Package 'atacInferCnv'

November 11, 2026

Type Package

Title Call CNV from single cell ATAC-seq data based on InferCNV adaptation

Version 1.0.0

Description The package prepares input scATAC-seq data and adapts for copy number variance profiling with InferCNV package usage. It has also various paramters to control the analysis (e.g. external normal reference usage, meta-cells, bin size, etc) and custom plot visualizations.

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Encoding UTF-8

Depends R (>= 4.6.0),utils

Imports infercnv (>= 1.3.1), Signac, Seurat, GenomicRanges, GenomeInfoDb, S4Vectors, config, stringr, ggplot2, SummarizedExperiment, SingleCellExperiment, Rcpp

biocViews Epigenetics, Sequencing, CopyNumberVariation, SingleCell,ImmunoOncology

VignetteBuilder knitr

URL https://github.com/kokonech/atacInferCNV

BugReports https://github.com/kokonech/atacInferCNV/issues

Suggests testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

RoxygenNote 7.3.3

LinkingTo Rcpp,RcppEigen

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/atacInferCnv

git_branch RELEASE_3_23

git_last_commit e1f6773

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`aggregateBins` *Combine ATAC signals across bins of specific size*

Description

Combine ATAC signals across bins of specific size

Usage

```
aggregateBins(sample, resDir, sId, bin_size, chrom_lengths)
```

Arguments

`sample`	Input Seurat object
`resDir`	Path to the result directory
`sId`	Result name
`bin_size`	Size of the bin e.g. 100000 for 100Kbp
`chrom_lengths`	Numeric vector of chromosome sizes, specific for genome

Value

Seurat object

atacInferCnv — *atacInferCnv: CNV inference from single-cell chromatin accessibility data*

Description

atacInferCnv provides tools for genome-wide inference, analysis, and visualization of copy number variation (CNV) from single cell and single nucleus ATAC-seq data. The package extends the use of infercnv for chromatin accessibility profiles and includes utilities for preparing input matrices, aggregating genomic regions into bins, constructing meta-cells, running CNV inference, and visualizing inferred CNV profiles.

Details

The package is intended for the analysis of tumor single-cell chromatin accessibility datasets and supports identification of large-scale chromosomal alterations, and subclonal CNV structure.

Value

The package-level help page is used for documentation only and does not return a value.

Key functions

prepareAtacInferCnvInput Prepare input matrices and annotations for CNV inference from scATAC-seq data.

runAtacInferCnv Run CNV calling.

plotCnvBlocks Visualize inferred CNV block profiles.

extractMetacells — *Compute meta-cells out of the main*

Description

Compute meta-cells out of the main

Usage

```
extractMetacells(
  resDir,
  sId,
  sample,
  targColumn,
  metacell_content = 5,
  verbose = TRUE
)
```

Arguments

resDir	Path to the result directory
sId	Result name
sample	Input Seurat object to split
targColumn	Name of annotation column to split
metacell_content	Amount of cells for adjustment, default n=5
verbose	Detailed output, progress messages, default TRUE

Value

Invisibly returns NULL.

---

plotCnvBlocks *Function to plot CNV blocks*

Description

This function creates a plot for CNV assigned/identified subclones

Usage

```
plotCnvBlocks(resDir, infercnvObj = NULL, save = FALSE, verbose = TRUE)
```

Arguments

resDir	Path to the result directory with input
infercnvObj	InferCnv result object. Default: NULL If NULL, then the object will be loaded from result directory.
save	Set TRUE to save plot to the result directory. Default: FALSE
verbose	Detailed output, progress messages, default TRUE

Value

Returns a list of plots

Examples

```
resPath = tempfile()
inPath = system.file("extdata", "MB183_ATAC_subset.tsv.gz",
                     package = "atacInferCnv")
sAnn = system.file("extdata", "MB183_ATAC_subset.CNV_blocks_ann_n30.txt",
                     package = "atacInferCnv")
prepareAtacInferCnvInput(inPath,sAnn,resPath, targColumn = "cnvBlock",
                       ctrlGrp = "Normal", performGA = FALSE)
runAtacInferCnv(resPath)
plotCnvBlocks(resPath)
```

prepareAtacInferCnvInput *Prepare input for the CNV calling from scATAC-seq data*

Description

Prepare input for the CNV calling from scATAC-seq data

Usage

```
prepareAtacInferCnvInput(
  dataPath = "",
  annPath = "",
  resDir = "",
  inObj = NULL,
  sId = "sample",
  targColumn = "CellType",
  ctrlGrp = "Normal",
  ctrlObj = NULL,
  binSize = NULL,
  chromLength = NULL,
  metaCells = FALSE,
  performGA = TRUE,
  verbose = TRUE
)
```

Arguments

dataPath	Path to the input data in 10X format or ATAC counts matrix in txt format (gzipped)
annPath	Path to annotation of the cells in tab-delimited format
resDir	Path to the result directory
inObj	Pre-computed Seurat/Signac or SingleCellExperiment object with required input data within (alternative for dataPath)
sId	Result name. Default: "Sample"
targColumn	Name of the target column in annotation. Default:CellType
ctrlGrp	Name for the reference control cell type. Could be several names, separated by comma. Default: "Normal"
ctrlObj	Seurat/Signac or SingleCellExperiment object to use as non-tumor control. Default:NULL
binSize	Apply custom bin size to combine signals in windows for CNV calling e.g. 500000 for 500 KBp. Default: NULL (not use this option)
chromLength	Numeric vector of chromosome sizes, specific for genome. Default: NULL

metaCells	Set TRUE to use meta cells (n=5 cells by default) or assign a number of cells. Default: FALSE
performGA	Perform general analysis of scATAC-data (clustering, UMAP). Default: TRUE
verbose	Detailed output, progress messages, and diagnostic information. Default: TRUE

Value

Invisibly returns NULL.

Examples

```
resPath = tempfile()
inPath = system.file("extdata", "MB183_ATAC_subset.tsv.gz",
                     package = "atacInferCnv")
sAnn = system.file("extdata", "MB183_ATAC_subset.CNV_blocks_ann_n30.txt",
                    package = "atacInferCnv" )
prepareAtacInferCnvInput(inPath,sAnn,resPath, targColumn = "cnvBlock",
                         ctrlGrp = "Normal",performGA = FALSE)
```

---

runAtacInferCnv *Wrapper function to run InferCNV calling*

Description

This function calls InferCNV from generated input. It has support for all original inferCnv options.

Usage

```
runAtacInferCnv(
  resDir,
  configFile = "infercnv_config.yml",
  numClusters = 1,
  chrToExclude = c("Y", "MT"),
  addDenoise = TRUE,
  clusterRefs = FALSE,
  smoothMethod = "runmeans",
  verbose = TRUE,
  returnObj = FALSE,
  ...
)
```

Arguments

resDir	Path to the result directory with input
configFile	Name of configuration file with InferCnv input data

numClusters	Number of clusters for hierarchical clustering. If equals one (by default) then no clustering is performed and provided annotation used for the formation of CNV groups.
chrToExclude	Chromosomes to exclude. Default: Y,MT
addDenoise	Activate denoise (InferCNV param). Default: TRUE
clusterRefs	Cluster also reference (InferCNV param). Default: FALSE
smoothMethod	Method for smoothing (InferCNV param). Default: runmeans
verbose	Detailed output, progress message and diagnostic information. If deactivated InferCnv log is saved to file infercnv.log. Default: TRUE
returnObj	Return InferCNV object to work with further. Default: FALSE
...	Other parameters to provide for infercnv::run, more details in documentation of this function

Value

Invisibly returns NULL by default.

Examples

```
resPath = tempfile()
inPath = system.file("extdata", "MB183_ATAC_subset.tsv.gz",
                     package = "atacInferCnv")
sAnn = system.file("extdata", "MB183_ATAC_subset.CNV_blocks_ann_n30.txt",
                     package = "atacInferCnv" )
prepareAtacInferCnvInput(inPath,sAnn,resPath, targColumn = "cnvBlock",
                         ctrlGrp = "Normal",performGA = FALSE)
resObj <- runAtacInferCnv(resPath, returnObj = TRUE)
```

---

writeConfig *Write InferCNV configuration*

Description

Write InferCNV configuration

Usage

```
writeConfig(resDir, sId, ctrlGrp = "Normal", binSize = NULL, meta = FALSE)
```

Arguments

resDir	Result directory path
sId	Result name
ctrlGrp	Name for the reference control cell type
binSize	Size of the bin e.g. 100000 for 100 Kbp
meta	True if use meta cells, default false

Value

Invisibly returns NULL.

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