

Package ‘peakCallingPipeline’

May 12, 2022

Title Call peaks for variety of ATAC-Seq data

Version 0.1

URL <https://github.com/>

Description ADD

License GPL-3

Depends ArchR,
parallel,
data.table,
assertthat

Suggests knitr,
rmarkdown,
testthat

Encoding UTF-8

LazyData true

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

R topics documented:

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.run_checks	<i>Check and sanitize user input</i>
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Description

Check and sanitize user input

Usage

.run_checks()

peakCaller

*Calls peaks currently utilizing ArchR***Description**

Sets global variables about specific genome build and number of threads to utilize on the machine.

Usage

```
peakCaller(
  archr.proj,
  archr.genome,
  groupBy,
  archr.threads = 4,
  arrow.file.dir = NULL,
  cell.annotation.file = NULL,
  archr.clustering = FALSE,
  varFeatures = 15000,
  resolution = c(0.2, 1, 2),
  tileSize = 25,
  normMethod = "ReadsInTSS",
  maxCells = NULL,
  archr.visualize = TRUE,
  output.folder = NULL
)
```

Arguments

archr.proj	An already setup ArchR project or a name (string) to build a new ArchR project. If passing an already defined archr.proj then arrow.file.dir and cell.annotation.file will not be used.
archr.genome	Valid genome name for ArchR: mm10, hg38
groupBy	Metadata field to group cells by
archr.threads	Number of threads to utilize, warning increases memory usage as well.
arrow.file.dir	Directory where all the Arrow files are stored
cell.annotation.file	File that contains sample_id and additional cell annotations to append to the ArchRProject
archr.clustering	Boolean (T/F) determining if clustering/LSI should be run.
varFeatures	Number of variable features to use for cluster
resolution	Vector of clustering resolutions for multi-round clusters
tileSize	Width of tiles that will section the genome
normMethod	Normalization method for fragment pileups
maxCells	Number of cells to use for each group.
archr.visualize	Should marker peak visualizations be produced
output.folder	If supplied we will save the marker peak table and ArchRProject to this location.

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Value

ArchRProject, markerPeaks

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