Package 'peakCallingPipeline'

August 4, 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,
    dplyr

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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annotatePeaks   *Post-pipeline annotation of marker peaks*

Description

Defines additional marker peak annotations and standardizes reporting tables.

Usage

```
annotatePeaks(
  marker.table,
  archr.proj,
  dataset,
  groupBy,
  publish,
  filename,
  shiny.dir = NULL,
  ucsc.user = NULL,
  ucsc.session = NULL
)
```

Arguments

marker.table	file.path to a tab-seperated file containing results of ArchR marker peak analysis
archr.proj	An already setup ArchR project or a string to build a new ArchR project.
dataset	Information about the dataset that these marker peaks belong to. E.g. Brain region, etc.
groupBy	The annotation level used to group data for peak calling. E.g. Class, Subclass, etc.
publish	Set to 'TRUE' if you are ready to make the marker peak table viewable on Shiny.
filename	filename to save annotated marker table
ucsc.user	A ucsc genome browser user/account which to contains the session to build links from.
ucsc.session	A registred session for the UCSC genome browser user/account specified in ucsc.user.

Value

annotated marker table

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peakCaller	*Calls peaks currently utilizing ArchR*

Description

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

Usage

```
peakCaller(
  archr.proj,
  archr.genome,
  groupBy,
  dataset,
  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 = FALSE,
    output.folder = NULL,
    publish = NULL,
    ucsc.user = NULL,
    ucsc.session = 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
dataset	Information about the dataset that these marker peaks belong to. E.g. Brain region, etc.
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.
publish	Set to 'TRUE' if you are ready to make the marker peak table viewable on Shiny.
ucsc.user	A ucsc genome browser user/account which to contains the session to build links from.
ucsc.session	A registred session for the UCSC genome browser user/account specified in ucsc.user.

Value

ArchRProject, markerPeaks

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