA. Default is NULL which will use the previously stored variable features.
seed	Random seed for reproducibility of results. Default NULL will use global seed in use by the R environment.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

**Value**

Updated SingleCellExperiment object which now contains the computed principal components

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")

## End(Not run)
```

---

runSeuratScaleData	<i>runSeuratScaleData Scales the input sce object according to the input parameters</i>
--------------------	---

---

**Description**

runSeuratScaleData Scales the input sce object according to the input parameters

**Usage**

```
runSeuratScaleData(
  inSCE,
  useAssay = "seuratNormData",
  scaledAssayName = "seuratScaledData",
  model = "linear",
  scale = TRUE,
  center = TRUE,
  scaleMax = 10,
  verbose = TRUE
)
```

## Arguments

inSCE	(sce) object to scale
useAssay	Assay containing normalized counts to scale.
scaledAssayName	Name of new assay containing scaled data. Default <code>seuratScaledData</code> .
model	selected model to use for scaling data. Default <code>"linear"</code> .
scale	boolean if data should be scaled or not. Default <code>TRUE</code> .
center	boolean if data should be centered or not. Default <code>TRUE</code> .
scaleMax	maximum numeric value to return for scaled data. Default <code>10</code> .
verbose	Logical value indicating if informative messages should be displayed. Default is <code>TRUE</code> .

## Value

Scaled `SingleCellExperiment` object

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")

## End(Not run)
```

---

`runSeuratSCTransform` *runSeuratSCTransform* Runs the *SCTransform* function to transform/normalize the input data

---

## Description

`runSeuratSCTransform` Runs the *SCTransform* function to transform/normalize the input data

## Usage

```
runSeuratSCTransform(  
  inSCE,  
  normAssayName = "SCTCounts",  
  useAssay = "counts",  
  verbose = TRUE  
)
```

**Arguments**

inSCE	Input SingleCellExperiment object
normAssayName	Name for the output data assay. Default "SCTCounts".
useAssay	Name for the input data assay. Default "counts".
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

**Value**

Updated SingleCellExperiment object containing the transformed data

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runSeuratSCTransform(mouseBrainSubsetSCE)
```

---

runSeuratTSNE	<i>runSeuratTSNE Computes tSNE from the given sce object and stores the tSNE computations back into the sce object</i>
---------------	--

---

**Description**

runSeuratTSNE Computes tSNE from the given sce object and stores the tSNE computations back into the sce object

**Usage**

```
runSeuratTSNE(
  inSCE,
  useReduction = c("pca", "ica"),
  reducedDimName = "seuratTSNE",
  dims = 10,
  perplexity = 30,
  externalReduction = NULL,
  seed = 1
)
```

**Arguments**

inSCE	(sce) object on which to compute the tSNE
useReduction	selected reduction algorithm to use for computing tSNE. One of "pca" or "ica". Default "pca".
reducedDimName	Name of new reducedDims object containing Seurat tSNE Default seuratTSNE.
dims	Number of reduction components to use for tSNE computation. Default 10.



perplexity	Adjust the perplexity tuneable parameter for the underlying tSNE call. Default 30.
externalReduction	Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.
seed	Random seed for reproducibility of results. Default 1.

**Value**

Updated sce object with tSNE computations stored

---

runSeuratUMAP	<i>runSeuratUMAP Computes UMAP from the given sce object and stores the UMAP computations back into the sce object</i>
---------------	--

---

**Description**

runSeuratUMAP Computes UMAP from the given sce object and stores the UMAP computations back into the sce object

**Usage**

```
runSeuratUMAP(
  inSCE,
  useReduction = c("pca", "ica"),
  reducedDimName = "seuratUMAP",
  dims = 10,
  minDist = 0.3,
  nNeighbors = 30L,
  spread = 1,
  externalReduction = NULL,
  seed = 42,
  verbose = TRUE
)
```

**Arguments**

inSCE	(sce) object on which to compute the UMAP
useReduction	Reduction to use for computing UMAP. One of "pca" or "ica". Default is "pca".
reducedDimName	Name of new reducedDims object containing Seurat UMAP Default seuratUMAP.
dims	Numerical value of how many reduction components to use for UMAP computation. Default 10.
minDist	Sets the "min.dist" parameter to the underlying UMAP call. See <a href="#">RunUMAP</a> for more information. Default 0.3.
nNeighbors	Sets the "n.neighbors" parameter to the underlying UMAP call. See <a href="#">RunUMAP</a> for more information. Default 30L.

spread	Sets the "spread" parameter to the underlying UMAP call. See <a href="#">RunUMAP</a> for more information. Default 1.
externalReduction	Pass DimReduc object if PCA/ICA computed through other libraries. Default NULL.
seed	Random seed for reproducibility of results. Default 42.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

### Value

Updated sce object with UMAP computations stored

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runSeuratNormalizeData(sce, useAssay = "counts")
sce <- runSeuratFindHVG(sce, useAssay = "counts")
sce <- runSeuratScaleData(sce, useAssay = "counts")
sce <- runSeuratPCA(sce, useAssay = "counts")
sce <- runSeuratFindClusters(sce, useAssay = "counts")
sce <- runSeuratUMAP(sce, useReduction = "pca")

## End(Not run)
```

---

runSingleR

*Label cell types with SingleR*

---

### Description

SingleR works with a reference dataset where the cell type labeling is given. Given a reference dataset of samples (single-cell or bulk) with known labels, it assigns those labels to new cells from a test dataset based on similarities in their expression profiles.

### Usage

```
runSingleR(
  inSCE,
  useAssay = "logcounts",
  useSCERef = NULL,
  labelColName = NULL,
  useBltinRef = c("hpca", "bpe", "mp", "dice", "immgen", "mouse", "zeisel"),
  level = c("main", "fine", "ont"),
  featureType = c("symbol", "ensembl"),
  labelByCluster = NULL
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	character. A string specifying which assay to use for expression profile identification. Required.
useSCERef	<a href="#">SingleCellExperiment</a> inherited object. An optional customized reference dataset. Default NULL.
labelColName	A single character. A string specifying the column in colData(useSCERef) that stores the cell type labeling. Default NULL.
useBltinRef	A single character. A string that specifies a reference provided by SingleR. Choose from "hpca", "bpe", "mp", "dice", "immgen", "mouse", "zeisel". See detail. Default "hpca".
level	A string for cell type labeling level. Used only when using some of the SingleR built-in references. Choose from "main", "fine", "ont". Default "main".
featureType	A string for whether to use gene symbols or Ensembl IDs when using a SingleR built-in reference. Should be set based on the type of rownames of inSCE. Choose from "symbol", "ensembl". Default "symbol".
labelByCluster	A single character. A string specifying the column name in colData(inSCE) that stores clustering labels. Use this when users want to only label cells on cluster level, instead of performing calculation on each cell. Default NULL.

**Value**

Input SCE object with cell type labeling updated in colData(inSCE), together with scoring metrics.

**Examples**

```
data("sceBatches")
logcounts(sceBatches) <- log(counts(sceBatches) + 1)
#sceBatches <- runSingleR(sceBatches, useBltinRef = "mp")
```

---

runSoupX

*Detecting and correct contamination with SoupX*


---

**Description**

A wrapper function for [autoEstCont](#) and [adjustCounts](#). Identify potential contamination from experimental factors such as ambient RNA. Visit [their vignette](#) for better understanding.

**Usage**

```
runSoupX(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  background = NULL,
```

```

bgAssayName = NULL,
bgBatch = NULL,
assayName = ifelse(is.null(background), "SoupX", "SoupX_bg"),
cluster = NULL,
reducedDimName = ifelse(is.null(background), "SoupX_UMAP_", "SoupX_bg_UMAP_"),
tfidfMin = 1,
soupQuantile = 0.9,
maxMarkers = 100,
contaminationRange = c(0.01, 0.8),
rhoMaxFDR = 0.2,
priorRho = 0.05,
priorRhoStdDev = 0.1,
forceAccept = FALSE,
adjustMethod = c("subtraction", "soupOnly", "multinomial"),
roundToInt = FALSE,
tol = 0.001,
pCut = 0.01
)

```

### Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
sample	A single character specifying a name that can be found in <code>colData(inSCE)</code> to directly use the cell annotation; or a character vector with as many elements as cells to indicate which sample each cell belongs to. SoupX will be run on cells from each sample separately. Default NULL.
useAssay	A single character string specifying which assay in <code>inSCE</code> to use. Default 'counts'.
background	A numeric matrix of counts or a <a href="#">SingleCellExperiment</a> object with the matrix in assay slot. It should have the same structure as <code>inSCE</code> except it contains the matrix including empty droplets. Default NULL.
bgAssayName	A single character string specifying which assay in background to use when background is a <a href="#">SingleCellExperiment</a> object. If NULL, the function will use the same value as <code>useAssay</code> . Default NULL.
bgBatch	The same thing as <code>sample</code> but for background. Can be a single character only when background is a <a href="#">SingleCellExperiment</a> object. Default NULL.
assayName	A single character string of the output corrected matrix. Default "SoupX" when not using a background, otherwise, "SoupX_bg".
cluster	Prior knowledge of clustering labels on cells. A single character string for specifying clustering label stored in <code>colData(inSCE)</code> , or a character vector with as many elements as cells. When not supplied, <a href="#">quickCluster</a> method will be applied.
reducedDimName	A single character string of the prefix of output corrected embedding matrix for each sample. Default "SoupX_UMAP_" when not using a background, otherwise, "SoupX_bg_UMAP_".
tfidfMin	Numeric. Minimum value of <code>tfidf</code> to accept for a marker gene. Default 1. See <code>?SoupX::autoEstCont</code> .

soupQuantile	Numeric. Only use genes that are at or above this expression quantile in the soup. This prevents inaccurate estimates due to using genes with poorly constrained contribution to the background. Default 0.9. See ?SoupX::autoEstCont.
maxMarkers	Integer. If we have heaps of good markers, keep only the best maxMarkers of them. Default 100. See ?SoupX::autoEstCont.
contaminationRange	Numeric vector of two elements. This constrains the contamination fraction to lie within this range. Must be between 0 and 1. The high end of this range is passed to <code>estimateNonExpressingCells</code> as <code>maximumContamination</code> . Default <code>c(0.01, 0.8)</code> . See ?SoupX::autoEstCont.
rhoMaxFDR	Numeric. False discovery rate passed to <code>estimateNonExpressingCells</code> , to test if rho is less than <code>maximumContamination</code> . Default 0.2. See ?SoupX::autoEstCont.
priorRho	Numeric. Mode of gamma distribution prior on contamination fraction. Default 0.05. See ?SoupX::autoEstCont.
priorRhoStdDev	Numeric. Standard deviation of gamma distribution prior on contamination fraction. Default 0.1. See ?SoupX::autoEstCont.
forceAccept	Logical. Should we allow very high contamination fractions to be used. Passed to <code>setContaminationFraction</code> . Default FALSE. See ?SoupX::autoEstCont.
adjustMethod	Character. Method to use for correction. One of 'subtraction', 'soupOnly', or 'multinomial'. Default 'subtraction'. See ?SoupX::adjustCounts.
roundToInt	Logical. Should the resulting matrix be rounded to integers? Default FALSE. See ?SoupX::adjustCounts.
tol	Numeric. Allowed deviation from expected number of soup counts. Don't change this. Default 0.001. See ?SoupX::adjustCounts.
pCut	Numeric. The p-value cut-off used when <code>method = 'soupOnly'</code> . Default 0.01. See ?SoupX::adjustCounts.

## Value

The input `inSCE` object with `soupX_nUMIs`, `soupX_clustrers`, `soupX_contamination` appended to `colData` slot; `soupX_{sample}_est` and `soupX_{sample}_counts` for each sample appended to `rowData` slot; and other computational metrics at `getSoupX(inSCE)`. Replace "soupX" to "soupX\_bg" when background is used.

## Author(s)

Yichen Wang

## Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
## Not run:
# SoupX does not work for toy example,
# can be tested with `sce <- importExampleData("pbmc3k")`
sce <- runSoupX(sce, sample = "sample")

## End(Not run)
```

runTSCAN

*Run runTSCAN function to obtain pseudotime values for cells***Description**

Wrapper for obtaining a pseudotime ordering of the cells by projecting them onto the MST

**Usage**

```
runTSCAN(inSCE, useReducedDim, cluster = NULL, seed = 12345)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useReducedDim	Character. Saved dimension reduction name in inSCE object. Required. Used for specifying which low-dimension representation to perform the clustering algorithm and building nearest neighbor graph on. Default "PCA"
cluster	Grouping for each cell in inSCE. A user may input a vector equal length to the number of the samples in inSCE, or can be retrieved from the colData slot. Default NULL.
seed	An integer. Set the seed for random process that happens only in "random" generation. Default 12345.

**Value**

A [SingleCellExperiment](#) object with pseudotime ordering of the cells along the paths

**Author(s)**

Nida Pervaiz

**Examples**

```
data("scExample", package = "singleCellTK")
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                   useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
                   reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
```

---

```
runTSCANClusterDEAnalysis
```

*Run runTSCANClusterDEAnalysis function to observe changes between paths and to obtain DE genes*

---

## Description

Wrapper for looking for differences in expression between paths of a branched trajectory. The differential expression analysis may highlight genes which are responsible for the branching event

## Usage

```
runTSCANClusterDEAnalysis(  
  inSCE,  
  useClusters,  
  useAssay = "logcounts",  
  fdrThreshold = 0.05  
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useClusters	Choose the cluster containing the branch point in the data in order to recompute the pseudotimes so that the root lies at the cluster center, allowing us to detect genes that are associated with the divergence of the branches.
useAssay	Character. The name of the assay to use. This assay should contain log normalized counts.
fdrThreshold	Only out put DEGs with FDR value smaller than this value. Default 0.05.

## Value

A [SingleCellExperiment](#) object with DE genes that are significant in our path of interest and are not significant and/or changing in the opposite direction in the other paths.

## Author(s)

Nida Pervaiz

## Examples

```
data("scExample", package = "singleCellTK")  
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")  
rowData(sce)$Symbol <- rowData(sce)$feature_name  
rownames(sce) <- rowData(sce)$Symbol  
sce <- scaterLogNormCounts(sce, assayName = "logcounts")  
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",  
  useAssay = "logcounts", reducedDimName = "PCA")
```

```
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
  reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
sce <- runTSCANClusterDEAnalysis(inSCE = sce, useClusters = 5)
```

---

runTSCANDEG

*Run runTSCANDEG function to obtain changes along a trajectory*


---

## Description

Wrapper for identifying genes with significant changes with respect to one of the TSCAN pseudo-times

## Usage

```
runTSCANDEG(
  inSCE,
  pathIndex,
  useAssay = "logcounts",
  discardCluster = NULL,
  log2fcThreshold = 0
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path number for which the pseudotime values should be used. PathIndex corresponds to one path from the root node to one of the terminal nodes.
useAssay	Character. The name of the assay to use. This assay should contain log normalized counts.
discardCluster	Optional. Clusters which are not of use or masks other interesting effects can be discarded.
log2fcThreshold	Only output DEGs with the absolute values of log2FC larger than this value. Default 0

## Value

A [SingleCellExperiment](#) object with genes that decrease and increase in expression with increasing pseudotime along the path in the MST.

## Author(s)

Nida Pervaiz



## Examples

```
data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rowData(sce)$Symbol <- rowData(sce)$feature_name
rownames(sce) <- rowData(sce)$Symbol
sce <- scaterLogNormCounts(sce, assayName = "logcounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
                  useAssay = "logcounts", reducedDimName = "PCA")
sce <- runDimReduce(inSCE = sce, method = "rTSNE", useReducedDim = "PCA",
                  reducedDimName = "TSNE")
sce <- runTSCAN (inSCE = sce, useReducedDim = "PCA", seed = NULL)
sce <- runTSCANDEG(inSCE = sce, pathIndex = 4)
```

runVAM

*Run VAM to score gene sets in single cell data*

## Description

Wrapper for the Variance-adjusted Mahalanobis (VAM), which is a fast and accurate method for cell-specific gene set scoring of single cell data. This algorithm computes distance statistics and one-sided p-values for all cells in the specified single cell gene expression matrix. Gene sets should already be imported and stored in the meta data using functions such as [importGeneSetsFromList](#) or [importGeneSetsFromMSigDB](#)

## Usage

```
runVAM(
  inSCE,
  geneSetCollectionName,
  useAssay,
  resultNamePrefix = NULL,
  center = TRUE,
  gamma = FALSE
)
```

## Arguments

**inSCE** Input [SingleCellExperiment](#) object.

**geneSetCollectionName** Character. The name of the gene set collection to use.

**useAssay** Character. The name of the assay to use. This assay should contain log normalized counts.

**resultNamePrefix** Character. Prefix to the name the VAM results which will be stored in the reducedDim slot of inSCE. The names of the output matrices will be resultNamePrefix\_Distance and resultNamePrefix\_CDF. If this parameter is set to NULL, then "VAM\_geneSetCollectionName\_" will be used. Default NULL.

center	Boolean. If TRUE, values will be mean centered when computing the Mahalanobis statistic. Default TRUE.
gamma	Boolean. If TRUE, a gamma distribution will be fit to the non-zero squared Mahalanobis distances computed from a row-permuted version of the gene expression matrix. The estimated gamma distribution will be used to compute a one-sided p-value for each cell. If FALSE, the p-value will be computed using the standard chi-square approximation for the squared Mahalanobis distance (or non-central if center = FALSE). Default FALSE.

**Value**

A [SingleCellExperiment](#) object with VAM metrics stored in reducedDim as VAM\_NameOfTheGeneset\_Distance and VAM\_NameOfTheGeneset\_CDF.

**Author(s)**

Nida Pervaiz

**See Also**

[importGeneSetsFromList](#), [importGeneSetsFromMSigDB](#), [importGeneSetsFromGMT](#), [importGeneSetsFromCollection](#) for importing gene sets. [sctkListGeneSetCollections](#), [getPathwayResultNames](#) and [getGenesetNamesFromCollection](#) for available related information in inSCE.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterlogNormCounts(sce, assayName = "logcounts")
gs1 <- rownames(sce)[seq(10)]
gs2 <- rownames(sce)[seq(11,20)]
gs <- list("geneset1" = gs1, "geneset2" = gs2)
sce <- importGeneSetsFromList(inSCE = sce, geneSetList = gs,
                             by = "rownames")
sce <- runVAM(inSCE = sce,
              geneSetCollectionName = "GeneSetCollection",
              useAssay = "logcounts")
```

---

runZINBWaVE

*Apply ZINBWaVE Batch effect correction method to SingleCellExperiment object*

---

**Description**

A general and flexible zero-inflated negative binomial model that can be used to provide a low-dimensional representations of scRNAseq data. The model accounts for zero inflation (dropouts), over-dispersion, and the count nature of the data. The model also accounts for the difference in library sizes and optionally for batch effects and/or other covariates.

**Usage**

```
runZINBWaVE(
  inSCE,
  useAssay = "counts",
  batch = "batch",
  nHVG = 1000L,
  nComponents = 50L,
  epsilon = 1000,
  nIter = 10L,
  reducedDimName = "zinbwave"
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object. Required.
useAssay	A single character indicating the name of the assay requiring batch correction. Note that ZINBWaVE works for counts (integer) input rather than logcounts that other methods prefer. Default "counts".
batch	A single character indicating a field in <a href="#">colData</a> that annotates the batches. Default "batch".
nHVG	An integer. Number of highly variable genes to use when fitting the model. Default 1000L.
nComponents	An integer. The number of principle components or dimensionality to generate in the resulting matrix. Default 50L.
epsilon	An integer. Algorithmic parameter. Empirically, a high epsilon is often required to obtain a good low-level representation. Default 1000L.
nIter	An integer, The max number of iterations to perform. Default 10L.
reducedDimName	A single character. The name for the corrected low-dimensional representation. Will be saved to <code>reducedDim(inSCE)</code> . Default "zinbwave".

**Value**

The input [SingleCellExperiment](#) object with `reducedDim(inSCE, reducedDimName)` updated.

**References**

Pollen, Alex A et al., 2014

**Examples**

```
data('sceBatches', package = 'singleCellTK')
## Not run:
  sceCorr <- runZINBWaVE(sceBatches, nIter = 5)

## End(Not run)
```

---

sampleSummaryStats      *Generate table of SCTK QC outputs.*

---

### Description

Creates a table of QC metrics generated from QC algorithms, which is stored within the metadata slot of the input SingleCellExperiment object.

### Usage

```
sampleSummaryStats(  
  inSCE,  
  sample = NULL,  
  useAssay = "counts",  
  simple = TRUE,  
  statsName = "qc_table"  
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved <a href="#">assay</a> data and/or <a href="#">colData</a> data. Required.
sample	Character vector. Indicates which sample each cell belongs to.
useAssay	A string specifying which assay in the SCE to use. Default 'counts'.
simple	Boolean. Indicates whether to generate a table of only basic QC stats (ex. library size), or to generate a summary table of all QC stats stored in the inSCE.
statsName	Character. The name of the slot that will store the QC stat table. Default "qc_table".

### Value

A SingleCellExperiment object with a summary table for QC statistics in the 'sample\_summary' slot of metadata.

### Examples

```
data(scExample, package = "singleCellTK")  
sce <- subsetSCEcols(sce, colData = "type != 'EmptyDroplet'")  
sce <- sampleSummaryStats(sce, simple = TRUE)  
getSampleSummaryStatsTable(sce, statsName = "qc_table")
```

---

scaterCPM	<i>scaterCPM Uses CPM from scater library to compute counts-per-million.</i>
-----------	--

---

**Description**

scaterCPM Uses CPM from scater library to compute counts-per-million.

**Usage**

```
scaterCPM(inSCE, assayName = "ScaterCPMCounts", useAssay = "counts")
```

**Arguments**

inSCE	Input SingleCellExperiment object
assayName	New assay name for cpm data.
useAssay	Input assay

**Value**

inSCE Updated SingleCellExperiment object

**Author(s)**

Irzam Sarfraz

**Examples**

```
data(sce_chc1, package = "scds")
sce_chc1 <- scaterCPM(sce_chc1, "countsCPM", "counts")
```

---

scaterlogNormCounts	<i>scaterlogNormCounts Uses <a href="#">logNormCounts</a> to log normalize input data</i>
---------------------	---

---

**Description**

scaterlogNormCounts Uses [logNormCounts](#) to log normalize input data

**Usage**

```
scaterlogNormCounts(  
  inSCE,  
  assayName = "ScaterLogNormCounts",  
  useAssay = "counts"  
)
```

**Arguments**

inSCE            Input SingleCellExperiment object  
assayName        New assay name for log normalized data  
useAssay         Input assay

**Value**

inSCE Updated SingleCellExperiment object that contains the new log normalized data

**Author(s)**

Irzam Sarfraz

**Examples**

```
data(sce_chcl, package = "scds")  
sce_chcl <- scaterlogNormCounts(sce_chcl, "logcounts", "counts")
```

---

scaterPCA	<i>Perform PCA on a SingleCellExperiment Object A wrapper to <a href="#">runPCA</a> function to compute principal component analysis (PCA) from a given <a href="#">SingleCellExperiment</a> object.</i>
-----------	--

---

**Description**

Perform PCA on a SingleCellExperiment Object A wrapper to [runPCA](#) function to compute principal component analysis (PCA) from a given [SingleCellExperiment](#) object.

**Usage**

```
scaterPCA(  
  inSCE,  
  useAssay = "logcounts",  
  useAltExp = NULL,  
  reducedDimName = "PCA",  
  nComponents = 50,  
  scale = FALSE,  
  ntop = NULL,  
  seed = NULL  
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useAssay</code>	Assay to use for PCA computation. If <code>useAltExp</code> is specified, <code>useAssay</code> has to exist in <code>assays(altExp(inSCE, useAltExp))</code> . Default "logcounts"
<code>useAltExp</code>	The subset to use for PCA computation, usually for the selected.variable features. Default NULL.
<code>reducedDimName</code>	Name to use for the reduced output assay. Default "PCA".
<code>nComponents</code>	Number of principal components to obtain from the PCA computation. Default 50.
<code>scale</code>	Logical scalar, whether to standardize the expression values. Default FALSE.
<code>ntop</code>	Number of top features to use as a further variable feature selection. Default NULL.
<code>seed</code>	Random seed for reproducibility of PCA results.

**Value**

A [SingleCellExperiment](#) object with PCA computation updated in `reducedDim(inSCE, reducedDimName)`.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterLogNormCounts(sce, "logcounts")
sce <- scaterPCA(sce, "logcounts")
```

---

sce

*Example Single Cell RNA-Seq data in SingleCellExperiment Object, subset of 10x public dataset <https://support.10xgenomics.com/single-cell-gene-expression/datasets/2.1.0/pbmc4k> A subset of 390 barcodes and top 200 genes were included in this example. Within 390 barcodes, 195 barcodes are empty droplet, 150 barcodes are cell barcode and 45 barcodes are doublets predicted by scrublet and doubletFinder package. This example only serves as a proof of concept and a tutorial on how to run the functions in this package. The results should not be used for drawing scientific conclusions.*

---

**Description**

Example Single Cell RNA-Seq data in SingleCellExperiment Object, subset of 10x public dataset <https://support.10xgenomics.com/single-cell-gene-expression/datasets/2.1.0/pbmc4k> A subset of 390 barcodes and top 200 genes were included in this example. Within 390 barcodes, 195 barcodes are empty droplet, 150 barcodes are cell barcode and 45 barcodes are doublets predicted by scrublet and doubletFinder package. This example only serves as a proof of concept and a tutorial on how to run the functions in this package. The results should not be used for drawing scientific conclusions.

**Usage**

```
data("scExample")
```

**Format**

A `SingleCellExperiment` object.

**Examples**

```
data("scExample")
```

---

sceBatches	<i>Example Single Cell RNA-Seq data in SingleCellExperiment object, with different batches annotated</i>
------------	--

---

**Description**

Two batches of pancreas scRNAseq dataset are combined with their original counts. Cell types and batches are annotated in `colData(sceBatches)`. Two batches came from Wang, et al., 2016, annotated as `'w'`; and Xin, et al., 2016, annotated as `'x'`. Two common cell types, `'alpha'` and `'beta'`, that could be found in both original studies with relatively large population were kept for cleaner demonstration.

**Usage**

```
data('sceBatches')
```

**Format**

An object of class `SingleCellExperiment` with 100 rows and 250 columns.

---

scranModelGeneVar	<i>scranModelGeneVar Generates and stores variability data from scran::modelGeneVar in the input singleCellExperiment object</i>
-------------------	--

---

**Description**

scranModelGeneVar Generates and stores variability data from `scran::modelGeneVar` in the input `singleCellExperiment` object

**Usage**

```
scranModelGeneVar(inSCE, assayName)
```



**Arguments**

inSCE            a singleCellExperiment object  
assayName        selected assay to compute variable features from

**Value**

inSCE updated singleCellExperiment object that contains variable feature metrics in rowData

**Author(s)**

Irzam Sarfraz

**Examples**

```
data(sce_chcl, package = "scds")  
sce_chcl <- scranModelGeneVar(sce_chcl, "counts")
```

---

sctkListGeneSetCollections

*Lists imported GeneSetCollections*

---

**Description**

Returns a vector of GeneSetCollections that have been imported and stored in metadata(inSCE)\$sctk\$genesets.

**Usage**

```
sctkListGeneSetCollections(inSCE)
```

**Arguments**

inSCE            A [SingleCellExperiment](#) object.

**Value**

Character vector.

**Author(s)**

Joshua D. Campbell

**See Also**

[importGeneSetsFromList](#) for importing from lists, [importGeneSetsFromGMT](#) for importing from GMT files, [GeneSetCollection](#) objects, and [importGeneSetsFromMSigDB](#) for importing MSigDB gene sets.

**Examples**

```

data(scExample)
library(GSEABase)
gs1 <- GeneSet(setName = "geneset1", geneIds = rownames(sce)[seq(10)])
gs2 <- GeneSet(setName = "geneset2", geneIds = rownames(sce)[seq(11,20)])
gsc1 <- GeneSetCollection(gs1)
gsc2 <- GeneSetCollection(gs2)
sce <- importGeneSetsFromCollection(inSCE = sce,
                                   geneSetCollection = gsc1,
                                   by = "rownames",
                                   collectionName = "Collection1")
sce <- importGeneSetsFromCollection(inSCE = sce,
                                   geneSetCollection = gsc2,
                                   by = "rownames",
                                   collectionName = "Collection2")
collections <- sctkListGeneSetCollections(sce)

```

---

sctkPythonInstallConda

*Installs Python packages into a Conda environment*


---

**Description**

Install all Python packages used in the [singleCellTK](#) package using `conda_install` from package [reticulate](#). This will create a new Conda environment with the name `envname` if not already present. Note that Anaconda or Miniconda already need to be installed on the local system.

**Usage**

```

sctkPythonInstallConda(
  envname = "sctk-reticulate",
  conda = "auto",
  packages = c("scipy", "numpy", "astroid", "six"),
  pipPackages = c("scrublet", "scanpy", "bbknn", "scanorama", "anndata"),
  selectConda = TRUE,
  forge = FALSE,
  pipIgnoreInstalled = TRUE,
  pythonVersion = NULL,
  ...
)

```

**Arguments**

<code>envname</code>	Character. Name of the conda environment to create.
<code>conda</code>	Character. Path to conda executable. Usue "auto" to find conda using the PATH and other conventional install locations. Default 'auto'.
<code>packages</code>	Character Vector. List of packages to install from Conda.

pipPackages	Character Vector. List of packages to install into the Conda environment using 'pip'.
selectConda	Boolean. Run <code>selectSCTKConda</code> after installing all packages to select the Conda environment. Default TRUE.
forge	Boolean. Include the Conda Forge repository.
pipIgnoreInstalled	Boolean. Ignore installed versions when using pip. This is TRUE by default so that specific package versions can be installed even if they are downgrades. The FALSE option is useful for situations where you don't want a pip install to attempt an overwrite of a conda binary package (e.g. SciPy on Windows which is very difficult to install via pip due to compilation requirements).
pythonVersion	Passed to <code>python_version</code> variable in <code>conda_install</code> . Default NULL.
...	Other parameters to pass to <code>conda_install</code> .

**Value**

None. Installation of Conda environment.

**See Also**

See `conda_create` for more information on creating a Conda environment. See `conda_install` for more description of the installation parameters. See <https://rstudio.github.io/reticulate/> for more information on package `reticulate`. See `selectSCTKConda` for reloading the Conda environment if R is restarted without going through the whole installation process again. See <https://docs.conda.io/en/latest/> for more information on Conda environments.

**Examples**

```
## Not run:
sctkPythonInstallConda(envname = "sctk-reticulate")

## End(Not run)
```

---

sctkPythonInstallVirtualEnv

*Installs Python packages into a virtual environment*

---

**Description**

Install all Python packages used in the `singleCellTK` package using `virtualenv_install` from package `reticulate`. This will create a new virtual environment with the name `envname` if not already present.

**Usage**

```
sctkPythonInstallVirtualEnv(
  envname = "sctk-reticulate",
  packages = c("scipy", "numpy", "astroid", "six", "scrublet", "scanpy", "scanorama",
    "bbknn", "anndata"),
  selectEnvironment = TRUE,
  python = NULL
)
```

**Arguments**

envname	Character. Name of the virtual environment to create.
packages	Character Vector. List of packages to install.
selectEnvironment	Boolean. Run <a href="#">selectSCTKVirtualEnvironment</a> after installing all packages to select the virtual environment. Default TRUE.
python	The path to a Python interpreter, to be used with the created virtual environment. When NULL, the Python interpreter associated with the current session will be used. Default NULL.

**Value**

None. Installation of virtual environment.

**See Also**

See [virtualenv\\_create](#) for more information on creating a Conda environment. See [virtualenv\\_install](#) for more description of the installation parameters. See <https://rstudio.github.io/reticulate/> for more information on package [reticulate](#). See [selectSCTKVirtualEnvironment](#) for reloading the virtual environment if R is restarted without going through the whole installation process again.

**Examples**

```
## Not run:
sctkPythonInstallVirtualEnv(envname = "sctk-reticulate")

## End(Not run)
```

---

 SEG

*Stably Expressed Gene (SEG) list object, with SEG sets for human and mouse.*

---

**Description**

The two gene sets came from dataset called 'segList' of package 'scMerge'.

**Usage**

```
data('SEG')
```

**Format**

list, with two entries "human" and "mouse", each is a character vector.

**Source**

```
data('segList', package='scMerge')
```

**Examples**

```
data('SEG')
humanSEG <- SEG$human
```

---

selectSCTKConda	<i>Selects a Conda environment</i>
-----------------	------------------------------------

---

**Description**

Selects a Conda environment with Python packages used in [singleCellTK](#).

**Usage**

```
selectSCTKConda(envname = "sctk-reticulate")
```

**Arguments**

envname            Character. Name of the conda environment to activate.

**Value**

None. Selects Conda environment.

**See Also**

[conda-tools](#) for more information on using Conda environments with package [reticulate](#). See <https://rstudio.github.io/reticulate/> for more information on package [reticulate](#).

See [sctkPythonInstallConda](#) for installation of Python modules into a Conda environment. See [conda-tools](#) for more information on using Conda environments with package [reticulate](#). See <https://rstudio.github.io/reticulate/> for more information on package [reticulate](#). See <https://docs.conda.io/en/latest/> for more information on Conda environments.

## Examples

```
## Not run:
sctkPythonInstallConda(envname = "sctk-reticulate", selectConda = FALSE)
selectSCTKConda(envname = "sctk-reticulate")

## End(Not run)
```

---

```
selectSCTKVirtualEnvironment
      Selects a virtual environment
```

---

## Description

Selects a virtual environment with Python packages used in [singleCellTK](#)

## Usage

```
selectSCTKVirtualEnvironment(envname = "sctk-reticulate")
```

## Arguments

envname            Character. Name of the virtual environment to activate.

## Value

None. Selects virtual environment.

## See Also

See [sctkPythonInstallVirtualEnv](#) for installation of Python modules into a virtual environment. See [virtualenv-tools](#) for more information on using virtual environments with package [reticulate](#). See <https://rstudio.github.io/reticulate/> for more information on package [reticulate](#).

## Examples

```
## Not run:
sctkPythonInstallVirtualEnv(envname = "sctk-reticulate", selectEnvironment = FALSE)
selectSCTKVirtualEnvironment(envname = "sctk-reticulate")

## End(Not run)
```

---

setRowNames	<i>Set rownames of SCE with a character vector or a rowData column</i>
-------------	--

---

### Description

Users can set rownames of an SCE object with either a character vector where the length equals to `nrow(x)`, or a single character specifying a column in `rowData(x)`. Also applicable to matrix like object where `rownames<-` method works, but only allows full size name vector. Users can set `dedup = TRUE` to remove duplicated entries in the specification, by adding `-1, -2, ..., -i` suffix to the duplication of the same identifier.

### Usage

```
setRowNames(x, rowNames, dedup = TRUE)
```

### Arguments

<code>x</code>	Input object where the rownames will be modified.
<code>rowNames</code>	Character vector of the rownames. If <code>x</code> is an <a href="#">SingleCellExperiment</a> object, a single character specifying a column in <code>rowData(x)</code> .
<code>dedup</code>	Logical. Whether to deduplicate the specified rowNames. Default TRUE

### Value

The input SCE object with rownames updated.

### Examples

```
data("scExample", package = "singleCellTK")
head(rownames(sce))
sce <- setRowNames(sce, "feature_name")
head(rownames(sce))
```

---

setSampleSummaryStatsTable<-	<i>Setter function which stores table of SCTK QC outputs to metadata.</i>
------------------------------	---

---

### Description

Stores table of QC metrics generated from QC algorithms within the metadata slot of the SingleCellExperiment object.

### Usage

```
setSampleSummaryStatsTable(inSCE, ...) <- value
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved <a href="#">assay</a> data and/or <a href="#">colData</a> data. Required.
...	Other arguments passed to the function.
value	The sample summary table of SCTK QC outputs

**Value**

A [SingleCellExperiment](#) object which contains a summary table for QC statistics generated from [SingleCellTK](#).

---

setSCTKDisplayRow	<i>Indicates which rowData to use for visualization</i>
-------------------	---

---

**Description**

This function is to be used to specify which

**Usage**

```
setSCTKDisplayRow(inSCE, featureDisplayRow)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
featureDisplayRow	Indicates which column name of <i>rowData</i> to be used for plots.

**Value**

A [SingleCellExperiment](#) object with the specific column name of *rowData* to be used for plotting stored in metadata.

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- setSCTKDisplayRow(inSCE = sce, featureDisplayRow = "feature_name")
plotSCEViolinAssayData(inSCE = sce, feature = "ENSG0000019582")
```



---

simpleLog	<i>A decorator that prints the arguments to the decorated function</i>
-----------	--

---

**Description**

A decorator that prints the arguments to the decorated function

**Usage**

```
simpleLog(f)
```

**Arguments**

f	A function to decorate
---	------------------------

**Value**

Prints message

---

singleCellTK	<i>Run the single cell analysis app</i>
--------------	---

---

**Description**

Use this function to run the single cell analysis app.

**Usage**

```
singleCellTK(inSCE = NULL, includeVersion = TRUE, theme = "yeti")
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
includeVersion	Include the version number in the SCTK header. The default is TRUE.
theme	The bootswatch theme to use for the singleCellTK UI. The default is 'flatly'.

**Value**

The shiny app will open

**Examples**

```
## Not run:
#Upload data through the app
singleCellTK()

# Load the app with a SingleCellExperiment object
data("mouseBrainSubsetSCE")
singleCellTK(mouseBrainSubsetSCE)

## End(Not run)
```

---

subDiffEx	<i>Passes the output of generateSimulatedData() to differential expression tests, picking either t-tests or ANOVA for data with only two conditions or multiple conditions, respectively.</i>
-----------	---

---

**Description**

Passes the output of generateSimulatedData() to differential expression tests, picking either t-tests or ANOVA for data with only two conditions or multiple conditions, respectively.

**Usage**

```
subDiffEx(tempData)

subDiffExttest(countMatrix, class.labels, test.type = "t.equalvar")

subDiffExANOVA(countMatrix, condition)
```

**Arguments**

tempData	Matrix. The output of generateSimulatedData(), where the first row contains condition labels.
countMatrix	Matrix. A simulated counts matrix, sans labels.
class.labels	Factor. The condition labels for the simulated cells. Will be coerced into 1's and 0's.
test.type	Type of test to perform. The default is t.equalvar.
condition	Factor. The condition labels for the simulated cells.

**Value**

subDiffEx(): A vector of fdr-adjusted p-values for all genes. Nonviable results (such as for genes with 0 counts in a simulated dataset) are coerced to 1.

subDiffExttest(): A vector of fdr-adjusted p-values for all genes. Nonviable results (such as for genes with 0 counts in a simulated dataset) are coerced to 1.

subDiffExANOVA(): A vector of fdr-adjusted p-values for all genes. Nonviable results (such as for genes with 0 counts in a simulated dataset) are coerced to 1.

**Functions**

- subDiffEx:
- subDiffExttest: Runs t-tests on all genes in a simulated dataset with 2 conditions, and adjusts for FDR.
- subDiffExANOVA: Runs ANOVA on all genes in a simulated dataset with more than 2 conditions, and adjusts for FDR.

**Examples**

```

data("mouseBrainSubsetSCE")
res <- generateSimulatedData(
  totalReads = 1000, cells=10,
  originalData = assay(mouseBrainSubsetSCE, "counts"),
  realLabels = colData(mouseBrainSubsetSCE)[, "level1class"])
tempSigDiff <- subDiffEx(res)

data("mouseBrainSubsetSCE")
#sort first 100 expressed genes
ord <- rownames(mouseBrainSubsetSCE)[
  order(rowSums(assay(mouseBrainSubsetSCE, "counts")),
    decreasing = TRUE)][seq(100)]
#subset to those first 100 genes
subset <- mouseBrainSubsetSCE[ord, ]
res <- generateSimulatedData(totalReads = 1000, cells=10,
  originalData = assay(subset, "counts"),
  realLabels = colData(subset)[, "level1class"])

realLabels <- res[1, ]
output <- res[-1, ]
fdr <- subDiffExttest(output, realLabels)

data("mouseBrainSubsetSCE")
#sort first 100 expressed genes
ord <- rownames(mouseBrainSubsetSCE)[
  order(rowSums(assay(mouseBrainSubsetSCE, "counts")),
    decreasing = TRUE)][seq(100)]
# subset to those first 100 genes
subset <- mouseBrainSubsetSCE[ord, ]
res <- generateSimulatedData(totalReads = 1000, cells=10,
  originalData = assay(subset, "counts"),
  realLabels = colData(subset)[, "level2class"])

realLabels <- res[1, ]
output <- res[-1, ]
fdr <- subDiffExANOVA(output, realLabels)

```

**Description**

Used to perform subsetting of a [SingleCellExperiment](#) object using a variety of methods that indicate the correct columns to keep. The various methods, `index`, `bool`, and `colData`, can be used in conjunction with one another.

**Usage**

```
subsetSCECols(inSCE, index = NULL, bool = NULL, colData = NULL)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>index</code>	Integer vector. Vector of indices indicating which columns to keep. If <code>NULL</code> , this will not be used for subsetting. Default <code>NULL</code> .
<code>bool</code>	Boolean vector. Vector of <code>TRUE</code> or <code>FALSE</code> indicating which columns should be kept. Needs to be the same length as the number of columns in <code>inSCE</code> . If <code>NULL</code> , this will not be used for subsetting. Default <code>NULL</code> .
<code>colData</code>	Character. An expression that will identify a subset of columns using variables found in the <code>colData</code> of <code>inSCE</code> . For example, if <code>x</code> is a numeric vector in <code>colData</code> , then <code>"x &lt; 5"</code> will return all columns with <code>x</code> less than 5. Single quotes should be used for character strings. For example, <code>"y == 'yes'"</code> will return all columns where <code>y</code> is "yes". Multiple expressions can be evaluated by placing them in a vector. For example <code>c("x &lt; 5", "y == 'yes'")</code> will apply both operations for subsetting. If <code>NULL</code> , this will not be used for subsetting. Default <code>NULL</code> .

**Value**

A [SingleCellExperiment](#) object that has been subsetted by `colData`.

**Author(s)**

Joshua D. Campbell

**Examples**

```
data(scExample)
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
```

---

subsetSCERows

*Subset a SingleCellExperiment object by rows*

---

**Description**

Used to perform subsetting of a [SingleCellExperiment](#) object using a variety of methods that indicate the correct rows to keep. The various methods, `index`, `bool`, and `rowData`, can be used in conjunction with one another. If `returnAsAltExp` is set to `TRUE`, then the returned object will have the same number of rows as the input `inSCE` as the subsetted object will be stored in the `altExp` slot.

**Usage**

```
subsetSCERows(
  inSCE,
  index = NULL,
  bool = NULL,
  rowData = NULL,
  returnAsAltExp = TRUE,
  altExpName = "subset",
  prependAltExpName = TRUE
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
index	Integer vector. Vector of indices indicating which rows to keep. If NULL, this will not be used for subsetting. Default NULL.
bool	Boolean vector. Vector of TRUE or FALSE indicating which rows should be kept. Needs to be the same length as the number of rows in inSCE. If NULL, this will not be used for subsetting. Default NULL.
rowData	Character. An expression that will identify a subset of rows using variables found in the rowData of inSCE. For example, if x is a numeric vector in rowData, then "x < 5" will return all rows with x less than 5. Single quotes should be used for character strings. For example, "y == 'yes'" will return all rows where y is "yes". Multiple expressions can be evaluated by placing them in a vector. For example c("x < 5", "y == 'yes'") will apply both operations for subsetting. If NULL, this will not be used for subsetting. Default NULL.
returnAsAltExp	Boolean. If TRUE, the subsetted <a href="#">SingleCellExperiment</a> object will be returned in the altExp slot of inSCE. If FALSE, the subsetted <a href="#">SingleCellExperiment</a> object will be directly returned.
altExpName	Character. Name of the alternative experiment object to add if returnAsAltExp = TRUE. Default subset.
prependAltExpName	Boolean. If TRUE, altExpName will be added to the beginning of the assay names in the altExp object. This is only utilized if returnAsAltExp = TRUE. Default TRUE.

**Value**

A [SingleCellExperiment](#) object that has been subsetted by rowData.

**Author(s)**

Joshua D. Campbell

## Examples

```
data(scExample)

# Set a variable up in the rowData indicating mitochondrial genes
rowData(sce)$isMito <- ifelse(grepl("^MT-", rowData(sce)$feature_name),
                             "yes", "no")
sce <- subsetSCERows(sce, rowData = "isMito == 'yes'")
```

---

summarizeSCE

*Summarize an assay in a [SingleCellExperiment](#)*

---

## Description

Creates a table of summary metrics from an input [SingleCellExperiment](#)

## Usage

```
summarizeSCE(inSCE, useAssay = NULL, sampleVariableName = NULL)
```

## Arguments

**inSCE**            Input [SingleCellExperiment](#) object.

**useAssay**        Indicate which assay to summarize. If NULL, then the first assay in `inSCE` will be used. Default NULL.

**sampleVariableName**    Variable name in `colData` denoting which sample each cell belongs to. If NULL, all cells will be assumed to come from the same sample. Default "sample".

## Value

A `data.frame` object of summary metrics.

## Examples

```
data("mouseBrainSubsetSCE")
summarizeSCE(mouseBrainSubsetSCE, sample = NULL)
```



# Index

## \* datasets

- MitoGenes, 95
- mouseBrainSubsetSCE, 95
- msigdb\_table, 96
- sce, 271
- sceBatches, 272
- SEG, 276
- .addSeuratToMetaDataSCE, 7
- .checkDiffExpResultExists, 8
- .computeSignificantPC, 9
- .extractSCEAnnotation, 9
- .formatDEAList, 10
- .GetComponentNames, 11
- .ggBar, 12
- .ggDensity, 13
- .ggScatter, 14
- .ggViolin, 16, 141
- .sce2adata, 18
- .seuratGetVariableFeatures, 19
- .seuratInvalidate, 20
- .updateAssaySCE, 21
- addPerCellQC, 234
- adjustCounts, 259
- altExp, 241, 284
- assay, 21, 58, 210, 231, 232, 237, 240, 241, 268, 280
- autoEstCont, 259
- barcodeRanks, 205
- bcds, 207, 208
- BiocParallelParam, 236, 238
- buildSNNGraph, 240
- calcEffectSizes, 21
- colData, 29, 30, 58, 64, 104, 185, 186, 205, 206, 208–210, 212, 213, 220, 223, 225, 227, 230–232, 236–239, 241, 244, 267, 268, 280
- colorRamp2, 155

- combineSCE, 22
- computeHeatmap, 23
- computeZScore, 24
- conda\_create, 275
- conda\_install, 274, 275
- constructSCE, 25
- convertSCEToSeurat, 25
- convertSeuratToSCE, 26
- cxds, 211, 212
- cxds\_bcds\_hybrid, 212, 213
- data.frame, 218
- data.table, 25
- dataAnnotationColor, 27
- DataFrame-class, 236
- dbscan, 219, 220
- decontX, 29, 218, 219
- dedupRowNames, 28
- DelayedArray, 66, 67, 72–76, 78, 86, 88, 89, 91, 183
- DelayedArray-class, 68
- detectCellOutlier, 29
- diffAbundanceFET, 30, 54
- DimHeatmap, 248, 249
- discreteColorPalette, 31
- distinctColors, 27, 31, 32
- downSampleCells, 32
- downSampleDepth, 34
- emptyDrops, 88, 205, 224, 225
- estimateNonExpressingCells, 261
- expData, 35
- expData, ANY, character-method, 36
- expData<-, 36
- expData<-, ANY, character, CharacterOrNullOrMissing, logical-method, 37
- expDataNames, 38
- expDataNames, ANY-method, 38
- expDeleteDataTag, 39
- exportSCE, 40



- exportSCEtoAnnData, 41
- exportSCEtoFlatFile, 42
- exportSCEtoSeurat, 43
- expSetDataTag, 44
- expTaggedData, 44
  
- featureIndex, 45, 79, 81, 82, 84, 85, 235
- FindIntegrationAnchors, 251
- findMarkerDiffExp, 47, 124, 126, 188
- findMarkerTopTable, 48
- fit\_dirichlet, 219
  
- generateHTANMeta, 49
- generateMeta, 50
- generateSimulatedData, 51
- GeneSetCollection, 79–86, 273
- getBiomarker, 51
- getDEGTopTable, 52
- getDiffAbundanceResults, 54
- getDiffAbundanceResults, SingleCellExperiment-method (getDiffAbundanceResults), 54
- getDiffAbundanceResults<- (getDiffAbundanceResults), 54
- getDiffAbundanceResults<-, SingleCellExperiment-method (getDiffAbundanceResults), 54
- getEnrichRResult, 226
- getEnrichRResult (getEnrichRResult<-), 55
- getEnrichRResult, SingleCellExperiment-method (getEnrichRResult<-), 55
- getEnrichRResult<-, 55
- getEnrichRResult<-, SingleCellExperiment-method (getEnrichRResult<-), 55
- getGenesetNamesFromCollection, 56, 266
- getGmt, 81, 235
- getMSigDBTable, 56
- getPathwayResultNames, 57, 266
- getSampleSummaryStatsTable, 57
- getSampleSummaryStatsTable, SingleCellExperiment-method (getSampleSummaryStatsTable), 57
- getSceParams, 58
- getSeuratVariableFeatures, 59
- getSoupX (getSoupX<-), 59
- getSoupX, SingleCellExperiment-method (getSoupX<-), 59
- getSoupX<-, 59
- getSoupX<-, SingleCellExperiment-method (getSoupX<-), 59
- getTopHVG, 60
- getTSCANResults, 62
- getTSCANResults, SingleCellExperiment-method (getTSCANResults), 62
- getTSCANResults<- (getTSCANResults), 62
- getTSCANResults<-, SingleCellExperiment-method (getTSCANResults), 62
- getTSNE, 62, 221
- getUMAP, 64, 221
- ggplot, 104, 113, 155
- grep, 46, 204
- GSEABase, 79, 81, 83, 84, 86
  
- Heatmap, 126, 155
  
- importAlevin, 65
- importAnnData, 66
- importBUSTools, 68
- importCellRanger, 69
- importCellRangerV2 (importCellRanger), 69
- importCellRangerV2Sample, 73
- importCellRangerV3 (importCellRanger), 69
- importCellRangerV3Sample, 74
- importDropEst, 75
- importExampleData, 76
- importFromFiles, 77
- importGeneSetsFromCollection, 79, 81, 83, 266
- importGeneSetsFromGMT, 80, 80, 83, 85, 86, 266, 273
- importGeneSetsFromList, 80, 81, 82, 85, 86, 265, 266, 273
- importGeneSetsFromMSigDB, 56, 80, 81, 83, 83, 96, 265, 266, 273
- importMitoGeneSet, 85
- importMultipleSources, 86
- importTopo, 87
- importSEQC, 88
- importSTARsolo, 90
- IntegrateData, 251
- isOutlier, 29
- iterateSimulations, 92
  
- kmeans, 229
  
- list.dirs, 70
- listSampleSummaryStatsTables, 93

- listSampleSummaryStatsTables, SingleCellExperiment-method (listSampleSummaryStatsTables), 93
- listTSCANResults (getTSCANResults), 62
- listTSCANResults, SingleCellExperiment-method (getTSCANResults), 62
- logNormCounts, 64, 269
- Matrix, 76
- matrix, 66–68, 71, 73–75, 78, 88, 89, 91
- mergeSCEColData, 94
- metadata, 80, 81, 83, 84, 86, 93
- MitoGenes, 95
- modelGeneVar, 220
- mouseBrainSubsetSCE, 95
- msigdb\_table, 96
- msigdbr, 84
- msigdbr\_show\_species, 84
- plotBarcodeRankDropsResults, 96
- plotBarcodeRankScatter, 97
- plotBatchCorrCompare, 99
- plotBatchVariance, 100
- plotBcdfsResults, 101
- plotClusterAbundance, 104
- plotClusterPseudo, 105
- plotCxlsResults, 106
- plotDecontXResults, 108
- plotDEGHeatmap, 111, 218
- plotDEGRegression, 113, 218
- plotDEGViolin, 115, 218
- plotDEGVolcano, 116, 218
- plotDimRed, 117
- plotDoubletFinderResults, 118
- plotEmptyDropsResults, 120
- plotEmptyDropsScatter, 122
- plotMarkerDiffExp, 124
- plotMASTThresholdGenes, 127
- plotPathway, 128
- plotPCA, 129
- plotRunPerCellQCResults, 130
- plotScDbfFinderResults, 132
- plotScdsHybridResults, 135
- plotSCEBarAssayData, 138
- plotSCEBarColData, 139
- plotSCEBatchFeatureMean, 141
- plotSCEDensity, 142
- plotSCEDensityAssayData, 143
- plotSCEDensityColData, 145
- plotSCEDimReduceColData, 147, 174
- plotSCEDimReduceFeatures, 149
- plotSCEDimReduceHeatmap (plotSCEHeatmap), 152
- plotSCEHeatmap, 113, 126, 152
- plotSCEScatter, 155
- plotSCEViolin, 158
- plotSCEViolinAssayData, 160
- plotSCEViolinColData, 163
- plotScrubletResults, 165
- plotSeuratElbow, 168
- plotSeuratGenes, 169
- plotSeuratHeatmap, 170
- plotSeuratHVG, 170
- plotSeuratJackStraw, 171
- plotSeuratReduction, 172
- plotSoupXResults, 173
- plotTopHVG, 175
- plotTSCANDEgenes, 176
- plotTSCANPseudotimeGenes, 177
- plotTSCANPseudotimeHeatmap, 178
- plotTSCANResults, 179
- plotTSNE, 180
- plotUMAP, 181
- qcInputProcess, 182
- quickCluster, 260
- rainbow, 27
- readMM, 66–68, 71, 73–75, 78, 88, 89, 91
- readSingleCellMatrix, 183
- reducedDim, 241
- reportCellQC, 184
- reportClusterAbundance, 185
- reportDiffAbundanceFET, 186
- reportDiffExp, 187
- reportDropletQC, 187
- reportFindMarker, 188
- reportQCTool, 189
- reportSeurat, 190
- reportSeuratClustering, 192
- reportSeuratDimRed, 194
- reportSeuratFeatureSelection, 195
- reportSeuratMarkerSelection, 196
- reportSeuratNormalization, 198
- reportSeuratResults, 199
- reportSeuratRun, 200
- reportSeuratScaling, 203
- ReprocessedAllenData, 77

- ReprocessedFluidigmData, 76
- reticulate, 274–278
- retrieveFeatureIndex, 204
- retrieveFeatureInfo, 46
- retrieveSCEIndex, 204
- runANOVA (runDEAnalysis), 214
- runBarcodeRankDrops, 97, 98, 205
- runBBKNN, 206
- runBcdfs, 102, 207
- runCellQC, 79, 81, 83, 84, 86, 208
- runComBatSeq, 210
- runCxls, 107, 211
- runCxlsBcdfsHybrid, 136, 212
- runDEAnalysis, 187, 214
- runDecontX, 109, 218
- runDESeq2 (runDEAnalysis), 214
- runDimReduce, 220
- runDoubletFinder, 119, 222
- runDropletQC, 223
- runEmptyDrops, 123, 224
- runEnrichR, 55, 225
- runFastMNN, 226
- runFeatureSelection, 227
- runGSVA, 228
- runKMeans, 229
- runLimmaBC, 230
- runLimmaDE (runDEAnalysis), 214
- runMAST (runDEAnalysis), 214
- runMNNCorrect, 226, 231
- runNormalization, 232
- runPCA, 270
- runPerCellQC, 209, 234
- runSCANORAMA, 237
- runScDbtFinder, 133, 238
- runSCMerge, 239
- runScranSNN, 240
- runScrublet, 121, 166, 242
- runSeuratFindClusters, 244
- runSeuratFindHVG, 246
- runSeuratFindMarkers, 247
- runSeuratHeatmap, 248
- runSeuratICA, 221, 249
- runSeuratIntegration, 250
- runSeuratJackStraw, 251
- runSeuratNormalizeData, 252
- runSeuratPCA, 221, 253
- runSeuratScaleData, 254
- runSeuratSCTransform, 255
- runSeuratTSNE, 221, 256
- runSeuratUMAP, 221, 257
- runSingleR, 258
- runSoupX, 60, 174, 259
- runTSCAN, 179, 262
- runTSCANClusterDEAnalysis, 105, 263
- runTSCANDEG, 177, 178, 264
- RunUMAP, 257, 258
- runVAM, 265
- runWilcox (runDEAnalysis), 214
- runZINBWave, 266
- sampleSummaryStats, 268
- scaterCPM, 269
- scaterlogNormCounts, 269
- scaterPCA, 221, 270
- scDbtFinder, 238, 239
- sce, 271
- sceBatches, 272
- scrnModelGeneVar, 272
- scRNAseq, 76
- scSEGIndex, 240
- sctkListGeneSetCollections, 266, 273
- sctkPythonInstallConda, 274, 277
- sctkPythonInstallVirtualEnv, 275, 278
- SCTransform, 255
- SEG, 276
- selectSCTKConda, 275, 277
- selectSCTKVirtualEnvironment, 276, 278
- setContaminationFraction, 261
- setRowNames, 279
- setSampleSummaryStatsTable<-, 279
- setSCTKDisplayRow, 280
- simpleLog, 281
- SingleCellExperiment, 8–10, 15, 21, 22, 25, 27, 29, 30, 33, 34, 40–43, 45–48, 50, 52–58, 60, 62–66, 68, 69, 76–88, 90, 92, 93, 97–100, 102, 104, 105, 107, 109, 110, 112, 114–116, 119, 121, 123, 125, 128, 130, 131, 133, 134, 136, 138, 140–142, 144, 146, 148, 150, 153, 156, 158, 161, 163, 166, 174, 176–182, 184–190, 192–213, 216–221, 223–225, 227–232, 235–241, 243, 244, 259, 260, 262–268, 270–273, 279–281, 284–286
- singleCellTK, 79, 80, 82, 83, 85, 274, 275, 277, 278, 281

subDiffEx, [282](#)  
subDiffExANOVA (subDiffEx), [282](#)  
subDiffExttest (subDiffEx), [282](#)  
subsetSCECols, [283](#)  
subsetSCERows, [284](#)  
SummarizedExperiment, [45](#), [46](#)  
summarizeSCE, [286](#)

TENxPBMCData, [76](#), [77](#)  
thresholdSCRNACountMatrix, [127](#)  
trimCounts, [287](#)

umap, [219](#)  
unit, [155](#)

virtualenv\_create, [276](#)  
virtualenv\_install, [275](#), [276](#)

with\_seed, [220](#)