

# Package ‘singleCellTK’

May 19, 2026

**Type** Package

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

**Version** 2.23.0

**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).

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**Encoding** UTF-8

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

**LazyData** FALSE

**Imports** ape, anndata, AnnotationHub, batchelor, BiocParallel, celldex, colourpicker, colorspace, cowplot, cluster, ComplexHeatmap, data.table, DelayedMatrixStats, DESeq2, dplyr, DT, ExperimentHub, ensemblDb, fields, ggplot2, ggplotify, ggrepel, ggtree, gridExtra, grid, GSVA (>= 1.50.0), GSVAdata, igraph, KernSmooth, limma, MAST, Matrix (>= 1.6-1), matrixStats, methods, msgdbr, multtest, plotly, plyr, ROCR, Rtsne, S4Vectors, scater, scMerge (>= 1.2.0), scran, Seurat (>= 3.1.3), shiny, shinyjs, SingleR, stringr, SoupX, sva, reshape2, shinyalert, circlize, enrichR (>= 3.2), celda, shinycssloaders, DropletUtils, scds (>= 1.2.0), reticulate (>= 1.14), tools,

tximport, tidy, eds, withr, GSEABase, R.utils, zinbwave,  
 scRNAseq (>= 2.0.2), TENxPBMCDData, yaml, rmarkdown, magrittr,  
 scDbfFinder, metap, VAM (>= 0.5.3), tibble, rlang, TSCAN,  
 TrajectoryUtils, scuttle, utils, stats, zellkonverter,  
 lifecycle

**RoxygenNote** 7.3.3

**Suggests** testthat, Rsubread, BiocStyle, knitr, lintr, spelling,  
 org.Mm.eg.db, kableExtra, shinythemes, shinyBS, shinyjqui,  
 shinyWidgets, shinyFiles, BiocGenerics, RColorBrewer, fastmap  
 (>= 1.1.0), harmony, SeuratObject, optparse

**VignetteBuilder** knitr

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

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

**Language** en-US

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

**git\_branch** devel

**git\_last\_commit** 3ac722f

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-18

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## Contents

calcEffectSizes . . . . .	7
combineSCE . . . . .	8
computeHeatmap . . . . .	9
computeZScore . . . . .	10
constructSCE . . . . .	10

convertSCEToSeurat . . . . .	11
convertSeuratToSCE . . . . .	12
dedupRowNames . . . . .	13
detectCellOutlier . . . . .	13
diffAbundanceFET . . . . .	14
discreteColorPalette . . . . .	15
distinctColors . . . . .	16
downSampleCells . . . . .	16
downSampleDepth . . . . .	18
expData . . . . .	19
expData,ANY,character-method . . . . .	19
expData<- . . . . .	20
expData<-,ANY,character,CharacterOrNullOrMissing,logical-method . . . . .	21
expDataNames . . . . .	21
expDataNames,ANY-method . . . . .	22
expDeleteDataTag . . . . .	23
exportSCE . . . . .	23
exportSCEtoAnnData . . . . .	24
exportSCEtoFlatFile . . . . .	25
exportSCEToSeurat . . . . .	26
expSetDataTag . . . . .	27
expTaggedData . . . . .	28
featureIndex . . . . .	29
generateHTANMeta . . . . .	30
generateMeta . . . . .	31
generateSimulatedData . . . . .	31
getBiomarker . . . . .	32
getDEGTopTable . . . . .	33
getDiffAbundanceResults . . . . .	34
getEnrichRResult<- . . . . .	35
getFindMarkerTopTable . . . . .	36
getGenesetNamesFromCollection . . . . .	37
getMSigDBTable . . . . .	38
getPathwayResultNames . . . . .	38
getSampleSummaryStatsTable . . . . .	39
getSceParams . . . . .	40
getSeuratVariableFeatures . . . . .	40
getSoupX<- . . . . .	41
getTopHVG . . . . .	42
getTSCANResults . . . . .	44
importAlevin . . . . .	45
importAnnData . . . . .	46
importBUStools . . . . .	47
importCellRanger . . . . .	49
importCellRangerV2Sample . . . . .	52
importCellRangerV3Sample . . . . .	53
importDropEst . . . . .	54
importExampleData . . . . .	55
importFromFiles . . . . .	56
importGeneSetsFromCollection . . . . .	58
importGeneSetsFromGMT . . . . .	59
importGeneSetsFromList . . . . .	61

importGeneSetsFromMSigDB . . . . .	62
importMitoGeneSet . . . . .	64
importMultipleSources . . . . .	65
importOptimus . . . . .	66
importSEQC . . . . .	67
importSTARsolo . . . . .	69
iterateSimulations . . . . .	70
listSampleSummaryStatsTables . . . . .	71
mergeSCEColData . . . . .	72
MitoGenes . . . . .	73
mouseBrainSubsetSCE . . . . .	73
msigdb_table . . . . .	74
plotBarcodeRankDropsResults . . . . .	75
plotBarcodeRankScatter . . . . .	76
plotBatchCorrCompare . . . . .	77
plotBatchVariance . . . . .	78
plotBcdsResults . . . . .	79
plotBubble . . . . .	82
plotClusterAbundance . . . . .	83
plotCxlsResults . . . . .	84
plotDecontXResults . . . . .	86
plotDEGHeatmap . . . . .	89
plotDEGRegression . . . . .	91
plotDEGViolin . . . . .	92
plotDEGVolcano . . . . .	94
plotDimRed . . . . .	95
plotDoubletFinderResults . . . . .	96
plotEmptyDropsResults . . . . .	98
plotEmptyDropsScatter . . . . .	100
plotEnrichR . . . . .	101
plotFindMarkerHeatmap . . . . .	102
plotMASTThresholdGenes . . . . .	105
plotPathway . . . . .	106
plotPCA . . . . .	107
plotRunPerCellQCResults . . . . .	108
plotScanpyDotPlot . . . . .	110
plotScanpyEmbedding . . . . .	111
plotScanpyHeatmap . . . . .	112
plotScanpyHVG . . . . .	113
plotScanpyMarkerGenes . . . . .	114
plotScanpyMarkerGenesDotPlot . . . . .	115
plotScanpyMarkerGenesHeatmap . . . . .	116
plotScanpyMarkerGenesMatrixPlot . . . . .	117
plotScanpyMarkerGenesViolin . . . . .	119
plotScanpyMatrixPlot . . . . .	119
plotScanpyPCA . . . . .	121
plotScanpyPCAGeneRanking . . . . .	122
plotScanpyPCAVariance . . . . .	122
plotScanpyViolin . . . . .	123
plotScDbfFinderResults . . . . .	124
plotScdsHybridResults . . . . .	126
plotSCEBarAssayData . . . . .	129

plotSCEBarColData . . . . .	130
plotSCEBatchFeatureMean . . . . .	132
plotSCEDensity . . . . .	133
plotSCEDensityAssayData . . . . .	134
plotSCEDensityColData . . . . .	136
plotSCEDimReduceColData . . . . .	137
plotSCEDimReduceFeatures . . . . .	140
plotSCEHeatmap . . . . .	142
plotSCEScatter . . . . .	145
plotSCEViolin . . . . .	147
plotSCEViolinAssayData . . . . .	150
plotSCEViolinColData . . . . .	152
plotScrubletResults . . . . .	154
plotSeuratElbow . . . . .	157
plotSeuratGenes . . . . .	158
plotSeuratHeatmap . . . . .	159
plotSeuratHVG . . . . .	159
plotSeuratJackStraw . . . . .	160
plotSeuratReduction . . . . .	161
plotSoupXResults . . . . .	162
plotTopHVG . . . . .	164
plotTSCANClusterDEG . . . . .	165
plotTSCANClusterPseudo . . . . .	166
plotTSCANDimReduceFeatures . . . . .	167
plotTSCANPseudotimeGenes . . . . .	168
plotTSCANPseudotimeHeatmap . . . . .	170
plotTSCANResults . . . . .	171
plotTSNE . . . . .	172
plotUMAP . . . . .	173
qcInputProcess . . . . .	174
readSingleCellMatrix . . . . .	175
reportCellQC . . . . .	176
reportClusterAbundance . . . . .	177
reportDiffAbundanceFET . . . . .	177
reportDiffExp . . . . .	178
reportDropletQC . . . . .	179
reportFindMarker . . . . .	180
reportQCTool . . . . .	181
reportSeurat . . . . .	182
reportSeuratClustering . . . . .	184
reportSeuratDimRed . . . . .	185
reportSeuratFeatureSelection . . . . .	187
reportSeuratMarkerSelection . . . . .	188
reportSeuratNormalization . . . . .	189
reportSeuratResults . . . . .	190
reportSeuratRun . . . . .	192
reportSeuratScaling . . . . .	194
retrieveSCEIndex . . . . .	195
runBarcodeRankDrops . . . . .	196
runBBKNN . . . . .	197
runBcbs . . . . .	198
runCellQC . . . . .	199

runClusterSummaryMetrics . . . . .	200
runComBatSeq . . . . .	201
runCxls . . . . .	203
runCxlsBcbsHybrid . . . . .	204
runDEAnalysis . . . . .	205
runDecontX . . . . .	209
runDimReduce . . . . .	211
runDoubletFinder . . . . .	212
runDropletQC . . . . .	214
runEmptyDrops . . . . .	215
runEnrichR . . . . .	216
runFastMNN . . . . .	217
runFeatureSelection . . . . .	219
runFindMarker . . . . .	220
runGSVA . . . . .	222
runHarmony . . . . .	223
runKMeans . . . . .	224
runLimmaBC . . . . .	225
runMNNCorrect . . . . .	226
runModelGeneVar . . . . .	227
runNormalization . . . . .	228
runPerCellQC . . . . .	230
runSCANORAMA . . . . .	232
runScanpyFindClusters . . . . .	233
runScanpyFindHVG . . . . .	235
runScanpyFindMarkers . . . . .	236
runScanpyNormalizeData . . . . .	237
runScanpyPCA . . . . .	238
runScanpyScaleData . . . . .	239
runScanpyTSNE . . . . .	240
runScanpyUMAP . . . . .	241
runScDblFinder . . . . .	242
runSCMerge . . . . .	243
runScranSNN . . . . .	244
runScrublet . . . . .	246
runSeuratFindClusters . . . . .	249
runSeuratFindHVG . . . . .	250
runSeuratFindMarkers . . . . .	251
runSeuratHeatmap . . . . .	252
runSeuratICA . . . . .	253
runSeuratIntegration . . . . .	254
runSeuratJackStraw . . . . .	255
runSeuratNormalizeData . . . . .	256
runSeuratPCA . . . . .	257
runSeuratScaleData . . . . .	258
runSeuratSCTransform . . . . .	259
runSeuratTSNE . . . . .	260
runSeuratUMAP . . . . .	261
runSingleR . . . . .	262
runSoupX . . . . .	263
runTSCAN . . . . .	265
runTSCANClusterDEAnalysis . . . . .	266

runTSCANDEG . . . . .	267
runTSNE . . . . .	268
runUMAP . . . . .	270
runVAM . . . . .	273
runZINBWaVE . . . . .	274
sampleSummaryStats . . . . .	275
scaterCPM . . . . .	276
scaterlogNormCounts . . . . .	277
scaterPCA . . . . .	277
sce . . . . .	279
sceBatches . . . . .	279
sctkListGeneSetCollections . . . . .	280
sctkPythonInstallConda . . . . .	281
sctkPythonInstallVirtualEnv . . . . .	282
SEG . . . . .	283
selectSCTKConda . . . . .	284
selectSCTKVirtualEnvironment . . . . .	284
setRowNames . . . . .	285
setSCTKDisplayRow . . . . .	286
singleCellTK . . . . .	286
subDiffEx . . . . .	287
subsetSCECols . . . . .	288
subsetSCERows . . . . .	289
summarizeSCE . . . . .	291
trimCounts . . . . .	291

**Index** **293**

---

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>Computes heatmap for a set of features against dimensionality reduction components</i>
----------------	---

---

### Description

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	Specify the name of the assay that will be scaled by this function for the features that are used in the heatmap.
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 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 [data.table](#) object containing the count matrix.  
 samplename            The sample name of the data.

**Value**

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

---

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

---

## 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)
```

---

dedupRowNames	<i>Deduplicate the rownames of a matrix or SingleCellExperiment object</i>
---------------	--

---

### Description

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

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

### Value

By default, a matrix or [SingleCellExperiment](#) object with rownames deduplicated. When x is a [SingleCellExperiment](#) 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	<i>Detecting outliers within the SingleCellExperiment object.</i>
-------------------	---

---

### 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

*Calculate Differential Abundance with FET***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 <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.

**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`, `[randomcolorR](SCTK_PerformingQC_Ce` 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 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(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 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(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	<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**

```
## 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`

*expDataNames* 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	<i>Export data in SingleCellExperiment object</i>
-----------	---

---

### Description

Export data in SingleCellExperiment object

### Usage

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

**Arguments**

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

**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**

sce	<a href="#">SingleCellExperiment</a> R object to be exported.
useAssay	Character. The name of assay of interests that will be set as the primary matrix of the output AnnData. Default "counts".
outputDir	Path to the directory where .h5ad outputs will be written. Default is the current working directory.
prefix	Prefix to use for the name of the output file. Default "sample".
overwrite	Boolean. Default TRUE.
compression	If output file compression is required, this variable accepts 'gzip', 'lzf' or "None" as inputs. Default "gzip".
compressionOpts	Integer. Sets the compression level
forceDense	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_chc1, package = "scds")
## Not run:
exportSCEtoAnnData(sce=sce_chc1, 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 <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_chc1, package = "scds")
## Not run:
exportSCEToFlatFile(sce_chc1, "sce_chc1")

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

---

### 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")
```

---

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

---

**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	<i>Generates a single simulated dataset, bootstrapping from the input counts matrix.</i>
-----------------------	--

---

### 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	<i>Given a list of genes and a SingleCellExperiment object, return the binary or continuous expression of the genes.</i>
--------------	--

---

**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 = S4Vectors::metadata(inSCE)$featureDisplay,
  onlyPos = FALSE,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL
)
```

### Arguments

`inSCE` [SingleCellExperiment](#) 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. Leave `NULL` for `rownames`. Default `metadata(inSCE)$featureDisplay` (see [setSCTKDisplayRow](#)).

`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.

**Examples**

```
data("sceBatches")
sceBatches <- scaterlogNormCounts(sceBatches, "logcounts")
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type",
                  classGroup1 = "alpha", classGroup2 = "beta",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
getDEGTopTable(sce.w, "w.aVSb")
```

---

`getDiffAbundanceResults`

*Get/Set diffAbundanceFET result table*

---

**Description**

Get/Set diffAbundanceFET result table

**Usage**

```
getDiffAbundanceResults(x, analysisName)

## S4 method for signature 'SingleCellExperiment'
getDiffAbundanceResults(x, analysisName)

getDiffAbundanceResults(x, analysisName) <- value

## S4 replacement method for signature 'SingleCellExperiment'
getDiffAbundanceResults(x, analysisName) <- value
```

**Arguments**

x                    A [SingleCellExperiment](#) object.  
analysisName        A single character string specifying an analysis performed with [diffAbundanceFET](#)  
value                The output table of [diffAbundanceFET](#)

**Value**

The differential abundance table for getter method, or update the SCE object with new result for setter method.

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- diffAbundanceFET(inSCE = mouseBrainSubsetSCE,
                                         cluster = "tissue",
                                         variable = "level1class",
                                         case = "oligodendrocytes",
                                         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 [SingleCellExperiment](#) 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 = c("Vamp7", "Cntn2", "Olig1"),
                                   db = "GO_Cellular_Component_2025",
                                   analysisName = "analysis1")
  result <- getEnrichRResult(mouseBrainSubsetSCE, "analysis1")
}

```

---

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

---

**Description**

Fetch the table of top markers that pass the filtering

**Usage**

```

getFindMarkerTopTable(
  inSCE,
  log2fcThreshold = 0,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.5,
  maxCtrlExprPerc = 0.5,
  minMeanExpr = 0,
  topN = 1
)

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

```

**Arguments**

**inSCE** [SingleCellExperiment](#) 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 [runFindMarker](#) prior to using this function to extract a top marker table.

**Value**

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

**See Also**

[runFindMarker](#), [plotFindMarkerHeatmap](#)

**Examples**

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

---

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	<i>Shows MSigDB categories</i>
----------------	--------------------------------

---

**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	<i>List pathway analysis result names</i>
-----------------------	---

---

**Description**

List pathway analysis result names

**Usage**

```
getPathwayResultNames(inSCE, stopIfNone = FALSE, verbose = 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.
verbose	Show warning if no result found. Default FALSE

**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.

**Examples**

```
data(scExample)
getPathwayResultNames(sce)
```

---

```
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, ...)

setSampleSummaryStatsTable(inSCE, statsName, ...) <- value

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

## S4 replacement method for signature 'SingleCellExperiment'
setSampleSummaryStatsTable(inSCE, statsName, ...) <- value
```

**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 metadata of the SingleCellExperiment object. Required.
...	Other arguments passed to the function.
value	The summary table for QC statistics generated from SingleCellTK to be added to the SCE object.

**Value**

For `getSampleSummaryStatsTable`, A matrix/array object. Contains a summary table for QC statistics generated from SingleCellTK. For `setSampleSummaryStatsTable<-`, A SingleCellExperiment object where the summary table is updated in the metadata slot.

**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("runScrublet", "runDecontX", "runBarcodeRanksMetaOutput", "genesets",
    "runSoupX"),
  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 SCTK_runQC.R 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<-	<i>Get or Set SoupX Result</i>
------------	--------------------------------

---

**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**

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object. For getter method, <a href="#">runSoupX</a> must have been already applied.
<code>sampleID</code>	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.
<code>background</code>	Logical. Whether background was applied when running <a href="#">runSoupX</a> . Default FALSE.
<code>value</code>	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.

**See Also**

[runSoupX](#), [plotSoupXResults](#)

**Examples**

```
## Not run:
sce <- importExampleData("pbmc3k")
sce <- runSoupX(sce, sample = "sample")
soupXResults <- getSoupX(sce)

## End(Not run)
```

getTopHVG

*Get or set top HVG after calculation***Description**

Extracts or select 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. `getTopHVG` only returns a character vector of the HVG selection, while with `setTopHVG`, a logical vector of the selection will be saved in the `rowData`, and optionally, a subset object for the HVGs can be stored in the `altExps` slot at the same time.

**Usage**

```
getTopHVG(
  inSCE,
  method = c("vst", "dispersion", "mean.var.plot", "modelGeneVar", "seurat", "seurat_v3",
    "cell_ranger"),
  hvgNumber = 2000,
  useFeatureSubset = "hvf",
  featureDisplay = metadata(inSCE)$featureDisplay
)

setTopHVG(
  inSCE,
  method = c("vst", "dispersion", "mean.var.plot", "modelGeneVar", "seurat", "seurat_v3",
    "cell_ranger"),
  hvgNumber = 2000,
  featureSubsetName = "hvg2000",
  genes = NULL,
  genesBy = NULL,
  altExp = FALSE
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object
<code>method</code>	Specify which method to use for variable gene extraction from Seurat "vst", "mean.var.plot", "dispersion" or Scran "modelGeneVar" or Scanpy "seurat", "cell_ranger", "seurat_v3". Default "vst"
<code>hvgNumber</code>	Specify the number of top variable genes to extract.
<code>useFeatureSubset</code>	Get the feature names in the HVG list set by <code>setTopHVG</code> . <code>method</code> and <code>hvgNumber</code> will not be used if not this is not NULL. Default "hvf".

featureDisplay	A character string for the rowData variable name to indicate what type of feature ID should be displayed. If set by <code>setSCTKDisplayRow</code> , will by default use it. If NULL, will use <code>rownames(inSCE)</code> .
featureSubsetName	A character string for the rowData variable name to store a logical index of selected features. Default "hvg2000".
genes	A customized character vector of gene list to be set as a rowData variable. Will ignore method and hvgNumber if set. Default NULL.
genesBy	If setting customized genes, where should it be found in rowData? Leave NULL for matching rownames. Default NULL.
altExp	TRUE for also creating a subset inSCE object with the selected HVGs and store this subset in the altExps slot, named by hvgListName. Default FALSE.

**Value**

getTopHVG	A character vector of the top hvgNumber variable feature names
setTopHVG	The input inSCE object with the logical vector of HVG selection updated in rowData, and related parameter updated in metadata. If altExp is TRUE, an altExp is also added

**Author(s)**

Irzam Sarfraz, Yichen Wang

**See Also**

[runFeatureSelection](#), [runSeuratFindHVG](#), [runModelGeneVar](#), [plotTopHVG](#)

**Examples**

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

# Create a "highly variable feature" subset using Seurat's vst method:
sce <- runSeuratFindHVG(sce, method = "vst", hvgNumber = 2000,
  createFeatureSubset = "hvf")

# Get the list of genes for a feature subset:
hvgs <- getTopHVG(sce, useFeatureSubset = "hvf")

# Create a new feature subset on the fly without rerunning the algorithm:
sce <- setTopHVG(sce, method = "vst", hvgNumber = 100,
  featureSubsetName = "hvf100")
hvgs <- getTopHVG(sce, useFeatureSubset = "hvf100")

# Get a list of variable features without creating a new feature subset:
hvgs <- getTopHVG(sce, useFeatureSubset = NULL,
  method = "vst", hvgNumber = 10)
```

---

```
getTSCANResults      getTSCANResults accessor function
```

---

### Description

SCTK allows user to access all TSCAN related results with "getTSCANResults". See details.

### 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)

listTSCANTerminalNodes(x)

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

### Arguments

x	Input <a href="#">SingleCellExperiment</a> object.
analysisName	Algorithm name implemented, should be one of "Pseudotime", "DEG", or "ClusterDEAnalysis".
pathName	Sub folder name within the analysisName. See details.
value	Value to be stored within the pathName or analysisName

### Details

When analysisName = "Pseudotime", returns the list result from [runTSCAN](#), including the MST structure.

When analysisName = "DEG", returns the list result from [runTSCANDEG](#), including DataFrames containing genes that increase/decrease along each the pseudotime paths. pathName indicates the path index, the available options of which can be listed by [listTSCANTerminalNodes](#).

When analysisName = "ClusterDEAnalysis", returns the list result from [runTSCANClusterDEAnalysis](#). Here pathName needs to match with the useCluster argument when running the algorithm.

### Value

Get or set TSCAN results

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
results <- getTSCANResults(mouseBrainSubsetSCE, "Pseudotime")
```

---

importAlevin	<i>Construct SCE object from Salmon-Alevin output</i>
--------------	---

---

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

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 down-grade 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

*Construct SCE object from BUStools output*


---

## 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: `./genecount`. Must have the same length as `samples`.

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

matrixFileNames	Filenames for the Market Exchange Format (MEX) sparse matrix files (.mtx files). Must have length 1 or the same length as samples.
featuresFileNames	Filenames for the feature annotation files. 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 BUSTools output files (barcodes.txt, genes.txt, and genes.mtx) 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 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-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	<p>Default NULL. Can be one of</p> <ul style="list-style-type: none"> <li>• NULL. All samples within cellRangerDirs will be imported. The order of samples will be first determined by the order of cellRangerDirs and then by <code>list.dirs</code>. This is only for the case where cellRangerDirs is specified.</li> <li>• 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.</li> <li>• A vector of folder paths for the samples to import. This is only for the case where cellRangerDirs is NULL.</li> </ul> <p>The cells in the final SCE object will be ordered in the same order of sampleDirs.</p>
sampleNames	<p>A vector of user-defined sample names for the samples to be imported. Must have the same length as <code>length(unlist(sampleDirs))</code> if sampleDirs is not 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>Supersedes</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 cellRangerOuts specifies the paths. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if sampleDirs 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 sampleDirs 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 <code>features.tsv.gz</code> or <code>genes.tsv</code>. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if sampleDirs 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 <code>barcodes.tsv.gz</code> or <code>barcodes.tsv</code>. Must have length 1 or the same length as <code>length(unlist(sampleDirs))</code> if sampleDirs is not NULL. Otherwise, make sure the length and order match the output of <code>unlist(lapply(cellRangerDirs, list.dirs, recursive = FALSE))</code>.</p>

<code>gzipped</code>	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> .
<code>class</code>	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <code>readMM</code> function), or "matrix" (as returned by <code>matrix</code> function). 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.
<code>dataTypeV2</code>	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 <code>reference</code> will be ignored.
<code>reference</code>	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.
<code>cellRangerOutsV2</code>	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, <code>reference</code> 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**

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

**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". 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')
```

---

```
importExampleData      Retrieve example datasets
```

---

**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).

**"NestorowaHSCData"** Retrieved with `NestorowaHSCData`. Returns a dataset of 1920 mouse haematopoietic stem cells from Nestorowa et al. 2015

- "**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")
```

---

<code>importFromFiles</code>	<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 readMM function), or "matrix" (as returned by matrix function). Default "Matrix".
delayedArray	Boolean. Whether to read the expression matrix as DelayedArray 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",
  noMatchError = TRUE
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
geneSetCollection	A <a href="#">GeneSetCollection</a> object. See <a href="#">GeneSetCollection</a> for more details.
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, character vector, or NULL. Describes the location within inSCE where the gene identifiers in geneSetCollection 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. by can be a vector the same length as the number of gene sets in the GeneSetCollection and the elements of the vector can point to different locations within inSCE. Finally, by can be NULL. In this case, the location of the gene identifiers in inSCE should be saved in the description slot for each gene set in the GeneSetCollection. See <a href="#">featureIndex</a> for more information. Default "rownames".
noMatchError	Boolean. Show an error if a collection does not have any matching features. Default TRUE.

## 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)
gs1 <- GSEABase::GeneSet(setName = "geneset1",
                        geneIds = rownames(sce)[seq(10)])
gs2 <- GSEABase::GeneSet(setName = "geneset2",
                        geneIds = rownames(sce)[seq(11,20)])
gsc <- GSEABase::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",
  noMatchError = TRUE
)
```

**Arguments**

`inSCE` Input [SingleCellExperiment](#) object.

`file` Character. Path to GMT file. See [getGmt](#) for more information on reading GMT files.

<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 <code>GeneSetCollection</code> .
<code>by</code>	Character, character vector, or <code>NULL</code> . Describes the location within <code>inSCE</code> where the gene identifiers in <code>geneSetList</code> should be mapped. If set to <code>"rownames"</code> 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 GMT file and the elements of the vector can point to different locations within <code>inSCE</code> . Finally, <code>by</code> can be <code>NULL</code> . In this case, the location of the gene identifiers in <code>inSCE</code> should be saved in the description (2nd column) of the GMT file. See <a href="#">featureIndex</a> for more information. Default <code>"rownames"</code> .
<code>sep</code>	Character. Delimiter of the GMT file. Default <code>"\t"</code> .
<code>noMatchError</code>	Boolean. Show an error if a collection does not have any matching features. Default <code>TRUE</code> .

### 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",  
  noMatchError = TRUE  
)
```

## Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>geneSetList</code>	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.
<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 <code>GeneSetCollection</code> .
<code>by</code>	Character or character vector. Describes the location within <code>inSCE</code> where the gene identifiers in <code>geneSetList</code> should be mapped. If set to <code>"rownames"</code> 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> . Finally, <code>by</code> can be a vector the same length as the number of gene sets in <code>geneSetList</code> and the elements of the vector can point to different locations within <code>inSCE</code> . See <a href="#">featureIndex</a> for more information. Default <code>"rownames"</code> .
<code>noMatchError</code>	Boolean. Show an error if a collection does not have any matching features. Default <code>TRUE</code> .

## 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 = "H",
  species = "Homo sapiens",
  mapping = c("gene_symbol", "human_gene_symbol", "entrez_gene"),
  by = "rownames",
  verbose = TRUE,
  noMatchError = 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. Default is "H".
species	Character. Species available can be found using the function <code>msigdbr_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 by parameter must be either in gene symbol or Entrez gene id format to match IDs from MSigDB.
by	Character. Describes the location within inSCE 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 identifies will be mapped to that column in the <code>rowData</code> of inSCE. See <a href="#">featureIndex</a> for more information. Default "rownames".
verbose	Boolean. Whether to display progress. Default TRUE.
noMatchError	Boolean. Show an error if a collection does not have any matching features. 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 = "mito",
  noMatchError = TRUE
)
```

### 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. Default "mito".
noMatchError	Boolean. Show an error if a collection does not have any matching features. Default TRUE.

### Details

The gene identifiers of mitochondrial genes will be loaded with "data(AllMito)". Currently, it supports human and mouse references. 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

*Construct SCE object from Optimus output***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\_

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

**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.g. 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 ( <code>empty_drops_result.csv</code> ). Default <code>call-RunEmptyDrops/empty_drops_result.csv</code> which works for <code>optimus_v1.4.0</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</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 gzip compressed. FALSE otherwise. Default seqc outputs are not gzipped. Default FALSE.
class	Character. The class of the expression matrix stored in the SCE object. Can be one of "Matrix" (as returned by <code>readMM</code> function), or "matrix" (as returned by <code>matrix</code> function). Default "Matrix".
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	<i>Construct SCE object from STARsolo outputs</i>
----------------	---

---

## Description

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

## Usage

```

importSTARsolo(
  STARsoloDirs,
  samples,
  STARsoloOuts = c("Gene", "GeneFull"),
  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: <i>/PATH/TO/prefixSolo.out</i> . For example: <i>./Solo.out</i> . Each sample should have its own path. Must have the same length as <code>samples</code> .
samples	A vector of user-defined sample names for the sample to be imported. Must have the same length as <code>STARsoloDirs</code> .
STARsoloOuts	Character. The intermediate folder to filtered or raw cell barcode, feature, and matrix files for each of samples. Default "Gene". It can be either Gene or GeneFull as the main folder from which data needs to be imported.
matrixFileNames	Filenames for the Market Exchange Format (MEX) sparse matrix file (.mtx file). Must have length 1 or the same length as <code>samples</code> .
featuresFileNames	Filenames for the feature annotation file. 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 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 <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</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 `SingleCellExperiment` object with saved table within the `metadata` 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)
```

---

<code>mergeSCEColData</code>	<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

*List of mitochondrial genes of multiple reference***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

**Value**

List of mitochondrial genes of multiple reference

**Examples**

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

mouseBrainSubsetSCE

*Example Single Cell RNA-Seq data in SingleCellExperiment Object, GSE60361 subset***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

**Value**

A subset of 30 cells from a single cell RNA-Seq experiment

**Source**

DOI: 10.1126/science.aaa1934

**Examples**

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

---

msigdb\_table

*MSigDB gene set Category table*

---

**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.

**Value**

A table of gene set categories

**Examples**

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

---

`plotBarcodeRankDropsResults`*Plots for runBarcodeRankDrops outputs.*

---

### Description

A wrapper function which visualizes outputs from the `runBarcodeRankDrops` function stored in the metadata slot of the [SingleCellExperiment](#) object.

### Usage

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

### Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results from <code>runBarcodeRankDrops</code> . Required.
<code>sample</code>	Character vector or <code>colData</code> variable name. Indicates which sample each cell belongs to. 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>dotSize</code>	Size of dots. Default 0.5.
<code>titleSize</code>	Size of title of plot. Default 18.
<code>axisSize</code>	Size of x/y-axis ticks. Default 15.
<code>axisLabelSize</code>	Size of x/y-axis labels. Default 18.
<code>legendSize</code>	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 = 0.1,
  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 or colData variable name. 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 0.1.
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	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".

sampleRelHeights

If there are multiple samples and combining by "all", the relative heights for each plot. Default 1.

sampleRelWidths

If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

### Value

a ggplot object of the scatter plot.

### See Also

[plotBarcodeRankDropsResults](#), [runBarcodeRankDrops](#)

### 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")
logcounts(sceBatches) <- log1p(counts(sceBatches))
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 colData(inSCE). 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="#">runBcde</a> . Required.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value. Default NULL.
groupBy	Groupings for each numeric value. 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.
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 inSCE. Default "UMAP".
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. Similar to dim1. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into bin groups. If more than one value, will bin numeric values using values as a cut point. Default NULL.
binLabel	Character vector. Labels for the bins created by bin. 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. Default 1.
relWidths	Relative widths of plots when combine is set. Default c(1, 1, 1).
plotNCols	Number of columns when plots are combined in a grid. Default NULL.
plotNRows	Number of rows when plots are combined in a grid. Default NULL.
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. Default 1.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

**Value**

list of .ggplot objects

**See Also**

[runBcDs](#)

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runQuickUMAP(sce)
sce <- runBcdfs(sce)
plotBcdfsResults(inSCE=sce, reducedDimName="UMAP")
```

---

plotBubble

*Plot Bubble plot*


---

**Description**

Plot a bubble plot with the color of the plot being the mean expression and the size of the dot being the percent of cells in the cluster expressing the gene.

**Usage**

```
plotBubble(
  inSCE,
  useAssay = "logcounts",
  featureNames,
  displayName = NULL,
  groupNames = "cluster",
  title = "",
  xlab = NULL,
  ylab = NULL,
  colorLow = "white",
  colorHigh = "blue",
  scale = FALSE
)
```

**Arguments**

inSCE	The single cell experiment to use.
useAssay	The assay to use.
featureNames	A string or vector of strings with each gene to aggregate.
displayName	A string that is the name of the column used for genes.
groupNames	The name of a colData entry that can be used as groupNames.
title	The title of the bubble plot
xlab	The x-axis label
ylab	The y-axis label
colorLow	The color to be used for lowest value of mean expression
colorHigh	The color to be used for highest value of mean expression
scale	Option to scale the data. Default: FALSE. Selected assay will not be scaled.

**Value**

A ggplot of the bubble plot.

## Examples

```
data("scExample")
plotBubble(inSCE=sce, useAssay="counts", featureNames=c("B2M", "MALAT1"),
displayName="feature_name", groupNames="type", title="cell type test",
xlab="gene", ylab="cluster", colorLow="white", colorHigh="blue")
```

---

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")
```

---

plotCxlsResults	<i>Plots for runCxls outputs.</i>
-----------------	-----------------------------------

---

### 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

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object with saved dimension reduction components or a variable with saved results from <code>runCxls</code> . Required.
--------------------	---

sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value. Default NULL.
groupBy	Groupings for each numeric value. 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.
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 inSCE. Default "UMAP".
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. Similar to dim1. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into bin groups. If more than one value, will bin numeric values using values as a cut point. Default NULL.
binLabel	Character vector. Labels for the bins created by bin. 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. Default 1.
relWidths	Relative widths of plots when combine is set. Default c(1, 1, 1).
plotNcols	Number of columns when plots are combined in a grid. Default NULL.
plotNrows	Number of rows when plots are combined in a grid. Default NULL.
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. Default 1.

sampleRelWidths

If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

### Value

list of .ggplot objects

### See Also

[runCxds](#)

### Examples

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runQuickUMAP(sce)
sce <- runCxds(sce)
plotCxdsResults(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 .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. Default = "UMAP"
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.
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.
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,
  onlyPos = FALSE,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL,
  useAssay = NULL,
  doLog = FALSE,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
  rowDataName = NULL,
  colDataName = NULL,
  colSplitBy = "condition",
  rowSplitBy = "regulation",
  rowLabel = S4Vectors::metadata(inSCE)$featureDisplay,
  title = paste0("DE Analysis: ", useResult),
  ...
)
```

**Arguments**

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
onlyPos	logical. Whether to only plot DEG with positive log <sub>2</sub> FC value. Default FALSE.
log2fcThreshold	numeric. Only plot DEGs with the absolute values of log <sub>2</sub> FC 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 then this value. Default NULL.
maxGroup2MeanExp	numeric. Only plot DEGs with mean expression in group2 less then this value. Default NULL.
minGroup1ExprPerc	numeric. Only plot DEGs expressed in greater then this fraction of cells in group1. Default NULL.
maxGroup2ExprPerc	numeric. Only plot DEGs expressed in less then 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.
doLog	Logical scalar. Whether to do $\log(\text{assay} + 1)$ transformation on the assay used for the analysis. Default FALSE.
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".
rowLabel	FALSE for not displaying; a variable in rowData to display feature identifiers stored there; if have run <code>setSCTKDisplayRow</code> , display the specified feature name; TRUE for the rownames of inSCE; NULL for auto-display rownames when the number of filtered feature is less than 60. Default looks for <code>setSCTKDisplayRow</code> information.
title	character. Main title of the heatmap. Default "DE Analysis: <useResult>".
...	Other arguments passed to <code>plotSCEHeatmap</code>

## 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) <- log1p(counts(sceBatches))
sce.w <- subsetSCEcols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type",
                  classGroup1 = "alpha", classGroup2 = "beta",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
plotDEGHeatmap(sce.w, "w.aVSb")
```

---

plotDEGRegression	<i>Create linear regression plot to show the expression the of top DEGs</i>
-------------------	---

---

## 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 $\log(\text{assay} + 1)$ transformation. Default TRUE.
check_sanity	Logical scalar. Whether to perform MAST's sanity check to see if the counts are logged. Default TRUE

**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) <- log1p(counts(sceBatches))
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type",
                  classGroup1 = "alpha", classGroup2 = "beta",
                  groupName1 = "w.alpha", groupName2 = "w.beta",
                  analysisName = "w.aVSb")
plotDEGRegression(sce.w, "w.aVSb")
```

---

plotDEGViolin

*Generate violin plot to show the expression of top DEGs*


---

**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) <- log1p(counts(sceBatches))
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type",
  classGroup1 = "alpha", classGroup2 = "beta",
  groupName1 = "w.alpha", groupName2 = "w.beta",
  analysisName = "w.aVSb")
plotDEGViolin(sce.w, "w.aVSb")
```

---

plotDEGVolcano      *Generate volcano plot for DEGs*

---

### Description

Generate volcano plot for DEGs

### Usage

```
plotDEGVolcano(
  inSCE,
  useResult,
  labelTopN = 10,
  log2fcThreshold = 0.25,
  fdrThreshold = 0.05,
  featureDisplay = S4Vectors::metadata(inSCE)$featureDisplay
)
```

### Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
useResult	character. A string specifying the analysisName used when running a differential expression analysis function.
labelTopN	Integer, label this number of top DEGs that pass the filters. FALSE for not labeling. Default 10.
log2fcThreshold	numeric. Label genes with the absolute values of log2FC greater than this value as regulated. Default 0.25.
fdrThreshold	numeric. Label genes with FDR value less than this value as regulated. Default 0.05.
featureDisplay	A character string to indicate a variable in rowData(inSCE) for feature labeling. NULL for using rownames. Default metadata(inSCE)\$featureDisplay (see <a href="#">setSCTKDisplayRow</a> )

### 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

### See Also

[runDEAnalysis](#), [plotDEGHeatmap](#)

**Examples**

```

data("sceBatches")
sceBatches <- scaterlogNormCounts(sceBatches, "logcounts")
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runWilcox(sce.w, class = "cell_type",
                  classGroup1 = "alpha", classGroup2 = "beta",
                  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 = "PCA",
  showLegend = FALSE,
  xDim = 1,
  yDim = 2,
  xAxisLabel = NULL,
  yAxisLabel = NULL
)

```

**Arguments**

inSCE	Input SCE object
useReduction	Reduction to plot. Default is "PCA".
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 or colData variable name. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value. Default NULL.
groupBy	Groupings for each numeric value. 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.
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 inSCE. Default "UMAP".
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. Similar to dim1. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into bin groups. If more than one value, will bin numeric values using values as a cut point. Default NULL.
binLabel	Character vector. Labels for the bins created by bin. 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. Default 1.
relWidths	Relative widths of plots when combine is set. Default c(1, 1, 1).
plotNcols	Number of columns when plots are combined in a grid. Default NULL.

plotNRows	Number of rows when plots are combined in a grid. Default NULL.
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. Default 1.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

**Value**

list of .ggplot objects

**See Also**

[runDoubletFinder](#)

**Examples**

```
data(scExample, package="singleCellTK")
options(future.globals.maxSize = 786432000)
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runQuickUMAP(sce)
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.

**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

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 or colData variable name. Indicates which sample each cell belongs to. Default NULL.
combinePlot	Must be either "all", "sample", or object, "none". "all" will combine all plots into a single .ggplot while "sample" will output a list of plots separated by sample. Default "all".
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.
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.
legendTitleSize	size of legend title. Default 16.
relHeights	Relative heights of plots when combine is set. Default 1.
relWidths	Relative widths of plots when combine is set. Default 1.
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. Default 1.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

### Value

list of .ggplot objects

### See Also

[runEmptyDrops](#), [plotEmptyDropsScatter](#)

### 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 col-Data slot of the [SingleCellExperiment](#) object via scatter plots.

### Usage

```
plotEmptyDropsScatter(
  inSCE,
  sample = NULL,
  fdrCutoff = 0.01,
  defaultTheme = TRUE,
  dotSize = 0.1,
  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 or colData variable name. 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 0.1.
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	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".
relHeights	Relative heights of plots when combine is set. Default 1.
relWidths	Relative widths of plots when combine is set. Default 1.
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. Default 1.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

**Value**

a ggplot object of the scatter plot.

**See Also**

[runEmptyDrops](#), [plotEmptyDropsResults](#)

**Examples**

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

---

plotEnrichR

*Plot EnrichR results*

---

**Description**

Plot results of EnrichR analysis as a barplot.

**Usage**

```
plotEnrichR(
  inSCE,
  analysisName,
  showTerms = 20,
  numChar = 40,
  y = "Count",
  orderBy = "Adjusted.P.value",
```

```

    xlab = NULL,
    ylab = NULL,
    title = NULL
  )

```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved EnrichR results. Required.
analysisName	A string that identifies the specific analysis to plot. Required.
showTerms	Number of enrichment terms to show. Default is 20.
numChar	Integer. Indicates the maximum number characters to be displayed in the term names. Default is 40.
y	Character string. Indicates the variable to be shown on the y-axis. Can be one of "Count" or "Ratio". Results that include background genes can only show "Count". Default is "Count".
orderBy	Character string. Indicates how to order the results prior to subsetting. Can be one of "P.value", "Adjusted.P.Value", or "Combined.Score". Default is "Adjusted.P.value".
xlab	Character vector. Label for x-axis. Default NULL.
ylab	Character vector. Label for y-axis. Default NULL.
title	Character string. Title of the plot. Default NULL.

### Value

A ggplot object of EnrichR results.

---

plotFindMarkerHeatmap *Plot a heatmap to visualize the result of [runFindMarker](#)*

---

### Description

This function will first reads the result saved in metadata slot, named by "findMarker" and generated by [runFindMarker](#). 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

```

plotFindMarkerHeatmap(
  inSCE,
  orderBy = "size",
  log2fcThreshold = 1,
  fdrThreshold = 0.05,
  minClustExprPerc = 0.7,
  maxCtrlExprPerc = 0.4,

```

```

    minMeanExpr = 1,
    topN = 10,
    decreasing = TRUE,
    rowLabel = TRUE,
    rowDataName = NULL,
    colDataName = NULL,
    featureAnnotations = NULL,
    cellAnnotations = NULL,
    featureAnnotationColor = NULL,
    cellAnnotationColor = NULL,
    colSplitBy = NULL,
    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 = NULL,
  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 unsplit 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.
rowLabel	TRUE for displaying rownames of inSCE, a rowData variable to use other feature identifiers, or a vector for customized row labels. Use FALSE for not displaying. 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 runFindMarker 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 plotSCEHeatmap.

**Value**A [Heatmap](#) object

**Author(s)**

Yichen Wang

**See Also**[runFindMarker](#), [getFindMarkerTopTable](#)**Examples**

```
data("sceBatches")
logcounts(sceBatches) <- log1p(counts(sceBatches))
sce.w <- subsetSCECols(sceBatches, colData = "batch == 'w'")
sce.w <- runFindMarker(sce.w, method = "wilcox", cluster = "cell_type")
plotFindMarkerHeatmap(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**

<code>inSCE</code>	SingleCellExperiment object
<code>useAssay</code>	character, default "logcounts"
<code>doPlot</code>	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.
<code>isLogged</code>	Logical scalar. Whether the assay used for the analysis is logged. If not, will do a $\log(\text{assay} + 1)$ transformation. Default TRUE.
<code>check_sanity</code>	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 <- scatterlogNormCounts(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 = NULL,
  shape = NULL,
  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 SingleCellExperiment 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 <a href="#">runPerCellQC</a> . Required.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
groupBy	Groupings for each numeric value. Users may input a vector equal length to the number of the samples in inSCE, 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. Default 1.
relWidths	Relative widths of plots when combine is set. Default 1.
labelSamples	Will label sample name in title of plot if TRUE. Default TRUE.
plotNcols	Number of columns when plots are combined in a grid. Default NULL.
plotNrows	Number of rows when plots are combined in a grid. Default NULL.
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. Default 1.

sampleRelWidths

If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

### Value

list of .ggplot objects

### See Also

[runPerCellQC](#)

### Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runPerCellQC(sce)
plotRunPerCellQCResults(inSCE = sce)
```

---

plotScanpyDotPlot

*plotScanpyDotPlot*

---

### Description

plotScanpyDotPlot

### Usage

```
plotScanpyDotPlot(
  inSCE,
  useAssay = NULL,
  features,
  groupBy,
  standardScale = NULL,
  title = "",
  vmin = NULL,
  vmax = NULL,
  colorBarTitle = "Mean expression in group"
)
```

### Arguments

inSCE	Input SingleCellExperiment object.
useAssay	Assay to use for plotting. By default it will use counts assay.
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes). The var_names could be a dictionary or a list.
groupBy	The key of the observation grouping to consider.

standardScale	Whether or not to standardize the given dimension between 0 and 1, meaning for each variable or group, subtract the minimum and divide each by its maximum. Default NULL means that it doesn't perform any scaling.
title	Provide title for the figure.
vmin	The value representing the lower limit of the color scale. Values smaller than vmin are plotted with the same color as vmin. Default NULL
vmax	The value representing the upper limit of the color scale. Values larger than vmax are plotted with the same color as vmax. Default NULL
colorBarTitle	Title for the color bar.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")
markers <- c("MALAT1" ,"RPS27" ,"CST3")
plotScanpyDotPlot(sce, features = markers, groupBy = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyEmbedding    *plotScanpyEmbedding*

---

**Description**

plotScanpyEmbedding

**Usage**

```
plotScanpyEmbedding(
  inSCE,
  reducedDimName,
  useAssay = NULL,
  color = NULL,
  legend = "right margin",
  title = ""
)
```

**Arguments**

<code>inSCE</code>	Input SingleCellExperiment object.
<code>reducedDimName</code>	Name of reducedDims object containing embeddings. Eg. scanpyUMAP.
<code>useAssay</code>	Specify name of assay to use. Default is NULL, which will use scaled assay by default.
<code>color</code>	Keys for annotations of observations/cells or variables/genes.
<code>legend</code>	Location of legend, either 'on data', 'right margin' or a valid keyword for the loc parameter of Legend.
<code>title</code>	Provide title for panels either as string or list of strings

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")
plotScanpyEmbedding(sce, reducedDimName = "scanpyUMAP", color = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyHeatmap      *plotScanpyHeatmap*

---

**Description**

plotScanpyHeatmap

**Usage**

```
plotScanpyHeatmap(
  inSCE,
  useAssay = NULL,
  features,
  groupBy,
  standardScale = "var",
  vmin = NULL,
  vmax = NULL
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	Assay to use for plotting. By default it will use counts assay.
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes). The var_names could be a dictionary or a list.
groupBy	The key of the observation grouping to consider.
standardScale	Whether or not to standardize the given dimension between 0 and 1, meaning for each variable or group, subtract the minimum and divide each by its maximum. Default NULL means that it doesn't perform any scaling.
vmin	The value representing the lower limit of the color scale. Values smaller than vmin are plotted with the same color as vmin. Default NULL
vmax	The value representing the upper limit of the color scale. Values larger than vmax are plotted with the same color as vmax. Default NULL

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")
markers <- c("MALAT1" , "RPS27" , "CST3")
plotScanpyHeatmap(sce, features = markers, groupBy = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyHVG

*plotScanpyHVG*

---

**Description**

plotScanpyHVG

**Usage**

```
plotScanpyHVG(inSCE, log = FALSE)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
log	Plot on logarithmic axes. Default FALSE.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
plotScanpyHVG(sce)

## End(Not run)
```

---

plotScanpyMarkerGenes *plotScanpyMarkerGenes*

---

**Description**

plotScanpyMarkerGenes

**Usage**

```
plotScanpyMarkerGenes(  
  inSCE,  
  groups = NULL,  
  nGenes = 10,  
  nCols = 4,  
  sharey = FALSE  
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
groups	The groups for which to show the gene ranking. Default NULL means that all groups will be considered.
nGenes	Number of genes to show. Default 10
nCols	Number of panels shown per row. Default 4
sharey	Controls if the y-axis of each panels should be shared. Default FALSE allows each panel to have its own y-axis range.

**Value**

plot object

**Examples**

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )
plotScanpyMarkerGenes(sce, groups = '0')

## End(Not run)

```

---

plotScanpyMarkerGenesDotPlot

*plotScanpyMarkerGenesDotPlot*


---

**Description**

plotScanpyMarkerGenesDotPlot

**Usage**

```

plotScanpyMarkerGenesDotPlot(
  inSCE,
  groups = NULL,
  nGenes = 10,
  groupBy,
  log2fcThreshold = NULL,
  parameters = "logfoldchanges",
  standardScale = NULL,
  features = NULL,
  title = "",
  vmin = NULL,
  vmax = NULL,
  colorBarTitle = "log fold change"
)

```

**Arguments**

inSCE	Input SingleCellExperiment object.
groups	The groups for which to show the gene ranking. Default NULL means that all groups will be considered.
nGenes	Number of genes to show. Default 10
groupBy	The key of the observation grouping to consider. By default, the groupby is chosen from the rank genes groups parameter.
log2fcThreshold	Only output DEGs with the absolute values of log2FC larger than this value. Default NULL.

parameters	The options for marker genes results to plot are: 'scores', 'logfoldchanges', 'pvals', 'pvals_adj', 'log10_pvals', 'log10_pvals_adj'. If NULL provided then it uses mean gene value to plot.
standardScale	Whether or not to standardize the given dimension between 0 and 1, meaning for each variable or group, subtract the minimum and divide each by its maximum. Default NULL means that it doesn't perform any scaling.
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes) to check their fold changes or p-values, instead of the top/bottom genes. The gene names could be a dictionary or a list. Default NULL
title	Provide title for the figure.
vmin	The value representing the lower limit of the color scale. Values smaller than vmin are plotted with the same color as vmin. Default NULL
vmax	The value representing the upper limit of the color scale. Values larger than vmax are plotted with the same color as vmax. Default NULL
colorBarTitle	Title for the color bar.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )
plotScanpyMarkerGenesDotPlot(sce, groupBy = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyMarkerGenesHeatmap

*plotScanpyMarkerGenesHeatmap*

---

**Description**

plotScanpyMarkerGenesHeatmap

**Usage**

```
plotScanpyMarkerGenesHeatmap(
  inSCE,
  groups = NULL,
  groupBy,
  nGenes = 10,
  features = NULL,
  log2fcThreshold = NULL
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
groups	The groups for which to show the gene ranking. Default NULL means that all groups will be considered.
groupBy	The key of the observation grouping to consider. By default, the groupby is chosen from the rank genes groups parameter.
nGenes	Number of genes to show. Default 10
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes). The var_names could be a dictionary or a list.
log2fcThreshold	Only output DEGs with the absolute values of log2FC larger than this value. Default NULL.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizedData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )
plotScanpyMarkerGenesHeatmap(sce, groupBy = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyMarkerGenesMatrixPlot

*plotScanpyMarkerGenesMatrixPlot*

---

**Description**

plotScanpyMarkerGenesMatrixPlot

**Usage**

```
plotScanpyMarkerGenesMatrixPlot(
  inSCE,
  groups = NULL,
  nGenes = 10,
  groupBy,
  log2fcThreshold = NULL,
  parameters = "logfoldchanges",
  standardScale = "var",
  features = NULL,
```

```

    title = "",
    vmin = NULL,
    vmax = NULL,
    colorBarTitle = "log fold change"
  )

```

### Arguments

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object.
<code>groups</code>	The groups for which to show the gene ranking. Default <code>NULL</code> means that all groups will be considered.
<code>nGenes</code>	Number of genes to show. Default <code>10</code>
<code>groupBy</code>	The key of the observation grouping to consider. By default, the <code>groupBy</code> is chosen from the <code>rank genes groups</code> parameter.
<code>log2fcThreshold</code>	Only output DEGs with the absolute values of <code>log2FC</code> larger than this value. Default <code>NULL</code> .
<code>parameters</code>	The options for marker genes results to plot are: <code>'scores'</code> , <code>'logfoldchanges'</code> , <code>'pvals'</code> , <code>'pvals_adj'</code> , <code>'log10_pvals'</code> , <code>'log10_pvals_adj'</code> . If <code>NULL</code> provided then it uses mean gene value to plot.
<code>standardScale</code>	Whether or not to standardize the given dimension between 0 and 1, meaning for each variable or group, subtract the minimum and divide each by its maximum. Default <code>NULL</code> means that it doesn't perform any scaling.
<code>features</code>	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes) to check their fold changes or p-values, instead of the top/bottom genes. The <code>var_names</code> could be a dictionary or a list. Default <code>NULL</code>
<code>title</code>	Provide title for the figure.
<code>vmin</code>	The value representing the lower limit of the color scale. Values smaller than <code>vmin</code> are plotted with the same color as <code>vmin</code> . Default <code>NULL</code>
<code>vmax</code>	The value representing the upper limit of the color scale. Values larger than <code>vmax</code> are plotted with the same color as <code>vmax</code> . Default <code>NULL</code>
<code>colorBarTitle</code>	Title for the color bar.

### Value

plot object

### Examples

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )
plotScanpyMarkerGenesMatrixPlot(sce, groupBy = 'Scanpy_louvain_1')

## End(Not run)

```

---

plotScanpyMarkerGenesViolin  
*plotScanpyMarkerGenesViolin*

---

### Description

plotScanpyMarkerGenesViolin

### Usage

```
plotScanpyMarkerGenesViolin(inSCE, groups = NULL, features = NULL, nGenes = 10)
```

### Arguments

inSCE	Input SingleCellExperiment object.
groups	The groups for which to show the gene ranking. Default NULL means that all groups will be considered.
features	List of genes to plot. Is only useful if interested in a custom gene list
nGenes	Number of genes to show. Default 10

### Value

plot object

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizedData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )
plotScanpyMarkerGenesViolin(sce, groups = '0')

## End(Not run)
```

---

plotScanpyMatrixPlot *plotScanpyMatrixPlot*

---

### Description

plotScanpyMatrixPlot

**Usage**

```
plotScanpyMatrixPlot(
  inSCE,
  useAssay = NULL,
  features,
  groupBy,
  standardScale = NULL,
  title = "",
  vmin = NULL,
  vmax = NULL,
  colorBarTitle = "Mean expression in group"
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	Assay to use for plotting. By default it will use counts assay.
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes). The var_names could be a dictionary or a list.
groupBy	The key of the observation grouping to consider.
standardScale	Whether or not to standardize the given dimension between 0 and 1, meaning for each variable or group, subtract the minimum and divide each by its maximum. Default NULL means that it doesn't perform any scaling.
title	Provide title for the figure.
vmin	The value representing the lower limit of the color scale. Values smaller than vmin are plotted with the same color as vmin. Default NULL
vmax	The value representing the upper limit of the color scale. Values larger than vmax are plotted with the same color as vmax. Default NULL
colorBarTitle	Title for the color bar.

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaledData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")
markers <- c("MALAT1" ,"RPS27" ,"CST3")
plotScanpyMatrixPlot(sce, features = markers, groupBy = 'Scanpy_louvain_1')

## End(Not run)
```

---

plotScanpyPCA	<i>plotScanpyPCA</i>
---------------	----------------------

---

## Description

plotScanpyPCA

## Usage

```
plotScanpyPCA(  
  inSCE,  
  reducedDimName = "scanpyPCA",  
  color = NULL,  
  title = "",  
  legend = "right margin"  
)
```

## Arguments

inSCE	Input SingleCellExperiment object.
reducedDimName	Name of new reducedDims object containing Scanpy PCA.
color	Keys for annotations of observations/cells or variables/genes.
title	Provide title for panels either as string or list of strings
legend	Location of legend, either 'on data', 'right margin' or a valid keyword for the loc parameter of Legend.

## Value

plot object

## Examples

```
data(scExample, package = "singleCellTK")  
## Not run:  
sce <- runScanpyNormalizeData(sce, useAssay = "counts")  
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")  
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")  
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")  
plotScanpyPCA(sce)  
  
## End(Not run)
```

---

plotScanpyPCAGeneRanking  
*plotScanpyPCAGeneRanking*

---

**Description**

plotScanpyPCAGeneRanking

**Usage**

```
plotScanpyPCAGeneRanking(inSCE, PC_comp = "1,2,3", includeLowest = TRUE)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
PC_comp	For example, '1,2,3' means [1, 2, 3], first, second, third principal component.
includeLowest	Whether to show the variables with both highest and lowest loadings. Default TRUE

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizedData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
plotScanpyPCAGeneRanking(sce)

## End(Not run)
```

---

plotScanpyPCAVariance *plotScanpyPCAVariance*

---

**Description**

plotScanpyPCAVariance

**Usage**

```
plotScanpyPCAVariance(inSCE, nPCs = 50, log = FALSE)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
nPCs	Number of PCs to show. Default 50.
log	Plot on logarithmic scale. Default FALSE

**Value**

plot object

**Examples**

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
plotScanpyPCAVariance(sce)

## End(Not run)
```

---

plotScanpyViolin

*plotScanpyViolin*

---

**Description**

plotScanpyViolin

**Usage**

```
plotScanpyViolin(
  inSCE,
  useAssay = NULL,
  features,
  groupBy,
  xlabel = "",
  ylabel = NULL
)
```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	Assay to use for plotting. By default it will use counts assay.
features	Genes to plot. Sometimes is useful to pass a specific list of var names (e.g. genes). The var_names could be a dictionary or a list.
groupBy	The key of the observation grouping to consider.
xlabel	Label of the x axis. Defaults to groupBy.
ylabel	Label of the y axis. If NULL and groupBy is NULL, defaults to 'value'. If NULL and groupBy is not NULL, defaults to features.

**Value**

plot object

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")
markers <- c("MALAT1" ,"RPS27" ,"CST3")
plotScanpyViolin(sce, features = markers, groupBy = "Scanpy_louvain_1")

## End(Not run)
```

---

plotScDblFinderResults

*Plots for runScDblFinder outputs.*

---

## Description

A wrapper function which visualizes outputs from the [runScDblFinder](#) function stored in the col-Data slot of the [SingleCellExperiment](#) object via various plots.

## Usage

```
plotScDblFinderResults(
  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="#">runScDblFinder</a> . Required.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value. Default NULL.
groupBy	Groupings for each numeric value. 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.
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 inSCE. Default "UMAP".
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. Similar to dim1. Default is NULL.
bin	Numeric vector. If single value, will divide the numeric values into bin groups. If more than one value, will bin numeric values using values as a cut point. Default NULL.
binLabel	Character vector. Labels for the bins created by bin. 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. Default 1.
relWidths	Relative widths of plots when combine is set. Default c(1, 1, 1).
plotNCols	Number of columns when plots are combined in a grid. Default NULL.
plotNRows	Number of rows when plots are combined in a grid. Default NULL.
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. Default 1.
sampleRelWidths	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

**Value**

list of .ggplot objects

**See Also**

[runScDbfFinder](#)

**Examples**

```
data(scExample, package="singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runQuickUMAP(sce)
sce <- runScDbfFinder(sce)
plotScDbfFinderResults(inSCE = sce, reducedDimName = "UMAP")
```

---

plotScdsHybridResults *Plots for runCxdsBcdsHybrid outputs.*

---

**Description**

A wrapper function which visualizes outputs from the runCxdsBcdsHybrid 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="#">runCxdsBcdsHybrid</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 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 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 <- runQuickUMAP(sce)
sce <- runCxdsBcndsHybrid(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 = 0.1,
  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 0.1.
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 = 0.1,
  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 SingleCellExperiment 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 0.1.
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 .ggViolin.

**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" slot-Name 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**

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 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, legendSize, legendTitleSize.
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.
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 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 = 0.1,
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

inSCE	Input <a href="#">SingleCellExperiment</a> object with saved dimension reduction components or a variable with saved results. Required.
colorBy	Color by a condition(any column of the annotation data). Required.
reducedDimName	Saved dimension reduction matrix name in the <a href="#">SingleCellExperiment</a> object. Required.
sample	Character vector. Indicates which sample each cell belongs to.
groupBy	Group by a condition(any column of the annotation data). Default NULL.
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.
shape	Add shapes to each condition.
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 0.1.
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'.
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.
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")
plotSCEDimReduceColData(
  inSCE = mouseBrainSubsetSCE, colorBy = "tissue",
  shape = NULL, conditionClass = "factor",
  reducedDimName = "TSNE_counts",
  xlab = "tsNE1", ylab = "tsNE2", labelClusters = TRUE
)
```

```
plotSCEDimReduceColData(
  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,  
  features,  
  feature = deprecated(),  
  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 = 0.1,  
  transparency = 1,  
  colorLow = "white",  
  colorMid = "gray",  
  colorHigh = "blue",  
  defaultTheme = TRUE,  
  title = NULL,  
  titleSize = 15,  
  legendTitle = NULL,  
  legendSize = 10,  
  legendTitleSize = 12,  
  ncols = NULL,  
  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.
features	Name of feature stored in assay of SingleCellExperiment object.
feature	Deprecated, use 'features' instead.
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 0.1.
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.

ncols	number of columns for multiple feature plotting. Default NULL.
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, features = "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",
  useReducedDim = NULL,
  doLog = FALSE,
  featureIndex = NULL,
  cellIndex = NULL,
  scale = TRUE,
  trim = c(-2, 2),
  featureIndexBy = "rownames",
  cellIndexBy = "rownames",
  cluster_columns = FALSE,
  cluster_rows = FALSE,
  rowDataName = NULL,
  colDataName = NULL,
  aggregateRow = NULL,
  aggregateCol = NULL,
  featureAnnotations = NULL,
  cellAnnotations = NULL,
  featureAnnotationColor = NULL,
  cellAnnotationColor = NULL,
```

```

palette = c("ggplot", "celda", "random"),
heatmapPalette = c("sequential", "diverging"),
addCellSummary = NULL,
rowSplitBy = NULL,
colSplitBy = NULL,
rowLabel = FALSE,
colLabel = FALSE,
rowLabelSize = 6,
colLabelSize = 6,
rowDend = TRUE,
colDend = TRUE,
title = NULL,
rowTitle = "Features",
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.
useReducedDim	character. A string indicating the reducedDim name that provides the expression level to plot. Only for plotSCEDimReduceHeatmap.
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 or min-max scaling on each row. Choose from "zscore", "min-max" or default TRUE or FALSE
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 plotSCEDimReduceHeatmap. Default "rownames".
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 "rownames".
cluster_columns	A logical scalar that turns on/off clustering of columns. Default FALSE. Clustering columns should be turned off when using reduced dim for plotting as it will be sorted by PCs

cluster_rows	A logical scalar that turns on/off clustering of rows. Default FALSE.
rowDataName	character. The column name(s) in rowData that need to be added to the annotation. Not applicable for plotSCEDimReduceHeatmap. Default NULL.
colDataName	character. The column name(s) in colData that need to be added to the annotation. Default NULL.
aggregateRow	Feature variable for aggregating the heatmap by row. Can be a vector or a rowData column name for feature variable. Multiple variables are allowed. Default NULL.
aggregateCol	Cell variable for aggregating the heatmap by column. Can be a vector or a colData column name for cell variable. Multiple variables are allowed. 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.
palette	Choose from "ggplot", "celda" or "random" to generate unique category colors.
heatmapPalette	Choose from "sequential", "diverging" or supply custom palette with colorScheme to generate unique category colors. Default is "sequential"
addCellSummary	Add summary barplots to column annotation. Supply the name of the column in colData as a character. This option will add summary for categorical variables as stacked barplots.
rowSplitBy	character. Do semi-heatmap based on the grouping of this(these) annotation(s). Should exist in either rowDataName or names(featureAnnotations). 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 NULL.
rowLabel	Use a logical for whether to display all the feature names, a single character to display a column of rowData(inSCE) annotation, a vector of the same length as full/subset nrow(inSCE) 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 colData(inSCE) annotation, a vector of the same length as full/subset ncol(inSCE) 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 <code>unit</code> object. For the gap size between rows of the splitted heatmap. Default <code>grid::unit(0, 'mm')</code> .
colGap	A numeric value or a <code>unit</code> 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 <code>colorRamp2</code> . Default NULL.
...	Other arguments passed to <code>Heatmap</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 = 0.1,
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 0.1.
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 = 0.1,
  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.
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(s) stored in the specified reducedDims. Either an integer which indicates the column(s) or a character vector specifies column name(s). By default, the 1st dimension/column will be used. Only used when "reduced-Dims" 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 0.1.
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 = 0.1,
  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 0.1.
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 = 0.1,
  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 <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.
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 0.1.
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.
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 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,
  reducedDimName,
  sample = NULL,
  shape = NULL,
  groupBy = NULL,
  combinePlot = "all",
  violin = TRUE,
  boxplot = FALSE,
  dots = TRUE,
  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> . Required.
reducedDimName	Saved dimension reduction name in inSCE. Default "UMAP".
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
shape	If provided, add shapes based on the value. Default NULL.
groupBy	Groupings for each numeric value. 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.
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.
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. Similar to dim1. Default is NULL.

<code>bin</code>	Numeric vector. If single value, will divide the numeric values into bin groups. If more than one value, will bin numeric values using values as a cut point. Default NULL.
<code>binLabel</code>	Character vector. Labels for the bins created by <code>bin</code> . 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 combine is set. Default 1.
<code>relWidths</code>	Relative widths of plots when combine is set. Default <code>c(1, 1, 1)</code> .
<code>plotNCols</code>	Number of columns when plots are combined in a grid. Default NULL.
<code>plotNRows</code>	Number of rows when plots are combined in a grid. Default NULL.
<code>labelSamples</code>	Will label sample name in title of plot if TRUE. Default TRUE.
<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.
<code>sampleRelHeights</code>	If there are multiple samples and combining by "all", the relative heights for each plot. Default 1.
<code>sampleRelWidths</code>	If there are multiple samples and combining by "all", the relative widths for each plot. Default 1.

**Value**

list of .ggplot objects

**See Also**

[runScrublet](#)

**Examples**

```

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

## End(Not run)

```

---

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

---

**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 = FALSE
)

```

**Arguments**

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

**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,
  useAssay = "seuratNormData",
  plotType,
  features,
  groupVariable = NULL,
  reducedDimName = "seuratUMAP",
  splitBy = NULL,
  cols = c("lightgrey", "blue"),
  ncol = 1,
  combine = FALSE
)

```

**Arguments**

inSCE	Input SingleCellExperiment object.
useAssay	Specify the name of the assay that will be scaled by this function.
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. Default is NULL.
reducedDimName	saved dimension reduction name in the SingleCellExperiment object. Default seuratUMAP.
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

---

<code>plotSeuratHeatmap</code>	<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**

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

**Value**

modified plot object

---

<code>plotSeuratHVG</code>	<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, useReduction = "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 <code>plotNRows</code> . Default 3.
plotNRows	Integer. Number of rows for the plot grid per sample. Will determine the number of top markers to show together with <code>plotNCols</code> . 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.

**See Also**

[runSoupX](#)

**Examples**

```
## Not run:
sce <- importExampleData("pbmc3k")
sce <- runSoupX(sce, sample = "sample")
plotSoupXResults(sce, sample = "sample")

## End(Not run)
```

---

plotTopHVG

*Plot highly variable genes*


---

**Description**

Plot highly variable genes

**Usage**

```
plotTopHVG(
  inSCE,
  method = "modelGeneVar",
  hvgNumber = 2000,
  useFeatureSubset = NULL,
  labelsCount = 10,
  featureDisplay = metadata(inSCE)$featureDisplay,
  labelSize = 2,
  dotSize = 2,
  textSize = 12
)
```

**Arguments**

inSCE	Input SingleCellExperiment object containing the computations.
method	Select either "vst", "mean.var.plot", "dispersion" or "modelGeneVar".
hvgNumber	Specify the number of top genes to highlight in red. Default 2000. See details.
useFeatureSubset	A character string for the rowData variable name to store a logical index of selected features. Default NULL. See details.
labelsCount	Specify the number of data points/genes to label. Should be less than hvgNumber. Default 10. See details.
featureDisplay	A character string for the rowData variable name to indicate what type of feature ID should be displayed. If set by <a href="#">setSCTKDisplayRow</a> , will by default use it. If NULL, will use rownames(inSCE).
labelSize	Numeric, size of the text label on top HVGs. Default 2.
dotSize	Numeric, size of the dots of the features. Default 2.
textSize	Numeric, size of the text of axis title, axis label, etc. Default 12.

**Details**

When `hvgNumber = NULL` and `useFeature = NULL`, only plot the mean VS variance/dispersion scatter plot. When only `hvgNumber` set, label the top `hvgNumber` HVGs ranked by the metrics calculated by method. When `useFeatureSubset` set, label the features in the subset on the scatter plot created with method and ignore `hvgNumber`.

**Value**

ggplot of HVG metrics and top HVG labels

**See Also**

[runFeatureSelection](#), [runSeuratFindHVG](#), [runModelGeneVar](#), [getTopHVG](#)

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runModelGeneVar(mouseBrainSubsetSCE)
plotTopHVG(mouseBrainSubsetSCE, method = "modelGeneVar")
```

---

`plotTSCANClusterDEG` *Plot features identified by [runTSCANClusterDEAnalysis](#) on cell 2D embedding with MST overlaid*

---

**Description**

A wrapper function which plot the top features expression identified by [runTSCANClusterDEAnalysis](#) on the 2D embedding of the cells cluster used in the analysis. The related MST edges are overlaid.

**Usage**

```
plotTSCANClusterDEG(
  inSCE,
  useCluster,
  pathIndex = NULL,
  useReducedDim = "UMAP",
  topN = 9,
  useAssay = NULL,
  featureDisplay = metadata(inSCE)$featureDisplay,
  combinePlot = c("all", "none")
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useCluster</code>	Choose a cluster used for identifying DEG with <a href="#">runTSCANClusterDEAnalysis</a> . Required.
<code>pathIndex</code>	Specifies one of the branching paths from <code>useCluster</code> and plot the top DEGs on this path. Usually presented by the terminal cluster of a path. By default NULL plot top DEGs of all paths.

useReducedDim	A single character for the matrix of 2D embedding. Should exist in reducedDims slot. Default "UMAP".
topN	Integer. Use top N genes identified. Default 9.
useAssay	A single character for the feature expression matrix. Should exist in assayNames(inSCE). Default NULL for using the one used in <a href="#">runTSCANClusterDEAnalysis</a> .
featureDisplay	Specify the feature ID type to display. Users can set default value with <a href="#">setSCTKDisplayRow</a> . NULL or "rownames" specifies the rownames of inSCE. Other character values indicates rowData variable.
combinePlot	Must be either "all" or "none". "all" will combine plots of each feature into a single .ggplot object, while "none" will output a list of plots. Default "all".

**Value**

A .ggplot object of cell scatter plot, colored by the expression of a gene identified by [runTSCANClusterDEAnalysis](#), with the layer of trajectory.

**Author(s)**

Yichen Wang

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
mouseBrainSubsetSCE <- runTSCANClusterDEAnalysis(inSCE = mouseBrainSubsetSCE,
                                                useCluster = 1)
plotTSCANClusterDEG(mouseBrainSubsetSCE, useCluster = 1,
                    useReducedDim = "TSNE_logcounts")
```

---

plotTSCANClusterPseudo

*Plot TSCAN pseudotime rooted from given cluster*

---

**Description**

This function finds all paths that root from a given cluster useCluster. For each path, this function plots the recomputed pseudotime starting from the root on a scatter plot which contains cells only in this cluster. MST has to be pre-calculated with [runTSCAN](#).

**Usage**

```
plotTSCANClusterPseudo(
  inSCE,
  useCluster,
  useReducedDim = "UMAP",
  combinePlot = c("all", "none")
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useCluster	The cluster to be regarded as the root, has to existing in colData(inSCE)\$TSCAN_clusters.
useReducedDim	Saved dimension reduction name in the SingleCellExperiment object. Required.
combinePlot	Must be either "all" or "none". "all" will combine plots of pseudotime along each path into a single .ggplot object, while "none" will output a list of plots. Default "all".

**Value**

combinePlot = "all"	A .ggplot object
combinePlot = "none"	A list of .ggplot

**Author(s)**

Nida Pervaiz

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
plotTSCANClusterPseudo(mouseBrainSubsetSCE, useCluster = 1,
                       useReducedDim = "TSNE_logcounts")
```

---

plotTSCANDimReduceFeatures

*Plot feature expression on cell 2D embedding with MST overlaid*

---

**Description**

A wrapper function which plots all cells or cells in chosen cluster. Each point is a cell colored by the expression of a feature of interest, the relevant edges of the MST are overlaid on top.

**Usage**

```
plotTSCANDimReduceFeatures(
  inSCE,
  features,
  useReducedDim = "UMAP",
  useAssay = "logcounts",
  by = "rownames",
  useCluster = NULL,
  featureDisplay = metadata(inSCE)$featureDisplay,
  combinePlot = c("all", "none")
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
features	Choose the feature of interest to explore the expression level on the trajectory. Required.
useReducedDim	A single character for the matrix of 2D embedding. Should exist in reducedDims slot. Default "UMAP".
useAssay	A single character for the feature expression matrix. Should exist in assayNames(inSCE). Default "logcounts".
by	Where should features be found? NULL, "rownames" for rownames(inSCE), otherwise will be regarded as rowData variable.
useCluster	Choose specific clusters where gene expression needs to be visualized. By default NULL, all clusters are chosen.
featureDisplay	Specify the feature ID type to display. Users can set default value with <a href="#">setSCTKDisplayRow</a> . NULL or "rownames" specifies the rownames of inSCE. Other character values indicates rowData variable.
combinePlot	Must be either "all" or "none". "all" will combine plots of each feature into a single .ggplot object, while "none" will output a list of plots. Default "all".

**Value**

A .ggplot object of cell scatter plot, colored by the expression of a gene of interest, with the layer of trajectory.

**Author(s)**

Yichen Wang

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
plotTSCANDimReduceFeatures(inSCE = mouseBrainSubsetSCE,
                           features = "Tshz1",
                           useReducedDim = "TSNE_logcounts")
```

---

plotTSCANPseudotimeGenes

*Plot expression changes of top features along a TSCAN pseudotime path*

---

**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. [runTSCANDEG](#) has to be run in advance with using the same pathIndex of interest.

**Usage**

```
plotTSCANPseudotimeGenes(
  inSCE,
  pathIndex,
  direction = c("increasing", "decreasing"),
  topN = 10,
  useAssay = NULL,
  featureDisplay = metadata(inSCE)$featureDisplay
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path index for which the pseudotime values should be used. Should have being used in <a href="#">runTSCANDEG</a> .
direction	Should we show features with expression increasing or decreasing along the increase in TSCAN pseudotime? Choices are "increasing" or "decreasing".
topN	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
useAssay	A single character to specify a feature expression matrix in assays slot. The expression of top features from here will be visualized. Default NULL use the one used for <a href="#">runTSCANDEG</a> .
featureDisplay	Specify the feature ID type to display. Users can set default value with <a href="#">setSCTKDisplayRow</a> . NULL or "rownames" specifies the rownames of inSCE. Other character values indicates rowData variable.

**Value**

A `ggplot` object with the facets of the top genes. Expression on y-axis, pseudotime on x-axis.

**Author(s)**

Nida Pervaiz

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
terminalNodes <- listTSCANTerminalNodes(mouseBrainSubsetSCE)
mouseBrainSubsetSCE <- runTSCANDEG(inSCE = mouseBrainSubsetSCE,
                                   pathIndex = terminalNodes[1])
plotTSCANPseudotimeGenes(mouseBrainSubsetSCE,
                          pathIndex = terminalNodes[1],
                          useAssay = "logcounts")
```

---

```
plotTSCANPseudotimeHeatmap
```

*Plot heatmap of genes with expression change along TSCAN pseudotime*

---

### Description

A wrapper function which visualizes outputs from the [runTSCANDEG](#) function. Plots the top genes that change in expression with increasing pseudotime along the path in the MST. [runTSCANDEG](#) has to be run in advance with using the same pathIndex of interest.

### Usage

```
plotTSCANPseudotimeHeatmap(
  inSCE,
  pathIndex,
  direction = c("both", "increasing", "decreasing"),
  topN = 50,
  log2fcThreshold = NULL,
  useAssay = NULL,
  featureDisplay = metadata(inSCE)$featureDisplay
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path index for which the pseudotime values should be used. Should have being used in <a href="#">runTSCANDEG</a> .
direction	Should we show features with expression increasing or decreasing along the increase in TSCAN pseudotime? Choices are "both", "increasing" or "decreasing".
topN	An integer. Only to plot this number of top genes along the path in the MST, in terms of FDR value. Use NULL to cancel the top N subscription. Default 30.
log2fcThreshold	Only output DEGs with the absolute values of log2FC larger than this value. Default NULL.
useAssay	A single character to specify a feature expression matrix in assays slot. The expression of top features from here will be visualized. Default NULL use the one used for <a href="#">runTSCANDEG</a> .
featureDisplay	Whether to display feature ID and what ID type to display. Users can set default ID type by <a href="#">setSCTKDisplayRow</a> . NULL will display when number of features to display is less than 60. FALSE for no display. Variable name in rowData to indicate ID type. "rownames" or TRUE for using rownames(inSCE).

### Value

A ComplexHeatmap in .ggplot class

### Author(s)

Nida Pervaiz

## Examples

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
terminalNodes <- listTSCANTerminalNodes(mouseBrainSubsetSCE)
mouseBrainSubsetSCE <- runTSCANDEG(inSCE = mouseBrainSubsetSCE,
                                   pathIndex = terminalNodes[1])
plotTSCANPseudotimeHeatmap(mouseBrainSubsetSCE,
                            pathIndex = terminalNodes[1])
```

---

plotTSCANResults	<i>Plot MST pseudotime values on cell 2D embedding</i>
------------------	--

---

## Description

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

## Usage

```
plotTSCANResults(inSCE, useReducedDim = "UMAP")
```

## Arguments

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

**useReducedDim**   Saved dimension reduction name in inSCE object. Required.

## Value

A `ggplot` object with the pseudotime ordering of the cells colored on a cell 2D embedding, and the MST path drawn on it.

## Author(s)

Nida Pervaiz

## Examples

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
plotTSCANResults(inSCE = mouseBrainSubsetSCE,
                 useReducedDim = "TSNE_logcounts")
```

---

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 = NULL,  
  shape = NULL,  
  reducedDimName = "TSNE",  
  runTSNE = FALSE,  
  useAssay = "counts"  
)
```

### 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 <code>SingleCellExperiment</code> object in the <code>reduced-Dims</code> slot. Required.
runTSNE	Run t-SNE if the <code>reducedDimName</code> 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 = NULL,  
  shape = NULL,  
  reducedDimName = "UMAP",  
  runUMAP = FALSE,  
  useAssay = "counts"  
)
```

### 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 <- runQuickUMAP(sce)  
plotUMAP(sce)
```

---

qcInputProcess      *Create SingleCellExperiment object from command line input arguments*

---

### Description

Create SingleCellExperiment object from command line input arguments

### Usage

```
qcInputProcess(
  preproc,
  samplename,
  path,
  raw,
  fil,
  ref,
  rawFile,
  filFile,
  flatFiles,
  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.
flatFiles	The full paths of the matrix, barcode, and features (in that order) files used to construct an SCE object.
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,
  sample = "sample",
  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
sample	Character. The name of the saved column from the colData indicating the sample grouping variable. Default is "sample"
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 <code>colData</code> .
<code>variable</code>	A single character, specifying the name to store the phenotype labels in <code>colData</code> .
<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,
  useReducedDim,
  featureDisplay = NULL,
  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.
useReducedDim	Specify an embedding for visualizing the relation ship between the conditions.
featureDisplay	The feature ID type to use for displaying. Should exists as a variable name of <code>rowData</code> . Default NULL use <code>rownames</code> of <code>inSCE</code> .
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 runFindMarker .html report</i>
------------------	---------------------------------------

---

**Description**

A function to generate .html Rmarkdown report containing the visualizations of the [runFindMarker](#) 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="#">runFindMarker</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

*Get .html report of the output of the selected QC algorithm*


---

## Description

A function to generate .html Rmarkdown report for the specified QC algorithm output

## Usage

```
reportQCTool(
  inSCE,
  algorithm = c("BarcodeRankDrops", "EmptyDrops", "QCMetrics", "Scrublet", "ScDbfFinder",
    "Cxls", "Bcfs", "CxlsBcfsHybrid", "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, runScDbfFinder, runCxls, runBcfs, runCxlsBcfsHybrid, runDecontX, runBarcodeRankDrops, runEmptyDrops
algorithm	Character. Specifies which QC algorithm report to generate. Available options are "BarcodeRankDrops", "EmptyDrops", "QCMetrics", "Scrublet", "ScDbfFinder", "Cxls", "Bcfs", "CxlsBcfsHybrid", "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 <- runQuickUMAP(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,
  outputPath = 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,
  numTopFeatures = 10,
  forceRun = TRUE
)
```

## Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object.
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.
variable.features	A numeric value indicating the number of top variable features to identify. Default 2000.
pc.count	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.
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.
outputPath	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.
runHVG	A logical value indicating if the feature selection computation should be run or not. Default is TRUE.
plotHVG	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.
runDimRed	A logical value indicating if PCA should be computed. Default is TRUE.
plotJackStraw	A logical value indicating if JackStraw plot be visualized for the principal components. Default is FALSE.
plotElbowPlot	A logical value indicating if the ElbowPlot be visualized for the principal components. Default is TRUE.
plotHeatmaps	A logical value indicating if heatmaps should be plotted for the principal components. Default is TRUE.
runClustering	A logical value indicating if clustering section should be run in the report. Default is TRUE.
plotTSNE	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.
numTopFeatures	A numeric value indicating the number of top features to visualize in each group. Default 10.
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 TRUE.

**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,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = TRUE
)
```

**Arguments**

`inSCE` Input [SingleCellExperiment](#) 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 <code>colData()</code> columns to use for differential expression in addition to the <code>biological.group</code> parameter.
runClustering	A logical value indicating if Clustering should be run or not in the report. Default is TRUE. If FALSE, parameters <code>plotTSNE</code> and <code>plotUMAP</code> 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.
outputPath	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 TRUE.

**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,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = TRUE
)
```

**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.
outputPath	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 TRUE.

**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,  
  outputPath = NULL,  
  subtitle = NULL,  
  authors = NULL,  
  showSession = FALSE,  
  pdf = FALSE,  
  forceRun = TRUE  
)
```

### 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.
outputPath	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 TRUE.

**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,
  numTopFeatures = 10,
  outputFile = NULL,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE
)
```

**Arguments**

`inSCE` Input [SingleCellExperiment](#) 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.
numTopFeatures	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.
outputPath	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,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = TRUE
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object previously passed through <code>reportSeuratRun()</code> .
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.
outputPath	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 TRUE.

**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,
  numTopFeatures = 10,
  outputFile = NULL,
  outputPath = NULL,
```

```

    subtitle = NULL,
    authors = NULL,
    showSession = FALSE,
    pdf = FALSE,
    forceRun = TRUE
  )

```

## Arguments

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object previously passed through <code>reportSeuratRun()</code> .
<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>pc.count</code>	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.
<code>plotTSNE</code>	A logical value indicating if TSNE plots should be visualized in the clustering section of the report. Default is TRUE.
<code>plotUMAP</code>	A logical value indicating if UMAP plots should be visualized in the clustering section of the report. Default is TRUE.
<code>runClustering</code>	A logical value indicating if Clustering should be run or not in the report. Default is TRUE. If FALSE, parameters <code>plotTSNE</code> and <code>plotUMAP</code> are also set to FALSE.
<code>runMSClusters</code>	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.
<code>runMSBioGroup</code>	A logical value indicating if the marker selection section for identifying marker genes between the <code>biological.group</code> parameter should be run and visualized in the report. Default TRUE.
<code>numTopFeatures</code>	A numeric value indicating the number of top features to visualize in each group. Default 10.
<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>outputPath</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.

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 TRUE.

**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,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = TRUE
)
```

**Arguments**

<code>inSCE</code>	Input <code>SingleCellExperiment</code> 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 tSNE & UMAP visualization.
<code>phenotype.groups</code>	A character value that specifies the name of the <code>colData()</code> column to use as additional phenotype variables in the Seurat report for tSNE & UMAP visualization.
<code>variable.features</code>	A numeric value indicating the number of top variable genes to identify in the report. Default is 2000.
<code>pc.count</code>	A numeric value indicating the number of principal components to use in the analysis workflow. Default is 50.
<code>runHVG</code>	A logical value indicating if feature selection should be run in the report. Default TRUE.
<code>plotHVG</code>	A logical value indicating if the top variable genes should be visualized through a mean-to-variance plot. Default is TRUE.
<code>runDimRed</code>	A logical value indicating if PCA should be computed in the report. Default is TRUE.
<code>plotJackStraw</code>	A logical value indicating if the JackStraw plot should be visualized for the principal components. Default is FALSE.
<code>plotElbowPlot</code>	A logical value indicating if the ElbowPlot should be visualized for the principal components. Default is FALSE.
<code>plotHeatmaps</code>	A logical value indicating if the Heatmaps should be visualized for the principal components. Default is FALSE.
<code>runClustering</code>	A logical value indicating if Clustering should be run over multiple resolutions as defined by the <code>minResolution</code> and <code>maxResolution</code> parameters. Default is TRUE.
<code>plotTSNE</code>	A logical value indicating if TSNE plot should be visualized for clusters. Default is TRUE.
<code>plotUMAP</code>	A logical value indicating if UMAP plot should be visualized for clusters. Default is TRUE.
<code>minResolution</code>	A numeric value indicating the minimum resolution to use for clustering. Default 0.3.
<code>maxResolution</code>	A numeric value indicating the maximum resolution to use for clustering. Default 1.5.
<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>outputPath</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.

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 TRUE.

**Value**

A [SingleCellExperiment](#) object with computations stored.

---

reportSeuratScaling	<i>Generates an HTML report for Seurat Scaling and returns the SCE object with the results computed and stored inside the object.</i>
---------------------	---

---

**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,
  outputPath = NULL,
  subtitle = NULL,
  authors = NULL,
  showSession = FALSE,
  pdf = FALSE,
  forceRun = TRUE
)
```

**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.
outputPath	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 TRUE.

**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**

inSCE	Input <a href="#">SingleCellExperiment</a> object. Required
IDs	Character vector of identifiers for features or cells to find in rowData or colData of inSCE
axis	A character scalar to specify whether to search for features or cells. Use "row", "feature" or "gene" for features; "col" or "cell" for cells.
by	Character. In which column to search for features/cells in rowData/colData. Default NULL for search the rownames/colnames
exactMatch	A logical scalar. Whether to only identify exact matches or to identify partial matches using <a href="#">grep</a> . Default TRUE
firstMatch	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, Yichen Wang

**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 or colData variable name. Indicates which sample each cell belongs to. Default NULL.
useAssay	A string specifying which assay in the SCE to use. Default "counts"
lower	See <a href="#">barcodeRanks</a> for more information. Default 100.
fitBounds	See <a href="#">barcodeRanks</a> for more information. Default NULL.
df	See <a href="#">barcodeRanks</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_inflection`. Please refer to the documentation of [barcodeRanks](#) for details.

### See Also

[barcodeRanks](#), [runDropletQC](#), [plotBarcodeRankDropsResults](#)

### Examples

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



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.
<code>sample</code>	Character vector or <code>colData</code> variable name. Indicates which sample each cell belongs to. Default NULL.
<code>seed</code>	Seed for the random number generator, can be NULL. 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.
<code>retRes</code>	See <a href="#">bcds</a> for more information. Default FALSE.
<code>nmax</code>	See <a href="#">bcds</a> for more information. Default "tune".
<code>varImp</code>	See <a href="#">bcds</a> for more information. Default FALSE.
<code>estNdbl</code>	See <a href="#">bcds</a> for more information. Default FALSE.
<code>useAssay</code>	A string specifying which assay in <code>inSCE</code> to use. Default "counts"

**Details**

When the argument `sample` is specified, [bcds](#) will be run on cells from each sample separately. If `sample = NULL`, then all cells will be processed together.

**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.

**See Also**

[bcds](#), [plotBcDsResults](#), [runCellQC](#)

**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", "scDbfFinder", "cxds", "bcds", "cxds_bcds_hybrid",
    "decontX", "decontX_bg", "soupX", "soupX_bg"),
  sample = NULL,
  collectionName = NULL,
  geneSetList = NULL,
  geneSetListLocation = "rownames",
  geneSetCollection = NULL,
  mitoRef = "human",
  mitoIDType = "ensembl",
  mitoPrefix = "MT-",
  mitoID = NULL,
  mitoGeneLocation = "rownames",
  useAssay = "counts",
  background = NULL,
  bgAssayName = NULL,
  bgBatch = NULL,
  seed = 12345,
  paramsList = NULL
)
```

**Arguments**

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>algorithms</code>	Character vector. Specify which QC algorithms to run. Available options are "QCMetrics", "scrublet", "doubletFinder", "scDbfFinder", "cxds", "bcds", "cxds_bcds_hybrid", "decontX" and "soupX".
<code>sample</code>	Character vector. Indicates which sample each cell belongs to. Algorithms will be run on cells from each sample separately.
<code>collectionName</code>	Character. Name of a <code>GeneSetCollection</code> obtained by using one of the <code>importGeneSet*</code> 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)
```

---

```
runClusterSummaryMetrics
```

*Run Cluster Summary Metrics*

---

**Description**

Calculates the mean expression of percent of cells that express the given genes for each cluster

**Usage**

```
runClusterSummaryMetrics(
  inSCE,
  useAssay = "logcounts",
  featureNames,
  displayName = NULL,
  groupNames = "cluster",
  scale = FALSE
)
```

**Arguments**

inSCE	The single cell experiment to use.
useAssay	The assay to use.
featureNames	A string or vector of strings with each gene to aggregate.
displayName	A string that is the name of the column used for genes.
groupNames	The name of a colData entry that can be used as groupNames.
scale	Option to scale the data. Default: FALSE. Selected assay will not be scaled.

**Value**

A dataframe with mean expression and percent of cells in cluster that express for each cluster.

**Examples**

```
data("scExample")
runClusterSummaryMetrics(inSCE=sce, useAssay="counts", featureNames=c("B2M", "MALAT1"),
  displayName="feature_name", groupNames="type")
```

---

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",
```



---

runCxds	<i>Find doublets/multiplets using <a href="#">cxds</a>.</i>
---------	---

---

### 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

```
runCxds(  
  inSCE,  
  sample = NULL,  
  seed = 12345,  
  ntop = 500,  
  binThresh = 0,  
  verb = FALSE,  
  retRes = FALSE,  
  estNdbl = FALSE,  
  useAssay = "counts"  
)
```

### Arguments

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>sample</code>	Character vector or <code>colData</code> variable name. Indicates which sample each cell belongs to. Default NULL.
<code>seed</code>	Seed for the random number generator, can be NULL. Default 12345.
<code>ntop</code>	See <a href="#">cxds</a> for more information. Default 500.
<code>binThresh</code>	See <a href="#">cxds</a> for more information. Default 0.
<code>verb</code>	See <a href="#">cxds</a> for more information. Default FALSE.
<code>retRes</code>	See <a href="#">cxds</a> for more information. Default FALSE.
<code>estNdbl</code>	See <a href="#">cxds</a> for more information. Default FALSE.
<code>useAssay</code>	A string specifying which assay in the SCE to use. Default "counts"

### Details

When the argument `sample` is specified, [cxds](#) will be run on cells from each sample separately. If `sample = NULL`, then all cells will be processed together.

### Value

A [SingleCellExperiment](#) object with [cxds](#) output appended to the `colData` slot. The columns include `cxds_score` and optionally `cxds_call`.

### See Also

[cxds](#), [plotCxdsResults](#), [runCellQC](#)

**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**

```
runCxlsBcDsHybrid(
  inSCE,
  sample = NULL,
  seed = 12345,
  nTop = 500,
  cxlsArgs = list(),
  bcDsArgs = list(),
  verb = FALSE,
  estNdbl = FALSE,
  force = 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="#">cxls_bcDs_hybrid</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>	The number of top variable genes to consider. Used in both <code>cxls</code> and <code>bcDs</code> . Default 500.
<code>cxlsArgs</code>	See <a href="#">cxls_bcDs_hybrid</a> for more information. Default NULL.
<code>bcDsArgs</code>	See <a href="#">cxls_bcDs_hybrid</a> for more information. Default NULL.
<code>verb</code>	See <a href="#">cxls_bcDs_hybrid</a> for more information. Default FALSE.
<code>estNdbl</code>	See <a href="#">cxls_bcDs_hybrid</a> for more information. Default FALSE.
<code>force</code>	See <a href="#">cxls_bcDs_hybrid</a> for more information. Default FALSE.
<code>useAssay</code>	A string specifying which assay in the SCE to use.

**Value**

A [SingleCellExperiment](#) object with [cxls\\_bcDs\\_hybrid](#) output appended to the `colData` slot. The columns include `hybrid_score` and optionally `hybrid_call`. Please refer to the documentation of [cxls\\_bcDs\\_hybrid](#) for details.

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runCxdsBcDsHybrid(sce)
```

---

**runDEAnalysis***Perform differential expression analysis on SCE object*

---

**Description**

Perform differential expression analysis on SCE object

**Usage**

```
runDEAnalysis(inSCE, method = "wilcox", ...)
```

```
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,
  verbose = TRUE
)
```

```
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,  
    verbose = TRUE  
)  
  
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,  
  verbose = TRUE  
)  
  
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,
verbose = TRUE
)

runWilcox(
  inSCE,
  useAssay = "logcounts",
  useReducedDim = NULL,
  index1 = NULL,
  index2 = NULL,
  class = "cluster",
  classGroup1 = c(1),
  classGroup2 = c(2),
  analysisName = "cluster1_VS_2",
  groupName1 = "cluster1",
  groupName2 = "cluster2",
  covariates = NULL,
  onlyPos = FALSE,
  log2fcThreshold = NULL,
  fdrThreshold = NULL,
  minGroup1MeanExp = NULL,
  maxGroup2MeanExp = NULL,
  minGroup1ExprPerc = NULL,
  maxGroup2ExprPerc = NULL,
  overwrite = FALSE,
  verbose = TRUE
)

```

## Arguments

inSCE	<a href="#">SingleCellExperiment</a> inherited object.
method	Character. Specify which method to use when using runDEAnalysis(). Choose from "wilcox", "MAST", "DESeq2", "Limma", "ANOVA". Default "wilcox".
...	Arguments to pass to specific methods when using the generic runDEAnalysis().
useAssay	character. A string specifying which assay to use for the DE regression. Ignored when useReducedDim is specified. Default "counts" for DESeq2, "logcounts" for other methods.
useReducedDim	character. A string specifying which reducedDim to use for DE analysis. Will treat the dimensions as features. 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.

<code>class</code>	A vector/factor with <code>ncol(inSCE)</code> elements, or a character scalar that specifies a column name of <code>colData(inSCE)</code> . Default <code>"cluster"</code> .
<code>classGroup1</code>	a vector specifying which "levels" given in <code>class</code> are of interests. Default <code>c(1)</code> .
<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. Default <code>c(2)</code> .
<code>analysisName</code>	A character scalar naming the DEG analysis. Default <code>"cluster1_vs_2"</code> .
<code>groupName1</code>	A character scalar naming the group of interests. Default <code>"cluster1"</code> .
<code>groupName2</code>	A character scalar naming the control group. Default <code>"cluster2"</code> .
<code>covariates</code>	A character vector of additional covariates to use when building the model. All covariates must exist in <code>names(colData(inSCE))</code> . Default NULL.
<code>fullReduced</code>	Logical, DESeq2 only argument. Whether to apply LRT (Likelihood ratio test) with a 'full' model. Default TRUE.
<code>onlyPos</code>	Whether to only output DEG with positive <code>log2_FC</code> value. Default FALSE.
<code>log2fcThreshold</code>	Only out put DEGs with the absolute values of <code>log2FC</code> greater than this value. Default NULL.
<code>fdrThreshold</code>	Only out put DEGs with FDR value less than this value. Default NULL.
<code>minGroup1MeanExp</code>	Only out put DEGs with mean expression in <code>group1</code> greater then this value. Default NULL.
<code>maxGroup2MeanExp</code>	Only out put DEGs with mean expression in <code>group2</code> less then this value. Default NULL.
<code>minGroup1ExprPerc</code>	Only out put DEGs expressed in greater then this fraction of cells in <code>group1</code> . Default NULL.
<code>maxGroup2ExprPerc</code>	Only out put DEGs expressed in less then this fraction of cells in <code>group2</code> . Default NULL.
<code>overwrite</code>	A logical scalar. Whether to overwrite result if exists. Default FALSE.
<code>verbose</code>	A logical scalar. Whether to show messages. Default TRUE.
<code>check_sanity</code>	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. Only use arguments `index1` and `index2`. 2. Annotation level selection. Only use arguments `class`, `classGroup1` and `classGroup2`.

### Value

The input [SingleCellExperiment](#) object, where `metadata(inSCE)$diffExp` is updated with a list named by `analysisName`, with elements of:

`$groupNames`      the naming of the two conditions

```

useAssay, useReducedDim
    the matrix name that was used for calculation
select
    the cell selection indices (logical) for each condition
result
    a data.frame of the DEGs table
method
    the method 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 <code>delta</code> in each iteration. If <code>estimateDelta = FALSE</code> , then <code>delta</code> is fixed with these values for the entire inference procedure. Fixing <code>delta</code> 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 <code>delta</code> 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	<i>Generic Wrapper function for running dimensionality reduction</i>
--------------	--

---

### Description

Generic Wrapper function for running dimensionality reduction

### Usage

```
runDimReduce(
  inSCE,
  method = c("scaterPCA", "seuratPCA", "seuratICA", "scanpyPCA", "rTSNE", "seuratTSNE",
             "scaterUMAP", "seuratUMAP", "scanpyUMAP", "scanpyTSNE"),
  useAssay = NULL,
  useReducedDim = NULL,
  useAltExp = NULL,
  reducedDimName = method,
  nComponents = 20,
  useFeatureSubset = NULL,
  scale = FALSE,
  seed = 12345,
  ...
)
```

### Arguments

inSCE	Input <code>SingleCellExperiment</code> object.
method	One from "scaterPCA", "seuratPCA", "seuratICA", "rTSNE", "seuratTSNE", "scaterUMAP", "seuratUMAP", "scanpyPCA", "scanpyUMAP" and "scanpyTSNE".
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.
useFeatureSubset	Subset of feature to use for dimension reduction. A character string indicating a rowData variable that stores the logical vector of HVG selection, or a vector that can subset the rows of inSCE. Default NULL.
scale	Logical scalar, whether to standardize the expression values. Default TRUE.
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](#), [runTSNE](#), [runSeuratTSNE](#), [runUMAP](#) 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",
  normalizationMethod = "logNormCounts")
sce <- runDimReduce(inSCE = sce, method = "scaterPCA",
  useAssay = "logcounts", scale = TRUE,
  reducedDimName = "PCA")
```

---

runDoubletFinder	<i>Generates a doublet score for each cell via doubletFinder</i>
------------------	--

---

### Description

Uses doubletFinder to determine cells within the dataset suspected to be doublets.

**Usage**

```
runDoubletFinder(
  inSCE,
  sample = NULL,
  useAssay = "counts",
  seed = 12345,
  seuratNfeatures = 2000,
  seuratPcs = seq(15),
  seuratRes = 1.5,
  sct = FALSE,
  formationRate = 0.075,
  nCores = NULL,
  verbose = FALSE
)
```

**Arguments**

inSCE	inSCE A <a href="#">SingleCellExperiment</a> object.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
useAssay	A string specifying which assay in the SCE to use. Default "counts".
seed	Seed for the random number generator, can be set to NULL. 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.
sct	Whether or not to use SCT. Default FALSE.
formationRate	Doublet formation rate used within algorithm. Default 0.075.
nCores	Number of cores used for running the function. Default NULL.
verbose	Boolean. Whether to print messages from Seurat and DoubletFinder. Default FALSE.

**Value**

[SingleCellExperiment](#) object containing the doublet\_finder\_doublet\_score variable in colData slot.

**See Also**

[runCellQC](#), [plotDoubletFinderResults](#)

**Examples**

```
data(scExample, package = "singleCellTK")
options(future.globals.maxSize = 786432000)
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runDoubletFinder(sce)
```

---

runDropletQC	<i>Perform comprehensive droplet QC</i>
--------------	---

---

### 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	A <a href="#">SingleCellExperiment</a> object. Must contain a raw counts matrix before empty droplets have been removed.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
useAssay	A string specifying which assay in the SCE to use. Default "counts"
lower	See <a href="#">emptyDrops</a> for more information. Default 100.
niters	See <a href="#">emptyDrops</a> for more information. Default 10000.
testAmbient	See <a href="#">emptyDrops</a> for more information. Default FALSE.
ignore	See <a href="#">emptyDrops</a> for more information. Default NULL.
alpha	See <a href="#">emptyDrops</a> for more information. Default NULL.
retain	See <a href="#">emptyDrops</a> for more information. Default NULL.
barcodeArgs	See <a href="#">emptyDrops</a> for more information. Default list().
BPPARAM	See <a href="#">emptyDrops</a> for more information. Default BiocParallel::SerialParam().

### 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.

**See Also**

[runDropletQC](#), [plotEmptyDropsResults](#), [plotEmptyDropsScatter](#)

**Examples**

```
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**

inSCE	A <a href="#">SingleCellExperiment</a> object.
features	Character vector, selected genes for enrichment analysis.
analysisName	A string that identifies each specific analysis.
db	Character vector. Selected database name(s) from the enrichR database list. If NULL then EnrichR will be run on all the available databases on the enrichR database. See details. Default NULL
by	Character. From where should we find the features? "rownames" for from rownames(inSCE), otherwise, from a column of feature metadata (rowData(inSCE)[[by]]). See details. Default "rownames".
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 = c("Vamp7", "Cntn2", "Olig1"),
                                   db = "GO_Cellular_Component_2025",
                                   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",
  useReducedDim = NULL,
  batch = "batch",
  reducedDimName = "fastMNN",
  k = 20,
  propK = NULL,
  ndist = 3,
  minBatchSkip = 0,
  cosNorm = TRUE,
  nComponents = 50,
  weights = NULL,
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
useReducedDim	A single character indicating the dimension reduction used for batch correction. Will ignore useAssay when using. Default NULL.
batch	A single character indicating a field in colData that annotates the batches of each cell; or a vector/factor with the same length as the number of cells. Default "batch".
reducedDimName	A single character. The name for the corrected low-dimensional representation. Default "fastMNN".
k	An integer scalar specifying the number of nearest neighbors to consider when identifying MNNs. See "See Also". Default 20.
propK	A numeric scalar in (0, 1) specifying the proportion of cells in each dataset to use for mutual nearest neighbor searching. See "See Also". Default NULL.
ndist	A numeric scalar specifying the threshold beyond which neighbours are to be ignored when computing correction vectors. See "See Also". Default 3.
minBatchSkip	Numeric scalar specifying the minimum relative magnitude of the batch effect, below which no correction will be performed at a given merge step. See "See Also". Default 0.
cosNorm	A logical scalar indicating whether cosine normalization should be performed on useAssay prior to PCA. See "See Also". Default TRUE.
nComponents	An integer scalar specifying the number of dimensions to produce. See "See Also". Default 50.
weights	The weighting scheme to use. Passed to <a href="#">multiBatchPCA</a> . Default NULL.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying whether the SVD should be parallelized.

**Value**

The input [SingleCellExperiment](#) object with `reducedDim(inSCE, reducedDimName)` updated.

**References**

Lun ATL, et al., 2016

**See Also**

[fastMNN](#) for using useAssay, and [reducedMNN](#) for using useReducedDim

**Examples**

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log1p(counts(sceBatches))
sceCorr <- runFastMNN(sceBatches, useAssay = 'logcounts')
```



---

runFindMarker	<i>Find the marker gene set for each cluster</i>
---------------	--

---

### Description

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. `runFindMarker` will be deprecated in the future.

### Usage

```
runFindMarker(
  inSCE,
  useAssay = "logcounts",
  useReducedDim = NULL,
  method = "wilcox",
  cluster = "cluster",
  covariates = NULL,
  log2fcThreshold = NULL,
  fdrThreshold = 0.05,
  minClustExprPerc = NULL,
  maxCtrlExprPerc = NULL,
  minMeanExpr = NULL,
  detectThresh = 0
)

findMarkerDiffExp(
  inSCE,
  useAssay = "logcounts",
  useReducedDim = NULL,
  method = c("wilcox", "MAST", "DESeq2", "Limma", "ANOVA"),
  cluster = "cluster",
  covariates = NULL,
  log2fcThreshold = NULL,
  fdrThreshold = 0.05,
  minClustExprPerc = NULL,
  maxCtrlExprPerc = NULL,
  minMeanExpr = NULL,
  detectThresh = 0
)
```

### Arguments

<code>inSCE</code>	<code>SingleCellExperiment</code> inherited object.
<code>useAssay</code>	character. A string specifying which assay to use for the MAST calculations. Default "logcounts".
<code>useReducedDim</code>	character. A string specifying which reducedDim to use for MAST calculations. Set useAssay to NULL when using. Required.
<code>method</code>	A single character for specific differential expression analysis method. Choose from 'wilcox', 'MAST', 'DESeq2', 'Limma', and 'ANOVA'. Default "wilcox".



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**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useAssay	Indicate which assay to use. The default is "logcounts"
resultNamePrefix	Character. Prefix to the name the GSVA results which will be stored in the reducedDim slot of inSCE. The names of the output matrix will be resultNamePrefix_Scores. If this parameter is set to NULL, then "GSVA_geneSetCollectionName_" will be used. Default NULL.
geneSetCollectionName	Character. The name of the gene set collection to use.
...	Parameters to pass to gsva()

**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")
```

---

runHarmony	<i>Apply Harmony batch effect correction method to SingleCellExperiment object</i>
------------	--

---

### Description

Harmony is an algorithm that projects cells into a shared embedding in which cells group by cell type rather than dataset-specific conditions.

### Usage

```
runHarmony(
  inSCE,
  useAssay = NULL,
  useReducedDim = NULL,
  batch = "batch",
  reducedDimName = "HARMONY",
  nComponents = 50,
  lambda = 0.1,
  theta = 5,
  sigma = 0.1,
  nIter = 10,
  seed = 12345,
  verbose = TRUE,
  ...
)
```

### Arguments

inSCE	Input <a href="#">SingleCellExperiment</a> object
useAssay	A single character indicating the name of the assay requiring batch correction. Default NULL. It is recommended to use a reducedDim such as PCA through the 'useReducedDim' parameter of this function.
useReducedDim	A single character indicating the name of the reducedDim to be used. It is recommended to use a reducedDim instead of a full assay as using an assay might cause the algorithm to not converge and throw error. Specifying this will ignore useAssay. Default NULL.
batch	A single character indicating a field in colData that annotates the batches of each cell; or a vector/factor with the same length as the number of cells. Default "batch".
reducedDimName	A single character. The name for the corrected low-dimensional representation. Will be saved to reducedDim(inSCE). Default "HARMONY".
nComponents	An integer. The number of PCs to use and generate. Default 50L.
lambda	A Numeric scalar. Ridge regression penalty parameter. Must be strictly positive. Smaller values result in more aggressive correction. Default 0.1.
theta	A Numeric scalar. Diversity clustering penalty parameter. Larger values of theta result in more diverse clusters. theta=0 does not encourage any diversity. Default 5.

sigma	A Numeric scalar. Width of soft kmeans clusters. Larger values of sigma result in cells assigned to more clusters. Smaller values of sigma make soft kmeans cluster approach hard clustering. Default 0.1.
nIter	An integer. The max number of iterations to perform. Default 10L.
seed	Set seed for reproducibility. Default is 12345.
verbose	Whether to print progress messages. Default TRUE.
...	Other arguments passed to <a href="#">HarmonyMatrix</a> . See details.

### Details

Since some of the arguments of [HarmonyMatrix](#) is controlled by this wrapper function. The additional arguments users can work with only include: `nclust`, `tau`, `block.size`, `max.iter.cluster`, `epsilon.cluster`, `epsilon.harmony`, `plot.convergence`, `reference_values` and `cluster_prior`.

### Value

The input [SingleCellExperiment](#) object with `reducedDim(inSCE, reducedDimName)` updated.

### References

Ilya Korsunsky, et al., 2019

### Examples

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log1p(counts(sceBatches))
## Not run:
if (require("harmony"))
  sceCorr <- runHarmony(sceBatches)

## End(Not run)
```

---

runKMeans

*Get clustering with KMeans*

---

### Description

Perform KMeans clustering on a [SingleCellExperiment](#) object, with `kmeans`.

### Usage

```
runKMeans(
  inSCE,
  nCenters,
  useReducedDim = "PCA",
  clusterName = "KMeans_cluster",
  nComp = 10,
  nIter = 10,
  nStart = 1,
  seed = 12345,
  algorithm = c("Hartigan-Wong", "Lloyd", "MacQueen")
)
```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object.
nCenters	An integer, the number of centroids (clusters).
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 <code>colData</code> . Default "KMeans_cluster".
nComp	An integer. The number of components to use for K-Means. Default 10. See Detail.
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	Input <a href="#">SingleCellExperiment</a> object
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 <code>assay</code> . Default "LIMMA".
batch	A single character indicating a field in <code>colData</code> that annotates the batches of each cell; or a vector/factor with the same length as the number of cells. 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) <- log1p(counts(sceBatches))
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,
  propK = NULL,
  sigma = 0.1,
  cosNormIn = TRUE,
  cosNormOut = TRUE,
  varAdj = TRUE,
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object
useAssay	A single character indicating the name of the assay requiring batch correction. Default "logcounts".
batch	A single character indicating a field in colData that annotates the batches of each cell; or a vector/factor with the same length as the number of cells. 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 scalar specifying the number of nearest neighbors to consider when identifying MNNs. See "See Also". Default 20.
propK	A numeric scalar in (0, 1) specifying the proportion of cells in each dataset to use for mutual nearest neighbor searching. See "See Also". Default NULL.
sigma	A numeric scalar specifying the bandwidth of the Gaussian smoothing kernel used to compute the correction vector for each cell. See "See Also". Default 0.1.
cosNormIn	A logical scalar indicating whether cosine normalization should be performed on the input data prior to calculating distances between cells. See "See Also". Default TRUE.
cosNormOut	A logical scalar indicating whether cosine normalization should be performed prior to computing corrected expression values. See "See Also". Default TRUE.
varAdj	A logical scalar indicating whether variance adjustment should be performed on the correction vectors. See "See Also". Default TRUE.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying whether the PCA and nearest-neighbor searches should be parallelized.

**Value**

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

**References**

Haghverdi L, Lun ATL, et. al., 2018

**See Also**

[mnnCorrect](#)

**Examples**

```
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log1p(counts(sceBatches))
sceCorr <- runMNNCorrect(sceBatches)
```

---

runModelGeneVar      *Calculate Variable Genes with Scran modelGeneVar*

---

**Description**

Generates and stores variability data in the input [SingleCellExperiment](#) object, using [modelGeneVar](#) method.

Also selects a specified number of top HVGs and store the logical selection in `rowData`.

**Usage**

```
runModelGeneVar(inSCE, useAssay = "logcounts")
```

**Arguments**

inSCE            A [SingleCellExperiment](#) object

useAssay        A character string to specify an assay to compute variable features from. Default "logcounts".

**Value**

inSCE updated with variable feature metrics in rowData

**Author(s)**

Irzam Sarfraz

**See Also**

[runFeatureSelection](#), [runSeuratFindHVG](#), [getTopHVG](#), [plotTopHVG](#)

**Examples**

```
data("scExample", package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- scaterlogNormCounts(sce, "logcounts")
sce <- runModelGeneVar(sce)
hvf <- getTopHVG(sce, method = "modelGeneVar", hvgNumber = 10,
                 useFeatureSubset = NULL)
```

---

runNormalization

*Run normalization/transformation with various methods*

---

**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 = "logcounts",
  normalizationMethod = "logNormCounts",
  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 'SC-Transform' 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, c(10, -10) 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",
  mitoGeneLocation = "rownames",
  mitoRef = c(NULL, "human", "mouse"),
  mitoIDType = c("ensembl", "symbol", "entrez", "ensemblTranscriptID"),
  mitoPrefix = "MT-",
  mitoID = NULL,
  collectionName = NULL,
  geneSetList = NULL,
  geneSetListLocation = "rownames",
  geneSetCollection = NULL,
  percent_top = c(50, 100, 200, 500),
  use_altexps = FALSE,
  flatten = TRUE,
  detectionLimit = 0,
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

<code>inSCE</code>	A <a href="#">SingleCellExperiment</a> object.
<code>useAssay</code>	A string specifying which assay in the SCE to use. Default "counts".
<code>mitoGeneLocation</code>	Character. Describes the location within <code>inSCE</code> where the gene identifiers in the mitochondrial gene sets should be located. 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. If this parameter is set to NULL, then no mitochondrial metrics will be calculated. Default "rownames".
<code>mitoRef</code>	Character. The species used to extract mitochondrial genes ID from build-in mitochondrial geneset in SCTK. Available species options are "human" and "mouse". Default is "human".
<code>mitoIDType</code>	Character. Types of mitochondrial gene id. SCTK supports "symbol", "entrez", "ensembl" and "ensemblTranscriptID". It is used with <code>mitoRef</code> to extract mitochondrial genes from build-in mitochondrial geneset in SCTK. 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 mitochondrial genes from the gene symbol. For

example, `mitoPrefix = "^MT-"` can be used to detect mito gene symbols like "MT-ND4". Note that case is ignored so "mt-" will still match "MT-ND4". Default `"^MT-"`.

<code>mitoID</code>	Character. A vector of mitochondrial genes to be quantified.
<code>collectionName</code>	Character. Name of a <code>GeneSetCollection</code> obtained by using one of the <code>importGeneSet*</code> functions. Default <code>NULL</code> .
<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 <code>NULL</code> .
<code>geneSetListLocation</code>	Character or numeric vector. If set to <code>'rownames'</code> , then the genes in <code>geneSetList</code> 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 <code>'rownames'</code> and <code>rowData(inSCE)</code> . An integer or integer vector can be supplied to denote the column index in <code>rowData(inSCE)</code> . Default <code>'rownames'</code> .
<code>geneSetCollection</code>	Class of <code>GeneSetCollection</code> from package <code>GSEABase</code> . The location of the gene IDs in <code>inSCE</code> should be in the <code>description</code> slot of each gene set and should follow the same notation as <code>geneSetListLocation</code> . The function <code>getGmt</code> 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>percent_top</code>	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. Default <code>c(50, 100, 200, 500)</code> .
<code>use_altexps</code>	Logical scalar indicating whether QC statistics should be computed for alternative Experiments in <code>inSCE</code> ( <code>altExps(inSCE)</code> ). If <code>TRUE</code> , statistics are computed for all alternative experiments. Alternatively, an integer or character vector specifying the alternative Experiments to use to compute QC statistics. Alternatively <code>NULL</code> , in which case alternative experiments are not used. Default <code>FALSE</code> .
<code>flatten</code>	Logical scalar indicating whether the nested <code>DataFrame-class</code> in the output should be flattened. Default <code>TRUE</code> .
<code>detectionLimit</code>	A numeric scalar specifying the lower detection limit for expression. Default <code>0</code>
<code>BPPARAM</code>	A <code>BiocParallelParam</code> object specifying whether the QC calculations should be parallelized. Default <code>BiocParallel::SerialParam()</code> .

## Details

This function allows multiple ways to import mitochondrial genes and quantify their expression in cells. `mitoGeneLocation` is required for all methods to point to the location within `inSCE` object that stores the mitochondrial gene IDs or Symbols. The various ways mito genes can be specified are:

- A combination of `mitoRef` and `mitoIDType` parameters can be used to load pre-built mitochondrial gene sets stored in the `SCTK` package. These parameters are used in the `importMitoGeneSet` function.
- The `mitoPrefix` parameter can be used to search for features matching a particular pattern. The default pattern is an "MT-" at the beginning of the ID.

- The `mitoID` parameter can be used to directly supply a vector of mitochondrial gene IDs or names. Only features that exactly match items in this vector will be included in the mitochondrial gene set.

### Value

A `SingleCellExperiment` object with cell QC metrics added to the `colData` slot.

### See Also

`addPerCellQC`, `link{plotRunPerCellQCResults}`, `runCellQC`

### 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",
  assayName = "SCANORAMA",
  SIGMA = 15,
  ALPHA = 0.1,
  KNN = 20,
  approx = TRUE
)
```

### Arguments

<code>inSCE</code>	Input <code>SingleCellExperiment</code> object
<code>useAssay</code>	A single character indicating the name of the assay requiring batch correction. Scanorama requires a transformed normalized expression assay. Default "logcounts".
<code>batch</code>	A single character indicating a field in <code>colData</code> that annotates the batches of each cell; or a vector/factor with the same length as the number of cells. Default "batch".

assayName	A single character. The name for the corrected assay. Will be saved to <a href="#">assay</a> . Default "SCANORAMA".
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 20.
approx	Boolean. Use approximate nearest neighbors, greatly speeds up matching runtime. Default TRUE.

**Value**

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

**References**

Brian Hie et al, 2019

**Examples**

```
## Not run:
data('sceBatches', package = 'singleCellTK')
logcounts(sceBatches) <- log1p(counts(sceBatches))
sceCorr <- runSCANORAMA(sceBatches, "ScaterLogNormCounts")

## End(Not run)
```

---

`runScanpyFindClusters` *runScanpyFindClusters* Computes the clusters from the input sce object and stores them back in sce object

---

**Description**

`runScanpyFindClusters` Computes the clusters from the input sce object and stores them back in sce object

**Usage**

```
runScanpyFindClusters(
  inSCE,
  useAssay = "scanpyScaledData",
  useReducedDim = "scanpyPCA",
  nNeighbors = 10,
  dims = 40,
  method = c("leiden", "louvain"),
  colDataName = NULL,
  resolution = 1,
  niterations = -1,
  flavor = "vtraag",
  use_weights = FALSE,
```

```

cor_method = "pearson",
inplace = TRUE,
externalReduction = NULL,
seed = 12345
)

```

### Arguments

inSCE	(sce) object from which clusters should be computed and stored in
useAssay	Assay containing scaled counts to use for clustering.
useReducedDim	Reduction method to use for computing clusters. Default "scanpyPCA".
nNeighbors	The size of local neighborhood (in terms of number of neighboring data points) 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 10.
dims	numeric value of how many components to use for computing clusters. Default 40.
method	selected method to compute clusters. One of "louvain", and "leiden". Default louvain.
colDataName	Specify the name to give to this clustering result. Default is NULL that will generate a meaningful name automatically.
resolution	A parameter value controlling the coarseness of the clustering. Higher values lead to more clusters Default 1.
niterations	How many iterations of the Leiden clustering method to perform. Positive values above 2 define the total number of iterations to perform, -1 has the method run until it reaches its optimal clustering. Default -1.
flavor	Choose between to packages for computing the clustering. Default vtraag
use_weights	Boolean. Use weights from knn graph. Default FALSE
cor_method	correlation method to use. Options are 'pearson', 'kendall', and 'spearman'. Default pearson.
inplace	If True, adds dendrogram information to annData object, else this function returns the information. Default TRUE
externalReduction	Pass DimReduce object if PCA computed through other libraries. Default NULL.
seed	Specify numeric value to set as a seed. Default 12345.

### Value

Updated sce object which now contains the computed clusters

### Examples

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")

## End(Not run)

```

---

runScanpyFindHVG	<i>runScanpyFindHVG Find highly variable genes and store in the input sce object</i>
------------------	--

---

### Description

runScanpyFindHVG Find highly variable genes and store in the input sce object

### Usage

```
runScanpyFindHVG(
  inSCE,
  useAssay = "scanpyNormData",
  method = c("seurat", "cell_ranger", "seurat_v3"),
  altExpName = "featureSubset",
  altExp = FALSE,
  hvgNumber = 2000,
  minMean = 0.0125,
  maxMean = 3,
  minDisp = 0.5,
  maxDisp = Inf
)
```

### 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 log normalized data, except when flavor='seurat_v3', in which counts data is expected.
method	selected method to use for computation of highly variable genes. One of 'seurat', 'cell_ranger', or 'seurat_v3'. Default "seurat".
altExpName	Character. Name of the alternative experiment object to add if returnAsAltExp = TRUE. Default featureSubset.
altExp	Logical value indicating if the input object is an altExperiment. Default FALSE.
hvgNumber	numeric value of how many genes to select as highly variable. Default 2000
minMean	If n_top_genes unequal None, this and all other cutoffs for the means and the normalized dispersions are ignored. Ignored if flavor='seurat_v3'. Default 0.0125
maxMean	If n_top_genes unequal None, this and all other cutoffs for the means and the normalized dispersions are ignored. Ignored if flavor='seurat_v3'. Default 3
minDisp	If n_top_genes unequal None, this and all other cutoffs for the means and the normalized dispersions are ignored. Ignored if flavor='seurat_v3'. Default 0.5
maxDisp	If n_top_genes unequal None, this and all other cutoffs for the means and the normalized dispersions are ignored. Ignored if flavor='seurat_v3'. Default Inf

### Value

Updated SingleCellExperiment object with highly variable genes computation stored [getTopHVG](#), [plotTopHVG](#)

**Examples**

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
g <- getTopHVG(sce, method = "seurat", hvgNumber = 500)

## End(Not run)

```

---

```
runScanpyFindMarkers  runScanpyFindMarkers
```

---

**Description**

runScanpyFindMarkers

**Usage**

```

runScanpyFindMarkers(
  inSCE,
  nGenes = NULL,
  useAssay = "scanpyNormData",
  colDataName,
  group1 = "all",
  group2 = "rest",
  test = c("wilcoxon", "t-test", "t-test_overestim_var", "logreg"),
  corr_method = c("benjamini-hochberg", "bonferroni")
)

```

**Arguments**

inSCE	Input SingleCellExperiment object.
nGenes	The number of genes that appear in the returned tables. Defaults to all genes.
useAssay	Specify the name of the assay to use for computation of marker genes. It is recommended to use log normalized assay.
colDataName	colData to use as the key of the observations grouping to consider.
group1	Name of group1. Subset of groups, to which comparison shall be restricted, or 'all' (default), for all groups.
group2	Name of group2. If 'rest', compare each group to the union of the rest of the group. If a group identifier, compare with respect to this group. Default is 'rest'
test	Test to use for DE. Default "t-test".
corr_method	p-value correction method. Used only for 't-test', 't-test_overestim_var', and 'wilcoxon'.

**Value**

A SingleCellExperiment object that contains marker genes populated in a data.frame stored inside metadata slot.

**Examples**

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyFindMarkers(sce, colDataName = "Scanpy_louvain_1" )

## End(Not run)

```

---

runScanpyNormalizeData

*runScanpyNormalizeData* Wrapper for *NormalizeData()* function from scanpy library Normalizes the sce object according to the input parameters

---

**Description**

runScanpyNormalizeData Wrapper for *NormalizeData()* function from scanpy library Normalizes the sce object according to the input parameters

**Usage**

```

runScanpyNormalizeData(
  inSCE,
  useAssay,
  targetSum = 10000,
  maxFraction = 0.05,
  normAssayName = "scanpyNormData"
)

```

**Arguments**

inSCE	(sce) object to normalize
useAssay	Assay containing raw counts to use for normalization.
targetSum	If NULL, after normalization, each observation (cell) has a total count equal to the median of total counts for observations (cells) before normalization. Default 1e4
maxFraction	Include cells that have more counts than max_fraction of the original total counts in at least one cell. Default 0.05
normAssayName	Name of new assay containing normalized data. Default scanpyNormData.

**Value**

Normalized SingleCellExperiment object

**Examples**

```

data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
rownames(sce) <- rowData(sce)$feature_name
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")

## End(Not run)

```

---

runScanpyPCA	<i>runScanpyPCA Computes PCA on the input sce object and stores the calculated principal components within the sce object</i>
--------------	---

---

**Description**

runScanpyPCA Computes PCA on the input sce object and stores the calculated principal components within the sce object

**Usage**

```

runScanpyPCA(
  inSCE,
  useAssay = "scanpyScaledData",
  reducedDimName = "scanpyPCA",
  nPCs = 50,
  method = c("arpack", "randomized", "auto", "lobpcg"),
  use_highly_variable = TRUE,
  seed = 12345
)

```

**Arguments**

inSCE	(sce) object on which to compute PCA
useAssay	Assay containing scaled counts to use in PCA. Default "scanpyScaledData".
reducedDimName	Name of new reducedDims object containing Scanpy PCA. Default scanpyPCA.
nPCs	numeric value of how many components to compute. Default 50.
method	selected method to use for computation of pca. One of 'arpack', 'randomized', 'auto' or 'lobpcg'. Default "arpack".
use_highly_variable	boolean value of whether to use highly variable genes only. By default uses them if they have been determined beforehand.
seed	Specify numeric value to set as a seed. Default 12345.

**Value**

Updated SingleCellExperiment object which now contains the computed principal components

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")

## End(Not run)
```

---

runScanpyScaleData	<i>runScanpyScaleData Scales the input sce object according to the input parameters</i>
--------------------	---

---

## Description

runScanpyScaleData Scales the input sce object according to the input parameters

## Usage

```
runScanpyScaleData(
  inSCE,
  useAssay = "scanpyNormData",
  scaledAssayName = "scanpyScaledData"
)
```

## Arguments

inSCE (sce) object to scale

useAssay Assay containing normalized counts to scale.

scaledAssayName Name of new assay containing scaled data. Default scanpyScaledData.

## Value

Scaled SingleCellExperiment object

## Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")

## End(Not run)
```

---

runScanpyTSNE	<i>runScanpyTSNE Computes tSNE from the given sce object and stores the tSNE computations back into the sce object</i>
---------------	--

---

### Description

runScanpyTSNE Computes tSNE from the given sce object and stores the tSNE computations back into the sce object

### Usage

```
runScanpyTSNE(
  inSCE,
  useAssay = NULL,
  useReducedDim = "scanpyPCA",
  reducedDimName = "scanpyTSNE",
  dims = 40,
  perplexity = 30,
  externalReduction = NULL,
  seed = 12345
)
```

### Arguments

inSCE	(sce) object on which to compute the tSNE
useAssay	Specify name of assay to use. Default is NULL, so useReducedDim param will be used instead.
useReducedDim	selected reduction method to use for computing tSNE. Default "scanpyPCA".
reducedDimName	Name of new reducedDims object containing Scanpy tSNE Default scanpyTSNE.
dims	Number of reduction components to use for tSNE computation. Default 40.
perplexity	Adjust the perplexity tuneable parameter for the underlying tSNE call. Default 30.
externalReduction	Pass DimReduc object if PCA computed through other libraries. Default NULL.
seed	Specify numeric value to set as a seed. Default 12345.

### Value

Updated sce object with tSNE computations stored

### Examples

```
data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyTSNE(sce, useReducedDim = "scanpyPCA")

## End(Not run)
```

---

runScanpyUMAP	<i>runScanpyUMAP Computes UMAP from the given sce object and stores the UMAP computations back into the sce object</i>
---------------	--

---

### Description

runScanpyUMAP Computes UMAP from the given sce object and stores the UMAP computations back into the sce object

### Usage

```
runScanpyUMAP(
  inSCE,
  useAssay = NULL,
  useReducedDim = "scanpyPCA",
  reducedDimName = "scanpyUMAP",
  dims = 40,
  minDist = 0.5,
  nNeighbors = 10,
  spread = 1,
  alpha = 1,
  gamma = 1,
  externalReduction = NULL,
  seed = 12345
)
```

### Arguments

inSCE	(sce) object on which to compute the UMAP
useAssay	Specify name of assay to use. Default is NULL, so useReducedDim param will be used instead.
useReducedDim	Reduction to use for computing UMAP. Default is "scanpyPCA".
reducedDimName	Name of new reducedDims object containing Scanpy UMAP Default scanpyUMAP.
dims	Numerical value of how many reduction components to use for UMAP computation. Default 40.
minDist	Sets the "min_dist" parameter to the underlying UMAP call. Default 0.5.
nNeighbors	Sets the "n_neighbors" parameter to the underlying UMAP call. Default 10.
spread	Sets the "spread" parameter to the underlying UMAP call. Default 1.
alpha	Sets the "alpha" parameter to the underlying UMAP call. Default 1.
gamma	Sets the "gamma" parameter to the underlying UMAP call. Default 1.
externalReduction	Pass DimReduce object if PCA computed through other libraries. Default NULL.
seed	Specify numeric value to set as a seed. Default 12345.

### Value

Updated sce object with UMAP computations stored

**Examples**

```

data(scExample, package = "singleCellTK")
## Not run:
sce <- runScanpyNormalizeData(sce, useAssay = "counts")
sce <- runScanpyFindHVG(sce, useAssay = "scanpyNormData", method = "seurat")
sce <- runScanpyScaleData(sce, useAssay = "scanpyNormData")
sce <- runScanpyPCA(sce, useAssay = "scanpyScaledData")
sce <- runScanpyFindClusters(sce, useReducedDim = "scanpyPCA")
sce <- runScanpyUMAP(sce, useReducedDim = "scanpyPCA")

## End(Not run)

```

runScDbfFinder

*Detect doublet cells using [scDbfFinder](#).***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(RNGseed = seed)
)

```

**Arguments**

inSCE	A <a href="#">SingleCellExperiment</a> object.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. Default NULL.
useAssay	A string specifying which assay in the SCE to use. Default "counts".
nNeighbors	Number of nearest neighbors used to calculate density for doublet detection. Default 50.
simDoublets	Number of simulated doublets created for doublet detection. Default 10000.
seed	Seed for the random number generator, can be set to NULL. Default 12345.
BPPARAM	A <a href="#">BiocParallelParam-class</a> object specifying whether the neighbour searches should be parallelized. Default <code>BiocParallel::SerialParam(RNGseed = seed)</code> .

**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 scDblFinder QC outputs added to the `colData` slot.

**References**

Lun ATL (2018). Detecting doublet cells with scran. [https://l1tla.github.io/SingleCellThoughts/software/doublet\\_detection/bycell.html](https://l1tla.github.io/SingleCellThoughts/software/doublet_detection/bycell.html)

**See Also**

[scDblFinder](#), [plotScDblFinderResults](#), [runCellQC](#)

**Examples**

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
sce <- runScDblFinder(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",
  hvgExprs = "counts",
  seg = NULL,
  kmeansK = NULL,
  cellType = NULL,
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object
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 <code>assay</code> . Default "scMerge".

hvgExprs	A single character. The assay that to be used for highly variable genes identification. Default "counts".
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 with <a href="#">segList</a> or <a href="#">segList_ensemblGeneID</a> . 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 kmeansK needs to be the same as the number of batches. Default NULL, and this value will be auto-detected by default, depending on cellType.
cellType	A single character. A string indicating a field in <code>colData(inSCE)</code> that defines different cell types. Default 'cell_type'.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying whether should be parallelized. Default <code>BiocParallel::SerialParam()</code> .

### Value

The input [SingleCellExperiment](#) object with `assay(inSCE, assayName)` updated.

### References

Hoa, et al., 2020

### Examples

```
data('sceBatches', package = 'singleCellTK')
## Not run:
logcounts(sceBatches) <- log1p(counts(sceBatches))
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,
  useReducedDim = "PCA",
  useAssay = NULL,
  useAltExp = NULL,
  altExpAssay = "counts",
  altExpRedDim = NULL,
  clusterName = "cluster",
  k = 14,
```

```

nComp = 10,
weightType = "jaccard",
algorithm = c("louvain", "leiden", "walktrap", "infomap", "fastGreedy", "labelProp",
             "leadingEigen"),
BPPARAM = BiocParallel::SerialParam(),
seed = 12345,
...
)

```

## Arguments

inSCE	A <a href="#">SingleCellExperiment</a> object.
useReducedDim	A single character, specifying which low-dimension representation ( <a href="#">reducedDim</a> ) to perform the clustering algorithm on. Default "PCA".
useAssay	A single character, specifying which <a href="#">assay</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 "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 14.
nComp	An integer. The number of components to use for graph construction. Default 10. See Detail.
weightType	A single character, that specifies the edge weighing scheme when constructing the Shared Nearest-Neighbor (SNN) graph. Choose from "rank", "number", "jaccard". Default "jaccard".
algorithm	A single character, that specifies the community detection algorithm to work on the SNN graph. Choose from "leiden", "louvain", "walktrap", "infomap", "fastGreedy", "labelProp", "leadingEigen". Default "louvain". See Detail.
BPPARAM	A <a href="#">BiocParallelParam</a> object to use for processing the SNN graph generation step in parallel.
seed	Random seed for reproducibility of results. Default NULL will use global seed in use by the R environment.
...	Other optional parameters passed to the <a href="#">igraph</a> clustering functions. See Details.

## Details

Different graph based clustering algorithms have diverse sets of parameters that users can tweak. The help information can be found here:

- for "louvain", see function help [cluster\\_louvain](#)
- for "leiden", see function help [cluster\\_leiden](#)

- for "walktrap", see function help [cluster\\_walktrap](#)
- for "infomap", see function help [cluster\\_infomap](#)
- for "fastGreedy", see function help [cluster\\_fast\\_greedy](#)
- for "labelProp", see function help [cluster\\_label\\_prop](#)
- for "leadingEigen", see function help [cluster\\_leading\\_eigen](#)

The Scrann SNN building method can work on specified nComp components. When users specify input matrix by useAssay or useAltExp + altExpAssay, the method will generate nComp components and use them all. When specifying useReducedDim or useAltExp + altExpReducedDim, this function will subset the top nComp components and pass them to the method.

### 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,
    minGeneVariabilityPct1 = 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.
sample	Character vector or colData variable name. Indicates which sample each cell belongs to. 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. See detail. 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 are excluded. Default 3.
minCells	Integer. Used for gene filtering prior to PCA. Genes expressed at fewer than minCounts in fewer than minCells are excluded. Default 3.

<code>minGeneVariabilityPctl</code>	Numeric. Used for gene filtering prior to PCA. Keep the most highly variable genes (in the top <code>minGeneVariabilityPctl</code> percentile), as measured by the v-statistic (Klein et al., Cell 2015). Default 85.
<code>logTransform</code>	Boolean. If TRUE, log-transform the counts matrix ( $\log_1p(\text{TPM})$ ). <code>sklearn.decomposition.TruncatedSVD</code> will be used for dimensionality reduction, unless <code>meanCenter</code> is TRUE. Default FALSE.
<code>meanCenter</code>	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.
<code>normalizeVariance</code>	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 <code>meanCenter</code> is TRUE. Default TRUE.
<code>nPrinComps</code>	Integer. Number of principal components used to embed the transcriptomes prior to k-nearest-neighbor graph construction. Default 30.
<code>tsneAngle</code>	Float. Determines angular size of a distant node as measured from a point in the t-SNE plot. If NULL, it is set to 0.5. Default NULL.
<code>tsnePerplexity</code>	Integer. The number of nearest neighbors that is used in other manifold learning algorithms. If NULL, it is set to 30. Default NULL.
<code>verbose</code>	Boolean. If TRUE, print progress updates. Default TRUE.
<code>seed</code>	Seed for the random number generator, can be set to NULL. Default 12345.

## Details

For the list of valid values for `distanceMetric`, see the documentation for [annoy](#) (if `useApproxNeighbors` is TRUE) or [sklearn.neighbors.NearestNeighbors](#) (if `useApproxNeighbors` is FALSE).

## Value

A [SingleCellExperiment](#) object with `scrub_doublets` output appended to the `colData` slot. The columns include `scrublet_score` and `scrublet_call`.

## See Also

[plotScrubletResults](#), [runCellQC](#)

## 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 = "seuratNormData",
  useReduction = c("pca", "ica"),
  dims = 10,
  algorithm = c("louvain", "multilevel", "SLM"),
  groupSingletons = TRUE,
  resolution = 0.8,
  seed = 12345,
  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.
seed	Specify the seed value. Default 12345.
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",
  method = c("vst", "dispersion", "mean.var.plot"),
  hvgNumber = 2000,
  createFeatureSubset = "hvf",
  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".
method	selected method to use for computation of highly variable genes. One of 'vst', 'dispersion', or 'mean.var.plot'. Default "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
createFeatureSubset	Specify a name of the subset to create for the identified variable features. Default is "hvf". Leave it NULL if you do not want to create a subset of variable features.
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

**See Also**

[runFeatureSelection](#), [runModelGeneVar](#), [getTopHVG](#), [plotTopHVG](#)

**Examples**

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

---

```
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</i> Computes the heatmap plot object from the pca slot in the input sce object
------------------	--

---

**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	Specify name of the assay that will be scaled by this function. The output scaled assay will be used for computation of the 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 <a href="#">DimHeatmap</a> for more information. Default TRUE.
raster	See <a href="#">DimHeatmap</a> 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 = "seuratScaledData",
  useFeatureSubset = NULL,
  scale = TRUE,
  reducedDimName = "seuratICA",
  nics = 20,
  seed = 12345,
  verbose = FALSE
)
```

**Arguments**

inSCE	(sce) object on which to compute ICA
useAssay	Assay containing scaled counts to use in ICA.
useFeatureSubset	Subset of feature to use for dimension reduction. A character string indicating a rowData variable that stores the logical vector of HVG selection, or a vector that can subset the rows of inSCE. Default NULL.
scale	Logical scalar, whether to standardize the expression values using <a href="#">ScaleData</a> . Default TRUE.
reducedDimName	Name of new reducedDims object containing Seurat ICA Default seuratICA.
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.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

### Details

For features used for computation, it can be controlled by `features` or `useFeatureSubset`. When `features` is specified, the scaling and dimensionality reduction will only be processed with these features. When `features` is NULL but `useFeatureSubset` is specified, will use the features that the HVG list points to. If both parameters are NULL, the function will see if any Seurat's variable feature detection has been ever performed, and use them if found. Otherwise, all features are used.

### 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</i> Compute jackstraw plot and store the computations in the input sce object
--------------------	---

---

**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	Specify name of the assay to use for scaling. Assay name provided against this parameter is scaled by the function and used for the computation of JackStraw scores along with the reduced dimensions specified by the dims parameter.
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)
```

---

runSeuratPCA	<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 = "seuratNormData",
  useFeatureSubset = "hvf",
  scale = TRUE,
  reducedDimName = "seuratPCA",
  nPCs = 20,
  seed = 12345,
  verbose = TRUE
)
```

### Arguments

inSCE            (sce) object on which to compute PCA  
 useAssay        Assay containing scaled counts to use in PCA. Default "seuratNormData".  
 useFeatureSubset      Subset of feature to use for dimension reduction. A character string indicating a rowData variable that stores the logical vector of HVG selection, or a vector that can subset the rows of inSCE. Default "hvf".  
 scale            Logical scalar, whether to standardize the expression values using [ScaleData](#). Default TRUE.  
 reducedDimName    Name of new reducedDims object containing Seurat PCA. Default seuratPCA.  
 nPCs            numeric value of how many components to compute. Default 20.

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.

### Details

For features used for computation, it can be controlled by `features` or `useFeatureSubset`. When `features` is specified, the scaling and dimensionality reduction will only be processed with these features. When `features` is NULL but `useFeatureSubset` is specified, will use the features that the HVG list points to. If both parameters are NULL, the function will see if any Seurat's variable feature detection has been ever performed, and use them if found. Otherwise, all features are used.

### 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 <- setTopHVG(sce, method = "vst", featureSubsetName = "hvf")
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 seuratScaledData.
model	selected model to use for scaling data. Default "linear".
scale	boolean if data should be scaled or not. Default TRUE.
center	boolean if data should be centered or not. Default TRUE
scaleMax	maximum numeric value to return for scaled data. Default 10.
verbose	Logical value indicating if informative messages should be displayed. Default is TRUE.

**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 = "fine",
  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 "fine".

- 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) <- log1p(counts(sceBatches))
#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 <code>?SoupX::autoEstCont</code> .
maxMarkers	Integer. If we have heaps of good markers, keep only the best <code>maxMarkers</code> of them. Default 100. See <code>?SoupX::autoEstCont</code> .
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 <a href="#">estimateNonExpressingCells</a> as <code>maximumContamination</code> . Default <code>c(0.01, 0.8)</code> . See <code>?SoupX::autoEstCont</code> .
rhoMaxFDR	Numeric. False discovery rate passed to <a href="#">estimateNonExpressingCells</a> , to test if <code>rho</code> is less than <code>maximumContamination</code> . Default 0.2. See <code>?SoupX::autoEstCont</code> .
priorRho	Numeric. Mode of gamma distribution prior on contamination fraction. Default 0.05. See <code>?SoupX::autoEstCont</code> .
priorRhoStdDev	Numeric. Standard deviation of gamma distribution prior on contamination fraction. Default 0.1. See <code>?SoupX::autoEstCont</code> .
forceAccept	Logical. Should we allow very high contamination fractions to be used. Passed to <a href="#">setContaminationFraction</a> . Default FALSE. See <code>?SoupX::autoEstCont</code> .
adjustMethod	Character. Method to use for correction. One of 'subtraction', 'soupOnly', or 'multinomial'. Default 'subtraction'. See <code>?SoupX::adjustCounts</code> .

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 method = 'soupOnly'. 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

### See Also

plotSoupXResults

### Examples

```
## Not run:
# SoupX does not work for toy example,
sce <- importExampleData("pbmc3k")
sce <- runSoupX(sce, sample = "sample")
plotSoupXResults(sce, sample = "sample")

## End(Not run)
```

---

runTSCAN

*Run TSCAN to obtain pseudotime values for cells*

---

### Description

Wrapper for obtaining a pseudotime ordering of the cells by projecting them onto the minimum spanning tree (MST)

### Usage

```
runTSCAN(
  inSCE,
  useReducedDim = "PCA",
  cluster = NULL,
  starter = NULL,
  seed = 12345
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useReducedDim	Character. A low-dimension representation in reducedDims, will be used for both clustering if cluster not specified and MST construction. Default "PCA".
cluster	Grouping for each cell in inSCE. A vector with equal length to the number of the cells in inSCE, or a single character for retrieving colData variable. Default NULL, will run runScranSNN to obtain.
starter	Character. Specifies the starting node from which to compute the pseudotime. Default NULL, will select an arbitrary node.
seed	An integer. Random seed for clustering if cluster is not specified. Default 12345.

**Value**

The input inSCE object with pseudotime ordering of the cells along the paths and the cluster label stored in colData, and other unstructured information in metadata.

**Author(s)**

Nida Pervaiz

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
```

---

runTSCANClusterDEAnalysis

*Find DE genes between all TSCAN paths rooted from given cluster*

---

**Description**

This function finds all paths that root from a given cluster useCluster, and performs tests to identify significant features for each path, and are not significant and/or changing in the opposite direction in the other paths. Using a branching cluster (i.e. a node with degree > 2) may highlight features which are responsible for the branching event. MST has to be pre-calculated with [runTSCAN](#).

**Usage**

```
runTSCANClusterDEAnalysis(
  inSCE,
  useCluster,
  useAssay = "logcounts",
  fdrThreshold = 0.05
)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
useCluster	The cluster to be regarded as the root, has to existing in <code>colData(inSCE)\$TSCAN_clusters</code> .
useAssay	Character. The name of the assay to use. This assay should contain log normalized counts. Default "logcounts".
fdrThreshold	Only out put DEGs with FDR value smaller than this value. Default 0.05.

**Value**

The input inSCE with results updated in metadata.

**Author(s)**

Nida Pervaiz

**Examples**

```
data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
mouseBrainSubsetSCE <- runTSCANclusterDEAnalysis(inSCE = mouseBrainSubsetSCE,
                                                useCluster = 1)
```

---

runTSCANDEG

*Test gene expression changes along a TSCAN trajectory path*


---

**Description**

Wrapper for identifying genes with significant changes with respect to one of the TSCAN pseudotime paths

**Usage**

```
runTSCANDEG(inSCE, pathIndex, useAssay = "logcounts", discardCluster = NULL)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> object.
pathIndex	Path index for which the pseudotime values should be used. This corresponds to the terminal node of specific path from the root node to the terminal node. Run <code>listTSCANTerminalNodes(inSCE)</code> for available options.
useAssay	Character. The name of the assay to use for testing the expression change. Should be log-normalized. Default "logcounts"
discardCluster	Cluster(s) which are not of use or masks other interesting effects can be discarded. Default NULL.

**Value**

The input inSCE with results updated in metadata.

**Author(s)**

Nida Pervaiz

**Examples**

```

data("mouseBrainSubsetSCE", package = "singleCellTK")
mouseBrainSubsetSCE <- runTSCAN(inSCE = mouseBrainSubsetSCE,
                               useReducedDim = "PCA_logcounts")
terminalNodes <- listTSCANTerminalNodes(mouseBrainSubsetSCE)
mouseBrainSubsetSCE <- runTSCANDEG(inSCE = mouseBrainSubsetSCE,
                                   pathIndex = terminalNodes[1])

```

runTSNE

*Run t-SNE embedding with Rtsne method***Description**

T-Stochastic Neighbour Embedding (t-SNE) algorithm is commonly for 2D visualization of single-cell data. This function wraps the Rtsne [Rtsne](#) function.

With this function, users can create tSNE embedding directly from raw count matrix, with necessary preprocessing including normalization, scaling, dimension reduction all automated. Yet we still recommend having the PCA as input, so that the result can match with the clustering based on the same input PCA, and will be much faster.

**Usage**

```

runTSNE(
  inSCE,
  useReducedDim = "PCA",
  useAssay = NULL,
  useAltExp = NULL,
  reducedDimName = "TSNE",
  logNorm = TRUE,
  useFeatureSubset = NULL,
  nTop = 2000,
  center = TRUE,
  scale = TRUE,
  pca = TRUE,
  partialPCA = FALSE,
  initialDims = 25,
  theta = 0.5,
  perplexity = 30,
  nIterations = 1000,
  numThreads = 1,
  seed = 12345
)

runQuickTSNE(inSCE, useAssay = "counts", ...)

getTSNE(
  inSCE,

```

```

    useReducedDim = "PCA",
    useAssay = NULL,
    useAltExp = NULL,
    reducedDimName = "TSNE",
    logNorm = TRUE,
    useFeatureSubset = NULL,
    nTop = 2000,
    center = TRUE,
    scale = TRUE,
    pca = TRUE,
    partialPCA = FALSE,
    initialDims = 25,
    theta = 0.5,
    perplexity = 30,
    nIterations = 1000,
    numThreads = 1,
    seed = 12345
)

```

### Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useReducedDim</code>	The low dimension representation to use for UMAP computation. Default "PCA".
<code>useAssay</code>	Assay to use for tSNE computation. If <code>useAltExp</code> is specified, <code>useAssay</code> has to exist in <code>assays(altExp(inSCE, useAltExp))</code> . Default NULL.
<code>useAltExp</code>	The subset to use for tSNE computation, usually for the selected.variable features. Default NULL.
<code>reducedDimName</code>	a name to store the results of the dimension reductions. Default "TSNE".
<code>logNorm</code>	Whether the counts will need to be log-normalized prior to generating the tSNE via <a href="#">scaterlogNormCounts</a> . Ignored when using <code>useReducedDim</code> . Default TRUE.
<code>useFeatureSubset</code>	Subset of feature to use for dimension reduction. A character string indicating a <code>rowData</code> variable that stores the logical vector of HVG selection, or a vector that can subset the rows of <code>inSCE</code> . Default NULL.
<code>nTop</code>	Automatically detect this number of variable features to use for dimension reduction. Ignored when using <code>useReducedDim</code> or using <code>useFeatureSubset</code> . Default 2000.
<code>center</code>	Whether data should be centered before PCA is applied. Ignored when using <code>useReducedDim</code> . Default TRUE.
<code>scale</code>	Whether data should be scaled before PCA is applied. Ignored when using <code>useReducedDim</code> . Default TRUE.
<code>pca</code>	Whether an initial PCA step should be performed. Ignored when using <code>useReducedDim</code> . Default TRUE.
<code>partialPCA</code>	Whether truncated PCA should be used to calculate principal components (requires the <code>irlba</code> package). This is faster for large input matrices. Ignored when using <code>useReducedDim</code> . Default FALSE.
<code>initialDims</code>	Number of dimensions from PCA to use as input in tSNE. Default 25.
<code>theta</code>	Numeric value for speed/accuracy trade-off (increase for less accuracy), set to 0.0 for exact TSNE. Default 0.5.

perplexity	perplexity parameter. Should not be bigger than $3 * \text{perplexity} < \text{ncol}(\text{inSCE}) - 1$ . Default 30. See <a href="#">Rtsne</a> details for interpretation.
nIterations	maximum iterations. Default 1000.
numThreads	Integer, number of threads to use using OpenMP, Default 1. 0 corresponds to using all available cores.
seed	Random seed for reproducibility of tSNE results. Default NULL will use global seed in use by the R environment.
...	Other parameters to be passed to runTSNE

### Value

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

### Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
# Run from raw counts
sce <- runQuickTSNE(sce)
## Not run:
# Run from PCA
sce <- scaterlogNormCounts(sce, "logcounts")
sce <- runModelGeneVar(sce)
sce <- setTopHVG(sce, method = "modelGeneVar", hvgNumber = 2000,
                featureSubsetName = "HVG_modelGeneVar2000")
sce <- scaterPCA(sce, useAssay = "logcounts",
                useFeatureSubset = "HVG_modelGeneVar2000", scale = TRUE)
sce <- runTSNE(sce, useReducedDim = "PCA")

## End(Not run)
```

---

runUMAP

*Run UMAP embedding with scater method*

---

### Description

Uniform Manifold Approximation and Projection (UMAP) algorithm is commonly for 2D visualization of single-cell data. These functions wrap the scater [calculateUMAP](#) function.

Users can use `runQuickUMAP` to directly create UMAP embedding from raw count matrix, with necessary preprocessing including normalization, variable feature selection, scaling, dimension reduction all automated. Therefore, `useReducedDim` is disabled for `runQuickUMAP`.

In a complete analysis, we still recommend having dimension reduction such as PCA created beforehand and select proper numbers of dimensions for using `runUMAP`, so that the result can match with the clustering based on the same input PCA.

### Usage

```
runUMAP(
  inSCE,
  useReducedDim = "PCA",
  useAssay = NULL,
```

```

    useAltExp = NULL,
    sample = NULL,
    reducedDimName = "UMAP",
    logNorm = TRUE,
    useFeatureSubset = NULL,
    nTop = 2000,
    scale = TRUE,
    pca = TRUE,
    initialDims = 10,
    nNeighbors = 30,
    nIterations = 200,
    alpha = 1,
    minDist = 0.01,
    spread = 1,
    seed = 12345,
    verbose = TRUE,
    BPPARAM = SerialParam()
)

runQuickUMAP(inSCE, useAssay = "counts", sample = "sample", ...)

getUMAP(
  inSCE,
  useReducedDim = "PCA",
  useAssay = NULL,
  useAltExp = NULL,
  sample = NULL,
  reducedDimName = "UMAP",
  logNorm = TRUE,
  useFeatureSubset = NULL,
  nTop = 2000,
  scale = TRUE,
  pca = TRUE,
  initialDims = 25,
  nNeighbors = 30,
  nIterations = 200,
  alpha = 1,
  minDist = 0.01,
  spread = 1,
  seed = 12345,
  BPPARAM = SerialParam()
)

```

### Arguments

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>useReducedDim</code>	The low dimension representation to use for UMAP computation. If <code>useAltExp</code> is specified, <code>useReducedDim</code> has to exist in <code>reducedDims(altExp(inSCE, useAltExp))</code> . Default "PCA".
<code>useAssay</code>	Assay to use for UMAP computation. If <code>useAltExp</code> is specified, <code>useAssay</code> has to exist in <code>assays(altExp(inSCE, useAltExp))</code> . Ignored when using <code>useReducedDim</code> . Default NULL.

useAltExp	The subset to use for UMAP computation, usually for the selected variable features. Default NULL.
sample	Character vector. Indicates which sample each cell belongs to. If given a single character, will take the annotation from colData. Default NULL.
reducedDimName	A name to store the results of the UMAP embedding coordinates obtained from this method. Default "UMAP".
logNorm	Whether the counts will need to be log-normalized prior to generating the UMAP via <a href="#">scatterlogNormCounts</a> . Ignored when using useReducedDim. Default TRUE.
useFeatureSubset	Subset of feature to use for dimension reduction. A character string indicating a rowData variable that stores the logical vector of HVG selection, or a vector that can subset the rows of inSCE. Default NULL.
nTop	Automatically detect this number of variable features to use for dimension reduction. Ignored when using useReducedDim or using useFeatureSubset. Default 2000.
scale	Whether useAssay matrix will need to be standardized. Default TRUE.
pca	Logical. Whether to perform dimension reduction with PCA before UMAP. Ignored when using useReducedDim. Default TRUE.
initialDims	Number of dimensions from PCA to use as input in UMAP. Default 10.
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 <a href="#">calculateUMAP</a> 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 <a href="#">calculateUMAP</a> 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 <a href="#">calculateUMAP</a> for more information.
seed	Random seed for reproducibility of UMAP results. Default NULL will use global seed in use by the R environment.
verbose	Logical. Whether to print log messages. Default TRUE.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying whether the PCA should be parallelized.
...	Parameters passed to runUMAP

### Value

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

### Examples

```
data(scExample, package = "singleCellTK")
sce <- subsetSCECols(sce, colData = "type != 'EmptyDroplet'")
# Run from raw counts
sce <- runQuickUMAP(sce)
plotDimRed(sce, "UMAP")
```

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 = "H",
  useAssay = "logcounts",
  resultNamePrefix = NULL,
  center = FALSE,
  gamma = TRUE
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>geneSetCollectionName</code>	Character. The name of the gene set collection to use. Default "H".
<code>useAssay</code>	Character. The name of the assay to use. This assay should contain log normalized counts. Default "logcounts".
<code>resultNamePrefix</code>	Character. Prefix to the name the VAM results which will be stored in the <code>reducedDim</code> slot of <code>inSCE</code> . The names of the output matrices will be <code>resultNamePrefix_Distance</code> and <code>resultNamePrefix_CDF</code> . If this parameter is set to NULL, then "VAM_geneSetCollectionName_" will be used. Default NULL.
<code>center</code>	Boolean. If TRUE, values will be mean centered when computing the Mahalanobis statistic. Default FALSE.
<code>gamma</code>	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 <code>center = FALSE</code> ). Default TRUE.

**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",
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object
<code>useAssay</code>	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 <code>colData</code> 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".
BPPARAM	A <code>BiocParallelParam</code> object specifying whether should be parallelized. Default <code>BiocParallel::SerialParam()</code> .

**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 <code>SingleCellExperiment</code> object with saved <code>assay</code> data and/or <code>colData</code> 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

*scaterCPM Uses CPM from scater library to compute counts-per-million.*

---

**Description**

scaterCPM Uses CPM from scater library to compute counts-per-million.

**Usage**

```
scaterCPM(inSCE, assayName = "ScaterCPMCounts", useAssay = "counts")
```

**Arguments**

inSCE	Input <code>SingleCellExperiment</code> 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_chc1, package = "scds")  
sce_chc1 <- scaterlogNormCounts(sce_chc1, "logcounts", "counts")
```

---

scaterPCA	<i>Perform scater PCA on a SingleCellExperiment Object</i>
-----------	--

---

### Description

A wrapper to [runPCA](#) function to compute principal component analysis (PCA) from a given [SingleCellExperiment](#) object.

**Usage**

```

scaterPCA(
  inSCE,
  useAssay = "logcounts",
  useFeatureSubset = "hvg2000",
  scale = TRUE,
  reducedDimName = "PCA",
  nComponents = 50,
  ntop = 2000,
  useAltExp = NULL,
  seed = 12345,
  BPPARAM = BiocParallel::SerialParam()
)

```

**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>useFeatureSubset</code>	Subset of feature to use for dimension reduction. A character string indicating a <code>rowData</code> variable that stores the logical vector of HVG selection, or a vector that can subset the rows of <code>inSCE</code> . Default "hvg2000".
<code>scale</code>	Logical scalar, whether to standardize the expression values. Default TRUE.
<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>ntop</code>	Automatically detect this number of variable features to use for dimension reduction. Ignored when using <code>useReducedDim</code> or using <code>useFeatureSubset</code> . Default 2000.
<code>useAltExp</code>	The subset to use for PCA computation, usually for the <code>selected.variable</code> features. Default NULL.
<code>seed</code>	Integer, random seed for reproducibility of PCA results. Default NULL.
<code>BPPARAM</code>	A <a href="#">BiocParallelParam</a> object specifying whether the PCA should be parallelized.

**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")

# Example of ranking variable genes, selecting the top variable features,
# and running PCA. Make sure to increase the number of highly variable
# features (hvgNumber) and the number of principal components (nComponents)
# for real datasets
sce <- runModelGeneVar(sce, useAssay = "logcounts")
sce <- setTopHVG(sce, method = "modelGeneVar", hvgNumber = 100,

```

```

featureSubsetName = "hvf")
sce <- scaterPCA(sce, useAssay = "logcounts", scale = TRUE,
useFeatureSubset = "hvf", nComponents = 5)

# Alternatively, let the scater PCA function select the top variable genes
sce <- scaterPCA(sce, useAssay = "logcounts", scale = TRUE,
useFeatureSubset = NULL, ntop = 100, nComponents = 5)

```

---

sce	<i>Example Single Cell RNA-Seq data in SingleCellExperiment Object, subset of 10x public dataset</i>
-----	--

---

### Description

<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.

### Value

Example Single Cell RNA-Seq data in SingleCellExperiment Object, subset of 10x public dataset

### 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')
```



```

                                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", "louvain", "leidenalg", "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. Use "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.
<code>pipPackages</code>	Character Vector. List of packages to install into the Conda environment using 'pip'.
<code>selectConda</code>	Boolean. Run <a href="#">selectSCTKConda</a> after installing all packages to select the Conda environment. Default TRUE.
<code>forge</code>	Boolean. Include the Conda Forge repository.
<code>pipIgnoreInstalled</code>	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).
<code>pythonVersion</code>	Passed to <code>python_version</code> variable in <a href="#">conda_install</a> . Default NULL.
<code>...</code>	Other parameters to pass to <a href="#">conda_install</a> .

**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", "louvain",
    "leidenalg", "scanorama", "bbknn", "anndata"),
  selectEnvironment = TRUE,
  python = NULL
)
```

**Arguments**

<code>envname</code>	Character. Name of the virtual environment to create.
<code>packages</code>	Character Vector. List of packages to install.
<code>selectEnvironment</code>	Boolean. Run <a href="#">selectSCTKVirtualEnvironment</a> after installing all packages to select the virtual environment. Default TRUE.
<code>python</code>	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	<i>Stably Expressed Gene (SEG) list object, with SEG sets for human and mouse.</i>
-----	--

---

**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.

**Value**

Stably Expressed Gene (SEG) list object, with SEG sets for human and mouse.

**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	<i>Selects a virtual environment</i>
------------------------------	--------------------------------------

---

**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 <code>rowNames</code> . 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))
```

---

setSCTKDisplayRow      *Indicates which rowData to use for visualization*

---

### Description

This function is to be used to specify which

### Usage

```
setSCTKDisplayRow(inSCE, featureDisplayRow)
```

### Arguments

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

**featureDisplayRow**                Indicates which column name of rowData 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")
```

---

singleCellTK                *Run the single cell analysis app*

---

### Description

Use this function to run the single cell analysis app.

### Usage

```
singleCellTK(inSCE = NULL, includeVersion = TRUE, theme = "yeti")
```

### Arguments

**inSCE**                Input [SingleCellExperiment](#) 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()`:
- `subDiffExtttest()`: 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 <- subDiffExtttest(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)
```

---

subsetSCECols

*Subset a SingleCellExperiment object by columns*


---

## 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**

`inSCE` Input [SingleCellExperiment](#) object.

`index` Integer vector. Vector of indices indicating which columns to keep. If `NULL`, this will not be used for subsetting. Default `NULL`.

`bool` Boolean vector. Vector of `TRUE` or `FALSE` indicating which columns should be kept. Needs to be the same length as the number of columns in `inSCE`. If `NULL`, this will not be used for subsetting. Default `NULL`.

`colData` Character. An expression that will identify a subset of columns using variables found in the `colData` of `inSCE`. For example, if `x` is a numeric vector in `colData`, then `"x < 5"` will return all columns with `x` less than 5. Single quotes should be used for character strings. For example, `"y == 'yes'"` will return all columns 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`.

**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	<i>Subset a SingleCellExperiment object by rows</i>
---------------	---

---

**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

<code>inSCE</code>	Input <a href="#">SingleCellExperiment</a> object.
<code>index</code>	Integer vector. Vector of indicies indicating which rows to keep. If NULL, this will not be used for subsetting. Default NULL.
<code>bool</code>	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 <code>inSCE</code> . If NULL, this will not be used for subsetting. Default NULL.
<code>rowData</code>	Character. An expression that will identify a subset of rows using variables found in the <code>rowData</code> of <code>inSCE</code> . For example, if <code>x</code> is a numeric vector in <code>rowData</code> , then <code>"x &lt; 5"</code> will return all rows with <code>x</code> less than 5. Single quotes should be used for character strings. For example, <code>"y == 'yes'"</code> will return all rows 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 NULL, this will not be used for subsetting. Default NULL.
<code>returnAsAltExp</code>	Boolean. If TRUE, the subsetted <a href="#">SingleCellExperiment</a> object will be returned in the <code>altExp</code> slot of <code>inSCE</code> . If FALSE, the subsetted <a href="#">SingleCellExperiment</a> object will be directly returned.
<code>altExpName</code>	Character. Name of the alternative experiment object to add if <code>returnAsAltExp = TRUE</code> . Default <code>subset</code> .
<code>prependAltExpName</code>	Boolean. If TRUE, <code>altExpName</code> will be added to the beginning of the assay names in the <code>altExp</code> object. This is only utilized if <code>returnAsAltExp = TRUE</code> . 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	<i>Summarize an assay in a <a href="#">SingleCellExperiment</a></i>
--------------	---

---

**Description**

Creates a table of summary metrics from an input [SingleCellExperiment](#)

**Usage**

```
summarizeSCE(inSCE, useAssay = NULL, sampleVariableName = NULL)
```

**Arguments**

inSCE	Input <a href="#">SingleCellExperiment</a> 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)
```

---

trimCounts	<i>Trim Counts</i>
------------	--------------------

---

**Description**

Trims an input count matrix such that each value greater than a threshold value and each value less than a provided lower threshold value is trimmed to the lower threshold value.

**Usage**

```
trimCounts(counts, trimValue = c(10, -10))
```

**Arguments**

counts	matrix
trimValue	where trimValue[1] for upper threshold and trimValue[2] as lower threshold. Default is c(10, -10)

**Value**

trimmed counts matrix



# Index

## \* datasets

- MitoGenes, [73](#)
- mouseBrainSubsetSCE, [73](#)
- msigdb\_table, [74](#)
- sce, [279](#)
- sceBatches, [279](#)
- SEG, [283](#)

[addPerCellQC](#), [230](#), [232](#)

[adjustCounts](#), [263](#)

[altExp](#), [245](#), [289](#)

[assay](#), [39](#), [202](#), [225](#), [226](#), [233](#), [243](#), [245](#), [276](#)

[autoEstCont](#), [263](#)

[barcodeRanks](#), [196](#)

[bcds](#), [198](#), [199](#)

[BiocParallelParam](#), [218](#), [227](#), [231](#), [244](#), [245](#), [272](#), [275](#), [278](#)

[buildSNNGraph](#), [244](#)

[calcEffectSizes](#), [7](#)

[calculateUMAP](#), [270](#), [272](#)

[cluster\\_fast\\_greedy](#), [246](#)

[cluster\\_infomap](#), [246](#)

[cluster\\_label\\_prop](#), [246](#)

[cluster\\_leading\\_eigen](#), [246](#)

[cluster\\_leiden](#), [245](#)

[cluster\\_louvain](#), [245](#)

[cluster\\_walktrap](#), [246](#)

[colData](#), [14](#), [39](#), [83](#), [177](#), [178](#), [196](#), [198](#), [200](#), [202–204](#), [211](#), [214](#), [215](#), [225](#), [232](#), [242](#), [243](#), [245](#), [248](#), [275](#), [276](#)

[colorRamp2](#), [145](#)

[combineSCE](#), [8](#)

[computeHeatmap](#), [9](#)

[computeZScore](#), [10](#)

[conda\\_create](#), [282](#)

[conda\\_install](#), [281](#), [282](#)

[constructSCE](#), [10](#)

[convertSCEToSeurat](#), [11](#)

[convertSeuratToSCE](#), [12](#)

[cxds](#), [203](#)

[cxds\\_bcds\\_hybrid](#), [204](#)

[data.table](#), [10](#)

[DataFrame-class](#), [231](#)

[dbscan](#), [210](#)

[decontX](#), [14](#), [209](#), [210](#)

[dedupRowNames](#), [13](#)

[DelayedArray](#), [45](#), [46](#), [51–55](#), [57](#), [65](#), [67](#), [68](#), [70](#), [175](#)

[DelayedArray-class](#), [48](#)

[detectCellOutlier](#), [13](#)

[diffAbundanceFET](#), [14](#), [35](#)

[DimHeatmap](#), [252](#)

[discreteColorPalette](#), [15](#)

[distinctColors](#), [15](#), [16](#)

[downSampleCells](#), [16](#)

[downSampleDepth](#), [18](#)

[emptyDrops](#), [67](#), [215](#)

[estimateNonExpressingCells](#), [264](#)

[expData](#), [19](#)

[expData](#), ANY, character-method, [19](#)

[expData<-](#), [20](#)

[expData<-](#), ANY, character, CharacterOrNullOrMissing, logical-method, [21](#)

[expDataNames](#), [21](#)

[expDataNames](#), ANY-method, [22](#)

[expDeleteDataTag](#), [23](#)

[exportSCE](#), [23](#)

[exportSCEtoAnnData](#), [24](#)

[exportSCEtoFlatFile](#), [25](#)

[exportSCEToSeurat](#), [26](#)

[expSetDataTag](#), [27](#)

[expTaggedData](#), [28](#)

[fastMNN](#), [218](#)

[featureIndex](#), [29](#), [58](#), [60](#), [61](#), [63](#), [64](#), [230](#)

[FindIntegrationAnchors](#), [255](#)

[findMarkerDiffExp](#) ([runFindMarker](#)), [220](#)

[findMarkerTopTable](#) ([getFindMarkerTopTable](#)), [36](#)

[fit\\_dirichlet](#), [210](#)

[generateHTANMeta](#), [30](#)

[generateMeta](#), [31](#)

[generateSimulatedData](#), [31](#)

[GeneSetCollection](#), [58–65](#), [280](#)

- getBiomarker, [32](#)
- getDEGTopTable, [33](#)
- getDiffAbundanceResults, [34](#)
- getDiffAbundanceResults, SingleCellExperiment-method [49](#)
- (getDiffAbundanceResults), [34](#)
- getDiffAbundanceResults<-
- (getDiffAbundanceResults), [34](#)
- getDiffAbundanceResults<- , SingleCellExperiment-method
- (getDiffAbundanceResults), [34](#)
- getEnrichRResult, [217](#)
- getEnrichRResult (getEnrichRResult<-), [35](#)
- getEnrichRResult, SingleCellExperiment-method
- (getEnrichRResult<-), [35](#)
- getEnrichRResult<- , [35](#)
- getEnrichRResult<- , SingleCellExperiment-method
- (getEnrichRResult<-), [35](#)
- getFindMarkerTopTable, [36](#), [105](#), [221](#)
- getGenesetNamesFromCollection, [37](#), [274](#)
- getGmt, [59](#), [231](#)
- getMSigDBTable, [38](#)
- getPathwayResultNames, [38](#), [274](#)
- getSampleSummaryStatsTable, [39](#)
- getSampleSummaryStatsTable, SingleCellExperiment-method
- (getSampleSummaryStatsTable), [39](#)
- getSceParams, [40](#)
- getSeuratVariableFeatures, [40](#)
- getSoupX (getSoupX<-), [41](#)
- getSoupX, SingleCellExperiment-method
- (getSoupX<-), [41](#)
- getSoupX<- , [41](#)
- getSoupX<- , SingleCellExperiment-method
- (getSoupX<-), [41](#)
- getTopHVG, [42](#), [165](#), [219](#), [228](#), [235](#), [251](#)
- getTSCANResults, [44](#)
- getTSCANResults, SingleCellExperiment-method
- (getTSCANResults), [44](#)
- getTSCANResults<- (getTSCANResults), [44](#)
- getTSCANResults<- , SingleCellExperiment-method
- (getTSCANResults), [44](#)
- getTSNE (runTSNE), [268](#)
- getUMAP (runUMAP), [270](#)
- ggplot, [83](#), [91](#), [145](#)
- grep, [29](#), [195](#)
- GSEABase, [58](#), [60](#), [61](#), [63](#), [64](#)
- HarmonyMatrix, [224](#)
- Heatmap, [104](#), [145](#)
- igraph, [245](#)
- importAlevin, [45](#)
- importAnnData, [46](#)
- importBUSTools, [47](#)
- importCellRanger, [49](#)
- importCellRangerV2 (importCellRanger), [49](#)
- importCellRangerV2Sample, [52](#)
- importCellRangerV3 (importCellRanger), [49](#)
- importCellRangerV3Sample, [53](#)
- importDropEst, [54](#)
- importExampleData, [55](#)
- importFromFiles, [56](#)
- importGeneSetsFromCollection, [58](#), [60](#), [62](#), [274](#)
- importGeneSetsFromGMT, [59](#), [59](#), [62](#), [63](#), [65](#), [274](#), [280](#)
- importGeneSetsFromList, [59](#), [60](#), [61](#), [63](#), [65](#), [273](#), [274](#), [280](#)
- importGeneSetsFromMSigDB, [38](#), [59](#), [60](#), [62](#), [62](#), [74](#), [273](#), [274](#), [280](#)
- importMitoGeneSet, [64](#), [231](#)
- importMultipleSources, [65](#)
- importOptimus, [66](#)
- importSEQC, [67](#)
- importSTARsolo, [69](#)
- IntegrateData, [255](#)
- isOutlier, [13](#)
- iterateSimulations, [70](#)
- kmeans, [224](#)
- list.dirs, [50](#)
- listSampleSummaryStatsTables, [71](#)
- listSampleSummaryStatsTables, SingleCellExperiment-method
- (listSampleSummaryStatsTables), [71](#)
- listTSCANResults (getTSCANResults), [44](#)
- listTSCANResults, SingleCellExperiment-method
- (getTSCANResults), [44](#)
- listTSCANTerminalNodes
- (getTSCANResults), [44](#)
- listTSCANTerminalNodes, SingleCellExperiment-method
- (getTSCANResults), [44](#)
- logNormCounts, [277](#)
- Matrix, [55](#)
- matrix, [45](#), [46](#), [48](#), [51–54](#), [57](#), [67](#), [68](#), [70](#)
- mergeSCEColData, [72](#)
- metadata, [59](#), [60](#), [62–64](#), [72](#)
- MitoGenes, [73](#)
- mnnCorrect, [227](#)
- modelGeneVar, [210](#), [227](#)
- mouseBrainSubsetSCE, [73](#)
- msigdb\_table, [74](#)

- msigdbr, [63](#)
- msigdbr\_species, [63](#)
- multiBatchPCA, [218](#)
  
- NestorowaHSCData, [55](#)
  
- plotBarcodeRankDropsResults, [75](#), [77](#), [196](#)
- plotBarcodeRankScatter, [76](#)
- plotBatchCorrCompare, [77](#)
- plotBatchVariance, [78](#)
- plotBcDsResults, [79](#), [199](#)
- plotBubble, [82](#)
- plotClusterAbundance, [83](#)
- plotCxdsResults, [84](#), [203](#)
- plotDecontXResults, [86](#)
- plotDEGHeatmap, [89](#), [94](#), [209](#)
- plotDEGRegression, [91](#), [209](#)
- plotDEGViolin, [92](#), [209](#)
- plotDEGVolcano, [94](#), [209](#)
- plotDimRed, [95](#)
- plotDoubletFinderResults, [96](#), [213](#)
- plotEmptyDropsResults, [98](#), [101](#), [216](#)
- plotEmptyDropsScatter, [99](#), [100](#), [216](#)
- plotEnrichR, [101](#)
- plotFindMarkerHeatmap, [37](#), [102](#), [221](#)
- plotMarkerDiffExp  
(plotFindMarkerHeatmap), [102](#)
- plotMASTThresholdGenes, [105](#)
- plotPathway, [106](#)
- plotPCA, [107](#)
- plotRunPerCellQCResults, [108](#)
- plotScanpyDotPlot, [110](#)
- plotScanpyEmbedding, [111](#)
- plotScanpyHeatmap, [112](#)
- plotScanpyHVG, [113](#)
- plotScanpyMarkerGenes, [114](#)
- plotScanpyMarkerGenesDotPlot, [115](#)
- plotScanpyMarkerGenesHeatmap, [116](#)
- plotScanpyMarkerGenesMatrixPlot, [117](#)
- plotScanpyMarkerGenesViolin, [119](#)
- plotScanpyMatrixPlot, [119](#)
- plotScanpyPCA, [121](#)
- plotScanpyPCAGeneRanking, [122](#)
- plotScanpyPCAVariance, [122](#)
- plotScanpyViolin, [123](#)
- plotScDbfFinderResults, [124](#), [243](#)
- plotScDsHybridResults, [126](#)
- plotSCEBarAssayData, [129](#)
- plotSCEBarColData, [130](#)
- plotSCEBatchFeatureMean, [132](#)
- plotSCEDensity, [133](#)
- plotSCEDensityAssayData, [134](#)
- plotSCEDensityColData, [136](#)
- plotSCEDimReduceColData, [137](#), [163](#)
- plotSCEDimReduceFeatures, [140](#)
- plotSCEHeatmap, [90](#), [91](#), [104](#), [142](#)
- plotSCEScatter, [145](#)
- plotSCEViolin, [147](#)
- plotSCEViolinAssayData, [150](#)
- plotSCEViolinColData, [152](#)
- plotScrubletResults, [154](#), [248](#)
- plotSeuratElbow, [157](#)
- plotSeuratGenes, [158](#)
- plotSeuratHeatmap, [159](#)
- plotSeuratHVG, [159](#)
- plotSeuratJackStraw, [160](#)
- plotSeuratReduction, [161](#)
- plotSoupXResults, [162](#)
- plotTopHVG, [43](#), [164](#), [219](#), [228](#), [235](#), [251](#)
- plotTSCANClusterDEG, [165](#)
- plotTSCANClusterPseudo, [166](#)
- plotTSCANDimReduceFeatures, [167](#)
- plotTSCANPseudotimeGenes, [168](#)
- plotTSCANPseudotimeHeatmap, [170](#)
- plotTSCANResults, [171](#)
- plotTSNE, [172](#)
- plotUMAP, [173](#)
  
- qcInputProcess, [174](#)
- quickCluster, [264](#)
  
- readMM, [45](#), [46](#), [48](#), [51–54](#), [57](#), [67](#), [68](#), [70](#)
- readSingleCellMatrix, [175](#)
- reducedDim, [245](#)
- reducedMNN, [218](#)
- reportCellQC, [176](#)
- reportClusterAbundance, [177](#)
- reportDiffAbundanceFET, [177](#)
- reportDiffExp, [178](#)
- reportDropletQC, [179](#)
- reportFindMarker, [180](#)
- reportQCTool, [181](#)
- reportSeurat, [182](#)
- reportSeuratClustering, [184](#)
- reportSeuratDimRed, [185](#)
- reportSeuratFeatureSelection, [187](#)
- reportSeuratMarkerSelection, [188](#)
- reportSeuratNormalization, [189](#)
- reportSeuratResults, [190](#)
- reportSeuratRun, [192](#)
- reportSeuratScaling, [194](#)
- ReprocessedAllenData, [55](#)
- ReprocessedFluidigmData, [55](#)
- reticulate, [281–285](#)
- retrieveFeatureIndex, [195](#)
- retrieveFeatureInfo, [30](#)

- retrieveSCEIndex, 195
- Rtsne, 268, 270
- runANOVA (runDEAnalysis), 205
- runBarcodeRankDrops, 75–77, 196
- runBBKNN, 197
- runBcnds, 79–81, 198
- runCellQC, 58, 60, 61, 63, 64, 199, 199, 203, 213, 232, 243, 248
- runClusterSummaryMetrics, 200
- runComBatSeq, 201
- runCxds, 84, 86, 155, 203
- runCxdsBcndsHybrid, 127, 204
- runDEAnalysis, 94, 178, 179, 205, 221
- runDecontX, 87, 209
- runDESeq2 (runDEAnalysis), 205
- runDimReduce, 211
- runDoubletFinder, 97, 98, 212
- runDropletQC, 196, 214, 216
- runEmptyDrops, 98–101, 215
- runEnrichR, 36, 216
- runFastMNN, 217
- runFeatureSelection, 43, 165, 219, 228, 251
- runFindMarker, 37, 102, 104, 105, 180, 220, 220
- runGSVA, 222
- runHarmony, 223
- runKMeans, 224
- runLimmaBC, 225
- runLimmaDE (runDEAnalysis), 205
- runMAST (runDEAnalysis), 205
- runMNNCorrect, 217, 226
- runModelGeneVar, 43, 165, 219, 227, 251
- runNormalization, 228
- runPCA, 277
- runPerCellQC, 109, 110, 200, 230
- runQuickTSNE (runTSNE), 268
- runQuickUMAP (runUMAP), 270
- runSCANORAMA, 232
- runScanpyFindClusters, 233
- runScanpyFindHVG, 235
- runScanpyFindMarkers, 236
- runScanpyNormalizeData, 237
- runScanpyPCA, 238
- runScanpyScaleData, 239
- runScanpyTSNE, 240
- runScanpyUMAP, 241
- runScDbtFinder, 124–126, 242
- runSCMerge, 243
- runScranSNN, 244
- runScrublet, 156, 246
- runSeuratFindClusters, 249
- runSeuratFindHVG, 43, 165, 219, 228, 250
- runSeuratFindMarkers, 251
- runSeuratHeatmap, 252
- runSeuratICA, 212, 253
- runSeuratIntegration, 254
- runSeuratJackStraw, 255
- runSeuratNormalizeData, 256
- runSeuratPCA, 212, 257
- runSeuratScaleData, 258
- runSeuratSCTransform, 259
- runSeuratTSNE, 212, 260
- runSeuratUMAP, 212, 261
- runSingleR, 262
- runSoupX, 41, 163, 263
- runTSCAN, 44, 166, 171, 265, 266
- runTSCANClusterDEAnalysis, 44, 165, 166, 266
- runTSCANDEG, 44, 168–170, 267
- runTSNE, 212, 268
- RunUMAP, 261
- runUMAP, 212, 270
- runVAM, 273
- runWilcox (runDEAnalysis), 205
- runZINBWave, 274
- sampleSummaryStats, 275
- ScaleData, 253, 257
- scaterCPM, 276
- scaterlogNormCounts, 269, 272, 277
- scaterPCA, 212, 277
- scDbtFinder, 242, 243
- sce, 279
- sceBatches, 279
- scRNAseq, 55
- scSEGIIndex, 244
- sctkListGeneSetCollections, 274, 280
- sctkPythonInstallConda, 281, 284
- sctkPythonInstallVirtualEnv, 282, 285
- SCTransform, 259
- SEG, 283
- segList, 244
- segList\_ensemblGeneID, 244
- selectSCTKConda, 281, 282, 284
- selectSCTKVirtualEnvironment, 282, 283, 284
- setContaminationFraction, 264
- setRowNames, 285
- setSampleSummaryStatsTable<-  
(getSampleSummaryStatsTable),  
39
- setSampleSummaryStatsTable<- ,SingleCellExperiment-method  
(getSampleSummaryStatsTable),  
39

setSCTKDisplayRow, [33](#), [43](#), [90](#), [94](#), [164](#), [166](#),  
[168–170](#), [286](#)  
setTopHVG, [219](#)  
setTopHVG (getTopHVG), [42](#)  
SingleCellExperiment, [8](#), [10](#), [13–15](#), [17](#), [18](#),  
[24–26](#), [29–33](#), [35–42](#), [44](#), [46](#), [47](#), [49](#),  
[55–67](#), [69](#), [71](#), [72](#), [75–77](#), [79](#), [80](#), [83](#),  
[84](#), [87](#), [89](#), [92–94](#), [97–100](#), [102](#), [103](#),  
[106](#), [108](#), [109](#), [124](#), [125](#), [127–129](#),  
[131–133](#), [135](#), [136](#), [138](#), [141](#), [143](#),  
[146](#), [148](#), [151](#), [153](#), [155](#), [163](#), [165](#),  
[167–174](#), [176–182](#), [184–200](#),  
[202–204](#), [207](#), [208](#), [210–216](#),  
[218–228](#), [230](#), [232](#), [233](#), [242–248](#),  
[262](#), [264](#), [266](#), [267](#), [269–280](#), [285](#),  
[286](#), [288–291](#)  
singleCellTK, [58](#), [59](#), [61](#), [62](#), [64](#), [281](#), [282](#),  
[284](#), [286](#)  
subDiffEx, [287](#)  
subDiffExANOVA (subDiffEx), [287](#)  
subDiffExttest (subDiffEx), [287](#)  
subsetSCECols, [288](#)  
subsetSCERows, [289](#)  
SummarizedExperiment, [29](#)  
summarizeSCE, [291](#)  
  
TENxPBMCData, [55](#), [56](#)  
thresholdSCRNACountMatrix, [105](#)  
trimCounts, [291](#)  
  
umap, [210](#)  
unit, [145](#)  
  
virtualenv\_create, [283](#)  
virtualenv\_install, [282](#), [283](#)  
  
with\_seed, [211](#)