

# Package ‘ChromSCape’

November 29, 2022

**Title** Analysis of single-cell epigenomics datasets with a Shiny App

**Version** 1.8.0

**Description** ChromSCape - Chromatin landscape profiling for Single Cells - is a ready-to-launch user-friendly Shiny Application for the analysis of single-cell epigenomics datasets (scChIP-seq, scATAC-seq, scCUT&Tag, ...) from aligned data to differential analysis & gene set enrichment analysis. It is highly interactive, enables users to save their analysis and covers a wide range of analytical steps: QC, preprocessing, filtering, batch correction, dimensionality reduction, visualization, clustering, differential analysis and gene set analysis.

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**biocViews** ShinyApps, Software, SingleCell, ChIPSeq, ATACSeq, MethylSeq, Classification, Clustering, Epigenetics, PrincipalComponent, SingleCell, ATACSeq, ChIPSeq, Annotation, BatchEffect, MultipleComparison, Normalization, Pathways, Preprocessing, QualityControl, ReportWriting, Visualization, GeneSetEnrichment, DifferentialPeakCalling

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annotation\_from\_merged\_peaks

*Find nearest peaks of each gene and return refined annotation*

**Description**

Find nearest peaks of each gene and return refined annotation

**Usage**

annotation\_from\_merged\_peaks(scExp, odir, merged\_peaks, geneTSS\_annotation)

**Arguments**

- scExp            A SingleCellExperiment object
- odir            An output directory where to write the mergedpeaks BED file
- merged\_peaks   A list of GRanges object containing the merged peaks
- geneTSS\_annotation  
                  A GRanges object with reference genes

**Value**

A data.frame with refined annotation

---

`annotToCol2`*annotToCol2*

---

### Description

`annotToCol2`

### Usage

```
annotToCol2(  
  annotS = NULL,  
  annotT = NULL,  
  missing = c("", NA),  
  anotype = NULL,  
  maxnumcateg = 2,  
  categCol = NULL,  
  quantitCol = NULL,  
  plotLegend = TRUE,  
  plotLegendFile = NULL  
)
```

### Arguments

|                             |                              |
|-----------------------------|------------------------------|
| <code>annotS</code>         | A color matrix               |
| <code>annotT</code>         | A color matrix               |
| <code>missing</code>        | Convert missing to NA        |
| <code>anotype</code>        | Annotation type              |
| <code>maxnumcateg</code>    | Maximum number of categories |
| <code>categCol</code>       | Categorical columns          |
| <code>quantitCol</code>     | Quantitative columns         |
| <code>plotLegend</code>     | Plot legend ?                |
| <code>plotLegendFile</code> | Which file to plot legend ?  |

### Value

A matrix of continuous or discrete colors

### Examples

```
data("scExp")  
annotToCol2(SingleCellExperiment::colData(scExp), plotLegend = FALSE)
```

---

|               |   |
|---------------|---|
| anocol_binary | <i>Helper binary column for anocol function</i> |
|---------------|---|

---

**Description**

Helper binary column for anocol function

**Usage**

```
anocol_binary(anocol, anotype, plotLegend, annotS)
```

**Arguments**

|            |                          |
|------------|--------------------------|
| anocol     | The color feature matrix |
| anotype    | The feature types        |
| plotLegend | Plot legend ?            |
| annotS     | A color matrix           |

**Value**

A color matrix similar to anocol with binary columns colored

---

|                    |   |
|--------------------|---|
| anocol_categorical | <i>Helper binary column for anocol function</i> |
|--------------------|---|

---

**Description**

Helper binary column for anocol function

**Usage**

```
anocol_categorical(anocol, categCol, anotype, plotLegend, annotS)
```

**Arguments**

|            |                                 |
|------------|---------------------------------|
| anocol     | The color feature matrix        |
| categCol   | Colors for categorical features |
| anotype    | The feature types               |
| plotLegend | Plot legend ?                   |
| annotS     | A color matrix                  |

**Value**

A color matrix similar to anocol with binary columns colored

---

bams\_to\_matrix\_indexes

*Count bam files on interval to create count indexes*

---

### Description

Count bam files on interval to create count indexes

### Usage

```
bams_to_matrix_indexes(dir, which, BPPARAM = BiocParallel::bpparam())
```

### Arguments

|         |   |
|---------|---|
| dir     | A directory containing single cell BAM files and BAI files  |
| which   | Genomic Range on which to count   |
| BPPARAM | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

### Value

A list containing a "feature index" data.frame and a count vector for non 0 entries, both used to form the sparse matrix

---

beds\_to\_matrix\_indexes

*Count bed files on interval to create count indexes*

---

### Description

Count bed files on interval to create count indexes

### Usage

```
beds_to_matrix_indexes(dir, which, BPPARAM = BiocParallel::bpparam())
```

### Arguments

|         |   |
|---------|---|
| dir     | A directory containing the single cell BED files  |
| which   | Genomic Range on which to count   |
| BPPARAM | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

### Value

A list containing a "feature index" data.frame and a names of cells as vector both used to form the sparse matrix



---

|               |  |
|---------------|--|
| calculate_CNA | <i>Estimate copy number alterations in cytobands</i> |
|---------------|--|

---

## Description

Cytobands are considered large enough in order that a variation at the cytoband level is not considered as an epigenetic event but as a genetic event, e.g. Copy Number Alterations. The function successively :

- Calculates the fraction of reads in each cytoband (FrCyto). See [calculate\\_cyto\\_mat](#)
- Calculates the log2-ratio FrCyto of each cell by the average FrCyto in normal cells. See [calculate\\_logRatio\\_CNA](#)
- Estimates if there was a gain or a loss of copy in each cyto band. See [calculate\\_gain\\_or\\_loss](#)

The corresponding matrices are accessible in the reducedDim slots "cytoBands", "logRatio\_cytoBands" and "gainOrLoss\_cytoBands" respectively.

## Usage

```
calculate_CNA(
  scExp,
  control_samples = unique(scExp$sample_id)[1],
  ref_genome = c("hg38", "mm10")[1],
  quantiles_to_define_gol = c(0.05, 0.95)
)
```

## Arguments

|                         |  |
|-------------------------|--|
| scExp                   | A SingleCellExperiment with "logRatio_cytoBand" reducedDim slot filled. See <a href="#">calculate_logRatio_CNA</a>   |
| control_samples         | Sample IDs of the normal sample to take as reference.  |
| ref_genome              | Reference genome ('hg38' or 'mm10')  |
| quantiles_to_define_gol | Quantiles of normal log2-ratio distribution below/above which cytoband is considered to be a loss/gain. (c(0.05,0.95)). See <a href="#">calculate_gain_or_loss</a> |

## Value

The SCE with the fraction of reads, log2-ratio and gain or loss in each cytobands in each cells (of dimension cell x cytoband) in the reducedDim slots.

**Examples**

```

data("scExp")
scExp = calculate_CNA(scExp, control_samples = unique(scExp$sample_id)[1],
ref_genome="hg38", quantiles_to_define_gol = c(0.05,0.95))
SingleCellExperiment::reducedDim(scExp, "cytoBand")
SingleCellExperiment::reducedDim(scExp, "logRatio_cytoBand")
SingleCellExperiment::reducedDim(scExp, "gainOrLoss_cytoBand")

```

---

|                    |  |
|--------------------|--|
| calculate_cyto_mat | <i>Calculate Fraction of reads in each cytobands</i> |
|--------------------|--|

---

**Description**

Re-Count binned reads onto cytobands and calculate the fraction of reads in each of the cytoband in each cell. For each cell, the fraction of reads in any given cytoband is calculated. Cytobands are considered large enough in order that a variation at the cytoband level is not considered as an epigenetic event but as a genetic event, e.g. Copy Number Alterations.

**Usage**

```
calculate_cyto_mat(scExp, ref_genome = c("hg38", "mm10")[1])
```

**Arguments**

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment with genomic coordinate as features (peaks or bins) |
| ref_genome | Reference genome ('hg38' or 'mm10')  |

**Value**

The SCE with the fraction of reads in each cytobands in each cells (of dimension cell x cytoband ) in the reducedDim slot "cytoBand".

**Examples**

```

data("scExp")
scExp = calculate_cyto_mat(scExp, ref_genome="hg38")
SingleCellExperiment::reducedDim(scExp, "cytoBand")

```

---

 calculate\_gain\_or\_loss

*Estimate the copy gains/loss of tumor vs normal based on log2-ratio of fraction of reads*

---

### Description

Given a SingleCellExperiment object with the slot "logRatio\_cytoBand" containing the log2-ratio of the fraction of reads in each cytoband, estimate if the cytoband was lost or acquired a gain in a non-quantitative way. To do so, the quantiles distribution of the normal cells are calculated, and any cytoband below or above will be considered as a loss/gain. The False Discovery Rate is directly proportional to the quantiles.

### Usage

```
calculate_gain_or_loss(scExp, controls, quantiles = c(0.05, 0.95))
```

### Arguments

|           |  |
|-----------|--|
| scExp     | A SingleCellExperiment with "logRatio_cytoBand" reducedDim slot filled. See <a href="#">calculate_logRatio_CNA</a>     |
| controls  | Sample IDs or Cell IDs of the normal sample to take as reference.  |
| quantiles | Quantiles of normal log2-ratio distribution below/above which cytoband is considered to be a loss/gain. (c(0.05,0.95)) |

### Value

The SCE with the gain or loss in each cytobands in each cells (of dimension cell x cytoband ) in the reducedDim slot "gainOrLoss\_cytoBand".

### Examples

```
data("scExp")
scExp = calculate_cyto_mat(scExp, ref_genome="hg38")
scExp = calculate_logRatio_CNA(scExp, controls=unique(scExp$sample_id)[1])
scExp = calculate_gain_or_loss(scExp, controls=unique(scExp$sample_id)[1])
SingleCellExperiment::reducedDim(scExp, "gainOrLoss_cytoBand")
```

---

 calculate\_logRatio\_CNA

*Calculate the log2-ratio of tumor vs normal fraction of reads in cyto-bands*

---

### Description

Given a SingleCellExperiment object with the slot "cytoBand" containing the fraction of reads in each cytoband, calculates the log2-ratio of tumor vs normal fraction of reads in cytobands, cell by cell. If the average signal in normal sample in a cytoband is 0, set this value to 1 so that the ratio won't affect the fraction of read value.

### Usage

```
calculate_logRatio_CNA(scExp, controls)
```

### Arguments

|          |  |
|----------|--|
| scExp    | A SingleCellExperiment with "cytoBand" reducedDim slot filled.<br>• see <a href="#">calculate_cyto_mat</a> |
| controls | Sample IDs or Cell IDs of the normal sample to take as reference.  |

### Value

The SCE with the log2-ratio of fraction of reads in each cytobands in each cells (of dimension cell x cytoband ) in the reducedDim slot "logRatio\_cytoBand".

### Examples

```
data("scExp")
scExp = calculate_cyto_mat(scExp, ref_genome="hg38")
scExp = calculate_logRatio_CNA(scExp, controls=unique(scExp$sample_id)[1])
SingleCellExperiment::reducedDim(scExp, "logRatio_cytoBand")
```

---

 call\_mac2\_merge\_peaks

*Calling MACS2 peak caller and merging resulting peaks*

---

### Description

Calling MACS2 peak caller and merging resulting peaks

**Usage**

```
call_mac2_merge_peaks(
  affectation,
  odir,
  p.value,
  format = c("scBED", "BAM")[1],
  ref,
  peak_distance_to_merge
)
```

**Arguments**

|                        |   |
|------------------------|---|
| affectation            | Annotation data.frame with cell cluster and cell id information |
| odir                   | Output directory to write MACS2 output                          |
| p.value                | P value to detect peaks, passed to MACS2                        |
| format                 | File format, either "BAM" or "scBED"                            |
| ref                    | Reference genome to get chromosome information from.            |
| peak_distance_to_merge | Distance to merge peaks   |

**Value**

A list of merged GRanges peaks

---

|             |                    |
|-------------|--------------------|
| changeRange | <i>changeRange</i> |
|-------------|--------------------|

---

**Description**

changeRange

**Usage**

```
changeRange(v, newmin = 1, newmax = 10)
```

**Arguments**

|        |                  |
|--------|------------------|
| v      | A numeric vector |
| newmin | New min          |
| newmax | New max          |

**Value**

A matrix with values scaled between newmin and newmax

---

CheA3\_TF\_nTargets      *A data.frame with the number of targets of each TF in ChEA3*

---

### Description

This data.frame was obtained by downloading datasets from ChEA3 database (<https://maayanlab.cloud/chea3/>) and merging targets for :

- ARCHS4\_Coexpression
- ENCODE\_ChIP-seq
- Enrichr\_Queries
- GTEX\_Coexpression
- Literature\_ChIP-seq
- ReMap\_ChIP-seq

### Usage

```
data("CheA3_TF_nTargets")
```

### Format

CheA3\_TF\_nTargets - a data.frame with 1632 rows (unique TFs) and 2 columns

### References

Keenan AB, Torre D, Lachmann A, Leong AK, Wojciechowicz M, Utti V, Jagodnik K, Kropiwnicki E, Wang Z, Ma'ayan A (2019) ChEA3: transcription factor enrichment analysis by orthogonal omics integration. *Nucleic Acids Research*. doi: 10.1093/nar/gkz446

The data.frame is composed of two columns:

- TF column containing the TF gene names (human)
- nTargets\_TF containing the number of targets for this TF in the combined database.

### Examples

```
data("CheA3_TF_nTargets")  
head(CheA3_TF_nTargets)
```

---

 check\_correct\_datamatrix

*Check if matrix rownames are well formatted and correct if needed*


---

**Description**

Throws warnings / error if matrix is in the wrong format

**Usage**

```
check_correct_datamatrix(datamatrix_single, sample_name = "")
```

**Arguments**

|                   |                                 |
|-------------------|---------------------------------|
| datamatrix_single | A sparse matrix                 |
| sample_name       | Matrix sample name for warnings |

**Value**

A sparseMatrix in the right rownames format

---

 choose\_cluster\_scExp *Choose a number of clusters*


---

**Description**

This functions takes as input a SingleCellExperiment object and a number of cluster to select. It outputs a SingleCellExperiment object with each cell assigned to a correlation cluster in colData. Also calculates a hierarchical clustering of the consensus associations calculated by Consensus-ClusterPlus.

**Usage**

```
choose_cluster_scExp(
  scExp,
  nclust = 3,
  consensus = FALSE,
  hc_linkage = "ward.D"
)
```

**Arguments**

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment object containing consclust in metadata.                      |
| nclust     | Number of cluster to pick (3)  |
| consensus  | Use consensus clustering results instead of simple hierarchical clustering ? (FALSE) |
| hc_linkage | A linkage method for hierarchical clustering. See <a href="#">cor</a> . ('ward.D')   |

**Value**

Returns a SingleCellExperiment object with each cell assigned to a correlation cluster in colData.

**Examples**

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = choose_cluster_scExp(scExp_cf, nclust=3, consensus=FALSE)
table(scExp_cf$cell_cluster)

scExp_cf = consensus_clustering_scExp(scExp)
scExp_cf_consensus = choose_cluster_scExp(scExp_cf, nclust=3, consensus=TRUE)
table(scExp_cf_consensus$cell_cluster)
```

---

|                   |  |
|-------------------|--|
| choose_perplexity | <i>Choose perplexity depending on number of cells for Tsne</i> |
|-------------------|--|

---

**Description**

Choose perplexity depending on number of cells for Tsne

**Usage**

```
choose_perplexity(dataset)
```

**Arguments**

dataset            A matrix of features x cells (rows x columns)

**Value**

A number between 5 and 30 to use in Rtsne function

---

|         |                |
|---------|----------------|
| col2hex | <i>Col2Hex</i> |
|---------|----------------|

---

**Description**

Transform character color to hexadecimal color code.

**Usage**

```
col2hex(cname)
```



**Arguments**

cname            Color name

**Value**

The HEX color code of a particular color

---

colors\_scExp            *Adding colors to cells & features*

---

**Description**

Adding colors to cells & features

**Usage**

```
colors_scExp(
  scExp,
  annotCol = "sample_id",
  color_by = "sample_id",
  color_df = NULL
)
```

**Arguments**

scExp            A SingleCellExperiment Object  
 annotCol        Column names to color  
 color\_by        If specifying color\_df, column names to color  
 color\_df        Color data.frame to specify which color for which condition

**Value**

A SingleCellExperiment with additionnal "color" columns in colData

**Examples**

```
data("scExp")
scExp = colors_scExp(scExp,annotCol = c("sample_id",
"total_counts"),
  color_by = c("sample_id","total_counts"))

#Specific colors using a manually created data.frame :
color_df = data.frame(sample_id=unique(scExp$sample_id),
  sample_id_color=c("red","blue","green","yellow"))
scExp = colors_scExp(scExp,annotCol="sample_id",
  color_by="sample_id",color_df=color_df)
```

---

combine\_datamatrix      *Combine two matrices and emit warning if no regions are in common*

---

**Description**

Combine two matrices and emit warning if no regions are in common

**Usage**

```
combine_datamatrix(datamatrix, datamatrix_single, file_names, i)
```

**Arguments**

|                   |  |
|-------------------|--|
| datamatrix        | A sparse matrix or NULL if empty                   |
| datamatrix_single | Another sparse matrix                              |
| file_names        | File name corresponding to the matrix for warnings |
| i                 | file number  |

**Value**

A combined sparse matrix

---

combine\_enrichmentTests  
*Run enrichment tests and combine into list*

---

**Description**

Run enrichment tests and combine into list

**Usage**

```
combine_enrichmentTests(
  diff,
  enrichment_qual,
  qual.th,
  logFC.th,
  min.percent,
  annotFeat_long,
  peak_distance,
  refined_annotation,
  GeneSets,
  GeneSetsDf,
  GenePool,
  progress = NULL
)
```

**Arguments**

|                    |  |
|--------------------|--|
| diff               | Differential list  |
| enrichment_qval    | Adjusted p-value threshold above which a pathway is considered significant list                          |
| qval.th            | Differential analysis adjusted p.value threshold   |
| logFC.th           | Differential analysis log-fold change threshold  |
| min.percent        | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01) |
| annotFeat_long     | Long annotation  |
| peak_distance      | Maximum gene to peak distance  |
| refined_annotation | Refined annotation data.frame if peak calling is done  |
| GeneSets           | List of pathways   |
| GeneSetsDf         | Data.frame of pathways   |
| GenePool           | Pool of possible genes for testing   |
| progress           | A shiny Progress instance to display progress bar.   |

**Value**

A list of list of pathway enrichment data.frames for Both / Over / Under and for each cluster

---

comparable\_variables *Find comparable variable scExp*

---

**Description**

Find comparable variable scExp

**Usage**

```
comparable_variables(scExp, allExp = TRUE)
```

**Arguments**

|        |   |
|--------|---|
| scExp  | A SingleCellExperiment  |
| allExp | A logical indicating whether alternative experiments comparable variables should also be fetch. |

**Value**

A character vector with the comparable variable names

---

|                 |   |
|-----------------|---|
| CompareedgeRGLM | <i>Creates a summary table with the number of genes under- or overexpressed in each group and outputs several graphical representations</i> |
|-----------------|---|

---

### Description

Creates a summary table with the number of genes under- or overexpressed in each group and outputs several graphical representations

### Usage

```
CompareedgeRGLM(
  dataMat = NULL,
  annot = NULL,
  ref_group = NULL,
  groups = NULL,
  featureTab = NULL,
  norm_method = "TMMwsp"
)
```

### Arguments

|             |  |
|-------------|--|
| dataMat     | reads matrix   |
| annot       | selected annotation of interest  |
| ref_group   | List containing one or more vectors of reference samples. Name of the vectors will be used in the results table. The length of this list should be 1 or the same length as the groups list |
| groups      | List containing the IDs of groups to be compared with the reference samples. Names of the vectors will be used in the results table  |
| featureTab  | Feature annotations to be added to the results table   |
| norm_method | Which method to use for normalizing ('upperquantile')  |

### Value

A dataframe containing the foldchange and p.value of each feature

### Author(s)

Eric Letouze & Celine Vallot

### Examples

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = choose_cluster_scExp(scExp_cf, nclust=2, consensus=FALSE)
featureTab = as.data.frame(SummarizedExperiment::rowRanges(scExp_cf))
```

```

rownames(featureTab) = featureTab$ID
ref_group = list("C1"=scExp_cf$cell_id[which(scExp_cf$cell_cluster=="C1")])
groups = list("C2"=scExp_cf$cell_id[which(scExp_cf$cell_cluster=="C2")])
myres = CompareedgeRGLM(as.matrix(SingleCellExperiment::counts(scExp_cf)),
  annot=as.data.frame(SingleCellExperiment::colData(scExp_cf)),
  ref_group=ref_group,groups=groups, featureTab=featureTab)

```

---

CompareWilcox

*CompareWilcox*


---

## Description

CompareWilcox

## Usage

```

CompareWilcox(
  dataMat = NULL,
  annot = NULL,
  ref_group = NULL,
  groups = NULL,
  featureTab = NULL,
  block = NULL,
  BPPARAM = BiocParallel::bpparam()
)

```

## Arguments

|            |   |
|------------|---|
| dataMat    | A raw count matrix  |
| annot      | A cell annotation data.frame  |
| ref_group  | List with cells in reference group(s)   |
| groups     | List with cells in group(s) to test   |
| featureTab | data.frame with feature annotation  |
| block      | Use a blocking factor to contract batch effect ?  |
| BPPARAM    | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

## Value

A dataframe containing the foldchange and p.value of each feature

## Author(s)

Eric Letouze & Celine Vallot & Pacome Prompsy

**Examples**

```

data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = choose_cluster_scExp(scExp_cf, nclust=2, consensus=FALSE)
featureTab = as.data.frame(SummarizedExperiment::rowRanges(scExp_cf))
rownames(featureTab) = featureTab$ID
ref_group = list("C1"=scExp_cf$cell_id[which(scExp_cf$cell_cluster=="C1")])
groups = list("C2"=scExp_cf$cell_id[which(scExp_cf$cell_cluster=="C2")])
myres = CompareWilcox(as.matrix(SingleCellExperiment::normcounts(scExp_cf)),
  annot=as.data.frame(SingleCellExperiment::colData(scExp_cf)),
  ref_group=ref_group, groups=groups, featureTab=featureTab)

```

---

concatenate\_scBed\_into\_clusters

*Concatenate single-cell BED into clusters*


---

**Description**

Concatenate single-cell BED into clusters

**Usage**

```
concatenate_scBed_into_clusters(affectation, files_list, odir)
```

**Arguments**

|             |  |
|-------------|--|
| affectation | Annotation data.frame containing cluster information   |
| files_list  | Named list of scBED file paths to concatenate. List Names must match affectation\$sample_id and basenames must match affectation\$barcode. |
| odir        | Output directory to write concatenate pseudo-bulk BEDs.  |

**Value**

Merge single-cell BED files into cluster BED files. Ungzip file if BED is gzipped.

---

 consensus\_clustering\_scExp

*Wrapper to apply ConsensusClusterPlus to scExp object*


---

## Description

Runs consensus hierarchical clustering on PCA feature space of scExp object. Plot consensus scores for each number of clusters. See [ConsensusClusterPlus](#) - Wilkerson, M.D., Hayes, D.N. (2010). ConsensusClusterPlus: a class discovery tool with confidence assessments and item tracking. *Bioinformatics*, 2010 Jun 15;26(12):1572-3.

## Usage

```
consensus_clustering_scExp(
  scExp,
  prefix = NULL,
  maxK = 10,
  reps = 100,
  pItem = 0.8,
  pFeature = 1,
  distance = "pearson",
  clusterAlg = "hc",
  innerLinkage = "ward.D",
  finalLinkage = "ward.D",
  plot_consclust = "pdf",
  plot_icl = "png"
)
```

## Arguments

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment object containing 'PCA' in reducedDims.   |
| prefix     | character value for output directory. Directory is created only if plot_consclust is not NULL. This title can be an absolute or relative path.   |
| maxK       | integer value. maximum cluster number to evaluate. (10)  |
| reps       | integer value. number of subsamples. (100)   |
| pItem      | numerical value. proportion of items to sample. (0.8)  |
| pFeature   | numerical value. proportion of features to sample. (1)   |
| distance   | character value. 'pearson': (1 - Pearson correlation), 'spearman' (1 - Spearman correlation), 'euclidean', 'binary', 'maximum', 'canberra', 'minkowski' or custom distance function. ('pearson')   |
| clusterAlg | character value. cluster algorithm. 'hc' heirarchical (hclust), 'pam' for partitioning around medoids, 'km' for k-means upon data matrix, 'kmdist' ('hc') for k-means upon distance matrices (former km option), or a function that returns a clustering. ('hc') |

|                |   |
|----------------|---|
| innerLinkage   | hierarchical linkage method for subsampling. ('ward.D')   |
| finalLinkage   | hierarchical linkage method for consensus matrix. ('ward.D')  |
| plot_consclust | character value. NULL - print to screen, 'pdf', 'png', 'pngBMP' for bitmap png, helpful for large datasets. ('pdf') |
| plot_icl       | same as above for item consensus plot. ('png')  |

### Details

This functions takes as input a SingleCellExperiment object that must have 'PCA' in reducedDims and outputs a SingleCellExperiment object containing consclust list calculated cluster consensus and item consensus scores in metadata.

### Value

Returns a SingleCellExperiment object containing consclust list, calculated cluster consensus and item consensus scores in metadata.

### References

ConsensusClusterPlus package by Wilkerson, M.D., Hayes, D.N. (2010). ConsensusClusterPlus: a class discovery tool with confidence assessments and item tracking. *Bioinformatics*, 2010 Jun 15;26(12):1572-3.

### Examples

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = consensus_clustering_scExp(scExp)
```

---

correlation\_and\_hierarchical\_clust\_scExp  
*Correlation and hierarchical clustering*

---

### Description

Calculates cell to cell correlation matrix based on the PCA feature space and runs hierarchical clustering taking 1 - correlation scores as distance.

### Usage

```
correlation_and_hierarchical_clust_scExp(scExp, hc_linkage = "ward.D")
```

### Arguments

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment object, containing 'PCA' in reducedDims.                    |
| hc_linkage | A linkage method for hierarchical clustering. See <a href="#">cor</a> . ('ward.D') |



**Details**

This function takes as input a SingleCellExperiment object that must have PCA calculated and outputs a SingleCellExperiment object with correlation matrix and hierarchical clustering.

**Value**

Return a SingleCellExperiment object with correlation matrix & hierarchical clustering.

**Examples**

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
```

---

|                |   |
|----------------|---|
| count_coverage | <i>Create a smoothed and normalized coverage track from a BAM file and given a bin GenomicRanges object (same as deepTools bamCoverage)</i> |
|----------------|---|

---

**Description**

Normalization is CPM, smoothing is done by averaging on n\_smoothBin regions left and right of any given region.

**Usage**

```
count_coverage(
  input,
  format = "BAM",
  bins,
  canonical_chr,
  norm_factor,
  n_smoothBin = 5,
  ref = "hg38",
  read_size = 101,
  original_bins = NULL
)
```

**Arguments**

|        |  |
|--------|--|
| input  | Either a named list of character vector of path towards single-cell BED files or a sparse raw matrix of small bins (<500bp). If a named list specifying scBEDn the names <b>MUST</b> correspond to the 'sample_id' column in your SingleCellExperiment object. The single-cell BED files names <b>MUST</b> match the barcode names in your SingleCellExperiment (column 'barcode'). The scBED files can be gzipped or not. |
| format | File format, either "BAM" or "BED"   |
| bins   | A GenomicRanges object of binned genome  |

|               |   |
|---------------|---|
| canonical_chr | GenomicRanges of the chromosomes to read the BAM file.                                |
| norm_factor   | Then number of cells or total number of reads in the given sample, for normalization. |
| n_smoothBin   | Number of bins left and right to smooth the signal.                                   |
| ref           | Genomic reference   |
| read_size     | Length of the reads   |
| original_bins | Original bins GenomicRanges in case the format is raw matrix.                         |

**Value**

A binned GenomicRanges that can be readily exported into bigwig file.

---

create\_project\_folder *Create ChromSCape project folder*

---

**Description**

Creates a project folder that will be recognizable by ChromSCape Shiny application.

**Usage**

```
create_project_folder(
  output_directory,
  analysis_name = "Analysis_1",
  ref_genome = c("hg38", "mm10")[1]
)
```

**Arguments**

|                  |  |
|------------------|--|
| output_directory | Path towards the directory to create the 'ChromSCape_Analyses' folder and the analysis subfolder. If this path already contains the 'ChromSCape_Analyses' folder, will only create the analysis subfolder. |
| analysis_name    | Name of the analysis. Must only contain alphanumeric characters or '_'.  |
| ref_genome       | Reference genome, either 'hg38' or 'mm10'.   |

**Value**

Creates the project folder and returns the root of the project.

**Examples**

```
dir = tempdir()
create_project_folder(output_directory = dir,
  analysis_name = "Analysis_1")
list.dirs(file.path(dir))
```

---

`create_sample_name_mat`*Create a sample name matrix*

---

**Description**

Create a sample name matrix

**Usage**

```
create_sample_name_mat(nb_samples, samples_names)
```

**Arguments**

`nb_samples`      Number of samples  
`samples_names`    Character vector of sample names

**Value**

A matrix

---

`create_scDataset_raw`    *Create a simulated single cell datamatrix & cell annotation*

---

**Description**

Create a simulated single cell datamatrix & cell annotation

**Usage**

```
create_scDataset_raw(  
  cells = 300,  
  features = 600,  
  featureType = c("window", "peak", "gene"),  
  sparse = TRUE,  
  nsamp = 4,  
  ref = "hg38",  
  batch_id = factor(rep(1, nsamp))  
)
```

**Arguments**

|             |                                  |
|-------------|----------------------------------|
| cells       | Number of cells (300)            |
| features    | Number of features (600)         |
| featureType | Type of feature (window)         |
| sparse      | Is matrix sparse ? (TRUE)        |
| nsamp       | Number of samples (4)            |
| ref         | Reference genome ('hg38')        |
| batch_id    | Batch origin (factor((1,1,1,1))) |

**Value**

A list composed of \* mat : a sparse matrix following an approximation of the negative binomial law (adapted to scChIPseq) \* annot : a data.frame of cell annotation \* batches : an integer vector with the batch number for each cell

**Examples**

```
# Creating a basic sparse 600 genomic bins x 300 cells matrix and annotation
l = create_scDataset_raw()
head(l$mat)
head(l$annot)
head(l$batches)

# Specifying number of cells, features and samples
l2 = create_scDataset_raw(cells = 500, features = 500, nsamp=2)

# Specifying species
mouse_l = create_scDataset_raw(ref="mm10")

# Specifying batches
batch_l = create_scDataset_raw(nsamp=4, batch_id = factor(c(1,1,2,2)))

# Peaks of different size as features
peak_l = create_scDataset_raw(featureType="peak")
head(peak_l$mat)

# Genes as features
gene_l = create_scDataset_raw(featureType="gene")
head(gene_l$mat)
```

---

create\_scExp

*Wrapper to create the single cell experiment from count matrix and feature dataframe*

---

**Description**

Create the single cell experiment from (sparse) datamatrix and feature dataframe containing feature names and location. Also optionally removes zero count Features, zero count Cells, non canonical chromosomes, and chromosome M. Calculates QC Metrics (scrn).

**Usage**

```
create_scExp(
  datamatrix,
  annot,
  remove_zero_cells = TRUE,
  remove_zero_features = TRUE,
  remove_non_canonical = TRUE,
  remove_chr_M = TRUE,
  mainExpName = "main",
  verbose = TRUE
)
```

**Arguments**

|                      |  |
|----------------------|--|
| datamatrix           | A matrix or sparseMatrix of raw counts. Features x Cells (rows x columns).   |
| annot                | A data.frame containing informations on cells. Should have the same number of rows as the number of columns in datamatrix. |
| remove_zero_cells    | remove cells with zero counts ? (TRUE)   |
| remove_zero_features | remove cells with zero counts ? (TRUE)   |
| remove_non_canonical | remove non canonical chromosomes ?(TRUE)   |
| remove_chr_M         | remove chromosomes M ? (TRUE)  |
| mainExpName          | Name of the mainExpName e.g. 'bins', 'peaks'... ("default")  |
| verbose              | (TRUE)   |

**Value**

Returns a SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp
```

DA\_custom

*Differential Analysis Custom in 'One vs One' mode***Description**

Differential Analysis Custom in 'One vs One' mode

**Usage**

```
DA_custom(
  affectation,
  by,
  counts,
  method,
  feature,
  block,
  ref,
  group,
  progress = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

|             |   |
|-------------|---|
| affectation | An annotation data.frame with cell_id and   |
| by          | = A character specifying the column of the object containing the groups of cells to compare.  |
| counts      | Count matrix  |
| method      | DA method : Wilcoxon or EdgeR   |
| feature     | Feature tables  |
| block       | Blocking feature  |
| ref         | If de_type is custom, the reference to compare (data.frame), must be a one-column data.frame with cell_clusters or sample_id as character in rows |
| group       | If de_type is custom, the group to compare (data.frame), must be a one-column data.frame with cell_clusters or sample_id as character in rows     |
| progress    | A shiny Progress instance to display progress bar.  |
| BPPARAM     | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session.       |

**Value**

A list of results, groups compared and references

---

DA\_one\_vs\_rest      *Differential Analysis in 'One vs Rest' mode*

---

## Description

Differential Analysis in 'One vs Rest' mode

## Usage

```
DA_one_vs_rest(  
  affectation,  
  by,  
  counts,  
  method,  
  feature,  
  block,  
  progress = NULL,  
  BPPARAM = BiocParallel::bpparam()  
)
```

## Arguments

|             |   |
|-------------|---|
| affectation | An annotation data.frame with cell_id and cell_cluster columns  |
| by          | = A character specifying the column of the object containing the groups of cells to compare.  |
| counts      | Count matrix  |
| method      | DA method : Wilcoxon or EdgeR   |
| feature     | Feature tables  |
| block       | Blocking feature  |
| progress    | A shiny Progress instance to display progress bar.  |
| BPPARAM     | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

## Value

A list of results, groups compared and references

---

`DA_pairwise`*Run differential analysis in Pairwise mode*

---

**Description**

Run differential analysis in Pairwise mode

**Usage**

```
DA_pairwise(  
  affectation,  
  by,  
  counts,  
  method,  
  feature,  
  block,  
  progress = NULL,  
  BPPARAM = BiocParallel::bpparam()  
)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>affectation</code> | An annotation data.frame with <code>cell_cluster</code> and <code>cell_id</code> columns  |
| <code>by</code>          | = A character specifying the column of the object containing the groups of cells to compare.  |
| <code>counts</code>      | Count matrix  |
| <code>method</code>      | DA method, Wilcoxon or edgeR  |
| <code>feature</code>     | Feature data.frame  |
| <code>block</code>       | Blocking feature  |
| <code>progress</code>    | A shiny Progress instance to display progress bar.  |
| <code>BPPARAM</code>     | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Value**

A list of results, groups compared and references



---

|                |   |
|----------------|---|
| define_feature | <i>Define the features on which reads will be counted</i> |
|----------------|---|

---

**Description**

Define the features on which reads will be counted

**Usage**

```
define_feature(ref = c("hg38", "mm10")[1],
  peak_file = NULL,
  bin_width = NULL,
  genebody = FALSE,
  extendPromoter = 2500)
```

**Arguments**

|                |   |
|----------------|---|
| ref            | Reference genome  |
| peak_file      | A bed file if counting on peaks   |
| bin_width      | A number of bins if dividing genome into fixed width bins                     |
| genebody       | A logical indicating if feature should be counted in genebodies and promoter. |
| extendPromoter | Extension length before TSS (2500).   |

**Value**

A GRanges object

**Examples**

```
gr_bins = define_feature("hg38", bin_width = 50000)
gr_genes = define_feature("hg38", genebody = TRUE, extendPromoter = 5000)
```

---

|                |  |
|----------------|--|
| detect_samples | <i>Heuristic discovery of samples based on cell labels</i> |
|----------------|--|

---

**Description**

Identify a fixed number of common string (samples) in a set of varying strings (cells). E.g. in the set "Sample1\_cell1", "Sample1\_cell2", "Sample2\_cell1", "Sample2\_cell2" and with nb\_samples=2, the function returns "Sample1", "Sample1", "Sample2", "Sample2".

**Usage**

```
detect_samples(barcodes, nb_samples = 1)
```

**Arguments**

barcodes            Vector of cell barcode names (e.g. Sample1\_cell1, Sample1\_cell2...)  
 nb\_samples        Number of samples to find

**Value**

character vector of sample names the same length as cell labels

**Examples**

```
barcodes = c(paste0("HBCx22_BC_", seq_len(100)),
             paste0("mouse_sample_XX", 208:397))
samples = detect_samples(barcodes, nb_samples=2)
```

---

differential\_activation

*Find Differentially Activated Features (One vs All)*

---

**Description**

Based on the statement that single-cell epigenomic dataset are very sparse, specifically when analysis small bins or peaks, we can define each feature as being 'active' or not simply by the presence or the absence of reads in this feature. This is the equivalent of binarize the data. When trying to find differences in signal for a feature between multiple cell groups, this function simply compare the percentage of cells 'activating' the feature in each of the group. The p.values are then calculated using a Pearson's Chi-squared Test for Count Data (comparing the number of active cells in one group vs the other) and corrected using Benjamini-Hochberg correction for multiple testing.

**Usage**

```
differential_activation(
  scExp,
  by = c("cell_cluster", "sample_id")[1],
  verbose = TRUE,
  progress = NULL
)
```

**Arguments**

scExp            A SingleCellExperiment object containing consclust with selected number of cluster.  
 by                Which grouping to run the marker enrichment ?  
 verbose        Print ?  
 progress        A shiny Progress instance to display progress bar.

**Details**

To calculate the logFC, the percentage of activation of the features are corrected for total number of reads to correct for library size bias. For each cluster ('group') the function consider the rest of the cells as the reference.

**Value**

Returns a dataframe of differential activation results that contains the rowData of the SingleCellExperiment with additional logFC, q.value, group activation (fraction of cells active for each feature in the group cells), reference activation (fraction of cells active for each feature in the reference cells).

**See Also**

For Pearson's Chi-squared Test for Count Data [chisq.test](#). For other differential analysis see [differential\\_analysis\\_scExp](#).

**Examples**

```
data("scExp")
res = differential_activation(scExp, by = "cell_cluster")
res = differential_activation(scExp, by = "sample_id")
```

---

differential\_analysis\_scExp

*Runs differential analysis between cell clusters*

---

**Description**

Based on clusters of cell defined previously, runs non-parametric Wilcoxon Rank Sum test to find significantly depleted or enriched features, in 'one\_vs\_rest' mode or 'pairwise' mode. In pairwise mode, each cluster is compared to all other cluster individually, and then pairwise comparisons between clusters are combined to find overall differential features using combineMarkers function from scran.

**Usage**

```
differential_analysis_scExp(
  scExp,
  de_type = c("one_vs_rest_fast", "one_vs_rest", "pairwise", "custom")[1],
  by = "cell_cluster",
  method = "wilcox",
  block = NULL,
  group = NULL,
  ref = NULL,
  prioritize_genes = nrow(scExp) > 20000,
  max_distanceToTSS = 1000,
  progress = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

|                   |  |
|-------------------|--|
| scExp             | A SingleCellExperiment object containing consclust with selected number of cluster.  |
| de_type           | Type of comparisons. Either 'one_vs_rest', to compare each cluster against all others, or 'pairwise' to make 1 to 1 comparisons. ('one_vs_rest')   |
| by                | = A character specifying the column of the object containing the groups of cells to compare. Exclusive with de_type == custom  |
| method            | Differential testing method, either 'wilcox' for Wilcoxon non- parametric testing or 'neg.binomial' for edgeRGLM based testing. ('wilcox')   |
| block             | Use batches as blocking factors ? If TRUE, block will be taken as the column "batch_id" from the SCE. Cells will be compared only within samples belonging to the same batch.                              |
| group             | If de_type = "custom", the sample / cluster of interest as a one- column data.frame. The name of the column is the group name and the values are character either cluster ("C1", "C2", ...) or sample_id.  |
| ref               | If de_type = "custom", the sample / cluster of reference as a one- column data.frame. The name of the column is the group name and the values are character either cluster ("C1", "C2", ...) or sample_id. |
| prioritize_genes  | First filter by loci being close to genes ? E.g. for differential analysis, it is more relevant to keep features close to genes  |
| max_distanceToTSS | If prioritize_genes is TRUE, the maximum distance to consider a feature close to a gene.   |
| progress          | A shiny Progress instance to display progress bar.   |
| BPPARAM           | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session.  |

**Details**

This functions takes as input a SingleCellExperiment object with consclust, the type of comparison, either 'one\_vs\_rest' or 'pairwise', the adjusted p-value threshold (qval.th) and the fold-change threshold (logFC.th). It outputs a SingleCellExperiment object containing a differential list.

**Value**

Returns a SingleCellExperiment object containing a differential list.

**Examples**

```
data("scExp")
scExp_cf = differential_analysis_scExp(scExp)
```

---

|             |                    |
|-------------|--------------------|
| distPearson | <i>distPearson</i> |
|-------------|--------------------|

---

**Description**

distPearson

**Usage**

distPearson(m)

**Arguments**

m                    A matrix

**Value**

A dist object

---

|                |                       |
|----------------|-----------------------|
| enrichmentTest | <i>enrichmentTest</i> |
|----------------|-----------------------|

---

**Description**

enrichmentTest

**Usage**

enrichmentTest(gene.sets, mylist, possibleIds, sep = ";", silent = FALSE)

**Arguments**

gene.sets            A list of reference gene sets  
 mylist                A list of genes to test  
 possibleIds          All existing genes  
 sep                   Separator used to collapse genes  
 silent                Silent mode ?

**Value**

A dataframe with the gene sets and their enrichment p.value

---

enrich\_TF\_ChEA3\_genes *Find the TF that are enriched in the differential genes using ChEA3 API*

---

### Description

Find the TF that are enriched in the differential genes using ChEA3 API

### Usage

```
enrich_TF_ChEA3_genes(genes)
```

### Arguments

genes                    A character vector with the name of genes to enrich for TF.

### Value

Returns a SingleCellExperiment object containing list of enriched Gene Sets for each cluster, either in depleted features, enriched features or simply differential features (both).

### References

Keenan AB, Torre D, Lachmann A, Leong AK, Wojciechowicz M, Utti V, Jagodnik K, Kropiwnicki E, Wang Z, Ma'ayan A (2019) ChEA3: transcription factor enrichment analysis by orthogonal omics integration. *Nucleic Acids Research*. doi: 10.1093/nar/gkz446 +

### Examples

```
data(scExp)
enrich_TF_ChEA3_genes(head(unlist(strsplit(SummarizedExperiment::rowData(scExp)$Gene, split = ",", fixed = TRUE)
```

---

enrich\_TF\_ChEA3\_scExp *Find the TF that are enriched in the differential genes using ChEA3 database*

---

### Description

Find the TF that are enriched in the differential genes using ChEA3 database

**Usage**

```
enrich_TF_ChEA3_scExp(
  scExp,
  ref = "hg38",
  qval.th = 0.01,
  logFC.th = 1,
  min.percent = 0.01,
  peak_distance = 1000,
  use_peaks = FALSE,
  progress = NULL,
  verbose = TRUE
)
```

**Arguments**

|               |  |
|---------------|--|
| scExp         | A SingleCellExperiment object containing list of differential features.                                  |
| ref           | A reference annotation, either 'hg38' or 'mm10'. ('hg38')  |
| qval.th       | Adjusted p-value threshold to define differential features. (0.01)                                       |
| logFC.th      | Fold change threshold to define differential features. (1)   |
| min.percent   | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01) |
| peak_distance | Maximum distanceToTSS of feature to gene TSS to consider associated, in bp. (1000)                       |
| use_peaks     | Use peak calling method (must be calculated beforehand). (FALSE)   |
| progress      | A shiny Progress instance to display progress bar.   |
| verbose       | A logical to print message or not. (TRUE)  |

**Value**

Returns a SingleCellExperiment object containing list of enriched Gene Sets for each cluster, either in depleted features, enriched features or simply differential features (both).

**Examples**

```
data("scExp")

scExp = enrich_TF_ChEA3_scExp(
  scExp,
  ref = "hg38",
  qval.th = 0.01,
  logFC.th = 1,
  min.percent = 0.01)
```

---

 exclude\_features\_scExp

*Remove specific features (CNA, repeats)*


---

## Description

Remove specific features (CNA, repeats)

## Usage

```
exclude_features_scExp(
  scExp,
  features_to_exclude,
  by = "region",
  verbose = TRUE
)
```

## Arguments

|                     |   |
|---------------------|---|
| scExp               | A SingleCellExperiment object.  |
| features_to_exclude | A GenomicRanges object or data.frame containing genomic regions or features to exclude or path towards a BED file containing the features to exclude.   |
| by                  | Type of features. Either 'region' or 'feature_name'. If 'region', will look for genomic coordinates in columns 1-3 (chr,start,stop). If 'feature_name', will look for a genes in first column. ('region') |
| verbose             | (TRUE)  |

## Value

A SingleCellExperiment object without features to exclude.

## Examples

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
features_to_exclude = data.frame(chr=c("chr4", "chr7", "chr17"),
  start=c(50000, 8000000, 2000000),
  end=c(100000, 16000000, 2500000))
features_to_exclude = as(features_to_exclude, "GRanges")
scExp = exclude_features_scExp(scExp, features_to_exclude)
scExp
```



---

`feature_annotation_scExp`*Add gene annotations to features*

---

**Description**

Add gene annotations to features

**Usage**

```
feature_annotation_scExp(scExp, ref = "hg38", reference_annotation = NULL)
```

**Arguments**

`scExp` A SingleCellExperiment object.  
`ref` Reference genome. Either 'hg38' or 'mm10'. ('hg38')  
`reference_annotation` A data.frame containing gene (or else) annotation with genomic coordinates.

**Value**

A SingleCellExperiment object with annotated rowData.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = feature_annotation_scExp(scExp)
head(SummarizedExperiment::rowRanges(scExp))

# Mouse
raw = create_scDataset_raw(ref = "mm10")
scExp = create_scExp(raw$mat, raw$annot)
scExp = feature_annotation_scExp(scExp, ref="mm10")
head(SummarizedExperiment::rowRanges(scExp))
```

---

`filter_correlated_cell_scExp`*Filter lowly correlated cells*

---

**Description**

Remove cells that have a correlation score lower than what would be expected by chance with other cells.

**Usage**

```
filter_correlated_cell_scExp(scExp, random_iter = 5,
  corr_threshold = 99, percent_correlation = 1,
  downsample = 2500, verbose = TRUE, n_process = 250,
  BPPARAM = BiocParallel::bpparam())
```

**Arguments**

|                     |   |
|---------------------|---|
| scExp               | A SingleCellExperiment object containing 'Cor', a correlation matrix, in reducedDims.   |
| random_iter         | Number of random matrices to create to calculate random correlation scores. (50)  |
| corr_threshold      | Quantile of random correlation score above which a cell is considered to be 'correlated' with another cell. (99)                            |
| percent_correlation | Percentage of the cells that any cell must be 'correlated' to in order to not be filtered. (1)  |
| downsample          | Number of cells to calculate correlation filtering threshold ? (2500)   |
| verbose             | Print messages ? (TRUE)   |
| n_process           | Number of cell to proceed at a time. Increase this number to increase speed at memory cost  |
| BPPARAM             | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Details**

This functions takes as input a SingleCellExperiment object that must have correlation matrix calculated and outputs a SingleCellExperiment object without lowly correlated cells. TSNE is recalculated.

**Value**

Returns a SingleCellExperiment object without lowly correlated cells. The calculated correlation score limit threshold is saved in metadata.

**Examples**

```
data("scExp")
dim(scExp)
scExp_cf = filter_correlated_cell_scExp(scExp,
  corr_threshold = 99, percent_correlation = 1)
dim(scExp_cf)
```

---

 filter\_genes\_with\_refined\_peak\_annotation

*Filter genes based on peak calling refined annotation*


---

**Description**

Filter genes based on peak calling refined annotation

**Usage**

```
filter_genes_with_refined_peak_annotation(
  refined_annotation,
  peak_distance,
  signific,
  over,
  under
)
```

**Arguments**

|                    |   |
|--------------------|---|
| refined_annotation | A data.frame containing each gene distance to real peak     |
| peak_distance      | Minimum distance to an existing peak to accept a given gene |
| signific           | Indexes of all significantly differential genes             |
| over               | Indexes of all significantly overexpressed genes            |
| under              | Indexes of all significantly underexpressed genes           |

**Value**

List of significantly differential, overexpressed and underexpressed genes close enough to existing peaks

---

 filter\_scExp

*Filter cells and features*


---

**Description**

Function to filter out cells & features from SingleCellExperiment based on total count per cell, number of cells 'ON' in features and top covered cells that might be doublets.

**Usage**

```
filter_scExp(  
  scExp,  
  min_cov_cell = 1600,  
  quant_removal = 95,  
  min_count_per_feature = 10,  
  verbose = TRUE  
)
```

**Arguments**

|                       |  |
|-----------------------|--|
| scExp                 | A SingleCellExperiment object.                             |
| min_cov_cell          | Minimum counts for each cell. (1600)                       |
| quant_removal         | Centile of cell counts above which cells are removed. (95) |
| min_count_per_feature | Minimum number of reads per feature (10).                  |
| verbose               | (TRUE)   |

**Value**

Returns a filtered SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()  
scExp = create_scExp(raw$mat, raw$annot)  
scExp. = filter_scExp(scExp)  
  
# No feature filtering (all features are valuable)  
scExp. = filter_scExp(scExp,min_count_per_feature=30)  
  
# No cell filtering (all features are valuable)  
scExp. = filter_scExp(scExp,min_cov_cell=0,quant_removal=100)
```

---

find\_clusters\_louvain\_scExp

*Build SNN graph and find cluster using Louvain Algorithm*

---

**Description**

Build SNN graph and find cluster using Louvain Algorithm

**Usage**

```
find_clusters_louvain_scExp(
  scExp,
  k = 10,
  resolution = 1,
  use.dimred = "PCA",
  type = c("rank", "number", "jaccard")[3],
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

|            |   |
|------------|---|
| scExp      | A SingleCellExperiment with PCA calculated  |
| k          | An integer scalar specifying the number of nearest neighbors to consider during graph construction.   |
| resolution | A numeric specifying the resolution of clustering to pass to igraph::cluster_louvain function.  |
| use.dimred | A string specifying the dimensionality reduction to use.  |
| type       | A string specifying the type of weighting scheme to use for shared neighbors.   |
| BPPARAM    | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Value**

A SingleCellExperiment containing the vector of clusters (named C1, C2 ....)

**Examples**

```
data('scExp')
scExp = find_clusters_louvain_scExp(scExp, k = 10)
```

---

|                   |                                   |
|-------------------|-----------------------------------|
| find_top_features | <i>Find most covered features</i> |
|-------------------|-----------------------------------|

---

**Description**

Find the top most covered features that will be used for dimensionality reduction. Optionally remove non-top features.

**Usage**

```

find_top_features(
  scExp,
  n = 20000,
  keep_others = FALSE,
  prioritize_genes = FALSE,
  max_distanceToTSS = 10000,
  verbose = TRUE
)

```

**Arguments**

|                   |   |
|-------------------|---|
| scExp             | A SingleCellExperiment.   |
| n                 | Either an integer indicating the number of top covered regions to find or a character vector of the top percentile of features to keep (e.g. 'q20' to keep top 20% features). |
| keep_others       | Logical indicating if non-top regions are to be removed from the SCE or not (FALSE).  |
| prioritize_genes  | First filter by loci being close to genes ? E.g. for differential analysis, it is more relevant to keep features close to genes   |
| max_distanceToTSS | If prioritize_genes is TRUE, the maximum distance to consider a feature close to a gene.  |
| verbose           | Print ?   |

**Value**

A SCE with top features

**Examples**

```

data(scExp)
scExp_top = find_top_features(scExp, n = 4000, keep_others = FALSE)

```

---

|                   |  |
|-------------------|--|
| generate_analysis | <i>Generate a complete ChromSCape analysis</i> |
|-------------------|--|

---

**Description**

Generate a complete ChromSCape analysis

**Usage**

```

generate_analysis(input_data_folder,
analysis_name = "Analysis_1",
output_directory = "./",
input_data_type = c("scBED", "DenseMatrix", "SparseMatrix",
                    "scBAM")[1],
feature_count_on = c("bins", "genebody", "peaks")[1],
feature_count_parameter = 50000,
ref_genome = c("hg38", "mm10")[1],
run = c("filter", "CNA", "cluster", "consensus", "peak_call", "coverage",
        "DA", "GSA", "report")[c(1,3,6,7,8,9)],
min_reads_per_cell = 1000,
max_quantile_read_per_cell = 99,
n_top_features = 40000,
norm_type = "CPM",
subsample_n = NULL,
exclude_regions = NULL,
n_clust = NULL,
corr_threshold = 99,
percent_correlation = 1,
maxK = 10,
qval.th = 0.1,
logFC.th = 1,
enrichment_qval = 0.1,
doBatchCorr = FALSE,
batch_sels = NULL,
control_samples_CNA = NULL,
genes_to_plot = c("Krt8", "Krt5", "Tgfb1", "Foxq1", "Cdkn2b",
                  "Cdkn2a", "chr7:15000000-20000000")
)

```

**Arguments**

**input\_data\_folder** Directory containing the input data.

**analysis\_name** Name given to the analysis.

**output\_directory** Directory where to create the analysis and the HTML report.

**input\_data\_type** The type of input data.

**feature\_count\_on** For raw data type, on which features to count the cells.

**feature\_count\_parameter** Additional parameter corresponding to the 'feature\_count\_on' parameter. E.g. for 'bins' must be a numeric, e.g. 50000, for 'peaks' must be a character containing path towards a BED peak file.

**ref\_genome** The genome of reference.

|   |  |
|---|--|
| <code>run</code>                        | What steps to run. By default runs everything. Some steps are required in order to run downstream steps. |
| <code>min_reads_per_cell</code>         | Minimum number of reads per cell.  |
| <code>max_quantile_read_per_cell</code> | Upper quantile above which to consider cells doublets.   |
| <code>n_top_features</code>             | Number of features to keep in the analysis.  |
| <code>norm_type</code>                  | Normalization type.  |
| <code>subsample_n</code>                | Number of cells per condition to downsample to, for performance principally.                             |
| <code>exclude_regions</code>            | Path towards a BED file containing CNA to exclude from the analysis (optional).                          |
| <code>n_clust</code>                    | Number of clusters to force choice of clusters.  |
| <code>corr_threshold</code>             | Quantile of correlation above which two cells are considered as correlated.                              |
| <code>percent_correlation</code>        | Percentage of the total cells that a cell must be correlated with in order to be kept in the analysis.   |
| <code>maxK</code>                       | Upper cluster number to rest for ConsensusClusterPlus.   |
| <code>qval.th</code>                    | Adjusted p-value below which to consider features differential.  |
| <code>logFC.th</code>                   | Log2-fold-change above/below which to consider a feature depleted/enriched.                              |
| <code>enrichment_qval</code>            | Adjusted p-value below which to consider a gene set as significantly enriched in differential features.  |
| <code>doBatchCorr</code>                | Logical indicating if batch correction using fastMNN should be run.                                      |
| <code>batch_sels</code>                 | If <code>doBatchCorr</code> is TRUE, a named list containing the samples in each batch.                  |
| <code>control_samples_CNA</code>        | If running CopyNumber Analysis, a character vector of the sample names that are 'normal'.                |
| <code>genes_to_plot</code>              | A character vector containing genes of interest of which to plot the coverage.                           |

**Value**

Creates a ChromSCape-readable directory and saved objects, as well as a multi-tabbed HTML report resuming the analysis.

**Examples**

```
## Not run:
generate_analysis("/path/to/data/", "Analysis_1")

## End(Not run)
```



---

generate\_count\_matrix *Generate count matrix*

---

### Description

Generate count matrix

### Usage

```
generate_count_matrix(cells, features, sparse, cell_names, feature_names)
```

### Arguments

|               |                    |
|---------------|--------------------|
| cells         | Number of cells    |
| features      | Number of features |
| sparse        | Is matrix sparse ? |
| cell_names    | Cell names         |
| feature_names | Feature names      |

### Value

A matrix or a sparse matrix

---

generate\_coverage\_tracks  
*Generate cell cluster pseudo-bulk coverage tracks*

---

### Description

Generate cell cluster pseudo-bulk coverage tracks. First, scBED files are concatenated into cell clusters contained in the 'by' column of your SingleCellExperiment object. To do so, for each sample in the given list, the barcodes of each cluster are grepped and BED files are merged into pseudo-bulk of clusters (C1,C2...). Two cells from different can have the same barcode ID as cell affectation is done sample by sample. Then coverage of pseudo-bulk BED files is calculated by averaging & smoothing reads on small genomic window (150bp per default). The pseudo bulk BED and BigWigs coverage tracks are writtend to the output directory. This functionality is not available on Windows as it uses the 'cat' and 'gzip' utilities from Unix OS.

**Usage**

```
generate_coverage_tracks(
  scExp_cf,
  input,
  odir,
  format = "scBED",
  ref_genome = c("hg38", "mm10")[1],
  bin_width = 150,
  n_smoothBin = 5,
  read_size = 101,
  quantile_for_peak_calling = 0.85,
  by = "cell_cluster",
  progress = NULL
)
```

**Arguments**

|                           |   |
|---------------------------|---|
| scExp_cf                  | A SingleCellExperiment with cluster selected. (see <a href="#">choose_cluster_scExp</a> ). It is recommended having a minimum of ~100 cells per cluster in order to obtain smooth tracks.   |
| input                     | Either a named list of character vector of path towards single-cell BED files or a sparse raw matrix of small bins (<500bp). If a named list specifying scBED the names MUST correspond to the 'sample_id' column in your SingleCellExperiment object. The single-cell BED files names MUST match the barcode names in your SingleCellExperiment (column 'barcode'). The scBED files can be gzipped or not. |
| odir                      | The output directory to write the cumulative BED and BigWig files.  |
| format                    | File format, either "raw_mat", "BED" or "BAM"   |
| ref_genome                | The genome of reference, used to constrain to canonical chromosomes. Either 'hg38' or 'mm10'. 'hg38' per default.   |
| bin_width                 | The width of the bin to create the coverage track. The smaller the greater the resolution & runtime. Default to 150.  |
| n_smoothBin               | Number of bins left & right to average ('smooth') the signal on. Default to 5.  |
| read_size                 | The estimated size of reads. Default to 101.  |
| quantile_for_peak_calling | The quantile to define the threshold above which signal is considered as a peak.  |
| by                        | A character specifying a categorical column of scExp_cf metadata by which to group cells and generate coverage tracks and peaks.  |
| progress                  | A Progress object for Shiny. Default to NULL.   |

**Value**

Generate coverage tracks (.bigwig) for each group in the SingleCellExperiment "by" column.

**Examples**

```
## Not run:
data(scExp)
input_files_coverage = list(
  "scChIP_Jurkat_K4me3" = paste0("/path/to/", scExp$barcode[1:51], ".bed"),
  "scChIP_Ramos_K4me3" = paste0("/path/to/", scExp$barcode[52:106], ".bed")
)
generate_coverage_tracks(scExp, input_files_coverage, "/path/to/output",
  ref_genome = "hg38")

## End(Not run)
```

---

generate\_feature\_names

*Generate feature names*

---

**Description**

Generate feature names

**Usage**

```
generate_feature_names(featureType, ref, features)
```

**Arguments**

|             |                                |
|-------------|--------------------------------|
| featureType | Type of feature                |
| ref         | Reference genome               |
| features    | Number of features to generate |

**Value**

A character vector of feature names

---

generate\_report

*From a ChromSCape analysis directory, generate an HTML report.*

---

**Description**

From a ChromSCape analysis directory, generate an HTML report.

**Usage**

```
generate_report(
  ChromSCape_directory,
  prefix = NULL,
  run = c("filter", "CNA", "cluster", "consensus", "peak_call", "coverage", "DA",
    "GSA", "report")[c(1, 3, 6, 7, 8, 9)],
  genes_to_plot = c("Krt8", "Krt5", "Tgfb1", "Foxq1", "Cdkn2b", "Cdkn2a",
    "chr7:15000000-20000000"),
  control_samples_CNA = NULL
)
```

**Arguments**

|                      |  |
|----------------------|--|
| ChromSCape_directory | Path towards the ChromSCape directory of which you want to create the report. The report will be created at the root of this directory.  |
| prefix               | Name of the analysis with the filtering parameters (e.g. Analysis_3000_100000_99_uncorrected). You will find the prefix in the Filtering_Normalize_Reduce subfolder.   |
| run                  | Which steps to report ("filter", "CNA", "cluster", "consensus", "peak_call", "coverage", "DA", "GSA", "report"). Only indicate steps that were done in the analysis. By default do not report CNA, consensus and peak calling. |
| genes_to_plot        | For the UMAP, which genes do you want to see in the report.  |
| control_samples_CNA  | If running the Copy Number Alteration (CNA) part, which samples are the controls   |

**Value**

Generate an HTML report at the root of the analysis directory.

**Examples**

```
## Not run:
generate_analysis("/path/to/data/", "Analysis_1")

## End(Not run)
```

---

gene\_set\_enrichment\_analysis\_scExp

*Runs Gene Set Enrichment Analysis on genes associated with differential features*

---

**Description**

This function takes previously calculated differential features and runs hypergeometric test to look for enriched gene sets in the genes associated with differential features, for each cell cluster. This function takes as input a `SingleCellExperiment` object with `conclust`, the type of comparison, either `'one_vs_rest'` or `'pairwise'`, the adjusted p-value threshold (`qval.th`) and the fold-change threshold (`logFC.th`). It outputs a `SingleCellExperiment` object containing a differential list.

**Usage**

```
gene_set_enrichment_analysis_scExp(
  scExp,
  enrichment_qval = 0.1,
  ref = "hg38",
  GeneSets = NULL,
  GeneSetsDf = NULL,
  GenePool = NULL,
  qval.th = 0.01,
  logFC.th = 1,
  min.percent = 0.01,
  peak_distance = 1000,
  use_peaks = FALSE,
  GeneSetClasses = c("c1_positional", "c2_curated", "c3_motif", "c4_computational",
    "c5_G0", "c6_oncogenic", "c7_immunologic", "hallmark"),
  progress = NULL
)
```

**Arguments**

|                              |   |
|------------------------------|---|
| <code>scExp</code>           | A <code>SingleCellExperiment</code> object containing list of differential features.  |
| <code>enrichment_qval</code> | Adjusted p-value threshold for gene set enrichment. (0.1)   |
| <code>ref</code>             | A reference annotation, either <code>'hg38'</code> or <code>'mm10'</code> . ( <code>'hg38'</code> )   |
| <code>GeneSets</code>        | A named list of gene sets. If <code>NULL</code> will automatically load MSigDB list of gene sets for specified reference genome. ( <code>NULL</code> )                                  |
| <code>GeneSetsDf</code>      | A dataframe containing gene sets & class of gene sets. If <code>NULL</code> will automatically load MSigDB dataframe of gene sets for specified reference genome. ( <code>NULL</code> ) |
| <code>GenePool</code>        | The pool of genes to run enrichment in. If <code>NULL</code> will automatically load Gen-code list of genes from specified reference genome. ( <code>NULL</code> )                      |
| <code>qval.th</code>         | Adjusted p-value threshold to define differential features. (0.01)  |
| <code>logFC.th</code>        | Fold change threshold to define differential features. (1)  |
| <code>min.percent</code>     | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01)  |
| <code>peak_distance</code>   | Maximum distanceToTSS of feature to gene TSS to consider associated, in bp. (1000)  |
| <code>use_peaks</code>       | Use peak calling method (must be calculated beforehand). ( <code>FALSE</code> )   |

GeneSetClasses Which classes of MSIGdb to look for.  
progress A shiny Progress instance to display progress bar.

**Value**

Returns a SingleCellExperiment object containing list of enriched Gene Sets for each cluster, either in depleted features, enriched features or simply differential features (both).

**Examples**

```
data("scExp")

#Usually recommending qual.th = 0.01 & logFC.th = 1 or 2
## Not run: scExp_cf = gene_set_enrichment_analysis_scExp(scExp,
  qual.th = 0.4, logFC.th = 0.3)
## End(Not run)
```

---

getExperimentNames *Get experiment names from a SingleCellExperiment*

---

**Description**

Get experiment names from a SingleCellExperiment

**Usage**

```
getExperimentNames(scExp)
```

**Arguments**

scExp A SingleCellExperiment with named mainExp and altExps.

**Value**

Character vector of unique experiment names

**Examples**

```
data(scExp)
getExperimentNames(scExp)
```

---

getMainExperiment      *Get Main experiment of a SingleCellExperiment*

---

**Description**

Get Main experiment of a SingleCellExperiment

**Usage**

```
getMainExperiment(scExp)
```

**Arguments**

scExp                    A SingleCellExperiment with named mainExp and altExps.

**Value**

The swapped SingleCellExperiment towards "main" experiment

**Examples**

```
data(scExp)
getMainExperiment(scExp)
```

---

get\_color\_dataframe\_from\_input  
*Get color dataframe from shiny::colorInput*

---

**Description**

Get color dataframe from shiny::colorInput

**Usage**

```
get_color_dataframe_from_input(  
  input,  
  levels_selected,  
  color_by = c("sample_id", "total_counts"),  
  input_id_prefix = "color_"  
)
```

**Arguments**

|                 |                                      |
|-----------------|--------------------------------------|
| input           | Shiny input object                   |
| levels_selected | Names of the features                |
| color_by        | Which feature color to retrieve      |
| input_id_prefix | Prefix in front of the feature names |

**Value**

A data.frame with the feature levels and the colors of each level of this feature.

---

|                   |                                    |
|-------------------|------------------------------------|
| get_cyto_features | <i>Map features onto cytobands</i> |
|-------------------|------------------------------------|

---

**Description**

Map the features of a SingleCellExperiment onto the cytobands of a given genome. Some features might not be mapped to any cytobands (e.g. if they are not in the canonical chromosomes), and are removed from the returned object.

**Usage**

```
get_cyto_features(scExp, ref_genome = c("hg38", "mm10")[1])
```

**Arguments**

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment with genomic coordinate as features (peaks or bins) |
| ref_genome | Reference genome ('hg38' or 'mm10')  |

**Details**

The cytobands are an arbitrary cutting of the genome that dates back to staining metaphase chromosomes with Giemsa.

**Value**

A data.frame of the SCE features with their corresponding cytoband name

**Examples**

```
data("scExp")
matching_cyto = get_cyto_features(scExp, ref_genome="hg38")
```



---

`get_genomic_coordinates`*Get SingleCellExperiment's genomic coordinates*

---

**Description**

Get SingleCellExperiment's genomic coordinates

**Usage**

```
get_genomic_coordinates(scExp)
```

**Arguments**

`scExp` A SingleCellExperiment object.

**Value**

A GRanges object of genomic coordinates.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
feature_GRanges = get_genomic_coordinates(scExp)
```

---

`get_most_variable_cyto`*Retrieve the cytobands with the most variable fraction of reads*

---

**Description**

Given a SingleCellExperiment object with the slot "cytoBand" containing the fraction of reads in each cytoBand, calculates the variance of each cytoBand and returns a data.frame with the top variables cytoBands. Most cytoBands are expected to be unchanged between normal and tumor samples, therefore focusing on the top variable cytoBands enable to focus on the most interesting regions.

**Usage**

```
get_most_variable_cyto(scExp, top = 50)
```

**Arguments**

`scExp` A SingleCellExperiment with "cytoBand" reducedDim slot filled.  
`top` Number of cytobands to return (50).

**Value**

A data.frame of the top variable cytoBands and their variance

**Examples**

```
data("scExp")
scExp = calculate_cyto_mat(scExp, ref_genome="hg38")
get_most_variable_cyto(scExp, top=50)
```

---

get\_pathway\_mat\_scExp *Get pathway matrix*

---

**Description**

Get pathway matrix

**Usage**

```
get_pathway_mat_scExp(
  scExp,
  pathways,
  max_distanceToTSS = 1000,
  ref = "hg38",
  GeneSetClasses = c("c1_positional", "c2_curated", "c3_motif", "c4_computational",
    "c5_G0", "c6_oncogenic", "c7_immunologic", "hallmark"),
  progress = NULL
)
```

**Arguments**

|                   |  |
|-------------------|--|
| scExp             | A SingleCellExperiment   |
| pathways          | A character vector specifying the pathways to retrieve the cell count for.                           |
| max_distanceToTSS | Numeric. Maximum distance to a gene's TSS to consider a region linked to a gene. (1000)#' @param ref |
| ref               | Reference genome, either mm10 or hg38  |
| GeneSetClasses    | Which classes of MSIGdb to load  |
| progress          | A shiny Progress instance to display progress bar.   |

**Value**

A matrix of cell to pathway

**Examples**

```
data(scExp)  
mat = get_pathway_mat_scExp(scExp, pathways = "KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY")
```

---

*gg\_fill\_hue*                      *gg\_fill\_hue*

---

**Description**

*gg\_fill\_hue*

**Usage**

```
gg_fill_hue(n)
```

**Arguments**

n                      num hues

**Value**

A color in HEX format

---

*groupMat*                      *groupMat*

---

**Description**

*groupMat*

**Usage**

```
groupMat(mat = NA, margin = 1, groups = NA, method = "mean")
```

**Arguments**

mat                      A matrix  
margin                      By row or columns ?  
groups                      Groups  
method                      Method to group

**Value**

A grouped matrix

---

|              |                     |
|--------------|---------------------|
| H1proportion | <i>H1proportion</i> |
|--------------|---------------------|

---

**Description**

H1proportion

**Usage**

H1proportion(pv = NA, lambda = 0.5)

**Arguments**

|        |                |
|--------|----------------|
| pv     | P.value vector |
| lambda | Lambda value   |

**Value**

H1 proportion value

---

has\_genomic\_coordinates

*Does SingleCellExperiment has genomic coordinates in features ?*

---

**Description**

Does SingleCellExperiment has genomic coordinates in features ?

**Usage**

has\_genomic\_coordinates(scExp)

**Arguments**

|       |                               |
|-------|-------------------------------|
| scExp | A SingleCellExperiment object |
|-------|-------------------------------|

**Value**

TRUE or FALSE

**Examples**

```

raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
has_genomic_coordinates(scExp)
raw_genes = create_scDataset_raw(featureType="gene")
scExp_gene = create_scExp(raw_genes$mat, raw_genes$annot)
has_genomic_coordinates(scExp_gene)

```

---

hclustAnnotHeatmapPlot

*hclustAnnotHeatmapPlot*


---

**Description**

hclustAnnotHeatmapPlot

**Usage**

```

hclustAnnotHeatmapPlot(
  x = NULL,
  hc = NULL,
  hmColors = NULL,
  anocol = NULL,
  xpos = c(0.1, 0.9, 0.114, 0.885),
  ypos = c(0.1, 0.5, 0.5, 0.6, 0.62, 0.95),
  dendro.cex = 1,
  xlab.cex = 0.8,
  hmRowNames = FALSE,
  hmRowNames.cex = 0.5
)

```

**Arguments**

|                |                      |
|----------------|----------------------|
| x              | A correlation matrix |
| hc             | An hclust object     |
| hmColors       | A color palette      |
| anocol         | A matrix of colors   |
| xpos           | Xpos                 |
| ypos           | Ypos                 |
| dendro.cex     | Size of denro names  |
| xlab.cex       | Size of x label      |
| hmRowNames     | Write rownames ?     |
| hmRowNames.cex | Size of rownames ?   |

**Value**

A heatmap

---

|                  |   |
|------------------|---|
| hg38.chromosomes | <i>Data.frame of chromosome length - hg38</i> |
|------------------|---|

---

**Description**

This data frame provides the length of each "canonical" chromosomes of Homo Sapiens genome build hg38.

**Usage**

```
data("hg38.chromosomes")
```

**Format**

hg38.chromosomes - a data frame with 24 rows and 3 variables:

**chr** Chromosome - character

**start** Start of the chromosome (bp) - integer

**end** End of the chromosome (bp) - integer

---

|               |  |
|---------------|--|
| hg38.cytoBand | <i>Data.frame of cytoBandlocation - hg38</i> |
|---------------|--|

---

**Description**

This data frame provides the location of each cytoBands of Homo Sapiens genome build hg38.

**Usage**

```
data("hg38.cytoBand")
```

**Format**

hg38.cytoBand - a data frame with 862 rows and 4 variables:

**chr** Chromosome - character

**start** Start of the chromosome (bp) - integer

**end** End of the chromosome (bp) - integer

**cytoBand** Name of the cytoBand - character

---

|              |                                      |
|--------------|--------------------------------------|
| hg38.GeneTSS | <i>Data.frame of gene TSS - hg38</i> |
|--------------|--------------------------------------|

---

**Description**

This dataframe was extracted from Gencode v25 and report the Transcription Start Site of each gene in the Homo Sapiens genome build hg38.

**Usage**

```
data("hg38.GeneTSS")
```

**Format**

hg38.GeneTSS - a data frame with 24 rows and 3 variables:

**chr** Chromosome - character  
**start** Start of the gene (TSS) - integer  
**end** End of the gene - integer  
**gene** Gene symbol - character

---

|          |                 |
|----------|-----------------|
| imageCol | <i>imageCol</i> |
|----------|-----------------|

---

**Description**

imageCol

**Usage**

```
imageCol(  
  matcol = NULL,  
  strat = NULL,  
  xlab.cex = 0.5,  
  ylab.cex = 0.5,  
  drawLines = c("none", "h", "v", "b")[1],  
  ...  
)
```

**Arguments**

|           |                       |
|-----------|-----------------------|
| matcol    | A matrix of colors    |
| strat     | Strat                 |
| xlab.cex  | X label size          |
| ylab.cex  | Y label size          |
| drawLines | Draw lines ?          |
| ...       | Additional parameters |

**Value**

A rectangular image

---

import\_count\_input\_files

*Import and count input files depending on their format*

---

**Description**

Import and count input files depending on their format

**Usage**

```
import_count_input_files(  
  files_dir_list,  
  file_type,  
  which,  
  ref,  
  verbose,  
  progress,  
  BPPARAM = BiocParallel::bpparam()  
)
```

**Arguments**

|                |   |
|----------------|---|
| files_dir_list | A named list of directories containing the input files.   |
| file_type      | Input file type.  |
| which          | A GRanges object of features.   |
| ref            | Reference genome.   |
| verbose        | Print ?   |
| progress       | A progress object for Shiny.  |
| BPPARAM        | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Value**

A list with the feature indexes data.frame containing non-zeroes entries in the count matrix and the cell names



---

|              |  |
|--------------|--|
| import_scExp | <i>Read single-cell matrix(ces) into scExp</i> |
|--------------|--|

---

## Description

Combine one or multiple matrices together to create a sparse matrix and cell annotation data.frame.

## Usage

```
import_scExp(file_paths, remove_pattern = "", temp_path = NULL)
```

## Arguments

|                |   |
|----------------|---|
| file_paths     | A character vector of file names towards single cell epigenomic matrices (features x cells) (must be .txt / .tsv) |
| remove_pattern | A string pattern to remove from the sample names. Can be a regexp.  |
| temp_path      | In case matrices are stored in temporary folder, a character vector of path towards temporary files. (NULL)       |

## Value

A list containing:

- datamatrix: a sparseMatrix of features x cells
- annot\_raw: an annotation of cells as data.frame

## Examples

```
mat1 = mat2 = create_scDataset_raw()$mat
tmp1 = tempfile(fileext = ".tsv")
tmp2 = tempfile(fileext = ".tsv")
write.table(as.matrix(mat1),file=tmp1,sep = "\t",
row.names = TRUE,col.names = TRUE,quote = FALSE)
write.table(as.matrix(mat2),file=tmp2, sep = "\t",
row.names = TRUE,col.names = TRUE,quote = FALSE)
file_paths = c(tmp1,tmp2)
out = import_scExp(file_paths)
```

---

index\_peaks\_barcode\_to\_matrix\_indexes

*Read index-peaks-barcode trio files on interval to create count indexes*

---

### Description

Read index-peaks-barcode trio files on interval to create count indexes

### Usage

```
index_peaks_barcode_to_matrix_indexes(
  feature_file,
  matrix_file,
  barcode_file,
  binarize = FALSE
)
```

### Arguments

|              |  |
|--------------|--|
| feature_file | A file containing the features genomic locations   |
| matrix_file  | A file containing the indexes of non-zeroes values and their value (respectively i,j,x,see sparseMatrix) |
| barcode_file | A file containing the barcode ids  |
| binarize     | Binarize matrix ?  |

### Value

A list containing a "feature index" data.frame, name\_cells, and a region GenomicRange object used to form the sparse matrix

---

inter\_correlation\_scExp

*Calculate inter correlation between cluster or samples*

---

### Description

Calculate inter correlation between cluster or samples

**Usage**

```
inter_correlation_scExp(
  scExp_cf,
  by = c("sample_id", "cell_cluster")[1],
  reference_group = unique(scExp_cf[[by]][1]),
  other_groups = unique(scExp_cf[[by]]),
  fullCor = TRUE
)
```

**Arguments**

|                 |  |
|-----------------|--|
| scExp_cf        | A SingleCellExperiment   |
| by              | On which feature to calculate correlation ("sample_id" or "cell_cluster")  |
| reference_group | Reference group to calculate correlation with. Must be in accordance with "by".  |
| other_groups    | Groups on which to calculate correlation (can contain multiple groups, and also reference_group). Must be in accordance with "by". |
| fullCor         | A logical specifying if the correlation matrix was calculated on the entire set of cells (TRUE).                                   |

**Value**

A data.frame of average inter-correlation of cells in other\_groups with cells in reference\_group

**Examples**

```
data(scExp)
inter_correlation_scExp(scExp)
```

---

intra\_correlation\_scExp

*Calculate intra correlation between cluster or samples*

---

**Description**

Calculate intra correlation between cluster or samples

**Usage**

```
intra_correlation_scExp(
  scExp_cf,
  by = c("sample_id", "cell_cluster")[1],
  fullCor = TRUE
)
```

**Arguments**

|          |  |
|----------|--|
| scExp_cf | A SingleCellExperiment   |
| by       | On which feature to calculate correlation ("sample_id" or "cell_cluster")                          |
| fullCor  | Logical specifying if the correlation matrix was run on the entire number of cells or on a subset. |

**Value**

A data.frame of cell average intra-correlation

**Examples**

```
data(scExp)
intra_correlation_scExp(scExp, by = "sample_id")
intra_correlation_scExp(scExp, by = "cell_cluster")
```

---

|           |                          |
|-----------|--------------------------|
| launchApp | <i>Launch ChromSCape</i> |
|-----------|--------------------------|

---

**Description**

Main function to launch ChromSCape in your favorite browser. You can pass additional parameters that you would pass to shiny::runApp ([runApp](#))

**Usage**

```
launchApp(launch.browser = TRUE, ...)
```

**Arguments**

|                |  |
|----------------|--|
| launch.browser | Wether to launch browser or not                        |
| ...            | Additional parameters passed to <a href="#">runApp</a> |

**Value**

Launches the shiny application

**Examples**

```
## Not run:
launchApp()

## End(Not run)
```

---

|             |   |
|-------------|---|
| load_MSIGdb | <i>Load and format MSIGdb pathways using msigdb package</i> |
|-------------|---|

---

**Description**

Load and format MSIGdb pathways using msigdb package

**Usage**

```
load_MSIGdb(
  ref,
  GeneSetClasses = c("c1_positional", "c2_curated", "c3_motif", "c4_computational",
    "c5_G0", "c6_oncogenic", "c7_immunologic", "hallmark")
)
```

**Arguments**

ref                    Reference genome, either mm10 or hg38  
 GeneSetClasses    Which classes of MSIGdb to load

**Value**

A list containing the GeneSet (list), GeneSetDf (data.frame) and GenePool character vector of all possible genes

---

|                   |  |
|-------------------|--|
| merge_MACS2_peaks | <i>Merge peak files from MACS2 peak caller</i> |
|-------------------|--|

---

**Description**

Merge peak files from MACS2 peak caller

**Usage**

```
merge_MACS2_peaks(peak_file, peak_distance_to_merge, min_peak_size = 200, ref)
```

**Arguments**

peak\_file            A character specifying the path towards the peak file (BED or bedGraph format)  
 peak\_distance\_to\_merge    Maximum distance to merge two peaks  
 min\_peak\_size    An integer specifying the minimum size of peaks  
 ref                Reference genome

**Value**

Peaks as GRanges

---

mm10.chromosomes      *Data.frame of chromosome length - mm10*

---

**Description**

This data frame provides the length of each "canonical" chromosomes of Mus Musculus (Mouse) genome build mm10.

**Usage**

```
data("mm10.chromosomes")
```

**Format**

mm10.chromosomes - a data frame with 24 rows and 3 variables:

**chr** Chromosome - character

**start** Start of the chromosome (bp) - integer

**end** End of the chromosome (bp) - integer

---

mm10.cytoBand      *Data.frame of cytoBandlocation - mm10*

---

**Description**

This data frame provides the location of each cytoBands of Homo Sapiens genome build mm10.

**Usage**

```
data("mm10.cytoBand")
```

**Format**

mm10.cytoBand - a data frame with 862 rows and 4 variables:

**chr** Chromosome - character

**start** Start of the chromosome (bp) - integer

**end** End of the chromosome (bp) - integer

**cytoBand** Name of the cytoBand - character

---

|              |                                      |
|--------------|--------------------------------------|
| mm10.GeneTSS | <i>Data.frame of gene TSS - mm10</i> |
|--------------|--------------------------------------|

---

**Description**

This dataframe was extracted from Gencode v25 and report the Transcription Start Site of each gene in the Mus Musculus genome build mm10 (Mouse).

**Usage**

```
data("mm10.GeneTSS")
```

**Format**

mm10.GeneTSS - a data frame with 24 rows and 3 variables:

**chr** Chromosome name - character  
**start** Start of the gene (TSS) - integer  
**end** End of the gene - integer  
**gene** Gene symbol - character

---

|                 |                         |
|-----------------|-------------------------|
| normalize_scExp | <i>Normalize counts</i> |
|-----------------|-------------------------|

---

**Description**

Normalize counts

**Usage**

```
normalize_scExp(  
  scExp,  
  type = c("CPM", "TFIDF", "RPKM", "TPM", "feature_size_only")  
)
```

**Arguments**

**scExp** A SingleCellExperiment object.  
**type** Which normalization to apply. Either 'CPM', 'TFIDF', 'RPKM', 'TPM' or 'feature\_size\_only'. Note that for all normalization by size (RPKM, TPM, feature\_size\_only), the features must have defined genomic coordinates.

**Value**

A SingleCellExperiment object containing normalized counts. (See ?normcounts())

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = normalize_scExp(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

num\_cell\_after\_cor\_filt\_scExp

*Number of cells before & after correlation filtering*

---

**Description**

Number of cells before & after correlation filtering

**Usage**

```
num_cell_after_cor_filt_scExp(scExp, scExp_cf)
```

**Arguments**

scExp            SingleCellExperiment object before correlation filtering.  
scExp\_cf        SingleCellExperiment object after correlation filtering.

**Value**

A colored kable with the number of cells per sample before and after filtering for display

**Examples**

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = filter_correlated_cell_scExp(scExp_cf,
  corr_threshold = 99, percent_correlation = 1)
## Not run: num_cell_after_cor_filt_scExp(scExp,scExp_cf)
```



---

num\_cell\_after\_QC\_filt\_scExp  
*Table of cells before / after QC*

---

**Description**

Table of cells before / after QC

**Usage**

```
num_cell_after_QC_filt_scExp(scExp, annot, datamatrix)
```

**Arguments**

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment object.                         |
| annot      | A raw annotation data.frame of cells before filtering. |
| datamatrix | A matrix of cells per regions before filtering.        |

**Value**

A formatted kable in HTML.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp_filtered = filter_scExp(scExp)
## Not run: num_cell_after_QC_filt_scExp(
scExp_filtered, SingleCellExperiment::colData(scExp))
## End(Not run)
```

---

num\_cell\_before\_cor\_filt\_scExp  
*Table of number of cells before correlation filtering*

---

**Description**

Table of number of cells before correlation filtering

**Usage**

```
num_cell_before_cor_filt_scExp(scExp)
```

**Arguments**

scExp            A SingleCellExperiment Object

**Value**

A colored kable with the number of cells per sample for display

**Examples**

```
data("scExp")
## Not run: num_cell_before_cor_filt_scExp(scExp)
```

---

```
num_cell_in_cluster_scExp
      Number of cells in each cluster
```

---

**Description**

Number of cells in each cluster

**Usage**

```
num_cell_in_cluster_scExp(scExp)
```

**Arguments**

scExp            A SingleCellExperiment object containing chromatin groups.

**Value**

A formatted kable of cell assignation to each cluster.

**Examples**

```
data("scExp")
scExp_cf = correlation_and_hierarchical_clust_scExp(scExp)
scExp_cf = choose_cluster_scExp(scExp_cf, nclust=3, consensus=FALSE)
## Not run: num_cell_in_cluster_scExp(scExp_cf)
```

---

|                |                       |
|----------------|-----------------------|
| num_cell_scExp | <i>Table of cells</i> |
|----------------|-----------------------|

---

**Description**

Table of cells

**Usage**

```
num_cell_scExp(annot, datamatrix)
```

**Arguments**

|            |   |
|------------|---|
| annot      | An annotation of cells. Can be obtain through 'colData(scExp)'. |
| datamatrix | A matrix of cells per regions before filtering.                 |

**Value**

A formatted kable in HTML.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
## Not run: num_cell_scExp(SingleCellExperiment::colData(scExp))
```

---

|                            |                                       |
|----------------------------|---------------------------------------|
| pca_irlba_for_sparseMatrix | <i>Run sparse PCA using irlba SVD</i> |
|----------------------------|---------------------------------------|

---

**Description**

This function allows to run a PCA using IRLBA Singular Value Decomposition in a fast & memory efficient way. The incremental Lanczos bidiagonalisation algorithm allows to keep the matrix sparse as the "loci" centering is implicit. The function then multiplies by the approximate singular values (svd\$d) in order to get more importance to the first PCs proportionally to their singular values. This step is crucial for downstream approaches, e.g. UMAP or T-SNE.

**Usage**

```
pca_irlba_for_sparseMatrix(x, n_comp, work = 3 * n_comp)
```

**Arguments**

|        |   |
|--------|---|
| x      | A sparse normalized matrix (features x cells)   |
| n_comp | The number of principal components to keep  |
| work   | Working subspace dimension, larger values can speed convergence at the cost of more memory use. |

**Value**

The rotated data, e.g. the cells x PC column in case of sc data.

---

plot\_cluster\_consensus\_scExp  
*Plot cluster consensus*

---

**Description**

Plot cluster consensus score for each k as a bargraph.

**Usage**

```
plot_cluster_consensus_scExp(scExp)
```

**Arguments**

|       |                        |
|-------|------------------------|
| scExp | A SingleCellExperiment |
|-------|------------------------|

**Value**

The consensus score for each cluster for each k as a barplot

**Examples**

```
data("scExp")  
plot_cluster_consensus_scExp(scExp)
```

---

`plot_correlation_PCA_scExp`*Plotting correlation of PCs with a variable of interest*

---

**Description**

Plotting correlation of PCs with a variable of interest

**Usage**

```
plot_correlation_PCA_scExp(  
  scExp,  
  correlation_var = "total_counts",  
  color_by = NULL,  
  topPC = 10  
)
```

**Arguments**

|                              |   |
|------------------------------|---|
| <code>scExp</code>           | A SingleCellExperiment Object   |
| <code>correlation_var</code> | A string specifying with which numeric variable from <code>colData</code> of <code>scExp</code> to calculate and plot the correlation of each PC with. ('total_counts') |
| <code>color_by</code>        | A string specifying with which categorical variable to color the plot. ('NULL')   |
| <code>topPC</code>           | An integer specifying the number of PCs to plot correlation with 10   |

**Value**

A ggplot histogram representing the distribution of count per cell

**Examples**

```
data("scExp")  
plot_correlation_PCA_scExp(scExp, topPC = 25)  
plot_correlation_PCA_scExp(scExp, color_by = "cell_cluster")  
plot_correlation_PCA_scExp(scExp, color_by = "sample_id")
```

---

plot\_coverage\_BigWig *Coverage plot*

---

### Description

Coverage plot

### Usage

```
plot_coverage_BigWig(  
  coverages,  
  label_color_list,  
  peaks = NULL,  
  chrom,  
  start,  
  end,  
  ref = "hg38"  
)
```

### Arguments

|                  |   |
|------------------|---|
| coverages        | A list containing sample coverage as GenomicRanges            |
| label_color_list | List of colors, list names are labels                         |
| peaks            | A GRanges object containing peaks location to plot (optional) |
| chrom            | Chromosome  |
| start            | Start   |
| end              | End   |
| ref              | Genomic Reference   |

### Value

A coverage plot annotated with genes

### Examples

```
data(scExp)
```

---

plot\_differential\_summary\_scExp  
*Differential summary barplot*

---

**Description**

Differential summary barplot

**Usage**

```
plot_differential_summary_scExp(  
  scExp_cf,  
  qval.th = 0.01,  
  logFC.th = 1,  
  min.percent = 0.01  
)
```

**Arguments**

|             |  |
|-------------|--|
| scExp_cf    | A SingleCellExperiment object  |
| qval.th     | Adjusted p-value threshold. (0.01)   |
| logFC.th    | Fold change threshold. (1)   |
| min.percent | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01) |

**Value**

A barplot summary of differential analysis

**Examples**

```
data("scExp")  
plot_differential_summary_scExp(scExp)
```

---

plot\_differential\_volcano\_scExp  
*Volcano plot of differential features*

---

**Description**

Volcano plot of differential features

**Usage**

```
plot_differential_volcano_scExp(  
  scExp_cf,  
  group = "C1",  
  logFC.th = 1,  
  qval.th = 0.01,  
  min.percent = 0.01  
)
```

**Arguments**

|             |  |
|-------------|--|
| scExp_cf    | A SingleCellExperiment object  |
| group       | A character indicating the group for which to plot the differential volcano plot. ("C1")                 |
| logFC.th    | Fold change threshold. (1)   |
| qval.th     | Adjusted p-value threshold. (0.01)   |
| min.percent | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01) |

**Value**

A volcano plot of differential analysis of a specific cluster

**Examples**

```
data("scExp")  
plot_differential_volcano_scExp(scExp, "C1")
```

---

plot\_distribution\_scExp

*Plotting distribution of signal*

---

**Description**

Plotting distribution of signal

**Usage**

```
plot_distribution_scExp(  
  scExp,  
  raw = TRUE,  
  log10 = FALSE,  
  pseudo_counts = 1,  
  bins = 150  
)
```



**Arguments**

|               |                                    |
|---------------|------------------------------------|
| scExp         | A SingleCellExperiment Object      |
| raw           | Use raw counts ?                   |
| log10         | Transform using log10 ?            |
| pseudo_counts | Pseudo-count to add if using log10 |
| bins          | Number of bins in the histogram    |

**Value**

A ggplot histogram representing the distribution of count per cell

**Examples**

```
data("scExp")
plot_distribution_scExp(scExp)
```

---

```
plot_gain_or_loss_barplots
```

*Plot Gain or Loss of cytobands of the most variables cytobands*

---

**Description**

Plot Gain or Loss of cytobands of the most variables cytobands

Plot Gain or Loss of cytobands of the most variables cytobands

**Usage**

```
plot_gain_or_loss_barplots(scExp, cells = NULL, top = 20)
```

```
plot_gain_or_loss_barplots(scExp, cells = NULL, top = 20)
```

**Arguments**

|       |  |
|-------|--|
| scExp | A SingleCellExperiment with "logRatio_cytoBand" reducedDim slot filled. See <a href="#">calculate_logRatio_CNA</a> |
| cells | Cell IDs of the tumor samples to   |
| top   | Number of most variables cytobands to plot   |

**Value**

Plot the gains/lost in the selected cells of interest as multiple barplots

Plot the gains/lost in the selected cells of interest as multiple barplots

**Examples**

```
data("scExp")
scExp = calculate_CNA(scExp, control_samples = unique(scExp$sample_id)[1],
  ref_genome="hg38", quantiles_to_define_gol = c(0.05,0.95))
plot_gain_or_loss_barplots(scExp, cells = scExp$cell_id[which(
  scExp$sample_id %in% unique(scExp$sample_id)[2])])
```

```
data("scExp")
scExp = calculate_CNA(scExp, control_samples = unique(scExp$sample_id)[1],
  ref_genome="hg38", quantiles_to_define_gol = c(0.05,0.95))
plot_gain_or_loss_barplots(scExp, cells = scExp$cell_id[which(
  scExp$sample_id %in% unique(scExp$sample_id)[2])])
```

---

plot\_heatmap\_scExp      *Plot cell correlation heatmap with annotations*

---

**Description**

Plot cell correlation heatmap with annotations

**Usage**

```
plot_heatmap_scExp(
  scExp,
  name_hc = "hc_cor",
  corColors = (grDevices::colorRampPalette(c("royalblue", "white", "indianred1")))(256),
  color_by = NULL,
  downsample = 1000,
  hc_linkage = "ward.D"
)
```

**Arguments**

|            |  |
|------------|--|
| scExp      | A SingleCellExperiment Object  |
| name_hc    | Name of the hclust contained in the SingleCellExperiment object                    |
| corColors  | A palette of colors for the heatmap  |
| color_by   | Which features to add as additional bands on top of plot                           |
| downsample | Number of cells to downsample  |
| hc_linkage | A linkage method for hierarchical clustering. See <a href="#">cor</a> . ('ward.D') |

**Value**

A heatmap of cell to cell correlation, grouping cells by hierarchical clustering.

**Examples**

```
data("scExp")
plot_heatmap_scExp(scExp)
```

---

```
plot_inter_correlation_scExp
```

*Violin plot of inter-correlation distribution between one or multiple groups and one reference group*

---

**Description**

Violin plot of inter-correlation distribution between one or multiple groups and one reference group

**Usage**

```
plot_inter_correlation_scExp(
  scExp_cf,
  by = c("sample_id", "cell_cluster")[1],
  jitter_by = NULL,
  reference_group = unique(scExp_cf[[by]])[1],
  other_groups = unique(scExp_cf[[by]]),
  downsample = 5000
)
```

**Arguments**

|                 |   |
|-----------------|---|
| scExp_cf        | A SingleCellExperiment  |
| by              | Color by sample_id or cell_cluster  |
| jitter_by       | Add jitter points of another layer (cell_cluster or sample_id)                                    |
| reference_group | Character containing the reference group name to calculate correlation from.                      |
| other_groups    | Character vector of the other groups for which to calculate correlation with the reference group. |
| downsample      | Downsample for plotting   |

**Value**

A violin plot of inter-correlation

**Examples**

```
data(scExp)
plot_intra_correlation_scExp(scExp)
```

plot\_intra\_correlation\_scExp

*Violin plot of intra-correlation distribution*

---

### Description

Violin plot of intra-correlation distribution

### Usage

```
plot_intra_correlation_scExp(  
  scExp_cf,  
  by = c("sample_id", "cell_cluster")[1],  
  jitter_by = NULL,  
  downsample = 5000  
)
```

### Arguments

|            |  |
|------------|--|
| scExp_cf   | A SingleCellExperiment   |
| by         | Color by sample_id or cell_cluster                             |
| jitter_by  | Add jitter points of another layer (cell_cluster or sample_id) |
| downsample | Downsample for plotting  |

### Value

A violin plot of intra-correlation

### Examples

```
data(scExp)  
plot_intra_correlation_scExp(scExp)
```

---

plot\_most\_contributing\_features

*Plot Top/Bottom most contributing features to PCA*

---

### Description

Plot Top/Bottom most contributing features to PCA

**Usage**

```
plot_most_contributing_features(
  scExp,
  component = "Component_1",
  n_top_bot = 10
)
```

**Arguments**

|           |   |
|-----------|---|
| scExp     | A SingleCellExperiment containing "PCA" in reducedDims and gene annotation in rowRanges |
| component | The name of the component of interest   |
| n_top_bot | An integer number of top and bot regions to plot  |

**Details**

If a gene TSS is within 10,000bp of the region, the name of the gene(s) will be displayed instead of the region

**Value**

A barplot of top and bottom features with the largest absolute value in the component of interest

**Examples**

```
data(scExp)
plot_most_contributing_features(scExp, component = "Component_1")
```

---

```
plot_percent_active_feature_scExp
```

*Barplot of the % of active cells for a given features*

---

**Description**

Barplot of the % of active cells for a given features

**Usage**

```
plot_percent_active_feature_scExp(
  scExp,
  gene,
  by = c("cell_cluster", "sample_id")[1],
  highlight = NULL,
  downsample = 5000,
  max_distanceToTSS = 1000
)
```

**Arguments**

|                   |   |
|-------------------|---|
| scExp             | A SingleCellExperiment  |
| gene              | A character specifying the gene to plot   |
| by                | Color violin by cell_cluster or sample_id ("cell_cluster")                              |
| highlight         | A specific group to highlight in a one vs all fashion                                   |
| downsample        | Downsample for plotting (5000)  |
| max_distanceToTSS | Numeric. Maximum distance to a gene's TSS to consider a region linked to a gene. (1000) |

**Value**

A violin plot of intra-correlation

**Examples**

```
data(scExp)
plot_percent_active_feature_scExp(scExp, "UBXN10")
```

---

plot\_pie\_most\_contributing\_chr

*Pie chart of top contribution of chromosomes in the 100 most contributing features to PCA #'*

---

**Description**

Pie chart of top contribution of chromosomes in the 100 most contributing features to PCA #'

**Usage**

```
plot_pie_most_contributing_chr(
  scExp,
  component = "Component_1",
  n_top_bot = 100
)
```

**Arguments**

|           |   |
|-----------|---|
| scExp     | A SingleCellExperiment containing "PCA" in reducedDims and gene annotation in rowRanges |
| component | The name of the component of interest   |
| n_top_bot | An integer number of top and bot regions to plot (100)                                  |

**Value**

A pie chart showing the distribution of chromosomes in the top features with the largest absolute value in the component of interest

**Examples**

```
data(scExp)
plot_pie_most_contributing_chr(scExp, component = "Component_1")
```

---

```
plot_reduced_dim_scExp
```

*Plot reduced dimensions (PCA, TSNE, UMAP)*

---

**Description**

Plot reduced dimensions (PCA, TSNE, UMAP)

**Usage**

```
plot_reduced_dim_scExp(
  scExp,
  color_by = "sample_id",
  reduced_dim = c("PCA", "TSNE", "UMAP"),
  select_x = NULL,
  select_y = NULL,
  downsample = 5000,
  transparency = 0.6,
  size = 1,
  max_distanceToTSS = 1000,
  annotate_clusters = "cell_cluster" %in% colnames(colData(scExp)),
  min_quantile = 0.01,
  max_quantile = 0.99
)
```

**Arguments**

|              |   |
|--------------|---|
| scExp        | A SingleCellExperiment Object   |
| color_by     | Character of feature used for coloration. Can be cell metadata ('total_counts', 'sample_id', ...) or a gene name. |
| reduced_dim  | Reduced Dimension used for plotting   |
| select_x     | Which variable to select for x axis   |
| select_y     | Which variable to select for y axis   |
| downsample   | Number of cells to downsample   |
| transparency | Alpha parameter, between 0 and 1  |
| size         | Size of the points.   |

|                   |   |
|-------------------|---|
| max_distanceToTSS | The maximum distance to TSS to consider a gene linked to a region. Used only if "color_by" is a gene name.    |
| annotate_clusters | A logical indicating if clusters should be labelled. The 'cell_cluster' column should be present in metadata. |
| min_quantile      | The lower threshold to remove outlier cells, as quantile of cell embeddings (between 0 and 0.5).              |
| max_quantile      | The upper threshold to remove outlier cells, as quantile of cell embeddings (between 0.5 and 1).              |

**Value**

A ggplot geom\_point plot of reduced dimension 2D representation

**Examples**

```
data("scExp")
plot_reduced_dim_scExp(scExp, color_by = "sample_id")
plot_reduced_dim_scExp(scExp, color_by = "total_counts")
plot_reduced_dim_scExp(scExp, reduced_dim = "UMAP")
plot_reduced_dim_scExp(scExp, color_by = "CD52", reduced_dim = "UMAP")
```

---

plot\_reduced\_dim\_scExp\_CNA

*Plot UMAP colored by Gain or Loss of cytobands*

---

**Description**

Plot UMAP colored by Gain or Loss of cytobands

**Usage**

```
plot_reduced_dim_scExp_CNA(scExp, cytoBand)
```

**Arguments**

|          |  |
|----------|--|
| scExp    | A SingleCellExperiment with "gainOrLoss_cytoBand" reducedDim slot filled. See <a href="#">calculate_gain_or_loss</a> |
| cytoBand | Which cytoBand to color cells by   |

**Value**

Plot the gains/lost of the cytoband overlaid on the epigenetic UMAP.



**Examples**

```
data("scExp")
scExp = calculate_CNA(scExp, control_samples = unique(scExp$sample_id)[1],
ref_genome="hg38", quantiles_to_define_gol = c(0.05,0.95))
plot_reduced_dim_scExp_CNA(scExp, get_most_variable_cyto(scExp)$cytoBand[1])
```

---

plot\_top\_TF\_scExp      *Barplot of top TFs from ChEA3 TF enrichment analysis*

---

**Description**

Barplot of top TFs from ChEA3 TF enrichment analysis

**Usage**

```
plot_top_TF_scExp(
  scExp,
  group = unique(scExp$cell_cluster)[1],
  set = c("Differential", "Enriched", "Depleted")[1],
  type = c("Score", "nTargets", "nTargets_over_TF", "nTargets_over_genes")[1],
  n_top = 25
)
```

**Arguments**

|       |  |
|-------|--|
| scExp | A SingleCellExperiment   |
| group | A character string specifying the differential group to display the top TFs  |
| set   | A character string specifying the set of genes in which the TF were enriched, either 'Differential', 'Enriched' or 'Depleted'.   |
| type  | A character string specifying the Y axis of the plot, either the number of differential targets or the ChEA3 integrated mean score. E.g. either "Score", "nTargets", "nTargets_over_TF" for the number of target genes over the total number of genes targeted by the TF or "nTargets_over_genes" for the number of target genes over the number of genes in the gene set. |
| n_top | An integer specifying the number of top TF to display  |

**Value**

A bar plot of top TFs from ChEA3 TF enrichment analysis

**Examples**

```

data("scExp")

plot_top_TF_scExp(
  scExp,
  group = "C1",
  set = "Differential",
  type = "Score",
  n_top = 10)

plot_top_TF_scExp(
  scExp,
  group = "C1",
  set = "Enriched",
  type = "nTargets_over_genes",
  n_top = 20)

```

---

```

plot_violin_feature_scExp
Violin plot of features

```

---

**Description**

Violin plot of features

**Usage**

```

plot_violin_feature_scExp(
  scExp,
  gene,
  by = c("cell_cluster", "sample_id")[1],
  downsample = 5000,
  max_distanceToTSS = 1000
)

```

**Arguments**

|                   |   |
|-------------------|---|
| scExp             | A SingleCellExperiment  |
| gene              | A character specifying the gene to plot   |
| by                | Color violin by cell_cluster or sample_id ("cell_cluster")                              |
| downsample        | Downsample for plotting (5000)  |
| max_distanceToTSS | Numeric. Maximum distance to a gene's TSS to consider a region linked to a gene. (1000) |

**Value**

A violin plot of intra-correlation

**Examples**

```
data(scExp)
plot_violin_feature_scExp(scExp, "UBXN10")
```

---

```
preprocessing_filtering_and_reduction
```

*Preprocess and filter matrix annotation data project folder to SCE*

---

**Description**

Preprocess and filter matrix annotation data project folder to SCE

**Usage**

```
preprocessing_filtering_and_reduction(
  datamatrix,
  annot_raw,
  min_reads_per_cell = 1600,
  max_quantile_read_per_cell = 95,
  n_top_features = 40000,
  norm_type = "CPM",
  n_dims = 10,
  remove_PC = NULL,
  subsample_n = NULL,
  ref_genome = "hg38",
  exclude_regions = NULL,
  doBatchCorr = FALSE,
  batch_sels = NULL
)
```

**Arguments**

|   |  |
|---|--|
| <code>datamatrix</code>                 | A sparse count matrix of features x cells.                               |
| <code>annot_raw</code>                  | A data.frame with barcode, cell_id, sample_id, batch_id, total_counts    |
| <code>min_reads_per_cell</code>         | Minimum read per cell to keep the cell                                   |
| <code>max_quantile_read_per_cell</code> | Upper count quantile threshold above which cells are removed             |
| <code>n_top_features</code>             | Number of features to keep   |
| <code>norm_type</code>                  | Normalization type c("CPM", "TFIDF", "RPKM", "TPM", "feature_size_only") |

|                 |  |
|-----------------|--|
| n_dims          | An integer specifying the number of dimensions to keep for PCA   |
| remove_PC       | A vector of string indicating which principal components to remove before downstream analysis as probably correlated to library size. Should be under the form : 'Component_1', 'Component_2', ... Recommended when using 'TFIDF' normalization method. (NULL) |
| subsample_n     | Number of cells to subsample.  |
| ref_genome      | Reference genome ("hg38" or "mm10").   |
| exclude_regions | GenomicRanges with regions to remove from the object.  |
| doBatchCorr     | Run batch correction ? TRUE or FALSE   |
| batch_sels      | If doBatchCorr is TRUE, List of characters. Names are batch names, characters are sample names.  |

**Value**

A SingleCellExperiment object containing feature spaces.

**Examples**

```
raw <- create_scDataset_raw()
scExp = preprocessing_filtering_and_reduction(raw$mat, raw$annot)
```

---

```
preprocess_CPM          Preprocess scExp - Counts Per Million (CPM)
```

---

**Description**

Preprocess scExp - Counts Per Million (CPM)

**Usage**

```
preprocess_CPM(scExp)
```

**Arguments**

scExp                    A SingleCellExperiment Object

**Value**

A SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = preprocess_CPM(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

preprocess\_feature\_size\_only  
*Preprocess scExp - size only*

---

**Description**

Preprocess scExp - size only

**Usage**

```
preprocess_feature_size_only(scExp)
```

**Arguments**

scExp            A SingleCellExperiment Object

**Value**

A SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = preprocess_feature_size_only(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

preprocess\_RPKM            *Preprocess scExp - Read per Kilobase Per Million (RPKM)*

---

**Description**

Preprocess scExp - Read per Kilobase Per Million (RPKM)

**Usage**

```
preprocess_RPKM(scExp)
```

**Arguments**

scExp            A SingleCellExperiment Object

**Value**

A SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = preprocess_RPKM(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

preprocess\_TFIDF      *Preprocess scExp - TF-IDF*

---

**Description**

Preprocess scExp - TF-IDF

**Usage**

```
preprocess_TFIDF(scExp, scale = 10000, log = TRUE)
```

**Arguments**

|       |   |
|-------|---|
| scExp | A SingleCellExperiment Object   |
| scale | A numeric to multiply the matrix in order to have human readable numbers.<br>Has no impact on the downstream analysis |
| log   | Whether to use neperian log on the TF-IDF normalized data or not.   |

**Value**

A SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = preprocess_TFIDF(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

```
preprocess_TPM      Preprocess scExp - Transcripts per Million (TPM)
```

---

**Description**

Preprocess scExp - Transcripts per Million (TPM)

**Usage**

```
preprocess_TPM(scExp)
```

**Arguments**

```
scExp      A SingleCellExperiment Object
```

**Value**

A SingleCellExperiment object.

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = preprocess_TPM(scExp)
head(SingleCellExperiment::normcounts(scExp))
```

---

```
rawfile_ToBigWig      rawfile_ToBigWig : reads in BAM file and write out BigWig coverage  

                       file, normalized and smoothed
```

---

**Description**

rawfile\_ToBigWig : reads in BAM file and write out BigWig coverage file, normalized and smoothed

**Usage**

```
rawfile_ToBigWig(
  input,
  BigWig_filename,
  format = "BAM",
  bin_width = 150,
  norm_factor,
  n_smoothBin = 5,
  ref = "hg38",
  read_size = 101,
```

```

    original_bins = NULL,
    quantile_for_peak_calling = 0.85
)

```

### Arguments

|                           |  |
|---------------------------|--|
| input                     | Either a named list of character vector of path towards single-cell BED files or a sparse raw matrix of small bins (<500bp). If a named list specifying scBEDn the names MUST correspond to the 'sample_id' column in your SingleCellExperiment object. The single-cell BED files names MUST match the barcode names in your SingleCellExperiment (column 'barcode'). The scBED files can be gzipped or not. |
| BigWig_filename           | Path to write the output BigWig file   |
| format                    | File format, either "BAM" or "BED"   |
| bin_width                 | Bin size for coverage  |
| norm_factor               | Then number of cells or total number of reads in the given sample, for normalization.  |
| n_smoothBin               | Number of bins for smoothing values  |
| ref                       | Reference genome.  |
| read_size                 | Length of the reads.   |
| original_bins             | Original bins GenomicRanges in case the format is raw matrix.  |
| quantile_for_peak_calling | The quantile to define the threshold above which signal is considered as a peak.   |

### Value

Writes in the output directory a bigwig file displaying the cumulative coverage of cells and a basic set of peaks called by taking all peaks above a given threshold

Writes a BigWig file as output

---

raw\_counts\_to\_sparse\_matrix

*Create a sparse count matrix from various format of input data.*

---

### Description

This function takes three different type of single-cell input: - Single cell BAM files (sorted) - Single cell BED files (gzipped) - A combination of an index file, a peak file and cell barcode file (The index file is composed of three column: index i, index j and value x for the non zeroes entries in the sparse matrix.)



**Usage**

```
raw_counts_to_sparse_matrix(
  files_dir_list,
  file_type = c("scBED", "scBAM", "FragmentFile"),
  use_Signac = TRUE,
  peak_file = NULL,
  n_bins = NULL,
  bin_width = NULL,
  genebody = NULL,
  extendPromoter = 2500,
  verbose = TRUE,
  ref = c("hg38", "mm10")[1],
  progress = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

|                             |   |
|-----------------------------|---|
| <code>files_dir_list</code> | A named character vector of directories containing the files. The names correspond to sample names.   |
| <code>file_type</code>      | Input file(s) type(s) ('scBED', 'scBAM', 'FragmentFile')  |
| <code>use_Signac</code>     | Use Signac wrapper function 'FeatureMatrix' if the Signac package is installed (TRUE).  |
| <code>peak_file</code>      | A file containing genomic location of peaks (NULL)  |
| <code>n_bins</code>         | The number of bins to tile the genome (NULL)  |
| <code>bin_width</code>      | The size of bins to tile the genome (NULL)  |
| <code>genebody</code>       | Count on genes (body + promoter) ? (NULL)   |
| <code>extendPromoter</code> | If counting on genes, number of base pairs to extend up or downstream of TSS (2500).  |
| <code>verbose</code>        | Verbose (TRUE)  |
| <code>ref</code>            | reference genome to use (hg38)  |
| <code>progress</code>       | Progress object for Shiny   |
| <code>BPPARAM</code>        | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Details**

This functions re-counts signal on either fixed genomic bins, a set of user-defined peaks or around the TSS of genes.

**Value**

A sparse matrix of features x cells

**References**

Stuart et al., Multimodal single-cell chromatin analysis with Signac bioRxiv <https://doi.org/10.1101/2020.11.09.373613>

---

read\_count\_mat\_with\_separated\_chr\_start\_end

*Read a count matrix with three first columns (chr,start,end)*

---

**Description**

Read a count matrix with three first columns (chr,start,end)

**Usage**

```
read_count_mat_with_separated_chr_start_end(
  path_to_matrix,
  format_test,
  separator
)
```

**Arguments**

|                |                          |
|----------------|--------------------------|
| path_to_matrix | Path to the count matrix |
| format_test    | Sample of the read.table |
| separator      | Separator character      |

**Value**

A sparseMatrix with rownames in the form "chr1:1222-55555"

---

read\_sparse\_matrix      *Read in one or multiple sparse matrices (10X format)*

---

**Description**

Given one or multiple directories, look in each directory for a combination of the following files :

- A 'features' file containing unique feature genomic locations -in tab separated format (\*\_features.bed / .txt / .tsv / .gz), e.g. chr, start and end
- A 'barcodes' file containing unique barcode names (\_barcode.txt / .tsv / .gz)
- A 'matrix' A file containing indexes of non zero entries (\_matrix.mtx / .gz)

**Usage**

```
read_sparse_matrix(files_dir_list, ref = c("hg38", "mm10")[1], verbose = TRUE)
```

**Arguments**

files\_dir\_list A named character vector containing the full path towards folders. Each folder should contain only the Feature file, the Barcode file and the Matrix file (see description).

ref Reference genome (used to filter non-canonical chromosomes).

verbose Print ?

**Value**

Returns a list containing a datamatrix and cell annotation

**Examples**

```
## Not run:
sample_dirs = c("/path/to/folder1/", "/path/to/folder2/")
names(sample_dirs) = c("sample_1", "sample_2")
out <- read_sparse_matrix(sample_dirs, ref = "hg38")
head(out$datamatrix)
head(out$annot_raw)

## End(Not run)
```

---

|              |  |
|--------------|--|
| rebin_matrix | <i>Transforms a bins x cells count matrix into a larger bins x cells count matrix.</i> |
|--------------|--|

---

**Description**

This functions is best used to re-count large number of small bins or peaks (e.g.  $\leq 5000$ bp) into equal or larger sized bins. The genome is either cut in fixed bins (e.g. 50,000bp) or into an user defined number of bins. Bins are calculated based on the canonical chromosomes. Note that if peaks are larger than bins, or if peaks are overlapping multiple bins, the signal is added to each bin. Users can increase the minimum overlap to consider peaks overlapping bins (by default 150bp, size of a nucleosome) to diminish the number of peaks overlapping multiple region. Any peak smaller than the minimum overlapp threshold will be dismissed. Therefore, library size might be slightly different from peaks to bins if signal was duplicated into multiple bins or ommitted due to peaks smaller than minimum overlap.

**Usage**

```
rebin_matrix(
  mat,
  bin_width = 50000,
  custom_annotation = NULL,
  minoverlap = 500,
  verbose = TRUE,
  ref = "hg38"
)
```

**Arguments**

|                   |  |
|-------------------|--|
| mat               | A matrix of peaks x cells  |
| bin_width         | Width of bins to produce in base pairs (minimum 500) (50000)   |
| custom_annotation | A GenomicRanges object specifying the new features to count the matrix on instead of recounting on genomic bins. If not NULL, takes precedence over bin_width.   |
| minoverlap        | Minimum overlap between the original bins and the new features to consider the peak as overlapping the bin . We recommend to put this number at exactly half of the original bin size (e.g. 500bp for original bin size of 1000bp) so that no original bins are counted twice. (500) |
| verbose           | Verbose  |
| ref               | Reference genome to use (hg38)   |

**Value**

A sparse matrix of larger bins or peaks.

**Examples**

```
mat = create_scDataset_raw()$mat
binned_mat = rebin_matrix(mat,bin_width = 10e6)
dim(binned_mat)
```

---

reduce\_dims\_scExp      *Reduce dimensions (PCA, TSNE, UMAP)*

---

**Description**

Reduce dimensions (PCA, TSNE, UMAP)

**Usage**

```
reduce_dims_scExp(
  scExp,
  dimension_reductions = c("PCA", "UMAP"),
  n = 10,
  batch_correction = FALSE,
  batch_list = NULL,
  remove_PC = NULL,
  verbose = TRUE
)
```

**Arguments**

|                      |  |
|----------------------|--|
| scExp                | A SingleCellExperiment object.   |
| dimension_reductions | A character vector of methods to apply. (c('PCA','TSNE','UMAP'))   |
| n                    | Numbers of dimensions to keep for PCA. (50)  |
| batch_correction     | Do batch correction ? (FALSE)  |
| batch_list           | List of characters. Names are batch names, characters are sample names.  |
| remove_PC            | A vector of string indicating which principal components to remove before downstream analysis as probably correlated to library size. Should be under the form : 'Component_1', 'Component_2', ... Recommended when using 'TFIDF' normalization method. (NULL) |
| verbose              | Print messages ?(TRUE)   |

**Value**

A SingleCellExperiment object containing feature spaces. See ?reduceDims().

**Examples**

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp = normalize_scExp(scExp, "CPM")
scExp = reduce_dims_scExp(scExp,dimension_reductions=c("PCA","UMAP"))
```

---

reduce\_dim\_batch\_correction  
*Reduce dimension with batch corrections*

---

**Description**

Reduce dimension with batch corrections

**Usage**

```
reduce_dim_batch_correction(scExp, mat, batch_list, n)
```

**Arguments**

|            |                             |
|------------|-----------------------------|
| scExp      | SingleCellExperiment        |
| mat        | The normalized count matrix |
| batch_list | List of batches             |
| n          | Number of PCs to keep       |

**Value**

A list containing the SingleCellExperiment with batch info and the corrected pca

---

|                  |   |
|------------------|---|
| remove_chr_M_fun | <i>Remove chromosome M from scExprownames</i> |
|------------------|---|

---

**Description**

Remove chromosome M from scExprownames

**Usage**

```
remove_chr_M_fun(scExp, verbose)
```

**Arguments**

|         |                        |
|---------|------------------------|
| scExp   | A SingleCellExperiment |
| verbose | Print ?                |

**Value**

A SingleCellExperiment without chromosome M (mitochondrial chr)

---

|                          |  |
|--------------------------|--|
| remove_non_canonical_fun | <i>Remove non canonical chromosomes from scExp</i> |
|--------------------------|--|

---

**Description**

Remove non canonical chromosomes from scExp

**Usage**

```
remove_non_canonical_fun(scExp, verbose)
```

**Arguments**

|         |                        |
|---------|------------------------|
| scExp   | A SingleCellExperiment |
| verbose | Print ?                |

**Value**

A SingleCellExperiment without non canonical chromosomes (random,unknown, contigs etc...)

---

`results_enrichmentTest`*Results of hypergeometric gene set enrichment test*

---

**Description**

Run hypergeometric enrichment test and combine significant pathways into a data.frame

**Usage**

```
results_enrichmentTest(  
  differentialGenes,  
  enrichment_qval,  
  GeneSets,  
  GeneSetsDf,  
  GenePool  
)
```

**Arguments**

|                   |  |
|-------------------|--|
| differentialGenes | Genes significantly over / under expressed                                 |
| enrichment_qval   | Adjusted p-value threshold above which a pathway is considered significant |
| GeneSets          | List of pathways   |
| GeneSetsDf        | Data.frame of pathways   |
| GenePool          | Pool of possible genes for testing   |

**Value**

A data.frame with pathways passing q.value threshold

---

`retrieve_top_bot_features_pca`*Retrieve Top and Bot most contributing features of PCA*

---

**Description**

Retrieve Top and Bot most contributing features of PCA

**Usage**

```
retrieve_top_bot_features_pca(
  pca,
  counts,
  component,
  n_top_bot,
  absolute = FALSE
)
```

**Arguments**

|           |  |
|-----------|--|
| pca       | A matrix/data.frame of rotated data                          |
| counts    | the normalized counts used for PCA                           |
| component | the component of interest                                    |
| n_top_bot | the number of top & bot features to take                     |
| absolute  | If TRUE, return the top features in absolute values instead. |

**Value**

a data.frame of top bot contributing features in PCA

---

|                    |                           |
|--------------------|---------------------------|
| run_pairwise_tests | <i>Run pairwise tests</i> |
|--------------------|---------------------------|

---

**Description**

Run pairwise tests

**Usage**

```
run_pairwise_tests(
  affectation,
  by,
  counts,
  feature,
  method,
  progress = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```



**Arguments**

|             |   |
|-------------|---|
| affectation | An annotation data.frame with cell_cluster and cell_id columns  |
| by          | = A character specifying the column of the object containing the groups of cells to compare.  |
| counts      | Count matrix  |
| feature     | Feature data.frame  |
| method      | DA method, Wilcoxon or edgeR  |
| progress    | A shiny Progress instance to display progress bar.  |
| BPPARAM     | BPPARAM object for multiprocessing. See <a href="#">bpparam</a> for more informations. Will take the default BPPARAM set in your R session. |

**Value**

A list containing objects for DA function

---

|                |   |
|----------------|---|
| run_tsne_scExp | <i>Run tsne on single cell experiment</i> |
|----------------|---|

---

**Description**

Run tsne on single cell experiment

**Usage**

```
run_tsne_scExp(scExp, verbose = FALSE)
```

**Arguments**

|         |                               |
|---------|-------------------------------|
| scExp   | A SingleCellExperiment Object |
| verbose | Print ?                       |

**Value**

A colored kable with the number of cells per sample for display

---

 scExp

*A SingleCellExperiment outputed by ChromSCape*


---

### Description

Data from a single-cell ChIP-seq experiment against H3K4me3 active mark from two cell lines, Jurkat B cells and Ramos T cells from Grosselin et al., 2019. The count matrices, on 5kbp bins, were given to ChromSCape and the filtering parameter was set to 3% of cells active in regions and subsampled down to 150 cells per sample. After correlation filtering, the experiment is composed of respectively 51 and 55 cells from Jurkat & Ramos and 5499 5kbp-genomic bins where signal is located.

### Usage

```
data("scExp")
```

### Format

scExp - a SingleCellExperiment with 106 cells and 5499 features (genomic bins) in hg38:

**chr** A SingleCellExperiment

### Details

The scExp is composed of :

- counts and normcounts assays, PCA, UMAP, and Correlation matrix in reducedDims(scExp)
- Assignment of genes to genomic bins in rowRanges(scExp)
- Cluster information in colData(scExp) correlation
- Hierarchical clustering dendrogram in metadata\$hc\_cor
- Consensus clustering raw data in metadata\$consclust
- Consensus clustering cluster-consensus and item consensus dataframes in metadata\$icl
- Differential analysis in metadata\$diff
- Gene Set Analysis in metadata\$enr

### Examples

```
data("scExp")
plot_reduced_dim_scExp(scExp)
plot_reduced_dim_scExp(scExp,color_by = "cell_cluster")
plot_heatmap_scExp(scExp)
plot_differential_volcano_scExp(scExp, "C1")
plot_differential_summary_scExp(scExp)
```

---

```
separate_BAM_into_clusters
```

*Separate BAM files into cell cluster BAM files*

---

### Description

Separate BAM files into cell cluster BAM files

### Usage

```
separate_BAM_into_clusters(affectation, odir, merged_bam)
```

### Arguments

|             |   |
|-------------|---|
| affectation | An annotation data.frame containing cell_id and cell_cluster columns            |
| odir        | A valid output directory path   |
| merged_bam  | A list of merged bam file paths<br>@importFrom Rsamtools filterBam ScanBamParam |

### Value

Create one BAM per cluster from one BAM per condition

---

```
separator_count_mat
```

*Determine Count matrix separator ("tab" or ",")*

---

### Description

Determine Count matrix separator ("tab" or ",")

### Usage

```
separator_count_mat(path_to_matrix)
```

### Arguments

|                |  |
|----------------|--|
| path_to_matrix | A path towards the count matrix to check |
|----------------|--|

### Value

A character separator

---

|           |   |
|-----------|---|
| smoothBin | <i>Smooth a vector of values with nb_bins left and right values</i> |
|-----------|---|

---

**Description**

Smooth a vector of values with nb\_bins left and right values

**Usage**

```
smoothBin(bin_score, nb_bins = 10)
```

**Arguments**

|           |  |
|-----------|--|
| bin_score | A numeric vector of values to be smoothed                                |
| nb_bins   | Number of values to take left and right<br>@importFrom BiocParallel bvec |

**Value**

A smooth vector of the same size

---

|                 |                        |
|-----------------|------------------------|
| subsample_scExp | <i>Subsample scExp</i> |
|-----------------|------------------------|

---

**Description**

Randomly sample x cells from each sample in a SingleCellExperiment to return a subsampled SingleCellExperiment with all samples having maximum n cells. If n is higher than the number of cell in a sample, this sample will not be subsampled.

**Usage**

```
subsample_scExp(scExp, n_cell_per_sample = 500, n_cell_total = NULL)
```

**Arguments**

|                   |  |
|-------------------|--|
| scExp             | A SingleCellExperiment   |
| n_cell_per_sample | An integer number of cells to subsample for each sample. Exclusive with n_cells_total. (500) |
| n_cell_total      | An integer number of cells to subsample in total. Exclusive with n_cell_per_sample (NULL).   |

**Value**

A subsampled SingleCellExperiment

## Examples

```
raw <- create_scDataset_raw()
scExp = create_scExp(raw$mat, raw$annot)
scExp_sub = subsample_scExp(scExp, 50)
## Not run: num_cell_scExp(scExp_sub)
```

---

subset\_bam\_call\_peaks *Peak calling on cell clusters*

---

## Description

This function does peak calling on each cell population in order to refine gene annotation for large bins. For instance, a 50000bp bins might contain the TSS of several genes, while in reality only one or two of these genes are overlapping the signal (peak). To do so, first in-silico cell sorting is applied based on previously defined clusters contained in the SingleCellExperiment. Taking BAM files of each sample as input, samtools pools then splits reads from each cell barcode into 1 BAM file per cell cluster (pseudo-bulk). Then MACS2 calls peaks on each cluster. The peaks are aggregated and merged if closer to a certain distance defined by user (10000bp). Then,

This function takes as input a SingleCellExperiment, that must contain a 'cell\_cluster' column in its colData, an output directory where to store temporary files, the list of BAM files corresponding to each sample and containing the cell barcode information as a tag (for instance tag CB:Z:xxx, XB:Z:xxx or else...) or single-cell BED files containing the raw reads and corresponding to the 'barcode' column metadata, the p.value used by MACS2 to distinguish significant peaks, the reference genome (either hg38 or mm10), the maximal merging distance in bp and a data.frame containing gene TSS genomic coordinates of corresponding genome (if set to NULL, will automatically load geneTSS). The output is a SingleCellExperiment with GRanges object containing ranges of each merged peaks that falls within genomic bins of the SingleCellExperiment, saving the bin range as additional column (window\_chr, window\_start, window\_end), as well as the closest genes and their distance relative to the peak. The peaks may be present in several rows if multiple genes are close / overlap to the peaks.

Note that the user must have MACS2 installed and available in the PATH. Users can open command terminal and type 'which macs2' to verify the availability of these programs. Will only work on unix operating system. Check operating system with 'print(.Platform)'.

## Usage

```
subset_bam_call_peaks(
  scExp,
  odir,
  input,
  format = "BAM",
  p.value = 0.05,
  ref = "hg38",
  peak_distance_to_merge = 10000,
  geneTSS_annotation = NULL,
```

```

    run_coverage = FALSE,
    progress = NULL
  )

```

### Arguments

|                        |   |
|------------------------|---|
| scExp                  | A SingleCellExperiment object   |
| odir                   | Output directory where to write temporary files and each cluster's BAM file   |
| input                  | A character vector of file paths to each sample's BAM file, containing cell barcode information as tags. BAM files can be paired-end or single-end. |
| format                 | Format of the input data, either "BAM" or "scBED".  |
| p.value                | a p-value to use for MACS2 to determine significant peaks. (0.05)   |
| ref                    | A reference genome, either hg38 or mm10. ('hg38')   |
| peak_distance_to_merge | Maximal distance to merge peaks together after peak calling , in bp. (10000)  |
| geneTSS_annotation     | A data.frame annotation of genes TSS. If NULL will automatically load Gene-code list of genes fro specified reference genome.                       |
| run_coverage           | Create coverage tracks (.bw) for each cluster ?   |
| progress               | A shiny Progress instance to display progress bar.  |

### Details

The BED files of the peaks called for each clusters, as well as the merged peaks are written in the output directory.

### Value

A SingleCellExperiment with refinded annotation

### Examples

```

## Not run:
data("scExp")
subset_bam_call_peaks(scExp, "path/to/out/", list("sample1" =
  "path/to/BAM/sample1.bam", "sample2" = "path/to/BAM/sample2.bam"),
  p.value = 0.05, ref = "hg38", peak_distance_to_merge = 10000,
  geneTSS_annotation = NULL)

## End(Not run)

```

---

|            |   |
|------------|---|
| summary_DA | <i>Summary of the differential analysis</i> |
|------------|---|

---

**Description**

Summary of the differential analysis

**Usage**

```
summary_DA(scExp, qval.th = 0.01, logFC.th = 1, min.percent = 0.01)
```

**Arguments**

|             |  |
|-------------|--|
| scExp       | A SingleCellExperiment object containing consclust with selected number of cluster.                      |
| qval.th     | Adjusted p-value threshold. (0.01)   |
| logFC.th    | Fold change threshold. (1)   |
| min.percent | Minimum fraction of cells having the feature active to consider it as significantly differential. (0.01) |

**Value**

A table summary of the differential analysis

**Examples**

```
data('scExp')
summary_DA(scExp)
```

---

|                        |  |
|------------------------|--|
| swapAltExp_sameColData | <i>Swap main &amp; alternative Experiments, with fixed colData</i> |
|------------------------|--|

---

**Description**

Swap main & alternative Experiments, with fixed colData

**Usage**

```
swapAltExp_sameColData(scExp, alt)
```

**Arguments**

|       |                                    |
|-------|------------------------------------|
| scExp | A SingleCellExperiment             |
| alt   | Name of the alternative experiment |

**Value**

A swapped SingleCellExperiment with the exact same colData.

**Examples**

```
data(scExp)
swapAltExp_sameColData(scExp, "peaks")
```

---

```
table_enriched_genes_scExp
```

*Creates table of enriched genes sets*

---

**Description**

Creates table of enriched genes sets

**Usage**

```
table_enriched_genes_scExp(
  scExp,
  set = "Both",
  group = "C1",
  enr_class_sel = c("c1_positional", "c2_curated", "c3_motif", "c4_computational",
    "c5_G0", "c6_oncogenic", "c7_immunologic", "hallmark")
)
```

**Arguments**

|               |  |
|---------------|--|
| scExp         | A SingleCellExperiment object containing list of enriched gene sets.   |
| set           | A character vector, either 'Both', 'Overexpressed' or 'Underexpressed'. ('Both')   |
| group         | The "group" name from differential analysis. Can be the cluster name or the custom name in case of a custom differential analysis. |
| enr_class_sel | Which classes of gene sets to show. (c('c1_positional', 'c2_curated', ...))  |

**Value**

A DT::data.table of enriched gene sets.

**Examples**

```
data("scExp")
## Not run: table_enriched_genes_scExp(scExp)
```



---

|            |  |
|------------|--|
| warning_DA | <i>Warning for differential_analysis_scExp</i> |
|------------|--|

---

**Description**

Warning for differential\_analysis\_scExp

**Usage**

```
warning_DA(scExp, by, de_type, method, block, group, ref)
```

**Arguments**

|         |   |
|---------|---|
| scExp   | A SingleCellExperiment object containing consclust with selected number of cluster.   |
| by      | = A character specifying the column of the object containing the groups of cells to compare. Exclusive with de_type == custom                     |
| de_type | Type of comparisons. Either 'one_vs_rest', to compare each cluster against all others, or 'pairwise' to make 1 to 1 comparisons. ('one_vs_rest')  |
| method  | Wilcoxon or edgerGLM  |
| block   | Use batches as blocking factors ?   |
| group   | If de_type is custom, the group to compare (data.frame), must be a one-column data.frame with cell_clusters or sample_id as character in rows     |
| ref     | If de_type is custom, the reference to compare (data.frame), must be a one-column data.frame with cell_clusters or sample_id as character in rows |

**Value**

Warnings or Errors if the input are not correct

---

|                                      |   |
|--------------------------------------|---|
| warning_filter_correlated_cell_scExp | <i>warning_filter_correlated_cell_scExp</i> |
|--------------------------------------|---|

---

**Description**

warning\_filter\_correlated\_cell\_scExp

**Usage**

```
warning_filter_correlated_cell_scExp(
  scExp,
  random_iter,
  corr_threshold,
  percent_correlation,
  run_tsne,
  downsample,
  verbose
)
```

**Arguments**

|                     |  |
|---------------------|--|
| scExp               | A SingleCellExperiment object containing 'Cor', a correlation matrix, in reducedDims.                            |
| random_iter         | Number of random matrices to create to calculate random correlation scores. (50)                                 |
| corr_threshold      | Quantile of random correlation score above which a cell is considered to be 'correlated' with another cell. (99) |
| percent_correlation | Percentage of the cells that any cell must be 'correlated' to in order to not be filtered. (1)                   |
| run_tsne            | Re-run tsne ? (FALSE)  |
| downsample          | Number of cells to calculate correlation filtering threshold ? (2500)  |
| verbose             | (TRUE)   |

**Value**

Warnings or Errors if the input are not correct

---

warning\_plot\_reduced\_dim\_scExp

*A warning helper for plot\_reduced\_dim\_scExp*

---

**Description**

A warning helper for plot\_reduced\_dim\_scExp

**Usage**

```
warning_plot_reduced_dim_scExp(
  scExp,
  color_by,
  reduced_dim,
  downsample,
```

```

    transparency,
    size,
    max_distanceToTSS,
    annotate_clusters,
    min_quantile,
    max_quantile
)

```

### Arguments

|                   |   |
|-------------------|---|
| scExp             | A SingleCellExperiment Object   |
| color_by          | Feature used for coloration   |
| reduced_dim       | Reduced Dimension used for plotting   |
| downsample        | Number of cells to downsample   |
| transparency      | Alpha parameter, between 0 and 1  |
| size              | Size of the points.   |
| max_distanceToTSS | Numeric. Maximum distance to a gene's TSS to consider a region linked to a gene.                              |
| annotate_clusters | A logical indicating if clusters should be labelled. The 'cell_cluster' column should be present in metadata. |
| min_quantile      | The lower threshold to remove outlier cells, as quantile of cell embeddings (between 0 and 0.5).              |
| max_quantile      | The upper threshold to remove outlier cells, as quantile of cell embeddings (between 0.5 and 1).              |

### Value

Warning or errors if the inputs are not correct

---

```

warning_raw_counts_to_sparse_matrix

```

*Warning for raw\_counts\_to\_sparse\_matrix*

---

### Description

Warning for raw\_counts\_to\_sparse\_matrix

**Usage**

```
warning_raw_counts_to_sparse_matrix(
  files_dir_list,
  file_type = c("scBAM", "scBED", "SparseMatrix"),
  peak_file = NULL,
  n_bins = NULL,
  bin_width = NULL,
  genebody = NULL,
  extendPromoter = 2500,
  verbose = TRUE,
  ref = "hg38"
)
```

**Arguments**

|                |  |
|----------------|--|
| files_dir_list | A named character vector of directory containing the raw files                       |
| file_type      | Input file(s) type(s) ('scBED','scBAM','SparseMatrix')                               |
| peak_file      | A file containing genomic location of peaks (NULL)                                   |
| n_bins         | The number of bins to tile the genome (NULL)   |
| bin_width      | The size of bins to tile the genome (NULL)   |
| genebody       | Count on genes (body + promoter) ? (NULL)  |
| extendPromoter | If counting on genes, number of base pairs to extend up or downstream of TSS (2500). |
| verbose        | Verbose (TRUE)   |
| ref            | reference genome to use (hg38)   |

**Value**

Error or warnings if the input are not correct

---

wrapper\_Signac\_FeatureMatrix

*Wrapper around 'FeatureMatrix' function from Signac Package*

---

**Description**

Wrapper around 'FeatureMatrix' function from Signac Package

**Usage**

```

wrapper_Signac_FeatureMatrix(
  files_dir_list,
  which,
  ref = "hg38",
  process_n = 2000,
  set_future_plan = TRUE,
  verbose = TRUE,
  progress = NULL
)

```

**Arguments**

|                              |   |
|------------------------------|---|
| <code>files_dir_list</code>  | A named character vector of directories containing the files. The names correspond to sample names.   |
| <code>which</code>           | A <code>GenomicRanges</code> containing the features to count on.   |
| <code>ref</code>             | Reference genome to use (hg38). Chromosomes that are not present in the canonical chromosomes of the given reference genome will be excluded from the matrix. |
| <code>process_n</code>       | Number of regions to load into memory at a time, per thread. Processing more regions at once can be faster but uses more memory. (2000)                       |
| <code>set_future_plan</code> | Set 'multisession' plan within the function (TRUE). If TRUE, the previous plan (e.g. <code>future::plan()</code> ) will be set back on exit.                  |
| <code>verbose</code>         | Verbose (TRUE).   |
| <code>progress</code>        | Progress object for Shiny.  |

**Details**

Signac & future are not required packages for ChromSCape as they are required only for the fragment matrix calculations. To use this function, install Signac package first (future will be installed as a dependency). For the simplicity of the application & optimization, the function by default sets `future::plan("multisession")` with `workers = future::availableCores(omit = 1)` in order to allow parallel processing with Signac. On exit the plan is re-set to the previously set future plan. Note that future multisession may have trouble running when VPN is on. To run in parallel, first deactivate your VPN if you encounter long runtimes.

**Value**

A sparse matrix of features x cells

**References**

Stuart et al., Multimodal single-cell chromatin analysis with Signac bioRxiv <https://doi.org/10.1101/2020.11.09.373613>

**Examples**

```
## Not run:  
gr_bins = define_feature("hg38", bin_width = 50000)  
wrapper_Signac_FeatureMatrix("/path/to/dir_containing_fragment_files",  
  gr_bins, ref = "hg38")  
  
## End(Not run)
```

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