Package: Signac (via r-universe)

October 9, 2026

Title Analysis of Single-Cell Chromatin Data

Version 1.17.1

Date 2026-04-06

Description A framework for the analysis and exploration of single-cell chromatin data. The 'Signac' package contains functions for quantifying single-cell chromatin data, computing per-cell quality control metrics, dimension reduction and normalization, visualization, and DNA sequence motif analysis. Reference: Stuart et al. (2021) <doi:10.1038/s41592-021-01282-5>.

Depends R (>= 4.1.0), methods

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

URL https://github.com/stuart-lab/signac, https://stuartlab.org/signac

BugReports https://github.com/stuart-lab/signac/issues

LinkingTo Rcpp

Imports GenomeInfoDb (>= 1.29.3), GenomicRanges, IRanges, Matrix, Rsamtools, S4Vectors, SeuratObject (>= 5.0.2), data.table, dplyr (>= 1.0.0), future, future.apply, ggplot2, rlang, pbapply, tidyr, patchwork, stats, utils, BiocGenerics, stringi, fastmatch, RcppRoll, scales, Rcpp, grid, tidyselect, vctrs, lifecycle, sparseMatrixStats, RSpectra

Collate 'RcppExports.R' 'Signac-package.R' 'data.R' 'differential_accessibility.R' 'generics.R' 'dimension_reduction.R' 'footprinting.R' 'fragments.R' 'genomeinfodb-methods.R' 'granges-methods.R' 'heatmaps.R' 'iranges-methods.R' 'links.R' 'mito.R' 'motifs.R' 'objects.R' 'ontology.R' 'peaks.R' 'preprocessing.R' 'quantification.R' 'region-enrichment.R' 'utilities.R' 'visualization.R' 'zzz.R'

Suggests Seurat (>= 5.0.2), ggforce, ggrepel, ggseqlogo, testthat (>= 2.1.0), SummarizedExperiment, TFBSTools, motifmatchr, BSgenome, shiny, miniUI, rtracklayer, biovizBase, Biostrings, lsa, MASS, wrswoR, fgsea

NeedsCompilation yes

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Config/pak/sysreqs libbz2-dev liblzma-dev xz-utils zlib1g-dev

Repository https://cran.r-universe.dev

Date/Publication 2026-04-06 19:33:00 UTC

RemoteUrl https://github.com/cran/Signac

RemoteRef HEAD

RemoteSha a6b429553220ea5bd120479a33116bc6fcdb1521

Contents

AccessiblePeaks 5
AddMotifs 5
AggregateTiles 6
AlleleFreq 8
Annotation 9
AnnotationPlot 10
as.ChromatinAssay 11
atac_small 12
ATACqc 12
AverageCounts 13
BigwigTrack 14
BinarizeCounts 16
blacklist_ce10 17
blacklist_ce11 17
blacklist_dm3 18
blacklist_dm6 18
blacklist_hg19 19
blacklist_hg38 19
blacklist_hg38_unified 20
blacklist_mm10 20
CallPeaks 21
Cells.Fragment 24
Cells<- 24
CellsPerGroup 25
ChromatinAssay-class 25

ClosestFeature . . . 26
ClusterClonotypes . . . 27
CombineTracks . . . 27
ConnectionsToLinks . . . 28
ConvertMotifID . . . 29
CountFragments . . . 30
CountsInRegion . . . 31
coverage,ChromatinAssay-method . . . 31
CoverageBrowser . . . 33
CoveragePlot . . . 33
CreateChromatinAssay . . . 38
CreateFragmentObject . . . 39
CreateMotifMatrix . . . 40
CreateMotifObject . . . 42
DensityScatter . . . 43
DepthCor . . . 43
DownsampleFeatures . . . 44
EnrichedTerms . . . 45
ExpressionPlot . . . 46
Extend . . . 46
FeatureMatrix . . . 47
FilterCells . . . 48
FindClonotypes . . . 49
FindMotifs . . . 50
findOverlaps-methods . . . 51
FindTopFeatures . . . 55
FitMeanVar . . . 56
Footprint . . . 58
FractionCountsInRegion . . . 60
Fragment-class . . . 61
FragmentHistogram . . . 61
Fragments . . . 62
FRiP . . . 63
GeneActivity . . . 64
GenomeBinMatrix . . . 65
GetCellsInRegion . . . 66
GetFootprintData . . . 67
GetFragmentData . . . 68
GetGRangesFromEnsDb . . . 68
GetIntersectingFeatures . . . 69
GetLinkedGenes . . . 70
GetLinkedPeaks . . . 70
GetMotifData . . . 71
GetTSSPositions . . . 72
granges-methods . . . 72
GRangesToString . . . 73
head.Fragment . . . 74
IdentifyVariants . . . 74

InsertionBias . . . 76
inter-range-methods . . . 77
IntersectMatrix . . . 79
Jaccard . . . 80
LinkPeaks . . . 80
LinkPlot . . . 82
Links . . . 83
LookupGeneCoords . . . 84
MatchRegionStats . . . 84
Motif-class . . . 85
MotifCounts . . . 86
MotifPlot . . . 87
Motifs . . . 87
nearest-methods . . . 88
NucleosomeSignal . . . 92
PeakPlot . . . 93
PearsonResidualVar . . . 94
PlotFootprint . . . 96
ReadMGATK . . . 97
RegionHeatmap . . . 98
RegionMatrix . . . 99
RegionPlot . . . 101
RegionStats . . . 102
RunSVD . . . 103
RunTFIDF . . . 105
seqinfo-methods . . . 108
SetMotifData . . . 110
SortIdents . . . 111
SplitFragments . . . 112
StringToGRanges . . . 113
subset.Fragment . . . 114
subset.Motif . . . 114
SubsetMatrix . . . 115
theme_browser . . . 116
TilePlot . . . 117
TSSEnrichment . . . 118
TSSPlot . . . 119
UnifyPeaks . . . 120
UpdatePath . . . 121
ValidateCells . . . 121
ValidateFragments . . . 122
ValidateHash . . . 122
VariantPlot . . . 123

Index **124**

AccessiblePeaks *Accessible peaks*

Description

Find accessible peaks in a set of cells

Usage

```
AccessiblePeaks(
  object,
  assay = NULL,
  idents = NULL,
  cells = NULL,
  min.cells = 10
)
```

Arguments

object	A Seurat object
assay	Name of assay to use
idents	A set of identity classes to find accessible peaks for
cells	A vector of cells to find accessible peaks for
min.cells	Minimum number of cells with the peak accessible (>0 counts) for the peak to be called accessible

Value

Returns a vector of peak names

AddMotifs *Add DNA sequence motif information*

Description

Construct a `Motif()` object containing DNA sequence motif information and add it to an existing Seurat object or ChromatinAssay. If running on a Seurat object, `AddMotifs` will also run `RegionStats()` to compute the GC content of each peak and store the results in the feature metadata. PFMs or PWMs are matched to the genome sequence using the `motifmatchr::matchMotifs()` function with default parameters to construct a matrix of motif positions in genomic regions.

Usage

```
AddMotifs(object, ...)

## Default S3 method:
AddMotifs(object, genome, pfm, verbose = TRUE, ...)

## S3 method for class 'ChromatinAssay'
AddMotifs(object, genome, pfm, verbose = TRUE, ...)

## S3 method for class 'Assay'
AddMotifs(object, genome, pfm, verbose = TRUE, ...)

## S3 method for class 'StdAssay'
AddMotifs(object, genome, pfm, verbose = TRUE, ...)

## S3 method for class 'Seurat'
AddMotifs(object, genome, pfm, assay = NULL, verbose = TRUE, ...)
```

Arguments

object	A Seurat object or ChromatinAssay object
...	Additional arguments passed to other methods
genome	A BSgenome, DNAStringSet, FaFile, or string stating the genome build recognized by getBSgenome.
pfm	A PFMatrixList or PWMatrixList object containing position weight/frequency matrices to use
verbose	Display messages
assay	Name of assay to use. If NULL, use the default assay

Value

When running on a ChromatinAssay or Seurat object, returns a modified version of the input object. When running on a matrix, returns a Motif object.

See Also

motifmatchr

AggregateTiles *Quantify aggregated genome tiles*

Description

Quantifies fragment counts per cell in fixed-size genome bins across the whole genome, then removes bins with less than a desired minimum number of counts in the bin, then merges adjacent tiles into a single region.

Usage

```
AggregateTiles(object, ...)

## S3 method for class 'Seurat'
AggregateTiles(
  object,
  genome,
  assay = NULL,
  new.assay.name = "tiles",
  min_counts = 5,
  binsize = 5000,
  verbose = TRUE,
  ...
)

## S3 method for class 'ChromatinAssay'
AggregateTiles(
  object,
  genome,
  min_counts = 5,
  binsize = 5000,
  verbose = TRUE,
  ...
)

## Default S3 method:
AggregateTiles(
  object,
  genome,
  cells = NULL,
  min_counts = 5,
  binsize = 5000,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat object or ChromatinAssay object
...	Additional arguments passed to other methods
genome	genome A vector of chromosome sizes for the genome. This is used to construct the genome bin coordinates. The can be obtained by calling seqlengths on a BSgenome-class object.
assay	Name of assay to use
new.assay.name	Name of new assay to create containing aggregated genome tiles
min_counts	Minimum number of counts for a tile to be retained prior to aggregation
binsize	Size of the genome bins (tiles) in base pairs

verbose	Display messages
cells	Cells to include

Value

When running on a Seurat object, returns the Seurat object with a new ChromatinAssay() added.

When running on a ChromatinAssay(), returns a new ChromatinAssay containing the aggregated genome tiles.

When running on a fragment file, returns a sparse region x cell matrix.

AlleleFreq *Compute allele frequencies per cell*

Description

Collapses allele counts for each strand and normalize by the total number of counts at each nucleotide position.

Usage

```
AlleleFreq(object, ...)

## Default S3 method:
AlleleFreq(object, variants, ...)

## S3 method for class 'Assay'
AlleleFreq(object, variants, ...)

## S3 method for class 'StdAssay'
AlleleFreq(object, variants, ...)

## S3 method for class 'Seurat'
AlleleFreq(object, variants, assay = NULL, new.assay.name = "alleles", ...)
```

Arguments

object	A Seurat object, Assay, or matrix
...	Arguments passed to other methods
variants	A character vector of informative variants to keep. For example, c("627G>A","709G>A","1045G>A","17
assay	Name of assay to use
new.assay.name	Name of new assay to store variant data in

Value

Returns a SeuratObject::Seurat() object with a new assay containing the allele frequencies for the informative variants.

Annotation *Annotation*

Description

Get the annotation from a ChromatinAssay

Usage

```
Annotation(object, ...)

Annotation(object, ...) <- value

## S3 method for class 'ChromatinAssay'
Annotation(object, ...)

## S3 method for class 'Seurat'
Annotation(object, ...)

## S3 replacement method for class 'ChromatinAssay'
Annotation(object, ...) <- value

## S3 replacement method for class 'Seurat'
Annotation(object, ...) <- value
```

Arguments

object	A Seurat object or ChromatinAssay object
...	Arguments passed to other methods
value	A value to set. Can be NULL, to remove the current annotation information, or a GenomicRanges::GRanges() object. If a GRanges object is supplied and the genome information is stored in the assay, the genome of the new annotations must match the genome of the assay.

Value

Returns a GenomicRanges::GRanges() object if the annotation data is present, otherwise returns NULL

Examples

```
Annotation(atac_small[["peaks"]])


Annotation(atac_small)

genes <- Annotation(atac_small)
```

```
Annotation(atac_small[["peaks"]]) <- genes
genes <- Annotation(atac_small)
Annotation(atac_small) <- genes
```

`AnnotationPlot` *Plot gene annotations*

Description

Display gene annotations in a given region of the genome.

Usage

```
AnnotationPlot(
  object,
  region,
  assay = NULL,
  mode = "gene",
  sep = c("-", "-"),
  extend.upstream = 0,
  extend.downstream = 0
)
```

Arguments

`object`	A `SeuratObject::Seurat()` object
`region`	A genomic region to plot
`assay`	Name of assay to use. If NULL, use the default assay.
`mode`	Display mode. Choose either "gene" or "transcript" to determine whether genes or transcripts are plotted.
`sep`	Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.
`extend.upstream`	Number of bases to extend the region upstream.
`extend.downstream`	Number of bases to extend the region downstream.

Value

Returns a `ggplot2::ggplot()` object

Examples

```
AnnotationPlot(object = atac_small, region = c("chr1-29554-39554"))
```

`as.ChromatinAssay` *Convert objects to a ChromatinAssay*

Description

Convert objects to a ChromatinAssay

Usage

```
as.ChromatinAssay(x, ...)

## S3 method for class 'Assay'
as.ChromatinAssay(
  x,
  ranges = NULL,
  seqinfo = NULL,
  annotation = NULL,
  motifs = NULL,
  fragments = NULL,
  bias = NULL,
  positionEnrichment = NULL,
  sep = c("-", "-"),
  ...
)
```

Arguments

`x`	An object to convert to class `ChromatinAssay()`
`...`	Arguments passed to other methods
`ranges`	A GRanges object
`seqinfo`	A `Seqinfo` object containing basic information about the genome used. Alternatively, the name of a UCSC genome can be provided and the sequence information will be downloaded from UCSC.
`annotation`	Genomic annotation. It must have the following columns: • tx_id or transcript_id: Transcript ID • gene_name: Gene name • gene_id: Gene ID • gene_biotype: Gene biotype (e.g. "protein_coding", "lincRNA") • type: Annotation type (e.g. "exon", "gap")
`motifs`	A `Motif()` object
`fragments`	A list of `Fragment()` objects
`bias`	Tn5 integration bias matrix
`positionEnrichment`	A named list of position enrichment matrices.

sep	Characters used to separate the chromosome, start, and end coordinates in the row names of the data matrix

---

atac_small *A small example scATAC-seq dataset*

Description

A subsetted version of 10x Genomics 10k human (hg19) PBMC scATAC-seq dataset

Usage

```
atac_small
```

Format

A Seurat object with the following assays

peaks A peak x cell dataset

bins A 5 kb genome bin x cell dataset

RNA A gene x cell dataset

Source

https://www.10xgenomics.com/datasets/10k-human-pbmcs-atac-v2-chromium-controller-2-standard

---

ATACqc *Compute scATAC-seq QC metrics*

Description

Wrapper function to run `fragtk qc` and add the metadata to the Seurat object.

Usage

```
ATACqc(object, ...)

## Default S3 method:
ATACqc(
  object,
  annotations,
  fragtk.path = NULL,
  outdir = tempdir(),
  cleanup = TRUE,
  verbose = TRUE,
  ...
```

```
)

## S3 method for class 'ChromatinAssay'
ATACqc(
  object,
  annotations = NULL,
  fragtk.path = NULL,
  outdir = tempdir(),
  cleanup = TRUE,
  verbose = TRUE,
  ...
)

## S3 method for class 'Seurat'
ATACqc(
  object,
  assay = NULL,
  annotations = NULL,
  fragtk.path = NULL,
  outdir = tempdir(),
  cleanup = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat object, ChromatinAssay object, or path to a fragment file.
...	Arguments passed to other methods
annotations	GenomicRanges::GRanges() object containing gene annotations. If NULL, attempt to extract this from the ChromatinAssay object if provided.
fragtk.path	Path to fragtk executable. If NULL, try to find fragtk automatically.
outdir	Path for output directory
cleanup	Remove output files created by fragtk
verbose	Display messages
assay	Name of assay to use. If NULL, use the default assay.

AverageCounts *Average Counts*

Description

Compute the mean counts per group of cells for a given assay

Usage

```
AverageCounts(object, assay = NULL, group.by = NULL, verbose = TRUE)
```

Arguments

object	A Seurat object
assay	Name of assay to use. Default is the active assay
group.by	Grouping variable to use. Default is the active identities
verbose	Display messages

Value

Returns a dataframe

Examples

```
AverageCounts(atac_small)
```

BigwigTrack *Plot data from BigWig files*

Description

Create coverage tracks, heatmaps, or line plots from bigwig files.

Usage

```
BigwigTrack(
  region,
  bigwig,
  smooth = 200,
  extend.upstream = 0,
  extend.downstream = 0,
  type = "coverage",
  y_label = "bigWig",
  bigwig.scale = "common",
  ymax = NULL,
  max.downsample = 3000,
  downsample.rate = 0.1
)
```

Arguments

region	GRanges object specifying region to plot
bigwig	List of bigwig file paths. List should be named, and the name of each element in the list of files will be displayed alongside the track in the final plot.
smooth	Number of bases to smooth data over (rolling mean). If NULL, do not apply smoothing.
extend.upstream	Number of bases to extend the region upstream.
extend.downstream	Number of bases to extend the region downstream.
type	Plot type. Can be one of "line", "heatmap", or "coverage"
y_label	Y-axis label
bigwig.scale	Scaling to apply to data from different bigwig files. Can be: • common: plot each bigwig on a common scale (default) • separate: plot each bigwig on a separate scale ranging from zero to the maximum value for that bigwig file within the plotted region
ymax	Maximum value for Y axis. Can be one of: • NULL: set to the highest value among all the tracks (default) • qXX: clip the maximum value to the XX quantile (for example, q95 will set the maximum value to 95\ remove the effect of extreme values that may otherwise distort the scale. • numeric: manually define a Y-axis limit
max.downsample	Minimum number of positions kept when downsampling. Downsampling rate is adaptive to the window size, but this parameter will set the minimum possible number of positions to include so that plots do not become too sparse when the window size is small.
downsample.rate	Fraction of positions to retain when downsampling. Retaining more positions can give a higher-resolution plot but can make the number of points large, resulting in larger file sizes when saving the plot and a longer period of time needed to draw the plot.

Details

Note that this function does not work on windows.

Value

Returns a ggplot object

`BinarizeCounts` *Binarize counts*

Description

Set counts >1 to 1 in a count matrix

Usage

```
BinarizeCounts(object, ...)

## Default S3 method:
BinarizeCounts(object, assay = NULL, verbose = TRUE, ...)

## S3 method for class 'Assay'
BinarizeCounts(object, assay = NULL, verbose = TRUE, ...)

## S3 method for class 'Seurat'
BinarizeCounts(object, assay = NULL, verbose = TRUE, ...)
```

Arguments

`object`	A Seurat object
`...`	Arguments passed to other methods
`assay`	Name of assay to use. Can be a list of assays, and binarization will be applied to each.
`verbose`	Display messages

Value

Returns a `SeuratObject::Seurat()` object

Examples

```
x <- matrix(data = sample(0:3, size = 25, replace = TRUE), ncol = 5)
BinarizeCounts(x)
BinarizeCounts(atac_small[["peaks"]])
BinarizeCounts(atac_small)
```

blacklist_ce10 *Genomic blacklist regions for C. elegans ce10 (0-based)*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_ce10
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_ce11 *Genomic blacklist regions for C. elegans ce11 (0-based)*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_ce11
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_dm3 *Genomic blacklist regions for Drosophila dm3 (0-based)*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_dm3
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_dm6 *Genomic blacklist regions for Drosophila dm6 (0-based)*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_dm6
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_hg19 *Genomic blacklist regions for Human hg19 (0-based)*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_hg19
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_hg38 *Genomic blacklist regions for Human GRCh38*

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_hg38
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

blacklist_hg38_unified

Unified genomic blacklist regions for Human GRCh38

Description

Manually curated genomic blacklist regions for the hg38 genome by Anshul Kundaje and Anna Shcherbina. See https://www.encodeproject.org/files/ENCFF356LFX/ for a description of how this blacklist was curated.

Usage

```
blacklist_hg38_unified
```

Format

A GRanges object

Details

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Author(s)

Anshul Kundaje

Anna Shcherbina

Source

https://www.encodeproject.org/files/ENCFF356LFX/

doi:10.1038/s4159801945839z

blacklist_mm10

Genomic blacklist regions for Mouse mm10 (0-based)

Description

This dataset is deprecated and will be removed from Signac in the future. See https://github.com/dozmorovlab/excluderanges instead.

Usage

```
blacklist_mm10
```

Format

A GRanges object

Source

https://github.com/Boyle-Lab/Blacklist

doi:10.1038/s4159801945839z

`CallPeaks` *Call peaks*

Description

Call peaks using MACS. Fragment files linked to the specified assay will be used to call peaks. If multiple fragment files are present, all will be used in a single MACS invocation. Returns the `.narrowPeak` MACS output as a `GRanges` object.

Usage

```
CallPeaks(object, ...)

## S3 method for class 'Seurat'
CallPeaks(
  object,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  macs2.path = NULL,
  broad = FALSE,
  format = "BED",
  outdir = tempdir(),
  fragment.tempdir = tempdir(),
  combine.peaks = TRUE,
  effective.genome.size = 2.7e+09,
  extsize = 200,
  shift = -extsize/2,
  additional.args = NULL,
  name = Project(object),
  cleanup = TRUE,
  verbose = TRUE,
  ...
)

## S3 method for class 'ChromatinAssay'
CallPeaks(
  object,
```

```
  macs2.path = NULL,
  outdir = tempdir(),
  broad = FALSE,
  format = "BED",
  effective.genome.size = 2.7e+09,
  extsize = 200,
  shift = -extsize/2,
  additional.args = NULL,
  name = "macs2",
  cleanup = TRUE,
  verbose = TRUE,
  ...
)

## S3 method for class 'Fragment'
CallPeaks(
  object,
  macs2.path = NULL,
  outdir = tempdir(),
  broad = FALSE,
  format = "BED",
  effective.genome.size = 2.7e+09,
  extsize = 200,
  shift = -extsize/2,
  additional.args = NULL,
  name = "macs2",
  cleanup = TRUE,
  verbose = TRUE,
  ...
)

## Default S3 method:
CallPeaks(
  object,
  macs2.path = NULL,
  outdir = tempdir(),
  broad = FALSE,
  format = "BED",
  effective.genome.size = 2.7e+09,
  extsize = 200,
  shift = -extsize/2,
  additional.args = NULL,
  name = "macs2",
  cleanup = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat object, ChromatinAssay object, Fragment object, or the path to fragment file/s.
...	Arguments passed to other methods
assay	Name of assay to use
group.by	Grouping variable to use. If set, peaks will be called independently on each group of cells and then combined. Note that to call peaks using subsets of cells we first split the fragment file/s used, so using a grouping variable will require extra time to split the files and perform multiple MACS peak calls, and will store additional files on-disk that may be large. Note that we store split fragment files in the temp directory (base::tempdir()) by default, and if the program is interrupted before completing these temporary files will not be removed. If NULL, peaks are called using all cells together (pseudobulk).
idents	List of identities to include if grouping cells (only valid if also setting the group.by parameter). If NULL, peaks will be called for all cell identities.
macs2.path	Path to MACS program. If NULL, try to find MACS automatically.
broad	Call broad peaks (--broad parameter for MACS)
format	File format to use. Should be either "BED" or "BEDPE" (see MACS documentation).
outdir	Path for output files
fragment.tempdir	Path to write temporary fragment files. Only used if group.by is not NULL.
combine.peaks	Controls whether peak calls from different groups of cells are combined using GenomicRanges::reduce when calling peaks for different groups of cells (group.by parameter). If FALSE, a list of GRanges object will be returned. Note that metadata fields such as the p-value, q-value, and fold-change information for each peak will be lost if combining peaks.
effective.genome.size	Effective genome size parameter for MACS (-g). Default is the human effective genome size (2.7e9).
extsize	extsize parameter for MACS. Only relevant if format="BED"
shift	shift parameter for MACS. Only relevant if format="BED"
additional.args	Additional arguments passed to MACS. This should be a single character string
name	Name for output MACS files. This will also be placed in the name field in the GRanges output.
cleanup	Remove MACS output files
verbose	Display messages

Details

See https://macs3-project.github.io/MACS/ for MACS documentation.

If you call peaks using MACS2 please cite: doi:10.1186/gb200899r137

Value

Returns a GenomicRanges::GRanges() object

`Cells.Fragment` *Set and get cell barcode information for a* `Fragment()` *object*

Description

This returns the names of cells in the object that are contained in the fragment file. These cell barcodes may not match the barcodes present in the fragment file. The `Fragment()` object contains an internal mapping of the cell names in the `ChromatinAssay()` object to the cell names in the fragment file, so that cell names can be changed in the assay without needing to change the cell names on disk.

Usage

```
## S3 method for class 'Fragment'
Cells(x, ...)

## S3 replacement method for class 'Fragment'
Cells(x, ...) <- value
```

Arguments

`x`	A Fragment object
`...`	Arguments passed to other methods
`value`	A vector of cell names to store in the `Fragment()` object

Details

To access the cell names that are stored in the fragment file itself, use `GetFragmentData(object = x, name = "cells")`.

`Cells<-` *Set and get cell barcode information for a Fragment object*

Description

Set and get cell barcode information for a Fragment object

Usage

```
Cells(x, ...) <- value
```

Arguments

x	A Seurat object
...	Arguments passed to other methods
value	A character vector of cell barcodes

CellsPerGroup *Cells per group*

Description

Count the number of cells in each group

Usage

```
CellsPerGroup(object, group.by = NULL)
```

Arguments

object	A Seurat object
group.by	A grouping variable. Default is the active identities

Value

Returns a vector

Examples

```
CellsPerGroup(atac_small)
```

ChromatinAssay-class *The ChromatinAssay class*

Description

The ChromatinAssay object is an extended SeuratObject::Assay() for the storage and analysis of single-cell chromatin data.

Slots

`ranges` A `GenomicRanges::GRanges()` object describing the genomic location of features in the object

`motifs` A `Motif()` object

`fragments` A list of `Fragment()` objects.

`seqinfo` A `Seqinfo` object containing basic information about the genome sequence used.

`annotation` A `GenomicRanges::GRanges()` object containing genomic annotations. This should be a GRanges object with the following columns:

- tx_id: Transcript ID
- gene_name: Gene name
- gene_id: Gene ID
- gene_biotype: Gene biotype (e.g. "protein_coding", "lincRNA")
- type: Annotation type (e.g. "exon", "gap")

`bias` A vector containing Tn5 integration bias information (frequency of Tn5 integration at different kmers)

`positionEnrichment` A named list of matrices containing positional enrichment scores for Tn5 integration (for example, enrichment at the TSS)

`links` A `GenomicRanges::GRanges()` object describing linked genomic positions, such as co-accessible sites or enhancer-gene regulatory relationships. This should be a `GRanges` object, where the start and end coordinates are the two linked genomic positions, and must contain a "score" metadata column.

`ClosestFeature` *Closest Feature*

Description

Find the closest feature to a given set of genomic regions

Usage

```
ClosestFeature(object, regions, annotation = NULL, ...)
```

Arguments

`object`	A Seurat object
`regions`	A set of genomic regions to query
`annotation`	A GRanges object containing annotation information. If NULL, use the annotations stored in the object.
`...`	Additional arguments passed to `StringToGRanges()`
	[Deprecated]

Value

Returns a dataframe with the name of each region, the closest feature in the annotation, and the distance to the feature.

Examples

```
ClosestFeature(
  object = atac_small,
  regions = head(granges(atac_small))
)
```

`ClusterClonotypes` *Find relationships between clonotypes*

Description

Perform hierarchical clustering on clonotype data

Usage

```
ClusterClonotypes(object, assay = NULL, group.by = NULL)
```

Arguments

`object`	A Seurat object
`assay`	Name of assay to use
`group.by`	Grouping variable for cells

Value

Returns a list containing two objects of class `stats::hclust()`, one for the cell clustering and one for the feature (allele) clustering

---

`CombineTracks` *Combine genome region plots*

Description

This can be used to combine coverage plots, peak region plots, gene annotation plots, and linked element plots. The different tracks are stacked on top of each other and the x-axis combined.

Usage

```
CombineTracks(plotlist, expression.plot = NULL, heights = NULL, widths = NULL)
```

Arguments

plotlist	A list of plots to combine. Must be from the same genomic region.
expression.plot	Plot containing gene expression information. If supplied, this will be placed to the left of the coverage tracks and aligned with each track
heights	Relative heights for each plot. If NULL, the first plot will be 8x the height of the other tracks.
widths	Relative widths for each plot. Only required if adding a gene expression panel. If NULL, main plots will be 8x the width of the gene expression panel

Value

Returns a patchworked ggplot2 object

Examples

```
p1 <- PeakPlot(atac_small, region = "chr1-29554-39554")
p2 <- AnnotationPlot(atac_small, region = "chr1-29554-39554")
CombineTracks(plotlist = list(p1, p2), heights = c(1, 1))
```

ConnectionsToLinks *Cicero connections to links*

Description

Convert the output of Cicero connections to a set of genomic ranges where the start and end coordinates of the range are the midpoints of the linked elements. Only elements on the same chromosome are included in the output.

Usage

```
ConnectionsToLinks(conns, ccans = NULL, threshold = 0, sep = c("-", "-"))
```

Arguments

conns	A dataframe containing co-accessible elements. This would usually be the output of run_cicero or assemble_connections. Specifically, this should be a dataframe where the first column contains the genomic coordinates of the first element in the linked pair of elements, with chromosome, start, end coordinates separated by "-" characters. The second column should be the second element in the linked pair, formatted in the same way as the first column. A third column should contain the co-accessibility scores.
ccans	This is optional, but if supplied should be a dataframe containing the cis-co-accessibility network (CCAN) information generated by generate_ccans. Specifically, this should be a dataframe containing the name of the peak in the first column, and the CCAN that it belongs to in the second column.

threshold	Threshold for retaining a coaccessible site. Links with a value less than or equal to this threshold will be discarded.
sep	Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.

Details

See the Cicero package for more information: https://bioconductor.org/packages/cicero/

Value

Returns a GenomicRanges::GRanges() object

ConvertMotifID *Convert between motif name and motif ID*

Description

Converts from motif name to motif ID or vice versa. To convert common names to IDs, use the name parameter. To convert IDs to common names, use the id parameter.

Usage

```
ConvertMotifID(object, ...)

## Default S3 method:
ConvertMotifID(object, name, id, ...)

## S3 method for class 'Motif'
ConvertMotifID(object, ...)

## S3 method for class 'ChromatinAssay'
ConvertMotifID(object, ...)

## S3 method for class 'Assay'
ConvertMotifID(object, ...)

## S3 method for class 'StdAssay'
ConvertMotifID(object, ...)

## S3 method for class 'Seurat'
ConvertMotifID(object, assay = NULL, ...)
```

Arguments

object	A Seurat, ChromatinAssay, or Motif object
...	Arguments passed to other methods
name	A vector of motif names
id	A vector of motif IDs. Only one of name and id should be supplied
assay	For Seurat object. Name of assay to use. If NULL, use the default assay

Value

Returns a character vector with the same length and order as the input. Any names or IDs that were not found will be stored as NA.

CountFragments *Count fragments*

Description

Count total fragments per cell barcode present in a fragment file.

Usage

```
CountFragments(fragments, cells = NULL, max_lines = NULL, verbose = TRUE)
```

Arguments

fragments	Path to a fragment file. If a list of fragment files is provided, the total fragments for each cell barcode across all files will be returned
cells	Cells to include. If NULL, include all cells
max_lines	Maximum number of lines to read from the fragment file. If NULL, read all lines in the file.
verbose	Display messages

Value

Returns a data.frame with the following columns:

- CB: the cell barcode
- frequency_count: total number of fragments sequenced for the cell
- mononucleosome: total number of fragments with length between 147 bp and 294 bp
- nucleosome_free: total number of fragments with length <147 bp
- reads_count: total number of reads sequenced for the cell

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
counts <- CountFragments(fragments = fpath)
```

CountsInRegion *Counts in region*

Description

Count reads per cell overlapping a given set of regions

Usage

```
CountsInRegion(object, assay, regions, ...)
```

Arguments

object	A Seurat object
assay	Name of a chromatin assay in the object to use
regions	A GRanges object
...	Additional arguments passed to IRanges::findOverlaps() **[Deprecated]**

Value

Returns a numeric vector

Examples

```
CountsInRegion(
  object = atac_small,
  assay = 'bins',
  regions = blacklist_hg19
)
```

coverage,ChromatinAssay-method *Coverage of a ChromatinAssay object*

Description

This is the coverage method for ChromatinAssay() objects.

Usage

```
## S4 method for signature 'ChromatinAssay'
coverage(
  x,
  shift = 0L,
  width = NULL,
  weight = 1L,
  method = c("auto", "sort", "hash")
)

## S4 method for signature 'Seurat'
coverage(
  x,
  shift = 0L,
  width = NULL,
  weight = 1L,
  method = c("auto", "sort", "hash")
)
```

Arguments

x	A ChromatinAssay() object
shift	How much each range should be shifted before coverage is computed. See IRanges::coverage() in the **IRanges** package.
width	Specifies the length of the returned coverage vectors. See IRanges::coverage() in the **IRanges** package.
weight	Assigns weight to each range in x. See IRanges::coverage() in the **IRanges** package.
method	See IRanges::coverage() in the **IRanges** package

Functions

- coverage(ChromatinAssay): method for ChromatinAssay objects
- coverage(Seurat): method for Seurat objects

See Also

- coverage-methods in the **IRanges** package.
- coverage-methods in the **GenomicRanges** package
- ChromatinAssay

CoverageBrowser *Genome browser*

Description

Interactive version of the CoveragePlot() function. Allows altering the genome position interactively. The current view at any time can be saved to a list of ggplot2::ggplot() objects using the "Save plot" button, and this list of plots will be returned after ending the browser by pressing the "Done" button.

Usage

```
CoverageBrowser(object, region, assay = NULL, sep = c("-", "-"), ...)
```

Arguments

object	A Seurat object
region	A set of genomic coordinates
assay	Name of assay to use
sep	Separators for genomic coordinates if region supplied as a string rather than GRanges object
...	Parameters passed to CoveragePlot()

Value

Returns a list of ggplot objects

CoveragePlot *Plot Tn5 insertion frequency over a region*

Description

Plot frequency of Tn5 insertion events for different groups of cells within given regions of the genome. Tracks are normalized using a per-group scaling factor computed as the number of cells in the group multiplied by the mean sequencing depth for that group of cells. This accounts for differences in number of cells and potential differences in sequencing depth between groups.

Usage

```
CoveragePlot(
  object,
  region,
  features = NULL,
  assay = NULL,
  split.assays = FALSE,
  assay.scale = "common",
  show.bulk = FALSE,
  expression.assay = "RNA",
  expression.slot = "data",
  annotation = TRUE,
  peaks = TRUE,
  peaks.group.by = NULL,
  ranges = NULL,
  ranges.group.by = NULL,
  ranges.title = "Ranges",
  region.highlight = NULL,
  links = TRUE,
  tile = FALSE,
  tile.size = 100,
  tile.cells = 100,
  bigwig = NULL,
  bigwig.type = "coverage",
  bigwig.scale = "common",
  heights = NULL,
  group.by = NULL,
  split.by = NULL,
  window = 100,
  extend.upstream = 0,
  extend.downstream = 0,
  scale.factor = NULL,
  ymax = NULL,
  cells = NULL,
  idents = NULL,
  sep = c("-", "-"),
  max.downsample = 3000,
  downsample.rate = 0.1,
  ...
)
```

Arguments

object	A Seurat object
region	A set of genomic coordinates to show. Can be a GRanges object, a string encoding a genomic position, a gene name, or a vector of strings describing the genomic coordinates or gene names to plot. If a gene name is supplied, annotations must be present in the assay.

`features` A vector of features present in another assay to plot alongside accessibility tracks (for example, gene names).

`assay` Name of the assay to plot. If a list of assays is provided, data from each assay will be shown overlaid on each track. The first assay in the list will define the assay used for gene annotations, links, and peaks (if shown). The order of assays given defines the plotting order.

`split.assays` When plotting data from multiple assays, display each assay as a separate track. If FALSE, data from different assays are overlaid on a single track with transparancy applied.

`assay.scale` Scaling to apply to data from different assays. Can be:

- common: plot all assays on a common scale (default)
- separate: plot each assay on a separate scale ranging from zero to the maximum value for that assay within the plotted region

`show.bulk` Include coverage track for all cells combined (pseudo-bulk). Note that this will plot the combined accessibility for all cells included in the plot (rather than all cells in the object).

`expression.assay` Name of the assay containing expression data to plot alongside accessibility tracks. Only needed if supplying `features` argument.

`expression.slot` Name of slot to pull expression data from. Only needed if supplying the `features` argument.

`annotation` Display gene annotations. Set to TRUE or FALSE to control whether genes models are displayed, or choose "transcript" to display all transcript isoforms, or "gene" to display gene models only (same as setting TRUE).

`peaks` Display peaks

`peaks.group.by` Grouping variable to color peaks by. Must be a variable present in the feature metadata. If NULL, do not color peaks by any variable.

`ranges` Additional genomic ranges to plot

`ranges.group.by` Grouping variable to color ranges by. Must be a variable present in the metadata stored in the `ranges` genomic ranges. If NULL, do not color by any variable.

`ranges.title` Y-axis title for ranges track. Only relevant if `ranges` parameter is set.

`region.highlight` Region to highlight on the plot. Should be a GRanges object containing the coordinates to highlight. By default, regions will be highlighted in grey. To change the color of the highlighting, include a metadata column in the GRanges object named "color" containing the color to use for each region.

`links` Display links. This can be a TRUE/FALSE value which will determine whether a links track is displayed, and if TRUE links for all genes in the plotted region will be shown. Alternatively, a character vector can be provided, giving a list of gene names to plot links for. If this is provided, only links for those genes will be displayed in the plot.

`tile` Display per-cell fragment information in sliding windows. If plotting multi-assay data, only the first assay is shown in the tile plot.

`tile.size` Size of the sliding window for per-cell fragment tile plot

`tile.cells` Number of cells to display fragment information for in tile plot.

`bigwig` List of bigWig file paths to plot data from. Files can be remotely hosted. The name of each element in the list will determine the y-axis label given to the track.

`bigwig.type` Type of track to use for bigWig files ("line", "heatmap", or "coverage"). Should either be a single value, or a list of values giving the type for each individual track in the provided list of bigwig files.

`bigwig.scale` Same as `assay.scale` parameter, except for bigWig files when plotted with `bigwig.type="coverage"`

`heights` Relative heights for each track (accessibility, gene annotations, peaks, links).

`group.by` Name of one or more metadata columns to group (color) the cells by. Default is the current cell identities

`split.by` A metadata variable to split the tracks by. For example, grouping by "celltype" and splitting by "batch" will create separate tracks for each combination of cell-type and batch.

`window` Smoothing window size

`extend.upstream`
Number of bases to extend the region upstream.

`extend.downstream`
Number of bases to extend the region downstream.

`scale.factor` Scaling factor for track height. If NULL (default), use the median group scaling factor determined by total number of fragments sequences in each group.

`ymax` Maximum value for Y axis. Can be one of:

- NULL: set to the highest value among all the tracks (default)
- qXX: clip the maximum value to the XX quantile (for example, q95 will set the maximum value to 95\ remove the effect of extreme values that may otherwise distort the scale.
- numeric: manually define a Y-axis limit

`cells` Which cells to plot. Default all cells

`idents` Which identities to include in the plot. Default is all identities.

`sep` Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.

`max.downsample` Minimum number of positions kept when downsampling. Downsampling rate is adaptive to the window size, but this parameter will set the minimum possible number of positions to include so that plots do not become too sparse when the window size is small.

`downsample.rate`
Fraction of positions to retain when downsampling. Retaining more positions can give a higher-resolution plot but can make the number of points large, resulting in larger file sizes when saving the plot and a longer period of time needed to draw the plot.

... Additional arguments passed to patchwork::wrap_plots()

Details

Additional information can be layered on the coverage plot by setting several different options in the CoveragePlot function. This includes showing:

- gene annotations
- peak positions
- additional genomic ranges
- additional data stored in a bigWig file, which may be hosted remotely
- gene or protein expression data alongside coverage tracks
- peak-gene links
- the position of individual sequenced fragments as a heatmap
- data for multiple chromatin assays simultaneously
- a pseudobulk for all cells combined

Value

Returns a patchwork::patchwork() object

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
Fragments(atac_small) <- fragments

# Basic coverage plot
CoveragePlot(object = atac_small, region = c("chr1-713500-714500"))

# Show additional ranges
ranges.show <- StringToGRanges("chr1-713750-714000")
CoveragePlot(object = atac_small, region = c("chr1-713500-714500"), ranges = ranges.show)

# Highlight region
CoveragePlot(object = atac_small, region = c("chr1-713500-714500"), region.highlight = ranges.show)

# Change highlight color
ranges.show$color <- "orange"
CoveragePlot(object = atac_small, region = c("chr1-713500-714500"), region.highlight = ranges.show)

# Show expression data
CoveragePlot(object = atac_small, region = c("chr1-713500-714500"), features = "ELK1")
```

`CreateChromatinAssay` *Create ChromatinAssay object*

Description

Create a `ChromatinAssay()` object from a count matrix or normalized data matrix. The expected format of the input matrix is features x cells. A set of genomic ranges must be supplied along with the matrix, with the length of the ranges equal to the number of rows in the matrix. If a set of genomic ranges are not supplied, they will be extracted from the row names of the matrix.

Usage

```
CreateChromatinAssay(
  counts,
  data,
  min.cells = 0,
  min.features = 0,
  max.cells = NULL,
  ranges = NULL,
  motifs = NULL,
  fragments = NULL,
  genome = NULL,
  annotation = NULL,
  bias = NULL,
  positionEnrichment = NULL,
  sep = c("-", "-"),
  validate.fragments = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

`counts`	Unnormalized data (raw counts)
`data`	Normalized data; if provided, do not pass counts
`min.cells`	Include features detected in at least this many cells. Will subset the counts matrix as well. To reintroduce excluded features, create a new object with a lower cutoff.
`min.features`	Include cells where at least this many features are detected.
`max.cells`	Include features detected in less than this many cells. Will subset the counts matrix as well. To reintroduce excluded features, create a new object with a higher cutoff. This can be useful for chromatin assays where certain artefactual loci accumulate reads in all cells. A percentage cutoff can also be set using 'q' followed by the percentage of cells, for example 'q90' will discard features detected in 90 percent of cells. If NULL (default), do not apply any maximum value.

ranges — A set of GenomicRanges::GRanges() corresponding to the rows of the input matrix

motifs — A Motif object (not required)

fragments — Path to a tabix-indexed fragments file for the data contained in the input matrix. If multiple fragment files are required, you can add additional Fragment() object to the assay after it is created using the CreateFragmentObject() and Fragments() functions. Alternatively, a list of Fragment() objects can be provided.

genome — A Seqinfo object containing basic information about the genome used. Alternatively, the name of a UCSC genome can be provided and the sequence information will be downloaded from UCSC.

annotation — A set of GenomicRanges::GRanges() containing annotations for the genome used. It must have the following columns:

- tx_id or transcript_id: Transcript ID
- gene_name: Gene name
- gene_id: Gene ID
- gene_biotype: Gene biotype (e.g. "protein_coding", "lincRNA")
- type: Annotation type (e.g. "exon", "gap")

bias — A Tn5 integration bias matrix

positionEnrichment — A named list of matrices containing positional signal enrichment information for each cell. Should be a cell x position matrix, centered on an element of interest (for example, TSS sites).

sep — Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate. Only used if ranges is NULL.

validate.fragments — Check that cells in the assay are present in the fragment file.

verbose — Display messages

... — Additional arguments passed to CreateFragmentObject()

CreateFragmentObject *Create a Fragment object*

Description

Create a Fragment object to store fragment file information. This object stores a 32-bit MD5 hash of the fragment file and the fragment file index so that any changes to the files on-disk can be detected. A check is also performed to ensure that the expected cells are present in the fragment file.

Usage

```
CreateFragmentObject(
  path,
  cells = NULL,
  validate.fragments = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

path	A path to the fragment file. The file should contain a tabix index in the same directory.
cells	A named character vector containing cell barcodes contained in the fragment file. This does not need to be all cells in the fragment file, but there should be no cells in the vector that are not present in the fragment file. A search of the file will be performed until at least one fragment from each cell is found. If NULL, don't check for expected cells. Each element of the vector should be a cell barcode that appears in the fragment file, and the name of each element should be the corresponding cell name in the object.
validate.fragments	Check that expected cells are present in the fragment file.
verbose	Display messages
...	Additional arguments passed to ValidateCells

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
cells <- colnames(x = atac_small)
names(x = cells) <- paste0("test_", cells)
frags <- CreateFragmentObject(path = fpath, cells = cells, verbose = FALSE, tolerance = 0.5)
```

CreateMotifMatrix *Create motif matrix*

Description

Create a motif x feature matrix from a set of genomic ranges, the genome, and a set of position weight matrices.

Usage

```
CreateMotifMatrix(
  features,
  pwm,
  genome,
  score = FALSE,
  use.counts = FALSE,
  sep = c("-", "-"),
  ...
)
```

Arguments

features	A GRanges object containing a set of genomic features
pwm	A TFBSTools::PFMatrixList() or TFBSTools::PWMatrixList() object containing position weight/frequency matrices to use
genome	Any object compatible with the genome argument in motifmatchr::matchMotifs()
score	Record the motif match score, rather than presence/absence (default FALSE)
use.counts	Record motif counts per region. If FALSE (default), record presence/absence of motif. Only applicable if score=FALSE.
sep	A length-2 character vector containing the separators to be used when constructing matrix rownames from the GRanges
...	Additional arguments passed to motifmatchr::matchMotifs()

Details

Requires that motifmatchr is installed https://www.bioconductor.org/packages/motifmatchr/.

Value

Returns a sparse matrix

Examples

```
## Not run:
library(JASPAR2018)
library(TFBSTools)
library(BSgenome.Hsapiens.UCSC.hg19)

pwm <- getMatrixSet(
  x = JASPAR2018,
  opts = list(species = 9606, all_versions = FALSE)
)
motif.matrix <- CreateMotifMatrix(
  features = granges(atac_small),
  pwm = pwm,
  genome = BSgenome.Hsapiens.UCSC.hg19
)
```

```
## End(Not run)
```

`CreateMotifObject` *Create motif object*

Description

Create a `Motif-class()` object.

Usage

```
CreateMotifObject(
  data = NULL,
  pwm = NULL,
  motif.names = NULL,
  positions = NULL,
  meta.data = NULL
)
```

Arguments

`data`	A motif x region matrix
`pwm`	A named list of position weight matrices or position frequency matrices matching the motif names in `data`. Can be of class PFMatrixList.
`motif.names`	A named list of motif names. List element names must match the names given in `pwm`. If NULL, use the names from the list of position weight or position frequency matrices. This can be used to set a alternative common name for the motif. If a PFMatrixList is passed to `pwm`, it will pull the motif name from the PFMatrixList.
`positions`	A `GenomicRanges::GRangesList()` object containing exact positions of each motif.
`meta.data`	A data.frame containing metadata

Value

Returns a `Motif()` object

Examples

```
motif.matrix <- matrix(
  data = sample(c(0,1),
    size = 100,
    replace = TRUE),
  ncol = 5
)
rownames(motif.matrix) <- 1:nrow(motif.matrix)
motif <- CreateMotifObject(data = motif.matrix)
```

DensityScatter *Scatterplot colored by point density*

Description

Create a scatterplot using variables in the object metadata and color cells by the density of points in the x-y space.

Usage

```
DensityScatter(object, x, y, log_x = FALSE, log_y = FALSE, quantiles = NULL)
```

Arguments

object	A Seurat object
x	Name of metadata variable to plot on x axis
y	Name of metadata variable to plot on y axis
log_x	log10 transform x values
log_y	log10 transform y values
quantiles	Vector of quantiles to display for x and y data distribution. Must be integer values between 0 and 100. TRUE can be passed as a shorthand way to set `c(5, 10, 90, 95)`. If FALSE or NULL, no quantile information is displayed

Value

Returns a ggplot object

DepthCor *Plot sequencing depth correlation*

Description

Compute the correlation between total counts and each reduced dimension component.

Usage

```
DepthCor(object, assay = NULL, reduction = "lsi", n = 10, ...)
```

Arguments

object	A `SeuratObject::Seurat()` object
assay	Name of assay to use for sequencing depth. If NULL, use the default assay.
reduction	Name of a dimension reduction stored in the input object
n	Number of components to use. If `NULL`, use all components.
...	Additional arguments passed to `stats::cor()`

Value

Returns a ggplot2::ggplot() object

Examples

```
DepthCor(object = atac_small)
```

DownsampleFeatures *Downsample Features*

Description

Randomly downsample features and assign to VariableFeatures for the object. This will select n features at random.

Usage

```
DownsampleFeatures(object, assay = NULL, n = 20000, verbose = TRUE)
```

Arguments

object	A Seurat object
assay	Name of assay to use. Default is the active assay.
n	Number of features to retain (default 20000).
verbose	Display messages

Value

Returns a SeuratObject::Seurat() object with SeuratObject::VariableFeatures() set to the randomly sampled features.

Examples

```
DownsampleFeatures(atac_small, n = 10)
```

`EnrichedTerms` *Find enriched ontology terms*

Description

Run ontology term enrichment testing on differential features for each of the identity classes. Runs `fgsea::fgsea()` on differential testing results from each identity class.

Usage

```
EnrichedTerms(
  object,
  terms,
  group.by = NULL,
  assay = NULL,
  var.features = TRUE,
  scoreType = "std",
  top.n = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

`object`	A Seurat object.
`terms`	Ontology term list. The name of each element in the list should be an ontology term, and the list elements a vector of feature names present in the assay.
`group.by`	Name of grouping variable to use. If NULL, use the active cell identities.
`assay`	Name of assay to use. If NULL, use the default assay.
`var.features`	Subset to only variable features for ontology term enrichment.
`scoreType`	`scoreType` parameter for `fgsea::fgseaSimple()`. Options are "std", "pos", "neg" (two-tailed or one-tailed tests).
`top.n`	Number of top enriched terms to retain for each set of cells. If NULL, retain all terms.
`verbose`	Display messages.
`...`	Additional arguments passed to `Seurat::FindMarkers()`

Value

Returns a named list of dataframes. Each element of the list contains a dataframe with the term enrichment results for an identity class.

ExpressionPlot *Plot gene expression*

Description

Display gene expression values for different groups of cells and different genes. Genes will be arranged on the x-axis and different groups stacked on the y-axis, with expression value distribution for each group shown as a violin plot. This is designed to work alongside a genomic coverage track, and the plot will be able to be aligned with coverage tracks for the same groups of cells.

Usage

```
ExpressionPlot(
  object,
  features,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  slot = "data"
)
```

Arguments

object	A Seurat object
features	A list of features to plot
assay	Name of the assay storing expression information
group.by	A grouping variable to group cells by. If NULL, use the current cell identities
idents	A list of identities to include in the plot. If NULL, include all identities
slot	Which slot to pull expression data from

Examples

```
ExpressionPlot(atac_small, features = "TSPAN6", assay = "RNA")
```

Extend *Extend*

Description

Resize GenomicRanges upstream and or downstream. From https://support.bioconductor.org/p/78652/

Usage

```
Extend(x, upstream = 0, downstream = 0, from.midpoint = FALSE)
```

Arguments

x	A range
upstream	Length to extend upstream
downstream	Length to extend downstream
from.midpoint	Count bases from region midpoint, rather than the 5' or 3' end for upstream and downstream respectively.

Value

Returns a GenomicRanges::GRanges() object

Examples

```
Extend(x = blacklist_hg19, upstream = 100, downstream = 100)
```

FeatureMatrix *Feature Matrix*

Description

Construct a feature x cell matrix from a genomic fragments file

Usage

```
FeatureMatrix(
  fragments,
  features,
  keep_all_features = FALSE,
  cells = NULL,
  process_n = 2000,
  sep = c("-", "-"),
  verbose = TRUE
)
```

Arguments

fragments	A list of Fragment() objects. Note that if setting the cells parameter, the requested cells should be present in the supplied Fragment objects. However, if the cells information in the fragment object is not set (Cells(fragments) is NULL), then the fragment object will still be searched.
features	A GRanges object containing a set of genomic intervals. These will form the rows of the matrix, with each entry recording the number of unique reads falling in the genomic region for each cell.

keep_all_features
: By default, if a genomic region provided is on a chromosome that is not present in the fragment file, it will not be included in the returned matrix. Set keep_all_features to TRUE to force output to include all features in the input ranges. Note that features on chromosomes that are not present in the fragment file will be filled with zero counts.

cells
: Vector of cells to include. If NULL, include all cells found in the fragments file

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.

sep
: Vector of separators to use for genomic string. First element is used to separate chromosome and coordinates, second separator is used to separate start and end coordinates.

verbose
: Display messages

Value

Returns a sparse matrix

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(fpath)
FeatureMatrix(
  fragments = fragments,
  features = granges(atac_small)
)
```

FilterCells *Filter cells from fragment file*

Description

Remove all fragments that are not from an allowed set of cell barcodes from the fragment file. This will create a new file on disk that only contains fragments from cells specified in the cells argument. The output file is block gzip-compressed and indexed, ready for use with Signac functions.

Usage

```
FilterCells(
  fragments,
  cells,
  outfile = NULL,
  buffer_length = 256L,
  verbose = TRUE
)
```

Arguments

fragments	Path to a fragment file
cells	A vector of cells to keep
outfile	Name for output file
buffer_length	Size of buffer to be read from the fragment file. This must be longer than the longest line in the file.
verbose	Display messages

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
tmpf <- tempfile(fileext = ".gz")
FilterCells(
  fragments = fpath,
  cells = head(colnames(atac_small)),
  outfile = tmpf
)
file.remove(tmpf)
```

FindClonotypes *Find clonotypes*

Description

Identify groups of related cells from allele frequency data. This will cluster the cells based on their allele frequencies, reorder the factor levels for the cluster identities by hierarchical clustering the collapsed (pseudobulk) cluster allele frequencies, and set the variable features for the allele frequency assay to the order of features defined by hierarchical clustering.

Usage

```
FindClonotypes(
  object,
  assay = NULL,
  features = NULL,
  metric = "cosine",
  resolution = 1,
  k = 10,
  algorithm = 3
)
```

Arguments

object	A Seurat object
assay	Name of assay to use
features	Features to include when constructing neighbor graph

metric	Distance metric to use
resolution	Clustering resolution to use. See Seurat::FindClusters()
k	Passed to k.param argument in Seurat::FindNeighbors()
algorithm	Community detection algorithm to use. See Seurat::FindClusters()

Value

Returns a SeuratObject::Seurat() object

FindMotifs *FindMotifs*

Description

Find motifs over-represented in a given set of genomic features. Computes the number of features containing the motif (observed) and compares this to the total number of features containing the motif (background) using the hypergeometric test.

Usage

```
FindMotifs(
  object,
  features,
  background = 40000,
  assay = NULL,
  verbose = TRUE,
  p.adjust.method = "BH",
  ...
)
```

Arguments

object	A Seurat object
features	A vector of features to test for enrichments over background
background	Either a vector of features to use as the background set, or a number specify the number of features to randomly select as a background set. If a number is provided, regions will be selected to match the sequence characteristics of the query features. To match the sequence characteristics, these characteristics must be stored in the feature metadata for the assay. This can be added using the RegionStats() function. If NULL, use all features in the assay.
assay	Which assay to use. Default is the active assay
verbose	Display messages
p.adjust.method	Multiple testing correction method to be applied. Passed to stats::p.adjust().
...	Arguments passed to MatchRegionStats().

Value

Returns a data frame

Examples

```
de.motif <- head(rownames(atac_small))
bg.peaks <- tail(rownames(atac_small))
FindMotifs(
  object = atac_small,
  features = de.motif,
  background = bg.peaks
)
```

`findOverlaps-methods` *Find overlapping ranges for ChromatinAssay objects*

Description

The `findOverlaps, countOverlaps` methods are available for `ChromatinAssay()` objects. This allows finding overlaps between genomic ranges and the ranges stored in the ChromatinAssay.

Usage

```
## S4 method for signature 'Vector,ChromatinAssay'
findOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'ChromatinAssay,Vector'
findOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
findOverlaps(
```

```
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'Vector,Seurat'
findOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'Seurat,Vector'
findOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'Seurat,Seurat'
findOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  select = c("all", "first", "last", "arbitrary"),
  ignore.strand = FALSE
)

## S4 method for signature 'Vector,ChromatinAssay'
countOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
```

```
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)

## S4 method for signature 'ChromatinAssay,Vector'
countOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
countOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)

## S4 method for signature 'Seurat,Vector'
countOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)

## S4 method for signature 'Vector,Seurat'
countOverlaps(
  query,
  subject,
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)

## S4 method for signature 'Seurat,Seurat'
countOverlaps(
  query,
  subject,
```

```
  maxgap = -1L,
  minoverlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore.strand = FALSE
)
```

Arguments

`query`, `subject`	A `ChromatinAssay()` object
`maxgap`, `minoverlap`, `type`, `select`, `ignore.strand`	See `?[findOverlaps][GenomicRanges::findOverlaps]` in the **GenomicRanges** and **IRanges** packages.

Details

If a ChromatinAssay is set as the default assay in a `SeuratObject::Seurat()` object, you can also call `findOverlaps` directly on the Seurat object.

Value

See `GenomicRanges::findOverlaps()`

Functions

- `findOverlaps(query = ChromatinAssay, subject = Vector)`: method for ChromatinAssay, Vector
- `findOverlaps(query = ChromatinAssay, subject = ChromatinAssay)`: method for ChromatinAssay, ChromatinAssay
- `findOverlaps(query = Vector, subject = Seurat)`: method for Vector, Seurat
- `findOverlaps(query = Seurat, subject = Vector)`: method for Seurat, Vector
- `findOverlaps(query = Seurat, subject = Seurat)`: method for Seurat, Seurat
- `countOverlaps(query = Vector, subject = ChromatinAssay)`: method for Vector, ChromatinAssay
- `countOverlaps(query = ChromatinAssay, subject = Vector)`: method for ChromatinAssay, Vector
- `countOverlaps(query = ChromatinAssay, subject = ChromatinAssay)`: method for ChromatinAssay, ChromatinAssay
- `countOverlaps(query = Seurat, subject = Vector)`: method for Seurat, Vector
- `countOverlaps(query = Vector, subject = Seurat)`: method for Vector, Seurat
- `countOverlaps(query = Seurat, subject = Seurat)`: method for Seurat, Seurat

See Also

- findOverlaps-methods in the **IRanges** package.
- findOverlaps-methods in the **GenomicRanges** package
- ChromatinAssay

`FindTopFeatures` *Find most frequently observed features*

Description

Find top features for a given assay based on total number of counts for the feature. Can specify a minimum cell count, or a lower percentile bound to determine the set of variable features. Running this function will store the total counts and percentile rank for each feature in the feature metadata for the assay. To only compute the feature metadata, without changing the variable features for the assay, set `min.cutoff=NA`.

Usage

```
FindTopFeatures(object, ...)

## Default S3 method:
FindTopFeatures(object, assay = NULL, min.cutoff = "q5", verbose = TRUE, ...)

## S3 method for class 'Assay'
FindTopFeatures(object, assay = NULL, min.cutoff = "q5", verbose = TRUE, ...)

## S3 method for class 'StdAssay'
FindTopFeatures(object, assay = NULL, min.cutoff = "q5", verbose = TRUE, ...)

## S3 method for class 'Seurat'
FindTopFeatures(object, assay = NULL, min.cutoff = "q5", verbose = TRUE, ...)
```

Arguments

`object`	A Seurat object
`...`	Arguments passed to other methods
`assay`	Name of assay to use
`min.cutoff`	Cutoff for feature to be included in the VariableFeatures for the object. This can be a percentile specified as 'q' followed by the minimum percentile, for example 'q5' to set the top 95\ as the VariableFeatures for the object. Alternatively, this can be an integer specifying the minimum number of counts for the feature to be included in the set of VariableFeatures. For example, setting to 10 will include features with >10 total counts in the set of VariableFeatures. If NULL, include all features in VariableFeatures. If NA, VariableFeatures will not be altered, and only the feature metadata will be updated with the total counts and percentile rank for each feature.
`verbose`	Display messages

Value

Returns a `SeuratObject::Seurat()` object

Examples

```
FindTopFeatures(object = atac_small[["peaks"]]["data"])
FindTopFeatures(object = atac_small[["peaks"]])
FindTopFeatures(object = atac_small[["peaks"]])
FindTopFeatures(atac_small)
```

FitMeanVar *Find variable features fitting LOESS*

Description

Find highly variable features by fitting a locally polynomial regression model to the log(mean) and log(variance) of downsampled features.

Usage

```
FitMeanVar(object, ...)

## S3 method for class 'Seurat'
FitMeanVar(
  object,
  assay = NULL,
  layer = NULL,
  nfeatures = 20000,
  loess.span = 0.1,
  min.cutoff = 10,
  weight.mean = 0,
  bins = 1000,
  sample_per_bin = 50,
  key = "dsLoess",
  verbose = FALSE,
  ...
)

## S3 method for class 'StdAssay'
FitMeanVar(
  object,
  layer = NULL,
  loess.span = 0.1,
  nfeatures = 20000,
  min.cutoff = 10,
  weight.mean = 0,
  bins = 1000,
  sample_per_bin = 50,
  key = "dsLoess",
  verbose = FALSE,
  ...
```

```
)

## S3 method for class 'Assay'
FitMeanVar(
  object,
  layer = NULL,
  loess.span = 0.1,
  nfeatures = 20000,
  min.cutoff = 10,
  weight.mean = 0,
  bins = 1000,
  sample_per_bin = 50,
  key = "dsLoess",
  verbose = FALSE,
  ...
)

## Default S3 method:
FitMeanVar(
  object,
  nfeatures = 20000,
  loess.span = 0.1,
  min.cutoff = 10,
  weight.mean = 0,
  bins = 1000,
  sample_per_bin = 50,
  random.seed = 1234,
  verbose = FALSE,
  ...
)

## S3 method for class 'data.frame'
FitMeanVar(
  object,
  loess.span = 0.1,
  weight.mean = 0,
  bins = 1000,
  sample_per_bin = 50,
  random.seed = 1234,
  verbose = FALSE,
  ...
)
```

Arguments

object	A Seurat object
...	Arguments passed to other methods
assay	Name of assay to use. If NULL, use the default assay.

layer	Name of layer to use. If NULL, use the default layer(s).
nfeatures	Number of features to selected as top variable features.
loess.span	span parameter passed to the stats::loess() function
min.cutoff	Minimum number of counts for a feature to be eligible for variable feature selection.
weight.mean	How much to weight the ranking of features according to their mean. Setting weight.mean=0 will rank features according to their residual variance only.
bins	Number of bins to use when downsampling features across the range of mean count values.
sample_per_bin	Number of features to select per mean count bin in feature downsampling step.
key	Key to use when storing the highly variable feature information in the assay.
verbose	Display messages.
random.seed	Random seed to set for sampling.

Details

This function is similar to the Seurat::FindVariableFeatures() function (with selection.method="vst"), but downsamples the features evenly across the range of mean values. This speeds up fitting of the loess curve when the number of features is large.

The function also provides the ability to combine ranking of features according to their mean count and their residual variance, using a weighted rank sum with weights set by the weight.mean parameter. This can help to avoid selecting features with high residual variance but very low mean.

Value

Returns a SeuratObject::Seurat() object

Examples

```
FitMeanVar(atac_small)
FitMeanVar(object = atac_small[["peaks"]])
```

Footprint *Transcription factor footprinting analysis*

Description

Compute the normalized observed/expected Tn5 insertion frequency for each position surrounding a set of motif instances.

Usage

```
Footprint(object, ...)

## S3 method for class 'ChromatinAssay'
Footprint(
  object,
  genome,
  motif.name = NULL,
  key = motif.name,
  regions = NULL,
  assay = NULL,
  upstream = 250,
  downstream = 250,
  compute.expected = TRUE,
  in.peaks = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'Seurat'
Footprint(
  object,
  genome,
  regions = NULL,
  motif.name = NULL,
  assay = NULL,
  upstream = 250,
  downstream = 250,
  in.peaks = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat or ChromatinAssay object
...	Arguments passed to other methods
genome	A BSgenome object or any other object supported by getSeq. Do showMethods("getSeq") to get the list of all supported object types.
motif.name	Name of a motif stored in the assay to footprint. If not supplied, must supply a set of regions.
key	Key to store positional enrichment information under.
regions	A set of genomic ranges containing the motif instances. These should all be the same width.
assay	Name of assay to use
upstream	Number of bases to extend upstream

downstream	Number of bases to extend downstream
compute.expected	Find the expected number of insertions at each position given the local DNA sequence context and the insertion bias of Tn5
in.peaks	Restrict motifs to those that fall in peaks
verbose	Display messages

Value

Returns a SeuratObject::Seurat() object

FractionCountsInRegion

Fraction of counts in a genomic region

Description

Find the fraction of counts per cell that overlap a given set of genomic ranges

Usage

```
FractionCountsInRegion(object, regions, assay = NULL, ...)
```

Arguments

object	A Seurat object
regions	A GRanges object containing a set of genomic regions
assay	Name of assay to use
...	Additional arguments passed to CountsInRegion() **[Deprecated]**

Value

Returns a numeric vector

Examples

```
## Not run:
FractionCountsInRegion(
  object = atac_small,
  assay = 'bins',
  regions = blacklist_hg19
)

## End(Not run)
```

Fragment-class *The Fragment class*

Description

The Fragment class is designed to hold information needed for working with fragment files.

Slots

`path` Path to the fragment file on disk. See https://www.10xgenomics.com/support/software/cell-ranger-atac/latest/analysis/outputs/fragments-file

`hash` A vector of two md5sums: first element is the md5sum of the fragment file, the second element is the md5sum of the index.

`cells` A named vector of cells where each element is the cell barcode as it appears in the fragment file, and the name of each element is the corresponding cell barcode as stored in the ChromatinAssay object.

FragmentHistogram *Plot fragment length histogram*

Description

Plot the frequency that fragments of different lengths are present for different groups of cells.

Usage

```
FragmentHistogram(
  object,
  assay = NULL,
  region = "chr1-1-2000000",
  group.by = NULL,
  cells = NULL,
  log.scale = FALSE,
  ...
)
```

Arguments

`object`	A Seurat object
`assay`	Which assay to use. Default is the active assay.
`region`	Genomic range to use. Default is fist two megabases of chromosome 1. Can be a GRanges object, a string, or a vector of strings.
`group.by`	Name of one or more metadata columns to group (color) the cells by. Default is the current cell identities

cells	Which cells to plot. Default all cells
log.scale	Display Y-axis on log scale. Default is FALSE.
...	Arguments passed to other functions

Value

Returns a ggplot2::ggplot() object

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
Fragments(atac_small) <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
FragmentHistogram(object = atac_small, region = "chr1-10245-780007")
```

Fragments *Get the Fragment objects*

Description

Get the Fragment objects

Usage

```
Fragments(object, ...)

Fragments(object, ...) <- value

## S3 method for class 'ChromatinAssay'
Fragments(object, ...)

## S3 method for class 'Seurat'
Fragments(object, ...)

## S3 replacement method for class 'ChromatinAssay'
Fragments(object, ...) <- value

## S3 replacement method for class 'Seurat'
Fragments(object, ...) <- value
```

Arguments

object	A Seurat object or ChromatinAssay object
...	Arguments passed to other methods
value	A Fragment() object or list of Fragment objects

Value

Returns a list of `Fragment()` objects. If there are no Fragment objects present, returns an empty list.

Examples

```
Fragments(atac_small[["peaks"]])
Fragments(atac_small)
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
Fragments(atac_small[["bins"]]) <- fragments
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
Fragments(atac_small) <- fragments
```

FRiP *Calculate fraction of reads in peaks per cell*

Description

Calculate fraction of reads in peaks per cell

Usage

```
FRiP(object, assay, total.fragments, col.name = "FRiP", verbose = TRUE)
```

Arguments

`object`	A Seurat object
`assay`	Name of the assay containing a peak x cell matrix
`total.fragments`	Name of a metadata column containing the total number of sequenced fragments for each cell. This can be computed using the `CountFragments()` function.
`col.name`	Name of column in metadata to store the FRiP information.
`verbose`	Display messages

Value

Returns a `SeuratObject::Seurat()` object

Examples

```
FRiP(object = atac_small, assay = "peaks", total.fragments = "fragments")
```

`GeneActivity` *Create gene activity matrix*

Description

Compute counts per cell in gene body and promoter region.

Usage

```
GeneActivity(
  object,
  assay = NULL,
  features = NULL,
  extend.upstream = 2000,
  extend.downstream = 0,
  biotypes = "protein_coding",
  max.width = 5e+05,
  process_n = 2000,
  gene.id = FALSE,
  verbose = TRUE
)
```

Arguments

`object`	A Seurat object
`assay`	Name of assay to use. If NULL, use the default assay
`features`	Genes to include. If NULL, use all protein-coding genes in the annotations stored in the object
`extend.upstream`	Number of bases to extend upstream of the TSS
`extend.downstream`	Number of bases to extend downstream of the TTS
`biotypes`	Gene biotypes to include. If NULL, use all biotypes in the gene annotation.
`max.width`	Maximum allowed gene width for a gene to be quantified. Setting this parameter can avoid quantifying extremely long transcripts that can add a relatively long amount of time. If NULL, do not filter genes based on width.
`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.
`gene.id`	Record gene IDs in output matrix rather than gene name.
`verbose`	Display messages

Value

Returns a sparse matrix

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
Fragments(atac_small) <- fragments
GeneActivity(atac_small)
```

GenomeBinMatrix *Genome bin matrix*

Description

Construct a bin x cell matrix from a fragments file.

Usage

```
GenomeBinMatrix(
  fragments,
  genome,
  cells = NULL,
  binsize = 5000,
  process_n = 2000,
  sep = c("-", "-"),
  verbose = TRUE
)
```

Arguments

fragments	Path to tabix-indexed fragments file or a list of Fragment() objects
genome	A vector of chromosome sizes for the genome. This is used to construct the genome bin coordinates. The can be obtained by calling seqlengths on a BSgenome::BSgenome-class() object.
cells	Vector of cells to include. If NULL, include all cells found in the fragments file
binsize	Size of the genome bins to use
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.
sep	Vector of separators to use for genomic string. First element is used to separate chromosome and coordinates, second separator is used to separate start and end coordinates.
verbose	Display messages

Details

This function bins the genome and calls `FeatureMatrix()` to construct a bin x cell matrix.

Value

Returns a sparse matrix

Examples

```
genome <- 780007
names(genome) <- 'chr1'
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(fpath)
GenomeBinMatrix(
  fragments = fragments,
  genome = genome,
  binsize = 1000
)
```

GetCellsInRegion *Get cells in a region*

Description

Extract cell names containing reads mapped within a given genomic region

Usage

```
GetCellsInRegion(tabix, region, cells = NULL)
```

Arguments

`tabix`	Tabix object
`region`	A string giving the region to extract from the fragments file
`cells`	Vector of cells to include in output. If NULL, include all cells

Value

Returns a list

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
GetCellsInRegion(tabix = fpath, region = "chr1-10245-762629")
```

`GetFootprintData` *Get footprinting data*

Description

Extract footprint data for a set of transcription factors or metafeatures. This function will pull accessibility data for a given feature (eg, a TF), and perform background normalization for each identity class. This is the data that's used to create TF footprinting plots with the `PlotFootprint` function.

Usage

```
GetFootprintData(
  object,
  features,
  assay = NULL,
  group.by = NULL,
  idents = NULL
)
```

Arguments

`object`	A Seurat object
`features`	A vector of features to extract data for
`assay`	Name of assay to use
`group.by`	A grouping variable
`idents`	Set of identities to group cells by

Value

Returns a data.frame with the following columns:

- group: Cell group (determined by group.by parameter
- position: Position relative to motif center
- count: Normalized Tn5 insertion counts at each position
- norm.value: Normalized Tn5 insertion counts at each position (same as count)
- feature: Name of the footprinted motif
- class: observed or expected

GetFragmentData *Get Fragment object data*

Description

Extract data from a `Fragment-class()` object

Usage

```
GetFragmentData(object, slot = "path")
```

Arguments

`object`	A `Fragment()` object
`slot`	Information to pull from object (path, hash, cells, prefix, suffix)

GetGRangesFromEnsDb *Extract genomic ranges from EnsDb object*

Description

Pulls the transcript information for all chromosomes from an EnsDb object. This wraps `biovizBase::crunch()` and applies the extractor function to all chromosomes present in the EnsDb object.

Usage

```
GetGRangesFromEnsDb(
  ensdb,
  standard.chromosomes = TRUE,
  biotypes = c("protein_coding", "lincRNA", "rRNA", "processed_transcript"),
  verbose = TRUE
)
```

Arguments

`ensdb`	An EnsDb object
`standard.chromosomes`	Keep only standard chromosomes
`biotypes`	Biotypes to keep
`verbose`	Display messages

`GetIntersectingFeatures` *Find intersecting regions between two objects*

Description

Intersects the regions stored in the rownames of two objects and returns a vector containing the names of rows that intersect for each object. The order of the row names return corresponds to the intersecting regions, i.e. the nth feature of the first vector will intersect the nth feature in the second vector. A distance parameter can be given, in which case features within the given distance will be called as intersecting.

Usage

```
GetIntersectingFeatures(
  object.1,
  object.2,
  assay.1 = NULL,
  assay.2 = NULL,
  distance = 0,
  verbose = TRUE
)
```

Arguments

`object.1`	The first Seurat object
`object.2`	The second Seurat object
`assay.1`	Name of the assay to use in the first object. If NULL, use the default assay
`assay.2`	Name of the assay to use in the second object. If NULL, use the default assay
`distance`	Maximum distance between regions allowed for an intersection to be recorded. Default is 0.
`verbose`	Display messages **[Deprecated]**

Value

Returns a list of two character vectors containing the row names in each object that overlap each other.

Examples

```
GetIntersectingFeatures(
  object.1 = atac_small,
  object.2 = atac_small,
  assay.1 = 'peaks',
  assay.2 = 'bins'
)
```

GetLinkedGenes *Get genes linked to peaks*

Description

Retrieve peak-gene links for a given set of genes. Links must be first obtained by running the LinkPeaks function.

Usage

```
GetLinkedGenes(object, features, assay = NULL, min.abs.score = 0)
```

Arguments

object	A Seurat object
features	A list of peaks to find linked genes for
assay	Name of assay to use. If NULL, use the default assay
min.abs.score	Minimum absolute value of the link score for a link to be returned

Details

This function is designed to obtain the stored results from running the LinkPeaks function. Alternatively, custom peak-gene linkage methods can be used as long as they store the gene name, peak name, and a peak-gene score information as metadata columns named "gene," "peak," and "score" respectively.

See Also

GetLinkedPeaks

GetLinkedPeaks *Get peaks linked to genes*

Description

Retrieve peak-gene links for a given set of genes. Links must be first obtained by running the LinkPeaks function.

Usage

```
GetLinkedPeaks(object, features, assay = NULL, min.abs.score = 0)
```

Arguments

object	A Seurat object
features	A list of genes to find linked peaks for
assay	Name of assay to use. If NULL, use the default assay
min.abs.score	Minimum absolute value of the link score for a link to be returned

Details

This function is designed to obtain the stored results from running the LinkPeaks function. Alternatively, custom peak-gene linkage methods can be used as long as they store the gene name, peak name, and a peak-gene score information as metadata columns named "gene," "peak," and "score" respectively.

See Also

GetLinkedGenes

GetMotifData *Retrieve a motif matrix*

Description

Get motif matrix for given assay

Usage

```
GetMotifData(object, ...)

## S3 method for class 'Motif'
GetMotifData(object, slot = "data", ...)

## S3 method for class 'ChromatinAssay'
GetMotifData(object, slot = "data", ...)

## S3 method for class 'Seurat'
GetMotifData(object, assay = NULL, slot = "data", ...)
```

Arguments

object	A Seurat object
...	Arguments passed to other methods
slot	Information to pull from object (data, pwm, meta.data)
assay	Which assay to use. Default is the current active assay

Value

Returns a SeuratObject::Seurat() object

Examples

```
motif.obj <- SeuratObject::GetAssayData(
  object = atac_small[['peaks']], slot = "motifs"
)
GetMotifData(object = motif.obj)
GetMotifData(object = atac_small)
```

GetTSSPositions *Find transcriptional start sites*

Description

Get the TSS positions from a set of genomic ranges containing gene positions. Ranges can contain exons, introns, UTRs, etc, rather than the whole transcript. Only protein coding gene biotypes are included in output.

Usage

```
GetTSSPositions(ranges, biotypes = "protein_coding")
```

Arguments

ranges	A GRanges object containing gene annotations.
biotypes	Gene biotypes to include. If NULL, use all biotypes in the supplied gene annotation.

---

granges-methods *Access genomic ranges for ChromatinAssay objects*

Description

Methods for accessing GenomicRanges::GRanges() object information stored in a ChromatinAssay() object.

Usage

```
## S4 method for signature 'ChromatinAssay'
granges(x, use.names = TRUE, use.mcols = FALSE, ...)

## S4 method for signature 'Seurat'
granges(x, use.names = TRUE, use.mcols = FALSE, ...)
```

Arguments

x	A ChromatinAssay() object
use.names	Whether the names on the genomic ranges should be propagated to the returned object.
use.mcols	Not supported for ChromatinAssay() objects
...	Additional arguments

Value

Returns a GenomicRanges::GRanges() object

Functions

- granges(Seurat): method for Seurat objects

See Also

- granges in the **GenomicRanges** package.
- ChromatinAssay

Examples

```
granges(atac_small)
```

GRangesToString *GRanges to String*

Description

[Deprecated]

Usage

```
GRangesToString(grange, sep = c("-", "-"))
```

Arguments

grange	A GRanges object
sep	Vector of separators to use for genomic string. First element is used to separate chromosome and coordinates, second separator is used to separate start and end coordinates.

Details

Convert GRanges object to a vector of strings

Value

Returns a character vector

Examples

```
GRangesToString(grange = blacklist_hg19)
```

`head.Fragment` *Return the first rows of a fragment file*

Description

Returns the first `n` rows of a fragment file. This allows the content of a fragment file to be inspected.

Usage

```
## S3 method for class 'Fragment'
head(x, n = 6L, ...)
```

Arguments

`x`	a `Fragment` object
`n`	an integer specifying the number of rows to return from the fragment file
`...`	additional arguments passed to `utils::read.table()`

Value

The first `n` rows of a fragment file as a `data.frame` with the following columns: chrom, start, end, barcode, readCount.

`IdentifyVariants` *Identify mitochondrial variants*

Description

Identify mitochondrial variants present in single cells.

Usage

```
IdentifyVariants(object, ...)

## Default S3 method:
IdentifyVariants(
  object,
  refallele,
  stabilize_variance = TRUE,
  low_coverage_threshold = 10,
  verbose = TRUE,
  ...
)

## S3 method for class 'Assay'
IdentifyVariants(object, refallele, ...)

## S3 method for class 'StdAssay'
IdentifyVariants(object, refallele, ...)

## S3 method for class 'Seurat'
IdentifyVariants(object, refallele, assay = NULL, ...)
```

Arguments

object	A Seurat object
...	Arguments passed to other methods
refallele	A dataframe containing reference alleles for the mitochondrial genome.
stabilize_variance	Stabilize variance
low_coverage_threshold	Low coverage threshold
verbose	Display messages
assay	Name of assay to use. If NULL, use the default assay.

Value

Returns a dataframe

Examples

```
## Not run:
data.dir <- "path/to/data/directory"
mgatk <- ReadMGATK(dir = data.dir)
variant.df <- IdentifyVariants(
  object = mgatk$counts,
  refallele = mgatk$refallele
)

## End(Not run)
```

`InsertionBias` *Compute Tn5 insertion bias*

Description

Counts the Tn5 insertion frequency for each DNA hexamer.

Usage

```
InsertionBias(object, ...)

## S3 method for class 'ChromatinAssay'
InsertionBias(object, genome, region = "chr1-1-249250621", verbose = TRUE, ...)

## S3 method for class 'Seurat'
InsertionBias(
  object,
  genome,
  assay = NULL,
  region = "chr1-1-249250621",
  verbose = TRUE,
  ...
)
```

Arguments

`object`	A Seurat or ChromatinAssay object
`...`	Additional arguments passed to `StringToGRanges()`
`genome`	A `BSgenome` object or any other object supported by `getSeq`. Do `showMethods("getSeq")` to get the list of all supported object types.
`region`	Genomic region to use when assessing bias.
`verbose`	Display messages
`assay`	Name of assay to use

Value

Returns a Seurat object

Examples

```
## Not run:
library(BSgenome.Mmusculus.UCSC.mm10)

region.use <- GRanges(
  seqnames = c('chr1', 'chr2'),
  IRanges(start = c(1,1), end = c(195471971, 182113224))
```

```
)

InsertionBias(
 object = atac_small,
 genome = BSgenome.Mmusculus.UCSC.mm10,
 region = region.use
)

## End(Not run)
```

`inter-range-methods` *Inter-range transformations for ChromatinAssay objects*

Description

The `range`, `reduce`, `gaps`, `disjoin`, `isDisjoint`, `disjointBins` methods are available for `ChromatinAssay()` objects.

Usage

```
## S4 method for signature 'ChromatinAssay'
range(x, ..., with.revmap = FALSE, na.rm = FALSE)

## S4 method for signature 'Seurat'
range(x, ..., with.revmap = FALSE, na.rm = FALSE)

## S4 method for signature 'ChromatinAssay'
reduce(x, drop.empty.ranges = FALSE, ...)

## S4 method for signature 'Seurat'
reduce(x, drop.empty.ranges = FALSE, ...)

## S4 method for signature 'ChromatinAssay'
gaps(x, start = NA, end = NA)

## S4 method for signature 'Seurat'
gaps(x, start = NA, end = NA)

## S4 method for signature 'ChromatinAssay'
disjoin(x, ...)

## S4 method for signature 'Seurat'
disjoin(x, ...)

## S4 method for signature 'ChromatinAssay'
isDisjoint(x, ...)

## S4 method for signature 'Seurat'
```

```
isDisjoint(x, ...)

## S4 method for signature 'ChromatinAssay'
disjointBins(x, ...)

## S4 method for signature 'Seurat'
disjointBins(x, ...)
```

Arguments

x	A ChromatinAssay() object
...	Additional arguments
with.revmap	See IRanges::inter-range-methods() in the **IRanges** packages
na.rm	Ignored
drop.empty.ranges	See ?[inter-range-methods][IRanges::inter-range-methods]
start, end	See ?[inter-range-methods][IRanges::inter-range-methods]

Functions

- range(Seurat): method for Seurat objects
- reduce(ChromatinAssay): method for ChromatinAssay objects
- reduce(Seurat): method for Seurat objects
- gaps(ChromatinAssay): method for ChromatinAssay objects
- gaps(Seurat): method for Seurat objects
- disjoin(ChromatinAssay): method for ChromatinAssay objects
- disjoin(Seurat): method for Seurat objects
- isDisjoint(ChromatinAssay): method for ChromatinAssay objects
- isDisjoint(Seurat): method for Seurat objects
- disjointBins(ChromatinAssay): method for ChromatinAssay objects
- disjointBins(Seurat): method for Seurat objects

See Also

- inter-range-methods in the **IRanges** package.
- inter-range-methods in the **GenomicRanges** package
- ChromatinAssay

`IntersectMatrix` *Intersect genomic coordinates with matrix rows*

Description

Remove or retain matrix rows that intersect given genomic regions

Usage

```
IntersectMatrix(
  matrix,
  regions,
  invert = FALSE,
  sep = c("-", "-"),
  verbose = TRUE,
  ...
)
```

Arguments

`matrix`	A matrix with genomic regions in the rows
`regions`	A set of genomic regions to intersect with regions in the matrix. Either a vector of strings encoding the genomic coordinates, or a GRanges object.
`invert`	Discard rows intersecting the genomic regions supplied, rather than retain.
`sep`	A length-2 character vector containing the separators to be used for extracting genomic coordinates from a string. The first element will be used to separate the chromosome name from coordinates, and the second element used to separate start and end coordinates.
`verbose`	Display messages
`...`	Additional arguments passed to `IRanges::findOverlaps()` **[Deprecated]**

Value

Returns a sparse matrix

Examples

```
counts <- matrix(data = rep(0, 12), ncol = 2)
rownames(counts) <- c("chr1-565107-565550","chr1-569174-569639",
"chr1-713460-714823","chr1-752422-753038",
"chr1-762106-763359","chr1-779589-780271")
IntersectMatrix(matrix = counts, regions = blacklist_hg19)
```

Jaccard *Calculate the Jaccard index between two matrices*

Description

Finds the Jaccard similarity between rows of the two matrices. Note that the matrices must be binary, and any rows with zero total counts will result in an NaN entry that could cause problems in downstream analyses.

Usage

```
Jaccard(x, y)
```

Arguments

x	The first matrix
y	The second matrix

Details

This will calculate the raw Jaccard index, without normalizing for the expected similarity between cells due to differences in sequencing depth.

Value

Returns a matrix

Examples

```
x <- matrix(data = sample(c(0, 1), size = 25, replace = TRUE), ncol = 5)
Jaccard(x = x, y = x)
```

LinkPeaks *Link peaks to genes*

Description

Find peaks that are correlated with the expression of nearby genes. For each gene, this function computes the correlation coefficient between the gene expression and accessibility of each peak within a given distance from the gene TSS, and computes an expected correlation coefficient for each peak given the GC content, accessibility, and length of the peak. The expected coefficient values for the peak are then used to compute a z-score and p-value.

Usage

```
LinkPeaks(
  object,
  peak.assay,
  expression.assay,
  peak.slot = "counts",
  expression.slot = "data",
  method = "pearson",
  gene.coords = NULL,
  distance = 5e+05,
  min.distance = NULL,
  min.cells = 10,
  genes.use = NULL,
  n_sample = 200,
  pvalue_cutoff = 0.05,
  score_cutoff = 0.05,
  gene.id = FALSE,
  verbose = TRUE
)
```

Arguments

object	A Seurat object
peak.assay	Name of assay containing peak information
expression.assay	Name of assay containing gene expression information
peak.slot	Name of slot to pull chromatin data from
expression.slot	Name of slot to pull expression data from
method	Correlation method to use. One of "pearson" or "spearman"
gene.coords	GRanges object containing coordinates of genes in the expression assay. If NULL, extract from gene annotations stored in the assay.
distance	Distance threshold for peaks to include in regression model
min.distance	Minimum distance between peak and TSS to include in regression model. If NULL (default), no minimum distance is used.
min.cells	Minimum number of cells positive for the peak and gene needed to include in the results.
genes.use	Genes to test. If NULL, determine from expression assay.
n_sample	Number of peaks to sample at random when computing the null distribution.
pvalue_cutoff	Minimum p-value required to retain a link. Links with a p-value equal or greater than this value will be removed from the output.
score_cutoff	Minimum absolute value correlation coefficient for a link to be retained
gene.id	Set to TRUE if genes in the expression assay are named using gene IDs rather than gene names.
verbose	Display messages

Details

This function was inspired by the method originally described by SHARE-seq (Sai Ma et al. 2020, Cell). Please consider citing the original SHARE-seq work if using this function: doi:10.1016/j.cell.2020.09.056

Value

Returns a Seurat object with the `Links` information set. This is a `GenomicRanges::granges()` object accessible via the `Links()` function, with the following information:

- score: the correlation coefficient between the accessibility of the peak and expression of the gene
- zscore: the z-score of the correlation coefficient, computed based on the distribution of correlation coefficients from a set of background peaks
- pvalue: the p-value associated with the z-score for the link
- gene: name of the linked gene
- peak: name of the linked peak

`LinkPlot` *Plot linked genomic elements*

Description

Display links between pairs of genomic elements within a given region of the genome.

Usage

```
LinkPlot(
  object,
  region,
  assay = NULL,
  min.cutoff = 0,
  sep = c("-", "-"),
  extend.upstream = 0,
  extend.downstream = 0,
  scale.linewidth = FALSE
)
```

Arguments

`object`	A `SeuratObject::Seurat()` object
`region`	A genomic region to plot
`assay`	Name of assay to use. If NULL, use the default assay.
`min.cutoff`	Minimum absolute score for link to be plotted.

sep — Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.

extend.upstream — Number of bases to extend the region upstream.

extend.downstream — Number of bases to extend the region downstream.

scale.linewidth — Scale thickness of the line according to link score.

Value

Returns a ggplot2::ggplot() object

Links *Get or set links information*

Description

Get or set the genomic link information for a Seurat object or ChromatinAssay

Usage

```
Links(object, ...)

Links(object, ...) <- value

## S3 method for class 'ChromatinAssay'
Links(object, ...)

## S3 method for class 'Seurat'
Links(object, ...)

## S3 replacement method for class 'ChromatinAssay'
Links(object, ...) <- value

## S3 replacement method for class 'Seurat'
Links(object, ...) <- value
```

Arguments

object — A Seurat object

... — Arguments passed to other methods

value — A GenomicRanges::GRanges() object

Examples

```
Links(atac_small[["peaks"]])
Links(atac_small)
links <- Links(atac_small)
Links(atac_small[["peaks"]]) <- links
links <- Links(atac_small)
Links(atac_small) <- links
```

LookupGeneCoords *Get gene coordinates*

Description

Extract the coordinates of the longest transcript for a gene stored in the annotations within an object.

Usage

```
LookupGeneCoords(object, gene, assay = NULL)
```

Arguments

object	A Seurat object
gene	Name of a gene to extract
assay	Name of assay to use

Examples

```
LookupGeneCoords(atac_small, gene = "MIR1302-10")
```

MatchRegionStats *Match DNA sequence characteristics*

Description

Return a vector if genomic regions that match the distribution of a set of query regions for any given set of characteristics, specified in the input `meta.feature` dataframe.

Usage

```
MatchRegionStats(
  meta.feature,
  query.feature,
  features.match = c("GC.percent"),
  n = 10000,
  verbose = TRUE,
  ...
)
```

Arguments

meta.feature	A dataframe containing DNA sequence information for features to choose from
query.feature	A dataframe containing DNA sequence information for features to match.
features.match	Which features of the query to match when selecting a set of regions. A vector of column names present in the feature metadata can be supplied to match multiple characteristics at once. Default is GC content.
n	Number of regions to select, with characteristics matching the query
verbose	Display messages
...	Arguments passed to other functions

Details

For each requested feature to match, a density distribution is estimated using the stats::density() function, and a set of weights for each feature in the dataset estimated based on the density distribution. If multiple features are to be matched (for example, GC content and overall accessibility), a joint density distribution is then computed by multiplying the individual feature weights. A set of features with characteristics matching the query regions is then selected using the base::sample() function, with the probability of randomly selecting each feature equal to the joint density distribution weight.

Value

Returns a character vector

Examples

```
metafeatures <- SeuratObject::GetAssayData(
  object = atac_small[['peaks']], layer = 'meta.features'
)
query.feature <- metafeatures[1:10, ]
features.choose <- metafeatures[11:nrow(metafeatures), ]
MatchRegionStats(
  meta.feature = features.choose,
  query.feature = query.feature,
  features.match = "percentile",
  n = 10
)
```

Motif-class *The Motif class*

Description

The Motif class is designed to store DNA sequence motif information, including motif PWMs or PFMs, motif positions, and metadata.

Slots

`data` A sparse, binary, feature x motif matrix. Columns correspond to motif IDs, rows correspond to genomic features (peaks or bins). Entries in the matrix should be 1 if the genomic feature contains the motif, and 0 otherwise.

`pwm` A named list of position weight matrices

`motif.names` A list containing the name of each motif

`positions` A `GenomicRanges::GRangesList()` object containing exact positions of each motif.

`meta.data` A dataframe for storage of additional information related to each motif. This could include the names of proteins that bind the motif.

`MotifCounts` *Count fragments surrounding motif sites*

Description

Count the number of sequenced DNA fragments in a region surrounding each instance of a given DNA sequence motif.

Usage

```
MotifCounts(
  object,
  motifs,
  flanking.region = 1000,
  assay = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

`object`	A Seurat object
`motifs`	A list of DNA sequence motif names. One matrix will be generated for each motif
`flanking.region`	Amount of sequence to include surrounding the motif itself
`assay`	Name of assay to use. Must be a ChromatinAssay
`verbose`	Display messages
`...`	Additional arguments passed to `FeatureMatrix()`

Value

Returns a list of sparse matrices

[Deprecated]

MotifPlot *Plot DNA sequence motif*

Description

Plot position weight matrix or position frequency matrix for different DNA sequence motifs.

Usage

```
MotifPlot(object, motifs, assay = NULL, use.names = TRUE, ...)
```

Arguments

object	A Seurat object
motifs	A list of motif IDs or motif names to plot
assay	Name of the assay to use
use.names	Use motif names stored in the motif object
...	Additional parameters passed to ggseqlogo::ggseqlogo()

Value

Returns a ggplot2::ggplot() object

Examples

```
motif.obj <- Motifs(atac_small)
MotifPlot(atac_small, motifs = head(colnames(motif.obj)))
```

Motifs *Get or set a motif information*

Description

Get or set the Motif object for a Seurat object or ChromatinAssay.

Usage

```
Motifs(object, ...)

Motifs(object, ...) <- value

## S3 method for class 'ChromatinAssay'
Motifs(object, ...)
```

```
## S3 method for class 'Seurat'
Motifs(object, ...)

## S3 replacement method for class 'ChromatinAssay'
Motifs(object, ...) <- value

## S3 replacement method for class 'Seurat'
Motifs(object, ...) <- value
```

Arguments

object	A Seurat object
...	Arguments passed to other methods
value	A Motif() object

Examples

```
Motifs(atac_small[["peaks"]])
Motifs(atac_small)
motifs <- Motifs(atac_small)
Motifs(atac_small[["peaks"]]) <- motifs
motifs <- Motifs(atac_small)
Motifs(atac_small) <- motifs
```

---

nearest-methods *Find the nearest range neighbors for ChromatinAssay objects*

Description

The precede, follow, nearest, distance, distanceToNearest methods are available for ChromatinAssay() objects.

Usage

```
## S4 method for signature 'ANY,ChromatinAssay'
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ANY'
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,Seurat'
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,ANY'
```

```
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,Seurat'
precede(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,ChromatinAssay'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ANY'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,Seurat'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,ANY'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,Seurat'
follow(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,ChromatinAssay'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ANY'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,Seurat'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,ANY'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'Seurat,Seurat'
nearest(x, subject, select = c("arbitrary", "all"), ignore.strand = FALSE)

## S4 method for signature 'ANY,ChromatinAssay'
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'ChromatinAssay,ANY'
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
```

```
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'ANY,Seurat'
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'Seurat,ANY'
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'Seurat,Seurat'
distance(x, y, ignore.strand = FALSE, ...)

## S4 method for signature 'ANY,ChromatinAssay'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)

## S4 method for signature 'ChromatinAssay,ANY'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)

## S4 method for signature 'ChromatinAssay,ChromatinAssay'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)

## S4 method for signature 'ANY,Seurat'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)

## S4 method for signature 'Seurat,ANY'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)

## S4 method for signature 'Seurat,Seurat'
distanceToNearest(x, subject, ignore.strand = FALSE, ...)
```

Arguments

x	A query ChromatinAssay() object
subject	The subject GenomicRanges::GRanges() or ChromatinAssay() object. If missing, x is used as the subject.
select	Logic for handling ties. See GenomicRanges::nearest-methods() in the **GenomicRanges** package.
ignore.strand	Logical argument controlling whether strand information should be ignored.
y	For the distance method, a GenomicRanges::GRanges() object or a ChromatinAssay() object
...	Additional arguments for methods

Functions

- precede(x = ChromatinAssay, subject = ANY): method for ChromatinAssay, ANY
- precede(x = ChromatinAssay, subject = ChromatinAssay): method for ChromatinAssay, ChromatinAssay
- precede(x = ANY, subject = Seurat): method for ANY, Seurat

- precede(x = Seurat, subject = ANY): method for Seurat, ANY
- precede(x = Seurat, subject = Seurat): method for Seurat, Seurat
- follow(x = ANY, subject = ChromatinAssay): method for ANY, ChromatinAssay
- follow(x = ChromatinAssay, subject = ANY): method for ChromatinAssay, ANY
- follow(x = ChromatinAssay, subject = ChromatinAssay): method for ChromatinAssay, ChromatinAssay
- follow(x = ANY, subject = Seurat): method for ANY, Seurat
- follow(x = Seurat, subject = ANY): method for Seurat, ANY
- follow(x = Seurat, subject = Seurat): method for Seurat, Seurat
- nearest(x = ANY, subject = ChromatinAssay): method for ANY, ChromatinAssay
- nearest(x = ChromatinAssay, subject = ANY): method for ChromatinAssay, ANY
- nearest(x = ChromatinAssay, subject = ChromatinAssay): method for ChromatinAssay, ChromatinAssay
- nearest(x = ANY, subject = Seurat): method for ANY, Seurat
- nearest(x = Seurat, subject = ANY): method for Seurat, ANY
- nearest(x = Seurat, subject = Seurat): method for Seurat, Seurat
- distance(x = ANY, y = ChromatinAssay): method for ANY, ChromatinAssay
- distance(x = ChromatinAssay, y = ANY): method for ChromatinAssay, ANY
- distance(x = ChromatinAssay, y = ChromatinAssay): method for ChromatinAssay, ChromatinAssay
- distance(x = ANY, y = Seurat): method for ANY, Seurat
- distance(x = Seurat, y = ANY): method for Seurat, ANY
- distance(x = Seurat, y = Seurat): method for Seurat, Seurat
- distanceToNearest(x = ANY, subject = ChromatinAssay): method for ANY, ChromatinAssay
- distanceToNearest(x = ChromatinAssay, subject = ANY): method for ChromatinAssay, ANY
- distanceToNearest(x = ChromatinAssay, subject = ChromatinAssay): method for ChromatinAssay, ChromatinAssay
- distanceToNearest(x = ANY, subject = Seurat): method for ANY, Seurat
- distanceToNearest(x = Seurat, subject = ANY): method for Seurat, ANY
- distanceToNearest(x = Seurat, subject = Seurat): method for Seurat, Seurat

See Also

- nearest-methods in the **IRanges** package.
- nearest-methods in the **GenomicRanges** package
- ChromatinAssay

NucleosomeSignal *NucleosomeSignal*

Description

Calculate the strength of the nucleosome signal per cell. Computes the ratio of fragments between 147 bp and 294 bp (mononucleosome) to fragments < 147 bp (nucleosome-free)

Usage

```
NucleosomeSignal(
  object,
  assay = NULL,
  n = ncol(object) * 5000,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat object
assay	Name of assay to use. Only required if a fragment path is not provided. If NULL, use the active assay.
n	Number of lines to read from the fragment file. If NULL, read all lines. Default scales with the number of cells in the object.
verbose	Display messages
...	Arguments passed to other functions

Value

Returns a SeuratObject::Seurat() object with added metadata for the ratio of mononucleosomal to nucleosome-free fragments per cell, and the percentile rank of each ratio.

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package = "Signac")
Fragments(atac_small) <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  tolerance = 0.5
)
NucleosomeSignal(object = atac_small)
```

PeakPlot *Plot peaks in a genomic region*

Description

Display the genomic ranges in a ChromatinAssay() object that fall in a given genomic region

Usage

```
PeakPlot(
  object,
  region,
  assay = NULL,
  peaks = NULL,
  group.by = NULL,
  color = "dimgrey",
  sep = c("-", "-"),
  extend.upstream = 0,
  extend.downstream = 0
)
```

Arguments

object	A SeuratObject::Seurat() object
region	A genomic region to plot
assay	Name of assay to use. If NULL, use the default assay.
peaks	A GRanges object containing peak coordinates. If NULL, use coordinates stored in the Seurat object.
group.by	Name of variable in feature metadata (if using ranges in the Seurat object) or genomic ranges metadata (if using supplied ranges) to color ranges by. If NULL, do not color by any metadata variable.
color	Color to use. If group.by is not NULL, this can be a custom color scale (see examples).
sep	Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.
extend.upstream	Number of bases to extend the region upstream.
extend.downstream	Number of bases to extend the region downstream.

Value

Returns a ggplot2::ggplot() object

Examples

```
# plot peaks in assay
PeakPlot(atac_small, region = "chr1-710000-715000")

# manually set color
PeakPlot(atac_small, region = "chr1-710000-715000", color = "red")

# color by a variable in the feature metadata
PeakPlot(atac_small, region = "chr1-710000-715000", group.by = "count")
```

PearsonResidualVar *Compute analytic Pearson residual variance*

Description

Find the top features for a given assay based on analytic Pearson residual variance. This function computes the Pearson residual variance for each feature without constructing the entire dense matrix of Pearson residuals to reduce the memory required.

Usage

```
PearsonResidualVar(object, ...)

## Default S3 method:
PearsonResidualVar(
  object,
  assay = NULL,
  nfeatures = 20000,
  min.counts = 100,
  ncell.batch = 100,
  theta = 10,
  verbose = TRUE,
  ...
)

## S3 method for class 'Assay'
PearsonResidualVar(
  object,
  assay = NULL,
  nfeatures = 20000,
  theta = 10,
  min.counts = 100,
  weight.mean = 0,
  ncell.batch = 100,
  verbose = TRUE,
  ...
```

```
)

## S3 method for class 'StdAssay'
PearsonResidualVar(
  object,
  assay = NULL,
  min.counts = 100,
  weight.mean = 0,
  theta = 10,
  ncell.batch = 100,
  verbose = TRUE,
  ...
)

## S3 method for class 'Seurat'
PearsonResidualVar(
  object,
  assay = NULL,
  min.counts = 100,
  weight.mean = 0,
  theta = 10,
  ncell.batch = 100,
  verbose = TRUE,
  ...
)
```

Arguments

`object`	A Seurat object
`...`	Arguments passed to other methods
`assay`	Name of assay to use
`nfeatures`	Number of top features to set as the variable features
`min.counts`	Minimum number of counts for feature to be eligible for variable features
`ncell.batch`	Number of cells to process in each batch. Higher number increases speed but uses more memory.
`theta`	Theta value for analytic Pearson residual calculation
`verbose`	Display messages
`weight.mean`	Weighting to apply to the feature mean relative to the Pearson residual variance for ranking features. `weight.mean=0` will rank features based on the Pearson residual variance only.

Value

Returns a `SeuratObject::Seurat()` object

References

Lause, J., Berens, P. & Kobak, D. Analytic Pearson residuals for normalization of single-cell RNA-seq UMI data. Genome Biol 22, 258 (2021). doi:10.1186/s13059021024517

Examples

```
PearsonResidualVar(object = atac_small[["peaks"]]["counts"])
PearsonResidualVar(object = atac_small[["peaks"]])
PearsonResidualVar(object = atac_small[["peaks"]])
PearsonResidualVar(atac_small)
```

PlotFootprint *Plot motif footprinting results*

Description

Plot motif footprinting results

Usage

```
PlotFootprint(
  object,
  features,
  assay = NULL,
  group.by = NULL,
  split.by = NULL,
  idents = NULL,
  label = TRUE,
  repel = TRUE,
  show.expected = TRUE,
  normalization = "subtract",
  label.top = 3,
  label.idents = NULL
)
```

Arguments

object	A Seurat object
features	A vector of features to plot
assay	Name of assay to use
group.by	A grouping variable
split.by	A metadata variable to split the plot by. For example, grouping by "celltype" and splitting by "batch" will create separate plots for each celltype and batch.
idents	Set of identities to include in the plot
label	TRUE/FALSE value to control whether groups are labeled.

repel	Repel labels from each other
show.expected	Plot the expected Tn5 integration frequency below the main footprint plot
normalization	Method to normalize for Tn5 DNA sequence bias. Options are "subtract", "divide", or NULL to perform no bias correction.
label.top	Number of groups to label based on highest accessibility in motif flanking region.
label.idents	Vector of identities to label. If supplied, label.top will be ignored.

ReadMGATK *Read MGATK output*

Description

Read output files from MGATK (https://github.com/caleblareau/mgatk).

Usage

```
ReadMGATK(dir, verbose = TRUE)
```

Arguments

dir	Path to directory containing MGATK output files
verbose	Display messages

Value

Returns a list containing a sparse matrix (counts) and two dataframes (depth and refallele).

The sparse matrix contains read counts for each base at each position and strand.

The depth dataframe contains the total depth for each cell. The refallele dataframe contains the reference genome allele at each position.

Examples

```
## Not run:
data.dir <- system.file("extdata", "test_mgatk", package="Signac")
mgatk <- ReadMGATK(dir = data.dir)

## End(Not run)
```

RegionHeatmap *Region heatmap*

Description

Plot fragment counts within a set of regions.

Usage

```
RegionHeatmap(
  object,
  key,
  assay = NULL,
  idents = NULL,
  group.order = NULL,
  normalize = TRUE,
  upstream = 3000,
  downstream = 3000,
  max.cutoff = "q95",
  cols = NULL,
  min.counts = 1,
  window = (upstream + downstream)/30,
  order = TRUE,
  nrow = NULL
)
```

Arguments

object	A Seurat object
key	Name of key to pull data from. Stores the results from RegionMatrix()
assay	Name of assay to use. If a list or vector of assay names is given, data will be plotted from each assay. Note that all assays must contain RegionMatrix results with the same key. Sorting will be defined by the first assay in the list
idents	Cell identities to include. Note that cells cannot be regrouped, this will require re-running RegionMatrix to generate a new set of matrices
group.order	Order of groups to be shown in the plot. This should be a character vector. If NULL, the group order will not be changed.
normalize	Normalize by number of cells in each group
upstream	Number of bases to include upstream of region. If NULL, use all bases that were included in the RegionMatrix function call. Note that this value cannot be larger than the value for upstream given in the original RegionMatrix function call. If NULL, use parameters that were given in the RegionMatrix function call
downstream	Number of bases to include downstream of region. See documentation for upstream

max.cutoff	Maximum cutoff value. Data above this value will be clipped to the maximum value. A quantile maximum can be specified in the form of "q##" where "##" is the quantile (eg, "q90" for 90th quantile). If NULL, no cutoff will be set
cols	Vector of colors to use as the maximum value of the color scale. One color must be supplied for each assay. If NULL, the default ggplot2 colors are used.
min.counts	Minimum total counts to display region in plot
window	Smoothing window to apply
order	Order regions by the total number of fragments in the region across all included identities
nrow	Number of rows to use when creating plot. If NULL, chosen automatically by ggplot2

Value

Returns a ggplot2 object

See Also

RegionMatrix

RegionMatrix *Region enrichment analysis*

Description

Count fragments within a set of regions for different groups of cells.

Usage

```
RegionMatrix(object, ...)

## S3 method for class 'Seurat'
RegionMatrix(
  object,
  regions,
  key,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  upstream = 3000,
  downstream = 3000,
  verbose = TRUE,
  ...
)

## S3 method for class 'ChromatinAssay'
```

```
RegionMatrix(
  object,
  regions,
  key,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  upstream = 3000,
  downstream = 3000,
  verbose = TRUE,
  ...
)

## Default S3 method:
RegionMatrix(
  object,
  regions,
  key,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  upstream = 3000,
  downstream = 3000,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat or ChromatinAssay object
...	Arguments passed to other methods
regions	A GenomicRanges::GRanges() object containing the set of genomic ranges to quantify
key	Name to store resulting matrices under
assay	Name of assay to use. If NULL, use the default assay
group.by	Grouping variable to use when aggregating data across cells. If NULL, use the active cell identities
idents	Cell identities to include. If NULL, include all identities
upstream	Number of bases to extend regions upstream
downstream	Number of bases to extend regions downstream
verbose	Display messages

Value

Returns a SeuratObject::Seurat() object

RegionPlot *Region plot*

Description

Plot fragment counts within a set of regions.

Usage

```
RegionPlot(
  object,
  key,
  assay = NULL,
  idents = NULL,
  group.order = NULL,
  normalize = TRUE,
  upstream = NULL,
  downstream = NULL,
  window = (upstream + downstream)/500,
  nrow = NULL
)
```

Arguments

object	A Seurat object
key	Name of key to pull data from. Stores the results from RegionMatrix()
assay	Name of assay to use. If a list or vector of assay names is given, data will be plotted from each assay. Note that all assays must contain RegionMatrix results with the same key. Sorting will be defined by the first assay in the list
idents	Cell identities to include. Note that cells cannot be regrouped, this will require re-running RegionMatrix to generate a new set of matrices
group.order	Order of groups to be shown in the plot. This should be a character vector. If NULL, the group order will not be changed.
normalize	Normalize by number of cells in each group
upstream	Number of bases to include upstream of region. If NULL, use all bases that were included in the RegionMatrix function call. Note that this value cannot be larger than the value for upstream given in the original RegionMatrix function call. If NULL, use parameters that were given in the RegionMatrix function call
downstream	Number of bases to include downstream of region. See documentation for upstream
window	Smoothing window to apply
nrow	Number of rows to use when creating plot. If NULL, chosen automatically by ggplot2

Value

Returns a ggplot2 object

See Also

RegionMatrix

`RegionStats` *Compute base composition information for genomic ranges*

Description

Compute the GC content, region lengths, and dinucleotide base frequencies for regions in the assay and add to the feature metadata.

Usage

```
RegionStats(object, ...)

## Default S3 method:
RegionStats(object, genome, verbose = TRUE, ...)

## S3 method for class 'ChromatinAssay'
RegionStats(object, genome, verbose = TRUE, ...)

## S3 method for class 'Seurat'
RegionStats(object, genome, assay = NULL, verbose = TRUE, ...)
```

Arguments

`object`	A Seurat object, Assay object, or set of genomic ranges
`...`	Arguments passed to other methods
`genome`	A `BSgenome` object or any other object supported by `getSeq`. Do `showMethods("getSeq")` to get the list of all supported object types.
`verbose`	Display messages
`assay`	Name of assay to use

Value

Returns a dataframe

Examples

```
## Not run:
library(BSgenome.Hsapiens.UCSC.hg19)
RegionStats(
  object = rownames(atac_small),
  genome = BSgenome.Hsapiens.UCSC.hg19
)

## End(Not run)
## Not run:
library(BSgenome.Hsapiens.UCSC.hg19)
RegionStats(
  object = atac_small[["peaks"]],
  genome = BSgenome.Hsapiens.UCSC.hg19
)

## End(Not run)
## Not run:
library(BSgenome.Hsapiens.UCSC.hg19)
RegionStats(
  object = atac_small,
  assay = "bins",
  genome = BSgenome.Hsapiens.UCSC.hg19
)

## End(Not run)
```

RunSVD *Run singular value decomposition*

Description

Run partial singular value decomposition using RSpectra::svds

Usage

```
RunSVD(object, ...)

## Default S3 method:
RunSVD(
  object,
  assay = NULL,
  n = 50,
  scale.embeddings = !pca,
  pca = FALSE,
  reduction.key = ifelse(pca, "PCA_", "LSI_"),
  scale.max = NULL,
  verbose = TRUE,
```

```
  tol = 1e-05,
  ...
)

## S3 method for class 'Assay'
RunSVD(
  object,
  assay = NULL,
  features = NULL,
  pca = FALSE,
  n = 50,
  reduction.key = ifelse(pca, "PCA_", "LSI_"),
  scale.max = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'StdAssay'
RunSVD(
  object,
  assay = NULL,
  features = NULL,
  pca = FALSE,
  n = 50,
  reduction.key = ifelse(pca, "PCA_", "LSI_"),
  scale.max = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'Seurat'
RunSVD(
  object,
  assay = NULL,
  features = NULL,
  layer = "data",
  n = 50,
  pca = FALSE,
  reduction.key = ifelse(pca, "PCA_", "LSI_"),
  reduction.name = ifelse(pca, "pca", "lsi"),
  scale.max = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

object	A Seurat object

...	Arguments passed to other methods
assay	Which assay to use. If NULL, use the default assay
n	Number of singular values to compute
scale.embeddings	Scale cell embeddings within each component to mean 0 and SD 1 (default TRUE).
pca	Run PCA. Setting this option to TRUE will perform implicit scaling and centering of the input matrix to enable memory-efficient computation of the principal components.
reduction.key	Key for dimension reduction object
scale.max	Clipping value for cell embeddings. Default (NULL) is no clipping.
verbose	Print messages
tol	Tolerance (tol) parameter for RSpectra::svds(). Larger values speed up convergence due to greater amount of allowed error.
features	Which features to use. If NULL, use variable features
layer	Name of layer to use.
reduction.name	Name for stored dimension reduction object.

Value

Returns a SeuratObject::Seurat() object

Examples

```
x <- matrix(data = rnorm(100), ncol = 10)
RunSVD(x)
## Not run:
RunSVD(atac_small[['peaks']])

## End(Not run)
## Not run:
RunSVD(atac_small[['peaks']])

## End(Not run)
RunSVD(atac_small, features = rownames(atac_small))
```

RunTFIDF *Compute the term-frequency inverse-document-frequency*

Description

Run term frequency inverse document frequency (TF-IDF) normalization on a matrix.

Usage

```
RunTFIDF(object, ...)

## Default S3 method:
RunTFIDF(
  object,
  assay = NULL,
  method = 1,
  scale.factor = 10000,
  idf = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'Assay'
RunTFIDF(
  object,
  assay = NULL,
  method = 1,
  scale.factor = 10000,
  idf = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'StdAssay'
RunTFIDF(
  object,
  assay = NULL,
  method = 1,
  scale.factor = 10000,
  idf = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'Seurat'
RunTFIDF(
  object,
  assay = NULL,
  method = 1,
  scale.factor = 10000,
  idf = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

`object`	A Seurat object
`...`	Arguments passed to other methods
`assay`	Name of assay to use
`method`	Which TF-IDF implementation to use. Choice of: • 1: The TF-IDF implementation used by Stuart & Butler et al. 2019 (doi:10.1101/460147). This computes $\log(TF \times IDF)$. • 2: The TF-IDF implementation used by Cusanovich & Hill et al. 2018 (doi:10.1016/j.cell.2018.06.052). This computes $TF \times (\log(IDF))$. • 3: The log-TF method used by Andrew Hill. This computes $\log(TF) \times \log(IDF)$. • 4: The 10x Genomics method (no TF normalization). This computes IDF.
`scale.factor`	Which scale factor to use. Default is 10000.
`idf`	A precomputed IDF vector to use. If NULL, compute based on the input data matrix.
`verbose`	Print progress

Details

Four different TF-IDF methods are implemented. We recommend using method 1 (the default).

Value

Returns a `SeuratObject::Seurat()` object

References

https://en.wikipedia.org/wiki/Latent_semantic_analysis#Latent_semantic_indexing

Examples

```
mat <- matrix(data = rbinom(n = 25, size = 5, prob = 0.2), nrow = 5)
RunTFIDF(object = mat)
RunTFIDF(atac_small[["peaks"]])
RunTFIDF(atac_small[["peaks"]])
RunTFIDF(object = atac_small)
```

seqinfo-methods *Access and modify sequence information for ChromatinAssay objects*

Description

Methods for accessing and modifying Seqinfo object information stored in a ChromatinAssay() object.

Usage

```
## S4 method for signature 'ChromatinAssay'
seqinfo(x)

## S4 replacement method for signature 'ChromatinAssay'
seqinfo(x) <- value

## S4 method for signature 'ChromatinAssay'
seqlevels(x)

## S4 replacement method for signature 'ChromatinAssay'
seqlevels(x) <- value

## S4 method for signature 'ChromatinAssay'
seqnames(x)

## S4 replacement method for signature 'ChromatinAssay'
seqnames(x) <- value

## S4 method for signature 'ChromatinAssay'
seqlengths(x)

## S4 replacement method for signature 'ChromatinAssay'
seqlengths(x) <- value

## S4 method for signature 'ChromatinAssay'
genome(x)

## S4 replacement method for signature 'ChromatinAssay'
genome(x) <- value

## S4 method for signature 'ChromatinAssay'
isCircular(x)

## S4 replacement method for signature 'ChromatinAssay'
isCircular(x) <- value

## S4 method for signature 'Seurat'
```

```
seqinfo(x)

## S4 replacement method for signature 'Seurat'
seqinfo(x) <- value

## S4 method for signature 'Seurat'
seqlevels(x)

## S4 replacement method for signature 'Seurat'
seqlevels(x) <- value

## S4 method for signature 'Seurat'
seqnames(x)

## S4 replacement method for signature 'Seurat'
seqnames(x) <- value

## S4 method for signature 'Seurat'
seqlengths(x)

## S4 replacement method for signature 'Seurat'
seqlengths(x) <- value

## S4 method for signature 'Seurat'
genome(x)

## S4 replacement method for signature 'Seurat'
genome(x) <- value

## S4 method for signature 'Seurat'
isCircular(x)

## S4 replacement method for signature 'Seurat'
isCircular(x) <- value
```

Arguments

x	A ChromatinAssay() object
value	A Seqinfo object or name of a UCSC genome to store in the ChromatinAssay()

Functions

- seqinfo(ChromatinAssay) <- value: set method for ChromatinAssay objects
- seqlevels(ChromatinAssay): get method for ChromatinAssay objects
- seqlevels(ChromatinAssay) <- value: set method for ChromatinAssay objects
- seqnames(ChromatinAssay): get method for ChromatinAssay objects
- seqnames(ChromatinAssay) <- value: set method for ChromatinAssay objects

- `seqlengths(ChromatinAssay)`: get method for ChromatinAssay objects
- `seqlengths(ChromatinAssay) <- value`: set method for ChromatinAssay objects
- `genome(ChromatinAssay)`: get method for ChromatinAssay objects
- `genome(ChromatinAssay) <- value`: set method for ChromatinAssay objects
- `isCircular(ChromatinAssay)`: get method for ChromatinAssay objects
- `isCircular(ChromatinAssay) <- value`: set method for ChromatinAssay objects
- `seqinfo(Seurat)`: get method for Seurat objects
- `seqinfo(Seurat) <- value`: set method for Seurat objects
- `seqlevels(Seurat)`: get method for Seurat objects
- `seqlevels(Seurat) <- value`: set method for Seurat objects
- `seqnames(Seurat)`: get method for Seurat objects
- `seqnames(Seurat) <- value`: set method for Seurat objects
- `seqlengths(Seurat)`: get method for Seurat objects
- `seqlengths(Seurat) <- value`: set method for Seurat objects
- `genome(Seurat)`: get method for Seurat objects
- `genome(Seurat) <- value`: set method for Seurat objects
- `isCircular(Seurat)`: get method for Seurat objects
- `isCircular(Seurat) <- value`: set method for Seurat objects

See Also

- seqinfo in the **GenomeInfoDb** package.
- ChromatinAssay

`SetMotifData` *Set motif data*

Description

Set motif matrix for given assay

Usage

```
SetMotifData(object, ...)

## S3 method for class 'Motif'
SetMotifData(object, slot, new.data, ...)

## S3 method for class 'ChromatinAssay'
SetMotifData(object, slot, new.data, ...)

## S3 method for class 'Seurat'
SetMotifData(object, assay = NULL, ...)
```

Arguments

object	A Seurat object
...	Arguments passed to other methods
slot	Name of slot to use
new.data	motif matrix to add. Should be matrix or sparse matrix class
assay	Name of assay whose data should be set

Value

Returns a SeuratObject::Seurat() object

Examples

```
motif.obj <- SeuratObject::GetAssayData(
  object = atac_small[['peaks']], slot = "motifs"
)
SetMotifData(object = motif.obj, slot = 'data', new.data = matrix(1:2))
new.data <- matrix(sample(c(0, 1), size = nrow(atac_small[["peaks"]]) * 10,
                   replace = TRUE), nrow = nrow(atac_small[["peaks"]]))
rownames(new.data) <- rownames(atac_small[["peaks"]])
SetMotifData(
  object = atac_small[['peaks']], slot = 'data', new.data = new.data
)
motif.matrix <- GetMotifData(object = atac_small)
SetMotifData(
object = atac_small, assay = 'peaks', slot = 'data', new.data = motif.matrix
)
```

SortIdents *Sorts cell metadata variable by similarity using hierarchical clustering*

Description

Compute distance matrix from a feature/variable matrix and perform hierarchical clustering to order variables (for example, cell types) according to their similarity.

Usage

```
SortIdents(
  object,
  layer = "data",
  assay = NULL,
  label = NULL,
  dendrogram = FALSE,
  method = "euclidean",
  verbose = TRUE
)
```

Arguments

object	A Seurat object containing single-cell data.
layer	The layer of the data to use (default is "data").
assay	Name of assay to use. If NULL, use the default assay
label	Metadata attribute to sort. If NULL, uses the active identities.
dendrogram	Logical, whether to plot the dendrogram (default is FALSE).
method	The distance method to use for hierarchical clustering (default is 'euclidean', other options from stats::dist() are 'maximum', 'manhattan', 'canberra', 'binary' and 'minkowski').
verbose	Display messages

Value

The Seurat object with metadata variable reordered by similarity. If the metadata variable was a character vector, it will be converted to a factor and the factor levels set according to the similarity ordering. If active identities were used (label=NULL), the levels will be updated according to similarity ordering.

Examples

```
atac_small$test <- sample(1:10, ncol(atac_small), replace = TRUE)
atac_small <- SortIdents(object = atac_small, label = 'test')
print(levels(atac_small$test))
```

SplitFragments *Split fragment file by cell identities*

Description

Splits a fragment file into separate files for each group of cells. If splitting multiple fragment files containing common cell types, fragments originating from different files will be appended to the same file for one group of cell identities.

Usage

```
SplitFragments(
  object,
  assay = NULL,
  group.by = NULL,
  idents = NULL,
  outdir = getwd(),
  file.suffix = "",
  append = TRUE,
  buffer_length = 256L,
  verbose = TRUE
)
```

Arguments

object	A Seurat object
assay	Name of assay to use
group.by	Name of grouping variable to group cells by
idents	List of identities to include
outdir	Directory to write output files
file.suffix	Suffix to add to all file names (before file extension). If splitting multiple fragment files without the append option set to TRUE, an additional numeric suffix will be added to each file (eg, .1, .2).
append	If splitting multiple fragment files, append cells from the same group (eg cluster) to the same file. Note that this can cause the output file to be unsorted.
buffer_length	Size of buffer to be read from the fragment file. This must be longer than the longest line in the file.
verbose	Display messages

StringToGRanges *String to GRanges*

Description

[Deprecated]

Usage

```
StringToGRanges(regions, sep = c("-", "-"), ...)
```

Arguments

regions	Vector of genomic region strings
sep	Vector of separators to use for genomic string. First element is used to separate chromosome and coordinates, second separator is used to separate start and end coordinates.
...	Additional arguments passed to GenomicRanges::makeGRangesFromDataFrame()

Details

Convert a genomic coordinate string to a GRanges object

Value

Returns a GRanges object

Examples

```
regions <- c('chr1-1-10', 'chr2-12-3121')
StringToGRanges(regions = regions)
```

subset.Fragment *Subset a Fragment object*

Description

Returns a subset of a `Fragment-class()` object.

Usage

```
## S3 method for class 'Fragment'
subset(x, cells = NULL, ...)
```

Arguments

x	A Fragment object
cells	Vector of cells to retain
...	Arguments passed to other methods

Value

Returns a subsetted `Fragment()` object

See Also

`base::subset()`

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
cells <- colnames(x = atac_small)
names(x = cells) <- paste0("test_", cells)
frags <- CreateFragmentObject(path = fpath, cells = cells, verbose = FALSE, tolerance = 0.5)
subset(frags, head(names(cells)))
```

subset.Motif *Subset a Motif object*

Description

Returns a subset of a `Motif-class()` object.

Usage

```
## S3 method for class 'Motif'
subset(x, features = NULL, motifs = NULL, ...)

## S3 method for class 'Motif'
x[i, j, ...]
```

Arguments

x	A Motif object
features	Which features to retain
motifs	Which motifs to retain
...	Arguments passed to other methods
i	Which columns to retain
j	Which rows to retain

Value

Returns a subsetted Motif() object

See Also

base::subset()

Examples

```
motif.obj <- SeuratObject::GetAssayData(
  object = atac_small[['peaks']], layer = "motifs"
)
subset(x = motif.obj, features = head(rownames(motif.obj), 10))
motif.obj <- SeuratObject::GetAssayData(
  object = atac_small, assay = 'peaks', layer = 'motifs'
)
motif.obj[1:10,1:10]
```

SubsetMatrix *Subset matrix rows and columns*

Description

Subset the rows and columns of a matrix by removing rows and columns with less than the specified number of non-zero elements.

Usage

```
SubsetMatrix(
  mat,
  min.rows = 1,
  min.cols = 1,
  max.row.val = 10,
  max.col.val = NULL
)
```

Arguments

mat	A matrix
min.rows	Minimum number of non-zero elements for the row to be retained
min.cols	Minimum number of non-zero elements for the column to be retained
max.row.val	Maximum allowed value in a row for the row to be retained. If NULL, don't set any limit.
max.col.val	Maximum allowed value in a column for the column to be retained. If NULL, don't set any limit.

Value

Returns a matrix

Examples

```
SubsetMatrix(mat = volcano)
```

---

theme_browser *Genome browser theme*

Description

Theme applied to panels in the `CoveragePlot()` function.

Usage

```
theme_browser(..., legend = TRUE, axis.text.y = FALSE)
```

Arguments

...	Additional arguments
legend	Display plot legend
axis.text.y	Display y-axis text

Examples

```
PeakPlot(atac_small, region = "chr1-710000-715000") + theme_browser()
```

`TilePlot` *Plot integration sites per cell*

Description

Plots the presence/absence of Tn5 integration sites for each cell within a genomic region.

Usage

```
TilePlot(
  object,
  region,
  sep = c("-", "-"),
  tile.size = 100,
  tile.cells = 100,
  extend.upstream = 0,
  extend.downstream = 0,
  assay = NULL,
  cells = NULL,
  group.by = NULL,
  order.by = "total",
  idents = NULL
)
```

Arguments

`object`	A Seurat object
`region`	A set of genomic coordinates to show. Can be a GRanges object, a string encoding a genomic position, a gene name, or a vector of strings describing the genomic coordinates or gene names to plot. If a gene name is supplied, annotations must be present in the assay.
`sep`	Separators to use for strings encoding genomic coordinates. First element is used to separate the chromosome from the coordinates, second element is used to separate the start from end coordinate.
`tile.size`	Size of the sliding window for per-cell fragment tile plot
`tile.cells`	Number of cells to display fragment information for in tile plot.
`extend.upstream`	Number of bases to extend the region upstream.
`extend.downstream`	Number of bases to extend the region downstream.
`assay`	Name of assay to use
`cells`	Which cells to plot. Default all cells
`group.by`	Name of grouping variable to group cells by. If NULL, use the current cell identities

order.by	Option for determining how cells are chosen from each group. Options are "total" or "random". "total" will select the top cells based on total number of fragments in the region, "random" will select randomly.
idents	List of cell identities to include in the plot. If NULL, use all identities.

Value

Returns a ggplot2::ggplot() object

Examples

```
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
fragments <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  validate.fragments = FALSE
)
Fragments(atac_small) <- fragments
TilePlot(object = atac_small, region = c("chr1-713500-714500"))
```

TSSEnrichment *Compute TSS enrichment score per cell*

Description

Compute the transcription start site (TSS) enrichment score for each cell, as defined by ENCODE: https://www.encodeproject.org/data-standards/terms/.

Usage

```
TSSEnrichment(
  object,
  tss.positions = NULL,
  n = NULL,
  fast = TRUE,
  assay = NULL,
  cells = NULL,
  process_n = 2000,
  verbose = TRUE,
  region_extension = 1000
)
```

Arguments

object	A Seurat object
tss.positions	A GRanges object containing the TSS positions. If NULL, use the genomic annotations stored in the assay.

n	Number of TSS positions to use. This will select the first *n* TSSs from the set. If NULL, use all TSSs (slower).
fast	Just compute the TSS enrichment score, without storing the base-resolution matrix of integration counts at each site. This reduces the memory required to store the object but does not allow plotting the accessibility profile at the TSS.
assay	Name of assay to use
cells	A vector of cells to include. If NULL (default), use all cells in the object
process_n	Number of regions to process at a time if using `fast` option.
verbose	Display messages
region_extension	Distance extended upstream and downstream from TSS in which to calculate enrichment and background.

Details

The computed score will be added to the object metadata as "TSS.enrichment".

Value

Returns a `SeuratObject::Seurat()` object

Examples

```
## Not run:
fpath <- system.file("extdata", "fragments.tsv.gz", package="Signac")
Fragments(atac_small) <- CreateFragmentObject(
  path = fpath,
  cells = colnames(atac_small),
  tolerance = 0.5
)
TSSEnrichment(object = atac_small)

## End(Not run)
```

TSSPlot *Plot signal enrichment around TSSs*

Description

[Deprecated]

Usage

```
TSSPlot(object, assay = NULL, group.by = NULL, idents = NULL)
```

Arguments

object	A Seurat object
assay	Name of the assay to use. Should have the TSS enrichment information for each cell already computed by running TSSEnrichment()
group.by	Set of identities to group cells by
idents	Set of identities to include in the plot

Details

Plot the normalized TSS enrichment score at each position relative to the TSS. Requires that TSSEnrichment() has already been run on the assay.

Value

Returns a ggplot2::ggplot2() object

UnifyPeaks *Unify genomic ranges*

Description

Create a unified set of non-overlapping genomic ranges from multiple Seurat objects containing single-cell chromatin data.

Usage

```
UnifyPeaks(object.list, mode = "reduce")
```

Arguments

object.list	A list of Seurat objects or ChromatinAssay objects
mode	Function to use when combining genomic ranges. Can be "reduce" (default) or "disjoin". See GenomicRanges::reduce() and GenomicRanges::disjoin() for more information on these functions. **[Deprecated]**

Value

Returns a GRanges object

Examples

```
UnifyPeaks(object.list = list(atac_small, atac_small))
```

UpdatePath *Update the file path for a Fragment object*

Description

Change the path to a fragment file store in a `Fragment()` object. Path must be to the same file that was used to create the fragment object. An MD5 hash will be computed using the new path and compared to the hash stored in the Fragment object to verify that the files are the same.

Usage

```
UpdatePath(object, new.path, verbose = TRUE)
```

Arguments

`object`	A `Fragment()` object
`new.path`	Path to the fragment file
`verbose`	Display messages

ValidateCells *Validate cells present in fragment file*

Description

Search for a fragment from each cell that should exist in the fragment file. Will iterate through chunks of the fragment file until at least one fragment from each cell barcode requested is found.

Usage

```
ValidateCells(
  object,
  cells = NULL,
  tolerance = 0.5,
  max.lines = 5e+07,
  verbose = TRUE
)
```

Arguments

`object`	A `Fragment()` object
`cells`	A character vector containing cell barcodes to search for. If NULL, use the cells stored in the Fragment object.

tolerance	Fraction of input cells that can be unseen before returning TRUE. For example, tolerance = 0.01 will return TRUE when 99% of cells have observed fragments in the file. This can be useful if there are cells present that have much fewer total counts, and would require extensive searching before a fragment from those cells are found.
max.lines	Maximum number of lines to read in without finding the required number of cells before returning FALSE. Setting this value avoids having to search the whole file if it becomes clear that the expected cells are not present. Setting this value to NULL will enable an exhaustive search of the entire file.
verbose	Display messages

ValidateFragments *Validate Fragment object*

Description

Verify that the cells listed in the object exist in the fragment file and that the fragment file or index have not changed since creating the fragment object.

Usage

```
ValidateFragments(object, verbose = TRUE, ...)
```

Arguments

object	A Fragment() object
verbose	Display messages
...	Additional parameters passed to ValidateCells()

ValidateHash *Validate hashes for Fragment object*

Description

Validate hashes for Fragment object

Usage

```
ValidateHash(object, verbose = TRUE)
```

Arguments

object	A Fragment() object
verbose	Display messages

`VariantPlot` *Plot strand concordance vs. VMR*

Description

Plot the Pearson correlation between allele frequencies on each strand versus the log10 mean-variance ratio for the allele.

Usage

```
VariantPlot(
  variants,
  min.cells = 2,
  concordance.threshold = 0.65,
  vmr.threshold = 0.01
)
```

Arguments

`variants`	A dataframe containing variant information. This should be computed using `IdentifyVariants()`
`min.cells`	Minimum number of high-confidence cells detected with the variant for the variant to be displayed.
`concordance.threshold`	Strand concordance threshold
`vmr.threshold`	Mean-variance ratio threshold

Index

∗ **assay**
Annotation, 9
as.ChromatinAssay, 11
Cells<-, 24
ChromatinAssay-class, 25
CreateChromatinAssay, 38
Fragments, 62
GetFragmentData, 68
Links, 83
Motifs, 87
∗ **coverage**
coverage,ChromatinAssay-method, 31
∗ **datasets**
atac_small, 12
blacklist_ce10, 17
blacklist_ce11, 17
blacklist_dm3, 18
blacklist_dm6, 18
blacklist_hg19, 19
blacklist_hg38, 19
blacklist_hg38_unified, 20
blacklist_mm10, 20
∗ **data**
atac_small, 12
blacklist_ce10, 17
blacklist_ce11, 17
blacklist_dm3, 18
blacklist_dm6, 18
blacklist_hg19, 19
blacklist_hg38, 19
blacklist_hg38_unified, 20
blacklist_mm10, 20
∗ **dimension_reduction**
Jaccard, 80
RunSVD, 103
∗ **footprinting**
Footprint, 58
GetFootprintData, 67
InsertionBias, 76
PlotFootprint, 96
∗ **fragments**
Cells.Fragment, 24
CountFragments, 30
CreateFragmentObject, 39
FilterCells, 48
Fragment-class, 61
Fragments, 62
head.Fragment, 74
SplitFragments, 112
subset.Fragment, 114
UpdatePath, 121
ValidateCells, 121
ValidateFragments, 122
ValidateHash, 122
∗ **granges**
granges-methods, 72
∗ **heatmap**
RegionHeatmap, 98
RegionMatrix, 99
RegionPlot, 101
∗ **inter_range**
inter-range-methods, 77
∗ **links**
ConnectionsToLinks, 28
GetLinkedGenes, 70
GetLinkedPeaks, 70
LinkPeaks, 80
LinkPlot, 82
Links, 83
∗ **mito**
AlleleFreq, 8
ClusterClonotypes, 27
FindClonotypes, 49
IdentifyVariants, 74
ReadMGATK, 97
VariantPlot, 123
∗ **motifs**
AddMotifs, 5

ConvertMotifID, 29
CreateMotifMatrix, 40
CreateMotifObject, 42
FindMotifs, 50
GetMotifData, 71
MatchRegionStats, 84
Motif-class, 85
MotifCounts, 86
MotifPlot, 87
Motifs, 87
RegionStats, 102
SetMotifData, 110
subset.Motif, 114
* **nearest**
nearest-methods, 88
* **overlaps**
findOverlaps-methods, 51
* **preprocessing**
BinarizeCounts, 16
CreateMotifMatrix, 40
DownsampleFeatures, 44
FindTopFeatures, 55
FitMeanVar, 56
PearsonResidualVar, 94
RunTFIDF, 105
UnifyPeaks, 120
* **qc**
ATACqc, 12
FragmentHistogram, 61
FRiP, 63
NucleosomeSignal, 92
TSSEnrichment, 118
TSSPlot, 119
* **quantification**
AggregateTiles, 6
CallPeaks, 21
FeatureMatrix, 47
GenomeBinMatrix, 65
* **seqinfo**
seqinfo-methods, 108
* **utilities**
AccessiblePeaks, 5
AverageCounts, 13
CellsPerGroup, 25
ClosestFeature, 26
CountsInRegion, 31
EnrichedTerms, 45
Extend, 46
FractionCountsInRegion, 60
GeneActivity, 64
GetCellsInRegion, 66
GetGRangesFromEnsDb, 68
GetIntersectingFeatures, 69
GetTSSPositions, 72
GRangesToString, 73
IntersectMatrix, 79
LookupGeneCoords, 84
MatchRegionStats, 84
SortIdents, 111
StringToGRanges, 113
SubsetMatrix, 115
UnifyPeaks, 120
* **visualization**
AnnotationPlot, 10
BigwigTrack, 14
CombineTracks, 27
CoverageBrowser, 33
CoveragePlot, 33
DensityScatter, 43
DepthCor, 43
ExpressionPlot, 46
FragmentHistogram, 61
LinkPlot, 82
MotifPlot, 87
PeakPlot, 93
PlotFootprint, 96
RegionHeatmap, 98
RegionPlot, 101
theme_browser, 116
TilePlot, 117
TSSPlot, 119
VariantPlot, 123
[.Motif *(*subset.Motif*)*, 114

AccessiblePeaks, 5
AddMotifs, 5
AggregateTiles, 6
AlleleFreq, 8
Annotation, 9
Annotation<- *(*Annotation*)*, 9
AnnotationPlot, 10
as.ChromatinAssay, 11
atac_small, 12
ATACqc, 12
AverageCounts, 13

base::sample(), *85*

base::subset(), *114, 115*
base::tempdir(), *23*
BigwigTrack, 14
BinarizeCounts, 16
biovizBase::crunch(), *68*
blacklist_ce10, 17
blacklist_ce11, 17
blacklist_dm3, 18
blacklist_dm6, 18
blacklist_hg19, 19
blacklist_hg38, 19
blacklist_hg38_unified, 20
blacklist_mm10, 20

CallPeaks, 21
Cells.Fragment, 24
Cells<-, 24
Cells<-.Fragment *(*Cells.Fragment*)*, 24
CellsPerGroup, 25
ChromatinAssay, *32*, *54*, *73*, *78*, *91*, *110*
ChromatinAssay *(*ChromatinAssay-class*)*, 25
ChromatinAssay(), *8*, *11*, *24*, *31, 32*, *38*, *51*, *54*, *72, 73*, *77, 78*, *88*, *90*, *93*, *108, 109*
ChromatinAssay-class, 25
ClosestFeature, 26
ClusterClonotypes, 27
CombineTracks, 27
ConnectionsToLinks, 28
ConvertMotifID, 29
CountFragments, 30
CountFragments(), *63*
countOverlaps *(*findOverlaps-methods*)*, 51
countOverlaps,ChromatinAssay,ChromatinAssay-method *(*findOverlaps-methods*)*, 51
countOverlaps,ChromatinAssay,Vector-method *(*findOverlaps-methods*)*, 51
countOverlaps,Seurat,Seurat-method *(*findOverlaps-methods*)*, 51
countOverlaps,Seurat,Vector-method *(*findOverlaps-methods*)*, 51
countOverlaps,Vector,ChromatinAssay-method *(*findOverlaps-methods*)*, 51
countOverlaps,Vector,Seurat-method *(*findOverlaps-methods*)*, 51
CountsInRegion, 31
CountsInRegion(), *60*
coverage *(*coverage,ChromatinAssay-method*)*, 31
coverage,ChromatinAssay-method, 31
coverage,Seurat-method *(*coverage,ChromatinAssay-method*)*, 31
coverage-methods, *32*
CoverageBrowser, 33
CoveragePlot, 33
CoveragePlot(), *33*, *116*
CreateChromatinAssay, 38
CreateFragmentObject, 39
CreateFragmentObject(), *39*
CreateMotifMatrix, 40
CreateMotifObject, 42

DensityScatter, 43
DepthCor, 43
disjoin *(*inter-range-methods*)*, 77
disjoin,ChromatinAssay-method *(*inter-range-methods*)*, 77
disjoin,Seurat-method *(*inter-range-methods*)*, 77
disjointBins *(*inter-range-methods*)*, 77
disjointBins,ChromatinAssay-method *(*inter-range-methods*)*, 77
disjointBins,Seurat-method *(*inter-range-methods*)*, 77
distance *(*nearest-methods*)*, 88
distance,ANY,ChromatinAssay-method *(*nearest-methods*)*, 88
distance,ANY,Seurat-method *(*nearest-methods*)*, 88
distance,ChromatinAssay,ANY-method *(*nearest-methods*)*, 88
distance,ChromatinAssay,ChromatinAssay-method *(*nearest-methods*)*, 88
distance,Seurat,ANY-method *(*nearest-methods*)*, 88
distance,Seurat,Seurat-method *(*nearest-methods*)*, 88
distanceToNearest *(*nearest-methods*)*, 88
distanceToNearest,ANY,ChromatinAssay-method *(*nearest-methods*)*, 88
distanceToNearest,ANY,Seurat-method *(*nearest-methods*)*, 88
distanceToNearest,ChromatinAssay,ANY-method *(*nearest-methods*)*, 88

distanceToNearest,ChromatinAssay,ChromatinAssay-method (nearest-methods), 88
distanceToNearest,Seurat,ANY-method (nearest-methods), 88
distanceToNearest,Seurat,Seurat-method (nearest-methods), 88
DownsampleFeatures, 44

EnrichedTerms, 45
ExpressionPlot, 46
Extend, 46

FeatureMatrix, 47
FeatureMatrix(), *66*, *86*
fgsea::fgsea(), *45*
fgsea::fgseaSimple(), *45*
FilterCells, 48
FindClonotypes, 49
FindMotifs, 50
findOverlaps (findOverlaps-methods), 51
findOverlaps,ChromatinAssay,ChromatinAssay-method (findOverlaps-methods), 51
findOverlaps,ChromatinAssay,Vector-method (findOverlaps-methods), 51
findOverlaps,Seurat,Seurat-method (findOverlaps-methods), 51
findOverlaps,Seurat,Vector-method (findOverlaps-methods), 51
findOverlaps,Vector,ChromatinAssay-method (findOverlaps-methods), 51
findOverlaps,Vector,Seurat-method (findOverlaps-methods), 51
findOverlaps-methods, 51, *54*
FindTopFeatures, 55
FitMeanVar, 56
follow (nearest-methods), 88
follow,ANY,ChromatinAssay-method (nearest-methods), 88
follow,ANY,Seurat-method (nearest-methods), 88
follow,ChromatinAssay,ANY-method (nearest-methods), 88
follow,ChromatinAssay,ChromatinAssay-method (nearest-methods), 88
follow,Seurat,ANY-method (nearest-methods), 88
follow,Seurat,Seurat-method (nearest-methods), 88
Footprint, 58
FragmentCountsInRegion, 60
Fragment (Fragment-class), 61
Fragment(), *11*, *24*, *26*, *39*, *47*, *62*, *63*, *65*, *68*, *114*, *121*, *122*
Fragment-class, 61
FragmentHistogram, 61
Fragments, 62
Fragments(), *39*
Fragments<- (Fragments), 62
FRiP, 63

gaps (inter-range-methods), 77
gaps,ChromatinAssay-method (inter-range-methods), 77
gaps,Seurat-method (inter-range-methods), 77
GeneActivity, 64
genome (seqinfo-methods), 108
genome,ChromatinAssay-method (seqinfo-methods), 108
genome,Seurat-method (seqinfo-methods), 108
genome<-,ChromatinAssay-method (seqinfo-methods), 108
genome<-,Seurat-method (seqinfo-methods), 108
GenomeBinMatrix, 65
GenomicRanges::disjoin(), *120*
GenomicRanges::findOverlaps(), *54*
GenomicRanges::GRanges(), *9*, *13*, *24*, *26*, *29*, *39*, *47*, *72*, *73*, *83*, *90*, *100*
GenomicRanges::granges(), *82*
GenomicRanges::GRangesList(), *42*, *86*
GenomicRanges::makeGRangesFromDataFrame(), *113*
GenomicRanges::reduce(), *120*
GetCellsInRegion, 66
GetFootprintData, 67
GetFragmentData, 68
GetGRangesFromEnsDb, 68
GetIntersectingFeatures, 69
GetLinkedGenes, 70
GetLinkedPeaks, 70
GetMotifData, 71
GetTSSPositions, 72
ggplot2::ggplot(), *10*, *33*, *44*, *62*, *83*, *87*, *93*, *118*
ggplot2::ggplot2(), *120*
ggseqlogo::ggseqlogo(), *87*

granges, *73*
granges *(granges-methods)*, 72
granges,ChromatinAssay-method *(granges-methods)*, 72
granges,Seurat-method *(granges-methods)*, 72
granges-methods, 72
GRangesToString, 73

head.Fragment, 74

IdentifyVariants, 74
IdentifyVariants(), *123*
InsertionBias, 76
inter-range-methods, 77, *78*
IntersectMatrix, 79
IRanges::coverage(), *32*
IRanges::findOverlaps(), *31*, *79*
isCircular *(seqinfo-methods)*, 108
isCircular,ChromatinAssay-method *(seqinfo-methods)*, 108
isCircular,Seurat-method *(seqinfo-methods)*, 108
isCircular<-,ChromatinAssay-method *(seqinfo-methods)*, 108
isCircular<-,Seurat-method *(seqinfo-methods)*, 108
isDisjoint *(inter-range-methods)*, 77
isDisjoint,ChromatinAssay-method *(inter-range-methods)*, 77
isDisjoint,Seurat-method *(inter-range-methods)*, 77

Jaccard, 80

LinkPeaks, 80
LinkPlot, 82
Links, 83
Links(), *82*
Links<- *(Links)*, 83
LookupGeneCoords, 84

MatchRegionStats, 84
MatchRegionStats(), *50*
Motif *(Motif-class)*, 85
Motif(), *5*, *11*, *26*, *42*, *88*, *115*
Motif-class, 85
MotifCounts, 86
motifmatchr::matchMotifs(), *5*, *41*
MotifPlot, 87
Motifs, 87
Motifs<- *(Motifs)*, 87

nearest *(nearest-methods)*, 88
nearest,ANY,ChromatinAssay-method *(nearest-methods)*, 88
nearest,ANY,Seurat-method *(nearest-methods)*, 88
nearest,ChromatinAssay,ANY-method *(nearest-methods)*, 88
nearest,ChromatinAssay,ChromatinAssay-method *(nearest-methods)*, 88
nearest,Seurat,ANY-method *(nearest-methods)*, 88
nearest,Seurat,Seurat-method *(nearest-methods)*, 88
nearest-methods, 88, *91*
NucleosomeSignal, 92

patchwork::patchwork(), *37*
patchwork::wrap_plots(), *37*
PeakPlot, 93
PearsonResidualVar, 94
PlotFootprint, 96
precede *(nearest-methods)*, 88
precede,ANY,ChromatinAssay-method *(nearest-methods)*, 88
precede,ANY,Seurat-method *(nearest-methods)*, 88
precede,ChromatinAssay,ANY-method *(nearest-methods)*, 88
precede,ChromatinAssay,ChromatinAssay-method *(nearest-methods)*, 88
precede,Seurat,ANY-method *(nearest-methods)*, 88
precede,Seurat,Seurat-method *(nearest-methods)*, 88

range *(inter-range-methods)*, 77
range,ChromatinAssay-method *(inter-range-methods)*, 77
range,Seurat-method *(inter-range-methods)*, 77
ReadMGATK, 97
reduce *(inter-range-methods)*, 77
reduce,ChromatinAssay-method *(inter-range-methods)*, 77

reduce,Seurat-method
(inter-range-methods), 77
RegionHeatmap, 98
RegionMatrix, 99
RegionMatrix(), *98*, *101*
RegionPlot, 101
RegionStats, 102
RegionStats(), *5*, *50*
RSpectra::svds, *103*
RSpectra::svds(), *105*
RunSVD, 103
RunTFIDF, 105

seqinfo (seqinfo-methods), 108
seqinfo,ChromatinAssay-method
(seqinfo-methods), 108
seqinfo,Seurat-method
(seqinfo-methods), 108
seqinfo-methods, 108
seqinfo<-,ChromatinAssay-method
(seqinfo-methods), 108
seqinfo<-,Seurat-method
(seqinfo-methods), 108
seqlengths (seqinfo-methods), 108
seqlengths,ChromatinAssay-method
(seqinfo-methods), 108
seqlengths,Seurat-method
(seqinfo-methods), 108
seqlengths<-,ChromatinAssay-method
(seqinfo-methods), 108
seqlengths<-,Seurat-method
(seqinfo-methods), 108
seqlevels (seqinfo-methods), 108
seqlevels,ChromatinAssay-method
(seqinfo-methods), 108
seqlevels,Seurat-method
(seqinfo-methods), 108
seqlevels<-,ChromatinAssay-method
(seqinfo-methods), 108
seqlevels<-,Seurat-method
(seqinfo-methods), 108
seqnames (seqinfo-methods), 108
seqnames,ChromatinAssay-method
(seqinfo-methods), 108
seqnames,Seurat-method
(seqinfo-methods), 108
seqnames<-,ChromatinAssay-method
(seqinfo-methods), 108
seqnames<-,Seurat-method
(seqinfo-methods), 108
SetMotifData, 110
Seurat::FindClusters(), *50*
Seurat::FindMarkers(), *45*
Seurat::FindNeighbors(), *50*
Seurat::FindVariableFeatures(), *58*
SeuratObject::Assay(), *25*
SeuratObject::Seurat(), *8*, *10*, *16*, *43*, *44*, *50*, *54*, *55*, *58*, *60*, *63*, *72*, *82*, *92*, *93*, *95*, *100*, *105*, *107*, *111*, *119*
SeuratObject::VariableFeatures(), *44*
SortIdents, 111
SplitFragments, 112
stats::cor(), *43*
stats::density(), *85*
stats::dist(), *112*
stats::hclust(), *27*
stats::loess(), *58*
stats::p.adjust(), *50*
StringToGRanges, 113
StringToGRanges(), *26*, *76*
subset.Fragment, 114
subset.Motif, 114
SubsetMatrix, 115

TFBSTools::PFMatrixList(), *41*
TFBSTools::PWMatrixList(), *41*
theme_browser, 116
TilePlot, 117
TSSEnrichment, 118
TSSEnrichment(), *120*
TSSPlot, 119

UnifyPeaks, 120
UpdatePath, 121
utils::read.table(), *74*

ValidateCells, 121
ValidateCells(), *122*
ValidateFragments, 122
ValidateHash, 122
VariantPlot, 123