

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:

peakCaller	1
Index	3

peakCaller	<i>Calls peaks currently utilizing ArchR</i>
------------	--

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

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

Value

ArchRProject, markerPeaks

Index

peakCaller, [1](#)