

# Package ‘ChromSCape’

July 5, 2022

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

**Version** 1.7.0

**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** 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

<code>scExp</code>	A SingleCellExperiment with "logRatio_cytoBand" reducedDim slot filled. See <a href="#">calculate_logRatio_CNA</a>
<code>controls</code>	Sample IDs or Cell IDs of the normal sample to take as reference.
<code>quantiles</code>	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. • 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

---

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 counteract 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 functions 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(
  filename,
  format = "BAM",
  bins,
  canonical_chr,
  n_smoothBin = 5,
  ref = "hg38",
  read_size = 101
)
```

### Arguments

filename	Path towards the BAM to create coverage from
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.
n_smoothBin	Number of bins left and right to smooth the signal.
ref	Genomic reference
read_size	Length of the reads

### Value

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

---

create_project_folder	<i>Create ChromSCape project folder</i>
-----------------------	---

---

### 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	<i>Wrapper to create the single cell experiment from count matrix and feature dataframe</i>
--------------	---

---

## 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 in 'One vs Rest' mode*

---

**Description**

Differential Analysis in 'One vs Rest' mode

**Usage**

```

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

```

**Arguments**

affectation	An annotation data.frame with cell_id and cell_cluster columns
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	<i>Differential Analysis in 'One vs Rest' mode</i>
----------------	--

---

**Description**

Differential Analysis in 'One vs Rest' mode

**Usage**

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

**Arguments**

affectation	An annotation data.frame with cell_id and cell_cluster columns
nclust	Number of clusters
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	<i>Run differential analysis in Pairwise mode</i>
-------------	---

---

## Description

Run differential analysis in Pairwise mode

## Usage

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

## Arguments

affectation	An annotation data.frame with cell_cluster and cell_id columns
nclust	Number of clusters
counts	Count matrix
method	DA method, Wilcoxon or edgeR
feature	Feature data.frame
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

---

define\_feature            *Define the features on which reads will be counted*

---

### 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            *Heuristic discovery of samples based on cell labels*

---

### 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,
  group_by = c("cell_cluster", "sample_id")[1],
  verbose = TRUE,
  progress = NULL
)
```

**Arguments**

scExp            A SingleCellExperiment object containing consclust with selected number of cluster.  
 group\_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, group_by = "cell_cluster")
res = differential_activation(scExp, group_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 scan.

**Usage**

```
differential_analysis_scExp(
  scExp,
  de_type = c("one_vs_rest_fast", "one_vs_rest", "pairwise")[1],
  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 conclud 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')
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 conclud, 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,
  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.
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      *Find most covered features*

---

**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      *Generate a complete ChromSCape analysis*

---

**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.

`run` What steps to run. By default runs everything. Some steps are required in order to run downstream steps.

`min_reads_per_cell` Minimum number of reads per cell.

`max_quantile_read_per_cell` Upper quantile above which to consider cells doublets.

`n_top_features` Number of features to keep in the analysis.

`norm_type` Normalization type.

`subsample_n` Number of cells per condition to downsample to, for performance principally.

`exclude_regions` Path towards a BED file containing CNA to exclude from the analysis (optional).

n_clust	Number of clusters to force choice of clusters.
corr_threshold	Quantile of correlation above which two cells are considered as correlated.
percent_correlation	Percentage of the total cells that a cell must be correlated with in order to be kept in the analysis.
maxK	Upper cluster number to rest for ConsensusClusterPlus.
qval.th	Adjusted p-value below which to consider features differential.
logFC.th	Log2-fold-change above/below which to consider a feature depleted/enriched.
enrichment_qval	Adjusted p-value below which to consider a gene set as significantly enriched in differential features.
doBatchCorr	Logical indicating if batch correction using fastMNN should be run.
batch_sels	If doBatchCorr is TRUE, a named list containing the samples in each batch.
control_samples_CNA	If running CopyNumber Analysis, a character vector of the sample names that are 'normal'.
genes_to_plot	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 'cell\_cluster' 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,
  input_type = "scBED",
  ref_genome = c("hg38", "mm10")[1],
  bin_width = 150,
  n_smoothBin = 5,
  read_size = 101,
  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 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.
odir	The output directory to write the cumulative BED and BigWig files.
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.
progress	A Progress object for Shiny. Default to NULL.

**Value**

Generate coverage tracks (.bigwig) for each cluster in the SingleCellExperiment ("cell\_cluster" 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	<i>From a ChromSCape analysis directory, generate an HTML report.</i>
-----------------	---

---

**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 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.

**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**

scExp	A SingleCellExperiment object containing list of differential features.
enrichment_qval	Adjusted p-value threshold for gene set enrichment. (0.1)
ref	A reference annotation, either 'hg38' or 'mm10'. ('hg38')
GeneSets	A named list of gene sets. If NULL will automatically load MSigDB list of gene sets for specified reference genome. (NULL)

GeneSetsDf	A dataframe containing gene sets & class of gene sets. If NULL will automatically load MSigDB dataframe of gene sets for specified reference genome. (NULL)
GenePool	The pool of genes to run enrichment in. If NULL will automatically load GeneCode list of genes fro specified reference genome. (NULL)
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)
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 qval.th = 0.01 & logFC.th = 1 or 2
## Not run: scExp_cf = gene_set_enrichment_analysis_scExp(scExp,
  qval.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)
```

---

gg_fill_hue	<i>gg_fill_hue</i>
-------------	--------------------

---

**Description**

gg\_fill\_hue

**Usage**

```
gg_fill_hue(n)
```

**Arguments**

n                num hues

**Value**

A color in HEX format

---

groupMat	<i>groupMat</i>
----------	-----------------

---

**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	<i>Does SingleCellExperiment has genomic coordinates in features ?</i>
-------------------------	--

---

**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

<code>feature_file</code>	A file containing the features genomic locations
<code>matrix_file</code>	A file containing the indexes of non-zeroes values and their value (respectively i,j,x,see <code>sparseMatrix</code> )
<code>barcode_file</code>	A file containing the barcode ids
<code>binarize</code>	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)
```

**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(odir, class, peak_distance_to_merge, ref)
```

**Arguments**

odir	Output directory
class	Cell cluster
peak_distance_to_merge	Maximum distance to merge two 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**

<code>scExp_cf</code>	A SingleCellExperiment
<code>by</code>	Color by <code>sample_id</code> or <code>cell_cluster</code>
<code>jitter_by</code>	Add jitter points of another layer ( <code>cell_cluster</code> or <code>sample_id</code> )
<code>downsample</code>	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_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",
  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")

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. 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	<i>Preprocess scExp - Transcripts per Million (TPM)</i>
----------------	---

---

**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	<i>rawfile_ToBigWig : reads in BAM file and write out BigWig coverage file, normalized and smoothed</i>
------------------	---

---

**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,
  n_smoothBin = 5,
  ref = "hg38",
  read_size = 101
)
```

**Arguments**

input	Path to the BAM file (with index) or BED file or raw_matrix from which to generate coverage (must be small bins).
BigWig_filename	Path to write the output BigWig file
format	File format, either "BAM" or "BED"
bin_width	Bin size for coverage
n_smoothBin	Number of bins for smoothing values
ref	Reference genome.
read_size	Length of the reads.

**Value**

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**

files_dir_list	A named character vector of directories containing the files. The names correspond to sample names.
file_type	Input file(s) type(s) ('scBED', 'scBAM', 'FragmentFile')
use_Signac	Use Signac wrapper function 'FeatureMatrix' if the Signac package is installed (TRUE).
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)
progress	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.

**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 function 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 overlap threshold will be dismissed. Therefore, library size might be slightly different from peaks to bins if signal was duplicated into multiple bins or omitted 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      *Remove chromosome M from scExprownames*

---

**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  
*Remove non canonical chromosomes from scExp*

---

**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      *Run pairwise tests*

---

**Description**

Run pairwise tests

**Usage**

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

**Arguments**

affectation	An annotation data.frame with cell_cluster and cell_id columns
nclust	Number of clusters
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 @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 @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                      *Summary of the differential analysis*

---

**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  
*Swap main & alternative Experiments, with fixed colData*

---

**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, de_type, method, block, group, ref)
```

**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')
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**

files_dir_list	A named character vector of directories containing the files. The names correspond to sample names.
which	A GenomicRanges containing the features to count on.
ref	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.



process_n	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)
set_future_plan	Set 'multisession' plan within the function (TRUE). If TRUE, the previous plan (e.g. future::plan()) will be set back on exit.
verbose	Verbose (TRUE).
progress	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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