

Package ‘esATAC’

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Type Package

Title An Easy-to-use Systematic pipeline for ATACseq data analysis

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Description This package provides a framework and complete preset pipeline for quantification and analysis of ATAC-seq Reads. It covers raw sequencing reads preprocessing (FASTQ files), reads alignment (Rbowtie2), aligned reads file operations (SAM, BAM, and BED files), peak calling (F-seq), genome annotations (Motif, GO, SNP analysis) and quality control report. The package is managed by dataflow graph. It is easy for user to pass variables seamlessly between processes and understand the workflow. Users can process FASTQ files through end-to-end preset pipeline which produces a pretty HTML report for quality control and preliminary statistical results, or customize workflow starting from any intermediate stages with esATAC functions easily and flexibly.

Depends R (>= 4.0.0), Rsamtools, GenomicRanges, ShortRead, pipeFrame

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Encoding UTF-8

LazyData true

Imports Rcpp (>= 0.12.11), methods, knitr, Rbowtie2, rtracklayer, ggplot2, Biostrings, ChIPseeker, clusterProfiler, igraph, rJava, magrittr, digest, BSgenome, AnnotationDbi, GenomicAlignments, GenomicFeatures, R.utils, GenomeInfoDb, BiocGenerics, S4Vectors, IRanges, rmarkdown, tools, VennDiagram, grid, JASPAR2018, TFBSTools, grDevices, graphics, stats, utils, parallel, corrplot, BiocManager, motifmatchr

Suggests BSgenome.Hsapiens.UCSC.hg19, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db, testthat, webshot, prettydoc

LinkingTo Rcpp

SystemRequirements C++11

Collate ATACProc.R BamToBed.R BedToBigWig.R BedUtils.R ConfigVal.R CppInterface.R CutSiteCountR.R CutSitePre.R FRiPQC.R FastQC.R FregLenDistribute.R FindAdapter.R JavaExports.R JavaInterface.R

LibComplexQC.R Mapping.R Methods.R PeakCallingFseq.R
 PeakCallingMACS2.R PeakQC.R RGo.R RMotifScan.R RPeakAnno.R
 RPeakComp.R RSNPs.R RcppExports.R RemoveAdapter.R Renamer.R
 Rsortbam.R SamToBam.R SamToBed.R TSSQC.R UnzipAndMerge.R
 onLoad.R RMotifScanPair.R utilities.R SingleRepReport.R

biocViews ImmunoOncology, Sequencing, DNaseSeq, QualityControl,
 Alignment, Preprocessing, Coverage, ATACSeq, DNaseSeq

VignetteBuilder knitr

Archs x64

RoxygenNote 7.1.1

NeedsCompilation yes

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| | |
|----------------|---|
| esATAC-package | <i>An Easy-to-use Systematic pipeline for ATACseq data analysis</i> |
|----------------|---|

Description

This package provides a framework and complete preset pipeline for the quantification and analysis of ATAC-seq Reads. It covers raw sequencing reads preprocessing (FASTQ files), reads alignment (Rbowtie2), aligned reads file operation (SAM, BAM, and BED files), peak calling (fseq), genome annotations (Motif, GO, SNP analysis) and quality control report. The package is managed by dataflow graph. It is easy for user to pass variables seamlessly between processes and understand the workflow. Users can process FASTQ files through end-to-end preset pipeline which produces a pretty HTML report for quality control and preliminary statistical results, or customize workflow starting from any intermediate stages with esATAC functions easily and flexibly.

Preset pipeline for single replicate case study is shown below.

For multi-replicates case study, see [atacRepsPipe](#).

For single replicate case-control study, see [atacPipe2](#).

For multi-replicates case-control study, see [atacRepsPipe2](#).

NOTE: Build bowtie index in the function may take some time. If you already have bowtie2 index files or you want to download(ftp://ftp.ccb.jhu.edu/pub/data/bowtie2_indexes) instead of building, you can let esATAC skip the steps by renaming them following the format (genome+suffix) and put them in reference installation path (refdir). Example: hg19 bowtie2 index files

- hg19.1.bt2
- hg19.2.bt2
- hg19.3.bt2
- hg19.4.bt2
- hg19.rev.1.bt2
- hg19.rev.2.bt2

For single end reads FASTQ files, The required parameters are fastqInput1 and adapter1. For paired end reads non-interleaved FASTQ files (interleave=FALSE,default), The required parameters are fastqInput1 and fastqInput2. Otherwise, parameter fastqInput2 is not required (interleave=TRUE)

The paths of sequencing data replicates can be a Character vector. For example:

```
fastqInput1=c("file_1.rep1.fastq","file_1.rep2.fastq")
```

```
fastqInput2=c("file_2.rep1.fastq","file_2.rep2.fastq")
```

The result will be return by the function. An HTML report file will be created for paired end reads. Intermediate files will be save at tmpdir path (default is ./)

Usage

```

atacPipe(
  genome,
  fastqInput1,
  fastqInput2 = NULL,
  tmpdir = file.path(getwd(), "esATAC-pipeline"),
  refdir = file.path(tmpdir, "refdir"),
  threads = 2,
  adapter1 = NULL,
  adapter2 = NULL,
  interleave = FALSE,
  basicAnalysis = FALSE,
  createReport = TRUE,
  motifs = NULL,
  pipelineName = "pipe",
  chr = c(1:22, "X", "Y"),
  p.cutoff = 1e-06,
  ...
)

```

Arguments

| | |
|---------------|---|
| genome | Character scalar. The genome(like hg19, mm10, etc.) reference data in "refdir" to be used in the pipeline. |
| fastqInput1 | Character vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2. And it can also be interleaved file paths when argument interleaved=TRUE |
| fastqInput2 | Character vector. It contains file paths with #2 mates paired with file paths in fastqInput1. For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. |
| tmpdir | Character scalar. The temporary file storage path. |
| refdir | Character scalar. The path for reference data being installed to and storage. |
| threads | Integer scalar. The max threads allowed to be created. |
| adapter1 | Character scalar. It is an adapter sequence for file1. For single end data, it is required. |
| adapter2 | Character scalar. It is an adapter sequence for file2. |
| interleave | Logical scalar. Set TRUE when files are interleaved paired-end sequencing data. |
| basicAnalysis | Logical scalar. If it is TRUE, the pipeline will skip the time consuming steps like GO annotation and motif analysis |
| createReport | Logical scalar. If the HTML report file will be created. |
| motifs | either PFMatrix , PFMatrixList , PWMMatrix , PWMMatrixList , default: vertebrates motif from JASPAR. |
| pipelineName | Character scalar. Temporary file prefix for identifying files when multiple pipeline generating file in the same tmpdir. |
| chr | Which chromatin the program will processing. It must be identical with the filename of cut site information files or subset of . Default:c(1:22, "X", "Y"). |
| p.cutoff | p-value cutoff for returning motifs, default: 1e-6. |
| ... | Additional arguments, currently unused. |

Details

See `packageDescription('esATAC')` for package details.

Value

List scalar. It is a list that save the result of the pipeline. Slot "filelist": the input file paths. Slot "wholesummary": a dataframe that for quality control summary Slot "atacProcs": [ATACProc-class](#) objects generated by each process in the pipeline. Slot "filtstat": a dataframe that summary the reads filtered in each process.

Author(s)

Zheng Wei and Wei Zhang

See Also

[printMap](#), [atacPipe2](#), [atacRenamer](#), [atacRemoveAdapter](#), [atacBowtie2Mapping](#), [atacPeakCalling](#), [atacMotifScan](#), [atacRepsPipe](#), [atacRepsPipe2](#)

Examples

```
## Not run:
## These codes are time consuming so they will not be run and
## checked by bioconductor checker.

# call pipeline
# for a quick example(only CTCF and BATF3 will be processing)
conclusion <-
  atacPipe(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
    fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
    # MODIFY: Set the genome for your data
    genome = "hg19",
    motifs = getMotifInfo(motif.file = system.file("extdata", "CustomizedMotif.txt", package="esATAC"))
  )

# call pipeline
# for overall example(all vertebrates motif in JASPAR will be processed)
conclusion <-
  atacPipe(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
    fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
    # MODIFY: Set the genome for your data
    genome = "hg19")

## End(Not run)
```

atacPipe2

*Pipeline for single replicate case-control paired-end sequencing data***Description**

The preset pipeline to process case control study sequencing data. An HTML report file, result files(e.g. BED, BAM files) and conclusion list will generated. See detail for usage.

Usage

```
atacPipe2(
  genome,
  case = list(fastqInput1 = "paths/To/fastq1", fastqInput2 = "paths/To/fastq2",
    adapter1 = NULL, adapter2 = NULL),
  control = list(fastqInput1 = "paths/To/fastq1", fastqInput2 = "paths/To/fastq2",
    adapter1 = NULL, adapter2 = NULL),
  tmpdir = file.path(getwd(), "esATAC-pipeline"),
  refdir = file.path(tmpdir, "refdir"),
  threads = 2,
  interleave = FALSE,
  createReport = TRUE,
  motifs = NULL,
  chr = c(1:22, "X", "Y"),
  p.cutoff = 1e-06,
  ...
)
```

Arguments

| | |
|--------------|---|
| genome | Character scalar. The genome(like hg19, mm10, etc.) reference data in "refdir" to be used in the pipeline. |
| case | List scalar. Input for case sample. fastqInput1, the path(s) of the mate 1 fastq file(s), is required. fastqInput2, the path(s) of the mate 2 fastq file(s), is required, when interleave=FALSE. adapter1 and adapter2 are optional. |
| control | List scalar. Input for control sample. fastqInput1, the path(s) of the mate 1 fastq file(s), is required. fastqInput2, the path(s) of the mate 2 fastq file(s), is required, when interleave=FALSE. adapter1 and adapter2 are optional. |
| tmpdir | Character scalar. The temporary file storage path. |
| refdir | Character scalar. The path for reference data being installed to and storage. |
| threads | Integer scalar. The max threads allowed to be created. |
| interleave | Logical scalar. Set TRUE when files are interleaved paired-end sequencing data. |
| createReport | Logical scalar. If the HTML report file will be created. |
| motifs | either PFMatrix , PFMatrixList , PWMMatrix , PWMMatrixList , default: vertebrates motif from JASPAR. |
| chr | Which chromatin the program will processing. It must be identical with the filename of cut site information files or subset of . Default:c(1:22, "X", "Y"). |
| p.cutoff | p-value cutoff for returning motifs, default: 1e-6. |
| ... | Additional arguments, currently unused. |

Details

NOTE: Build bowtie index in this function may take some time. If you already have bowtie2 index files or you want to download(ftp://ftp.ccb.jhu.edu/pub/data/bowtie2_indexes) instead of building, you can let esATAC skip the steps by renaming them following the format (genome+suffix) and put them in reference installation path (refdir). Example: hg19 bowtie2 index files

- hg19.1.bt2
- hg19.2.bt2
- hg19.3.bt2
- hg19.4.bt2
- hg19.rev.1.bt2
- hg19.rev.2.bt2

For single end reads FASTQ files, The required parameters are fastqInput1 and adapter1. For paired end reads non-interleaved FASTQ files (interleave=FALSE,default), The required parameters are fastqInput1 and fastqInput2. Otherwise, parameter fastqInput2 is not required (interleave=TRUE)

The paths of sequencing data replicates can be a Character vector. For example:

```
fastqInput1=c("file_1.rep1.fastq", "file_1.rep2.fastq")
```

```
fastqInput2=c("file_2.rep1.fastq", "file_2.rep2.fastq")
```

The result will be return by the function. An HTML report file will be created for paired end reads. Intermediate files will be save at tmpdir path (default is ./)

Value

List scalar. It is a list that save the result of the pipeline. Slot "wholesummary": a dataframe for quality control summary of case and control data Slot "caselist" and "ctrlist": Each of them is a list that save the result for case or control data. Slots of "caselist" and "ctrlist": Slot "filelist": the input file paths. Slot "wholesummary": a dataframe for quality control summary of case or control data Slot "atacProcs": [ATACProc-class](#) objects generated by each process in the pipeline. Slot "filtstat": a dataframe that summary the reads filtered in each process.

Author(s)

Zheng Wei and Wei Zhang

See Also

[atacPipe](#)

Examples

```
## Not run:
## These codes are time consuming so they will not be run and
## checked by bioconductor checker.

# call pipeline
# for a quick example(only CTCF and BATF3 will be processed)
conclusion <-
  atacPipe2(
    # MODIFY: Change these paths to your own case files!
```

```

# e.g. fastqInput1 = "your/own/data/path.fastq"
case=list(fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
          fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz")),
# MODIFY: Change these paths to your own control files!
# e.g. fastqInput1 = "your/own/data/path.fastq"
control=list(fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2"),
             fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
# MODIFY: Set the genome for your data
genome = "hg19",
motifs = getMotifInfo(motif.file = system.file("extdata", "CustomizedMotif.txt", package="esATAC"))

# call pipeline
# for overall example(all vertebrates motif in JASPAR will be processed)
conclusion <-
  atacPipe2(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    case=list(fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
              fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz")),
    # MODIFY: Change these paths to your own control files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    control=list(fastqInput1 = system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2"),
                 fastqInput2 = system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
    # MODIFY: Set the genome for your data
    genome = "hg19")

## End(Not run)

```

| | |
|----------------|-----------------------------------|
| ATACProc-class | <i>Base class of this package</i> |
|----------------|-----------------------------------|

Description

This class is inherit from Step in pipeFrame package, no more method is extended or override. Please see Step class for detail.

| | |
|--------------|--|
| atacRepsPipe | <i>Pipeline for multi-replicates case paired-end sequencing data</i> |
|--------------|--|

Description

The preset pipeline to process multi-replicates case study sequencing data. HTML report files, result files(e.g. BED, BAM files) and conclusion list will generated. See detail for usage.

Usage

```

atacRepsPipe(
  genome,
  fastqInput1,
  fastqInput2 = NULL,
  rekdir = NULL,

```



```

    tmpdir = NULL,
    threads = 2,
    adapter1 = NULL,
    adapter2 = NULL,
    interleave = FALSE,
    createReport = TRUE,
    motifs = NULL,
    prefix = NULL,
    chr = c(1:22, "X", "Y"),
    p.cutoff = 1e-06,
    ...
)

```

Arguments

| | |
|--------------|---|
| genome | Character scalar. The genome(like hg19, mm10, etc.) reference data in "refdir" to be used in the pipeline. |
| fastqInput1 | List scalar. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2 And it can also be interleaved file paths when argument interleave=TRUE. Each element in the fastqInput1 List is for a replicate It can be a Character vector of FASTQ files paths to be merged. |
| fastqInput2 | List scalar. It contains file paths with #2 mates paired with file paths in fastqInput1. For single-end sequencing files and interleaved paired-end sequencing files(argument interleave=TRUE), it must be NULL. Each element in the fastqInput1 List is for a replicate It can be a Character vector of FASTQ files paths to be merged. |
| refdir | Character scalar. The path for reference data being installed to and storage. |
| tmpdir | Character scalar. The temporary file storage path. |
| threads | Integer scalar. The max threads allowed to be created. |
| adapter1 | Character scalar. It is an adapter sequence for file1. For single end data, it is required. |
| adapter2 | Character scalar. It is an adapter sequence for file2. |
| interleave | Logical scalar. Set TRUE when files are interleaved paired-end sequencing data. |
| createReport | Logical scalar. If the HTML report file will be created. |
| motifs | either PFMatrix , PFMatrixList , PWMMatrix , PWMMatrixList , default: vertebrates motif from JASPAR. |
| prefix | Character scalar. Temporary file prefix for identifying files when multiple pipeline generating file in the same tmpdir. |
| chr | Which chromatin the program will processing. It must be identical with the filename of cut site information files or subset of . Default:c(1:22, "X", "Y"). |
| p.cutoff | p-value cutoff for returning motifs, default: 1e-6. |
| ... | Additional arguments, currently unused. |

Value

List scalar. It is a list that save the result of the pipeline. Slot "filelist": the input file paths. Slot "wholesummary": a dataframe that for quality control summary Slot "atacProcs": [ATACProc-class](#) objects generated by each process in the pipeline. Slot "filtstat": a dataframe that summary the reads filtered in each process.

Author(s)

Zheng Wei and Wei Zhang

See Also

[printMap](#), [atacPipe2](#), [atacRenamer](#), [atacRemoveAdapter](#), [atacBowtie2Mapping](#), [atacPeakCalling](#), [atacMotifScan](#)

Examples

```
## Not run:
## These codes are time consuming so they will not be run and
## checked by bioconductor checker.

# call pipeline
# for a quick example(only CTCF and BATF3 will be processing)
conclusion <-
  atacRepsPipe(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    fastqInput1 = list(system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
                      system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2")),
    fastqInput2 = list(system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
                      system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
    # MODIFY: Set the genome for your data
    genome = "hg19",
    motifs = getMotifInfo(motif.file = system.file("extdata", "CustomizedMotif.txt", package="esATAC")))

# call pipeline
# for overall example(all vertebrates motif in JASPAR will be processed)
conclusion <-
  atacRepsPipe(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    fastqInput1 = list(system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
                      system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2")),
    fastqInput2 = list(system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
                      system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
    # MODIFY: Set the genome for your data
    genome = "hg19")

## End(Not run)
```

atacRepsPipe2

Pipeline for multi-replicates case-control paired-end sequencing data

Description

The preset pipeline to process multi-replicates case control study sequencing data. HTML report files, result files(e.g. BED, BAM files) and conclusion list will generated. See detail for usage.

Usage

```

atacRepsPipe2(
  genome,
  caseFastqInput1,
  caseFastqInput2,
  ctrlFastqInput1,
  ctrlFastqInput2,
  caseAdapter1 = NULL,
  caseAdapter2 = NULL,
  ctrlAdapter1 = NULL,
  ctrlAdapter2 = NULL,
  refdir = NULL,
  tmpdir = NULL,
  threads = 2,
  interleave = FALSE,
  createReport = TRUE,
  motifs = NULL,
  chr = c(1:22, "X", "Y"),
  p.cutoff = 1e-06,
  ...
)

```

Arguments

| | |
|-----------------|---|
| genome | Character scalar. The genome(like hg19, mm10, etc.) reference data in "refdir" to be used in the pipeline. |
| caseFastqInput1 | List scalar. Input for case samples. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2 And it can also be interleaved file paths when argument interleaved=TRUE. Each element in the caseFastqInput1 List is for a replicate It can be a Character vector of FASTQ files paths to be merged. |
| caseFastqInput2 | List scalar. Input for case samples. It contains file paths with #2 mates paired with file paths in caseFastqInput1 For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. Each element in the caseFastqInput2 List is for a replicate |
| ctrlFastqInput1 | List scalar. Input for control samples. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in ctrlFastqInput2 And it can also be interleaved file paths when argument interleaved=TRUE. Each element in the ctrlFastqInput1 List is for a replicate It can be a Character vector of FASTQ files paths to be merged. |
| ctrlFastqInput2 | List scalar. Input for control samples. It contains file paths with #2 mates paired with file paths in fastqInput1. For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. Each element in the ctrlFastqInput1 List is for a replicate |
| caseAdapter1 | Character scalar. Adapter for caseFastqInput1. |
| caseAdapter2 | Character scalar. Adapter for caseFastqInput2. |

| | |
|--------------|---|
| ctrlAdapter1 | Character scalar. Adapter for ctrlFastqInput1. |
| ctrlAdapter2 | Character scalar. Adapter for ctrlFastqInput2. |
| refdir | Character scalar. The path for reference data being installed to and storage. |
| tmpdir | Character scalar. The temporary file storage path. |
| threads | Integer scalar. The max threads allowed to be created. |
| interleave | Logical scalar. Set TRUE when files are interleaved paired-end sequencing data. |
| createReport | Logical scalar. If the HTML report file will be created. |
| motifs | either <code>PMatrix</code> , <code>PMatrixList</code> , <code>PWMatrix</code> , <code>PWMatrixList</code> , default: vertebrates motif from JASPAR. |
| chr | Which chromatin the program will processing. It must be identical with the filename of cut site information files or subset of . Default:c(1:22, "X", "Y"). |
| p.cutoff | p-value cutoff for returning motifs, default: 1e-6. |
| ... | Additional arguments, currently unused. |

Details

NOTE: Build bowtie index in this function may take some time. If you already have bowtie2 index files or you want to download(ftp://ftp.ccb.jhu.edu/pub/data/bowtie2_indexes) instead of building, you can let esATAC skip the steps by renaming them following the format (genome+suffix) and put them in reference installation path (refdir). Example: hg19 bowtie2 index files

- hg19.1.bt2
- hg19.2.bt2
- hg19.3.bt2
- hg19.4.bt2
- hg19.rev.1.bt2
- hg19.rev.2.bt2

For single end reads FASTQ files, The required parameters are fastqInput1 and adapter1. For paired end reads non-interleaved FASTQ files (interleave=FALSE,default), The required parameters are fastqInput1 and fastqInput2. Otherwise, parameter fastqInput2 is not required (interleave=TRUE)

The paths of sequencing data replicates can be a Character vector. For example:

```
fastqInput1=c("file_1.rep1.fastq","file_1.rep2.fastq")
```

```
fastqInput2=c("file_2.rep1.fastq","file_2.rep2.fastq")
```

The result will be return by the function. An HTML report file will be created for paired end reads. Intermediate files will be save at tmpdir path (default is ./)

Value

List scalar. It is a list that save the result of the pipeline. Slot "caselist" and "ctrlist": Each of them is a list that save the result for case or control data. Slot "comp_result": compare analysis result for case and control data

Author(s)

Zheng Wei and Wei Zhang

See Also[atacPipe](#)**Examples**

```

## Not run:
## These codes are time consuming so they will not be run and
## checked by bioconductor checker.

# call pipeline
# for a quick example(only CTCF will be processed)
conclusion <-
  atacRepsPipe2(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    caseFastqInput1=list(system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
                        system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz")),
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    caseFastqInput2=list(system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
                        system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz")),
    # MODIFY: Change these paths to your own control files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    ctrlFastqInput1=list(system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2"),
                        system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2")),
    # MODIFY: Change these paths to your own control files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    ctrlFastqInput2=list(system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2"),
                        system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
    # MODIFY: Set the genome for your data
    genome = "hg19",
    motifs = getMotifInfo(motif.file = system.file("extdata", "CustomizedMotif.txt", package="esATAC"))
  )

# call pipeline
# for overall example(all human motif in JASPAR will be processed)
conclusion <-
  atacRepsPipe2(
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    caseFastqInput1=list(system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz"),
                        system.file(package="esATAC", "extdata", "chr20_1.1.fq.gz")),
    # MODIFY: Change these paths to your own case files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    caseFastqInput2=list(system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz"),
                        system.file(package="esATAC", "extdata", "chr20_2.1.fq.gz")),
    # MODIFY: Change these paths to your own control files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    ctrlFastqInput1=list(system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2"),
                        system.file(package="esATAC", "extdata", "chr20_1.2.fq.bz2")),
    # MODIFY: Change these paths to your own control files!
    # e.g. fastqInput1 = "your/own/data/path.fastq"
    ctrlFastqInput2=list(system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2"),
                        system.file(package="esATAC", "extdata", "chr20_2.2.fq.bz2")),
    # MODIFY: Set the genome for your data
  )

```

```

        genome = "hg19"
    )

## End(Not run)

```

BamToBed

Convert bam format to bed format.

Description

This function is used to convert SAM file to BED file and merge interleaved paired end reads, shift reads, filter reads according to chromosome, filter reads according to fragment size, sort, remove duplicate reads before generating BED file.

Usage

```

atacBam2Bed(
  atacProc,
  bamInput = NULL,
  bedOutput = NULL,
  reportOutput = NULL,
  bsgenome = NULL,
  mergePairIntoFrag = c("auto", "yes", "no"),
  posOffset = +4,
  negOffset = -5,
  chrFilterList = "chrM|_",
  sortBed = TRUE,
  rmMultiMap = TRUE,
  minFragLen = 0,
  maxFragLen = 2000,
  saveExtLen = FALSE,
  uniqueBed = c("auto", "yes", "no"),
  ...
)

## S4 method for signature 'ATACProc'
atacBam2Bed(
  atacProc,
  bamInput = NULL,
  bedOutput = NULL,
  reportOutput = NULL,
  bsgenome = NULL,
  mergePairIntoFrag = c("auto", "yes", "no"),
  posOffset = +4,
  negOffset = -5,
  chrFilterList = "chrM|_",
  sortBed = TRUE,
  rmMultiMap = TRUE,
  minFragLen = 0,
  maxFragLen = 2000,
  saveExtLen = FALSE,

```

```

    uniqueBed = c("auto", "yes", "no"),
    ...
)

bam2bed(
  bamInput,
  bedOutput = NULL,
  reportOutput = NULL,
  bsgenome = NULL,
  mergePairIntoFrag = c("auto", "yes", "no"),
  posOffset = +4,
  negOffset = -5,
  chrFilterList = "chrM|_",
  sortBed = TRUE,
  rmMultiMap = TRUE,
  minFragLen = 0,
  maxFragLen = 2000,
  saveExtLen = FALSE,
  uniqueBed = c("auto", "yes", "no"),
  ...
)

```

Arguments

| | |
|-------------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacBamSort , atacSam2Bam . |
| bamInput | Character scalar. Bam file input path. |
| bedOutput | Character scalar. Bed file output path. If ignored, bed file will be put in the same path as the bam file. |
| reportOutput | Character scalar. Report file path. |
| bsgenome | Bsgenome object. This object from bioconductor |
| mergePairIntoFrag | Logical scalar Merge paired end reads. |
| posOffset | Integer scalar The offset that positive strand reads will shift. |
| negOffset | Integer scalar The offset that negative strand reads will shift. |
| chrFilterList | Character vector The chromatin(or regex of chromatin) will be discard |
| sortBed | Logical scalar Sort bed file in the order of chromatin, start, end |
| rmMultiMap | Logical scalar. Remove multi-map reads. |
| minFragLen | Integer scalar The minimum fragment size will be retained. |
| maxFragLen | Integer scalar The maximum fragment size will be retained. |
| saveExtLen | Logical scalar. Save the fragment that are not in the range of minFragLen and maxFragLen |
| uniqueBed | Logical scalar Remove duplicates reads in bed if TRUE. default: FALSE |
| ... | Additional arguments, currently unused. |

Details

The bam file will be automatically obtained from `object(atacProc)` or input by hand. Output can be ignored.

Value

An invisible `ATACProc-class` object scalar for downstream analysis.

Author(s)

Zheng Wei, Wei Zhang

See Also

`atacBamSort` `atacSam2Bam`

Examples

```
library(Rsamtools)
# change dataset !!
# ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
# bam2bed(bamInput = ex1_file)
```

BedToBigWig

generate BigWig file from BED file

Description

This function is used to generate BigWig file from BED reads file. The BigWig file can be shown reads coverage on genome browser.

Usage

```
atacBedToBigWig(
  atacProc,
  bedInput = NULL,
  bsgenome = NULL,
  bwOutput = NULL,
  toWig = FALSE,
  ...
)

## S4 method for signature 'ATACProc'
atacBedToBigWig(
  atacProc,
  bedInput = NULL,
  bsgenome = NULL,
  bwOutput = NULL,
  toWig = FALSE,
  ...
)

bedToBigWig(bedInput, bsgenome = NULL, bwOutput = NULL, toWig = FALSE, ...)
```


Arguments

| | |
|----------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed , atacBedUtils . |
| bedInput | Character scalar. Bed file input path. |
| bsgenome | BSGenome object scalar. BSGenome object for specific species. |
| bwOutput | Character scalar. BigWig file output path. |
| toWig | Logical scalar. |
| ... | Additional arguments, currently unused. Save as wig file instead of binary BigWig file |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(`atacProc`) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `bedToBigWig` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [samToBed](#) [atacBedUtils](#) [bedUtils](#)

Examples

```
library(R.utils)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
## Not run:
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)

library(BSgenome.Hsapiens.UCSC.hg19)
bedToBigWig(bedfile, BSgenome.Hsapiens.UCSC.hg19)

dir(td)

## End(Not run)
```

BedUtils

process bed file with limit memory

Description

This function is used to merge interleaved paired end reads in bed, downsample bed reads, shift bed reads, filter bed reads according to chromosome, filter bed reads according to fragment size, sort bed, remove duplicate reads in bed.

Usage

```

atacBedUtils(
  atacProc,
  bedInput = NULL,
  bedOutput = NULL,
  mergePair = FALSE,
  downSample = NULL,
  posOffset = 0L,
  negOffset = 0L,
  chrFilterList = c("chrM"),
  select = FALSE,
  sortBed = FALSE,
  uniqueBed = FALSE,
  minFragLen = 0,
  maxFragLen = 2e+09,
  newStepType = "BedUtils",
  ...
)

## S4 method for signature 'ATACProc'
atacBedUtils(
  atacProc,
  bedInput = NULL,
  bedOutput = NULL,
  mergePair = FALSE,
  downSample = NULL,
  posOffset = 0L,
  negOffset = 0L,
  chrFilterList = c("chrM"),
  select = FALSE,
  sortBed = FALSE,
  uniqueBed = FALSE,
  minFragLen = 0,
  maxFragLen = 2e+09,
  newStepType = "BedUtils",
  ...
)

bedUtils(
  bedInput,
  bedOutput = NULL,

```

```

mergePair = FALSE,
downSample = NULL,
reportOutput = NULL,
posOffset = 0L,
negOffset = 0L,
chrFilterList = c("chrM"),
select = FALSE,
sortBed = FALSE,
uniqueBed = FALSE,
minFragLen = 0,
maxFragLen = 2e+09,
newStepType = "BedUtils",
...
)

```

Arguments

| | |
|---------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacBam2Bed bam2bed atacSamToBed samToBed |
| bedInput | Character scalar. Bed file input path. |
| bedOutput | Character scalar. Bed file output path. |
| mergePair | Logical scalar Merge paired end interleave reads. |
| downSample | Integer scalar Down sample reads if the number is less than total number |
| posOffset | Integer scalar The offset that positive strand reads will shift. |
| negOffset | Integer scalar The offset that negative strand reads will shift. |
| chrFilterList | Character vector The chromatin(or regex of chromatin) will be retain/discard if select is TRUE/FALSE |
| select | Logical scalar The chromatin in chrFilterList will be retain if TRUE. default: FALSE |
| sortBed | Logical scalar Sort bed file in the order of chromatin, start, end |
| uniqueBed | Logical scalar Remove duplicates reads in bed if TRUE. default: FALSE |
| minFragLen | Integer scalar The minimum fragment size will be retained. |
| maxFragLen | Integer scalar The maximum fragment size will be retained. |
| newStepType | Character scalar. New step type name for different default parameters. |
| ... | Additional arguments, currently unused. |
| reportOutput | Character scalar. Report output file path. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(`atacProc`) or generated based on known parameters if their values are default(e.g. `NULL`). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `bedUtils` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacBam2Bed](#) [bam2bed](#) [atacSamToBed](#) [samToBed](#) [atacFragLenDistr](#) [atacExtractCutSite](#) [atacPeakCalling](#)
[atacTSSQC](#) [atacBedToBigWig](#)

Examples

```
library(R.utils)
library(magrittr)
td <- tempdir()
setTmpDir(td)

sambzfile <- system.file(package="esATAC", "extdata", "Example.sam.bz2")
samfile <- file.path(td,"Example.sam")
bunzip2(sambzfile,destname=samfile,overwrite=TRUE,remove=FALSE)
atacproc<-samToBed(samInput = samfile) %>%
atacBedUtils(maxFragLen = 100, chrFilterList = NULL)
```

Bowtie2Mapping

*Use bowtie2 aligner to map reads to reference genome***Description**

Use bowtie2 aligner to map reads to reference genome

Usage

```
atacBowtie2Mapping(
  atacProc,
  samOutput = NULL,
  reportOutput = NULL,
  bt2Idx = NULL,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  paramList = "--no-discordant --no-unal --no-mixed -X 2000",
  ...
)

## S4 method for signature 'ATACProc'
atacBowtie2Mapping(
  atacProc,
  samOutput = NULL,
  reportOutput = NULL,
  bt2Idx = NULL,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
```

```

interleave = FALSE,
threads = getThreads(),
paramList = "--no-discordant --no-unal --no-mixed -X 2000",
...
)

bowtie2Mapping(
  fastqInput1,
  fastqInput2 = NULL,
  samOutput = NULL,
  reportOutput = NULL,
  bt2Idx = NULL,
  interleave = FALSE,
  threads = getThreads(),
  paramList = "--no-discordant --no-unal --no-mixed -X 2000",
  ...
)

```

Arguments

| | |
|--------------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacRemoveAdapter removeAdapter |
| samOutput | Character scalar. A path to a SAM file used for the alignment output. |
| reportOutput | Character scalar. The prefix of report files path. |
| bt2Idx | Character scalar. bowtie2 index files prefix: 'dir/basename' (minus trailing '*.bt2' of 'dir/basename.*.bt2'). |
| fastqInput1 | Character vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2. And it can also be interleaved file paths when argument interleaved=TRUE |
| fastqInput2 | Character vector. It contains file paths with #2 mates paired with file paths in fastqInput1. For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. |
| interleave | Logical. Set TRUE when files are interleaved paired-end sequencing data. |
| threads | Integer scalar. The threads will be created in this process. default: getThreads() |
| paramList | Additional arguments to be passed on to the binaries. See below for details. |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use bowtie2Mapping instead. additional parameters to be passed on to bowtie2. You can put all additional arguments in one Character(e.g. "--threads 8 --no-mixed") with white space splited just like command line, or put them as Character vector (e.g. c("--threads","8","--no-mixed")). Note that some arguments("-x","-interleaved","-U","-1","-2","-S","threads") to the bowtie2 are invalid if they are already handled as explicit function arguments. See the output of bowtie2_usage() for details about available parameters.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacRemoveAdapter](#) [removeAdapter](#) [bowtie2](#) [bowtie2_build](#) [bowtie2_usage](#) [atacSam2Bam](#) [atacSamToBed](#)
[atacLibComplexQC](#)

Examples

```
td <- tempdir()
setTmpDir(td)

## Building a bowtie2 index
library("Rbowtie2")
refs <- dir(system.file(package="esATAC", "extdata", "bt2","refs"),
full=TRUE)
bowtie2_build(references=refs, bt2Index=file.path(td, "lambda_virus"),
"--threads 4 --quiet",overwrite=TRUE)
## Alignments
reads_1 <- system.file(package="esATAC", "extdata", "bt2", "reads",
"reads_1.fastq")
reads_2 <- system.file(package="esATAC", "extdata", "bt2", "reads",
"reads_2.fastq")
if(file.exists(file.path(td, "lambda_virus.1.bt2"))){
  (bowtie2Mapping(bt2Idx = file.path(td, "lambda_virus"),
  samOutput = file.path(td, "result.sam"),
  fastqInput1=reads_1,fastqInput2=reads_2,threads=3))
  head(readLines(file.path(td, "result.sam")))
}
```

CutSiteCountR

Count cut site number in given motif region and plot footprint.

Description

This function is used to count cut site number in given motif regions and plot footprint. Multi-motif is supported. NOTE: The input parameter is a little bit complex, [atacExtractCutSite](#) and [atacMotifScan](#) is recommended to use which makes the entire procedure easier.

Usage

```
atacCutSiteCount(
  atacProcCutSite,
  atacProcMotifScan = NULL,
  csInput = NULL,
  motif_info = NULL,
  chr = c(1:22, "X", "Y"),
  matrixOutput = NULL,
```

```

    strandLength = 100,
    FootPrint = TRUE,
    prefix = NULL,
    ...
)

## S4 method for signature 'ATACProc'
atacCutSiteCount(
  atacProcCutSite,
  atacProcMotifScan = NULL,
  csInput = NULL,
  motif_info = NULL,
  chr = c(1:22, "X", "Y"),
  matrixOutput = NULL,
  strandLength = 100,
  FootPrint = TRUE,
  prefix = NULL,
  ...
)

cutsitecount(
  csInput = NULL,
  motif_info = NULL,
  chr = c(1:22, "X", "Y"),
  matrixOutput = NULL,
  strandLength = 100,
  FootPrint = TRUE,
  prefix = NULL,
  ...
)

```

Arguments

| | |
|-------------------|--|
| atacProcCutSite | ATACProc-class object scalar. It has to be the return value of upstream process: atacExtractCutSite . |
| atacProcMotifScan | ATACProc-class object scalar. It has to be the return value of upstream process: atacMotifScan . |
| csInput | Your cut site information file(from atacExtractCutSite function, separated by chromatin name and all cut site are sorted) path with prefix. e.g. "/your_cut_site_information_path/pr |
| motif_info | A rds file from function atacMotifScan . In the rds file, it saves 3 column information(motif, motif exact position information file path and motif length). |
| chr | Which chromatin the program will processing. It must be identical with the filename of cut site information files or subset of . Default:c(1:22, "X", "Y"). |
| matrixOutput | The output directory, where to save your cut site count of every motif position. an empty folder would be great. Default:tmpdir/Footprint |
| strandLength | How many bp(base pair) do you want to count up/downstream of the motif. default:100. |
| FootPrint | TRUE or FALSE, plot footprint or not. |
| prefix | prefix for the pdf file. |
| ... | Additional arguments, currently unused. |

Details

The parameter is simplified because of too many input file. parameter `atacProcCutSite` and `atacProcMotifScan` contains all input information so function `atacExtractCutSite` and `atacMotifScan` is recommended to use together. For instance, if you want footprint of 3 TFs (transcription factor) of human in chr1-22, X, Y, then you need 24 chromatin cut site files, 3 motif position files as well as 3 integers of the motif. Function `atacExtractCutSite` and `atacMotifScan` will do all this, you just specify which motif you want. Therefore, `atacExtractCutSite` and `atacMotifScan` is recommended to use together.

Value

An invisible `ATACProc-class` object scalar.

Author(s)

Wei Zhang

See Also

`atacExtractCutSite` `atacMotifScan`

Examples

```
library(R.utils)
library(BSgenome.Hsapiens.UCSC.hg19)
## processing bed file
fra_path <- system.file("extdata", "chr20.50000.bed.bz2", package="esATAC")
frag <- as.vector(bunzip2(filename = fra_path,
  destname = file.path(getwd(), "chr20.50000.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
cs.data <- extractcutsite.bedInput = frag, prefix = "ATAC")

## find motif position
p1bz <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
peak1_path <- as.vector(bunzip2(filename = p1bz,
  destname = file.path(getwd(), "Example_peak1.bed"),
  ext="bz2", FUN = bzfile, overwrite=TRUE, remove = FALSE))
# motif <- readRDS(system.file("extdata", "MotifPFM.rds", package="esATAC"))
# motif.data <- motifsScan(peak = peak1_path, genome = BSgenome.Hsapiens.UCSC.hg19, motifs = motif)

## plot footprint
# atacCutSiteCount(atacProcCutSite = cs.data, atacProcMotifScan = motif.data)
```

CutSitePre

Extract ATAC-seq cutting site from bed file.

Description

Extract cutting site from ATAC-seq fragment bed file (from `atacSamToBed`).

Usage

```

    atacExtractCutSite(
        atacProc,
        bedInput = NULL,
        csOutput.dir = NULL,
        prefix = NULL,
        ...
    )

## S4 method for signature 'ATACProc'
atacExtractCutSite(
    atacProc,
    bedInput = NULL,
    csOutput.dir = NULL,
    prefix = NULL,
    ...
)

extractcutsite(bedInput, csOutput.dir = NULL, prefix = NULL, ...)

```

Arguments

| | |
|--------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed . |
| bedInput | Character scalar. Input bed file path, must be merged bed file(a line is a fragment). The input file should be UCSC bed format(0-based). |
| csOutput.dir | Character scalar. The output path, an empty folder would be great. Default: a folder in the same path as input bed file. |
| prefix | Character scalar. Output file name prefix, e.g. prefix_chr*.bed, default "Cut-site". |
| ... | Additional arguments, currently unused. |

Details

In ATAC-seq data, every line in merged bed file (from [atacSamToBed](#), the first 3 column is chr, start, end) means a DNA fragment, the cutting site is start+1 and end, this function extract and sort this information for the next step ([atacCutSiteCount](#)).

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also

[atacCutSiteCount](#)

Examples

```
library(R.utils)
fra_path <- system.file("extdata", "chr20.50000.bed.bz2", package="esATAC")
frag <- as.vector(bunzip2(filename = fra_path,
  destname = file.path(getwd(), "chr20.50000.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
extractcutsite.bedInput = frag, prefix = "ATAC")
```

FastQC

*Quality control for ATAC-seq data.***Description**

Generate quality control plots from fastq of ATAC-seq data.

Usage

```
atacQCReport(atacProc, input_file = NULL, output_file = NULL, ...)

## S4 method for signature 'ATACProc'
atacQCReport(atacProc, input_file = NULL, output_file = NULL, ...)

qcreport(input_file, output_file = NULL, ...)
```

Arguments

| | |
|-------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacUnzipAndMerge , atacRenamer |
| input_file | Character scalar. Input file path. One or more(vector) fastq file path. |
| output_file | Character scalar. output file path. Default:"input_file_QC.pdf" in the same folder as your input file. |
| ... | Additional arguments, currently unused. |

Details

Every highthroughput sequencing need quality control analysis, this function provide QC for ATAC-seq, such as GC content.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also

[atacUnzipAndMerge](#), [atacRenamer](#)

Examples

```

library(R.utils)
fra_path <- system.file("extdata", "chr20_1.2.fq.bz2", package="esATAC")
fq1 <- as.vector(bunzip2(filename = fra_path,
  destname = file.path(getwd(), "chr20_1.fq"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
fra_path <- system.file("extdata", "chr20_2.2.fq.bz2", package="esATAC")
fq2 <- as.vector(bunzip2(filename = fra_path,
  destname = file.path(getwd(), "chr20_2.fq"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
## Not run:
qcreport(input_file = c(fq1, fq2))

## End(Not run)

```

FindAdapter

Use AdapterRemoval to identify adapters

Description

Use AdapterRemoval to identify adapters for paired end data

Usage

```

atacFindAdapter(
  atacProc,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  reportPrefix = NULL,
  interleave = FALSE,
  findParamList = NULL,
  threads = getThreads(),
  ...
)

## S4 method for signature 'ATACProc'
atacFindAdapter(
  atacProc,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  reportPrefix = NULL,
  interleave = FALSE,
  findParamList = NULL,
  threads = getThreads(),
  ...
)

findAdapter(
  fastqInput1,
  fastqInput2 = NULL,

```

```

    reportPrefix = NULL,
    interleave = FALSE,
    findParamList = NULL,
    threads = getThreads(),
    ...
)

```

Arguments

| | |
|---------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacRenamer renamer atacUnzipAndMerge unzipAndMerge |
| fastqInput1 | Character vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2 And it can also be interleaved file paths when argument interleaved=TRUE |
| fastqInput2 | Character vector. It contains file paths with #2 mates paired with file paths in fastqInput1 For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. |
| reportPrefix | Character. The prefix of report files path. Default: generate from known parameters |
| interleave | Logical. Set TRUE when files are interleaved paired-end sequencing data. |
| findParamList | Additional arguments to be passed on to the binaries for identifying adapter. See below for details. |
| threads | The number of threads used in this step. |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `findAdapter` instead. You can put all additional arguments in one Character(e.g. `"-threads 8"`) with white space splited just like command line, or put them in Character vector(e.g. `c("-threads","8")`). Note that some arguments(`"-file1","-file2","-adapter1","-adapter2","-output1","-output2","-basename","-interleaved","thread"`) to the `findParamList` are invalid if they are already handled as explicit function arguments. See the output of `adapterremoval_usage()` for details about available parameters.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacRenamer renamer atacUnzipAndMerge unzipAndMerge atacBowtie2Mapping](#)

Examples

```

library(magrittr)
td <- tempdir()
setTmpDir(td)

# Identify adapters
prefix<-system.file(package="esATAC", "extdata", "uzmg")
(reads_1 <-file.path(prefix,"m1",dir(file.path(prefix,"m1"))))
(reads_2 <-file.path(prefix,"m2",dir(file.path(prefix,"m2"))))

reads_merged_1 <- file.path(td,"reads1.fastq")
reads_merged_2 <- file.path(td,"reads2.fastq")
atacproc <-
atacUnzipAndMerge(fastqInput1 = reads_1,fastqInput2 = reads_2) %>%
atacRenamer %>% atacFindAdapter

dir(td)

```

FragLenDistr

*Quality control for fragment length distribution***Description**

These functions are used to generate fragment distribution plot. The fourier transform of fragment distribution will be calculated. Strength distribution around period at 10.4bp and 180bp will be shown in another two plots.

Usage

```

atacFragLenDistr(atacProc, reportPrefix = NULL, bedInput = NULL, ...)

## S4 method for signature 'ATACProc'
atacFragLenDistr(atacProc, reportPrefix = NULL, bedInput = NULL, ...)

fragLenDistr(bedInput, reportPrefix = NULL, ...)

```

Arguments

| | |
|--------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed samToBed atacBedUtils bedUtils |
| reportPrefix | Character scalar. The prefix of report files path. |
| bedInput | Character scalar. BED file input path. |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use fragLenDistr instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [samToBed](#) [atacBedUtils](#) [bedUtils](#)

Examples

```
library(R.utils)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
## Not run:
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)
fragLenDistr(bedfile)

## End(Not run)

dir(td)
```

FRiPQC

Quality control for fraction of reads in peaks (FRiP)

Description

Calculate the fraction of reads falling within peak regions

Usage

```
atacFripQC(
  atacProc,
  atacProcPeak = NULL,
  bsgenome = NULL,
  reportOutput = NULL,
  readsBedInput = NULL,
  peakBedInput = NULL,
  ...
)

## S4 method for signature 'ATACProc'
atacFripQC(
  atacProc,
  atacProcPeak = NULL,
  bsgenome = NULL,
```

```

    reportOutput = NULL,
    readsBedInput = NULL,
    peakBedInput = NULL,
    ...
)

```

```
fripQC(readsBedInput, peakBedInput, bsgenome = NULL, reportOutput = NULL, ...)
```

Arguments

| | |
|---------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed samToBed atacBedUtils bedUtils |
| atacProcPeak | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling , peakCalling . |
| bsgenome | BSGenome object scalar. BSGenome object for specific species. |
| reportOutput | Character scalar. The report file path |
| readsBedInput | Character scalar. Reads BED file for peak calling. |
| peakBedInput | Character scalar. Peaks BED file |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(`atacProc`) or generated based on known parameters if their values are default(e.g. `NULL`). Otherwise, the generated values will be overwritten. If you want to use this function independently, or you can use `fripQC` instead.

Value

An invisible `fripQC` object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [atacBedUtils](#)

Examples

```

library(R.utils)
library(BSGenome.Hsapiens.UCSC.hg19)
library(magrittr)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td, "chr20.50000.bed")
bunzip2(bedbzfile, destname=bedfile, overwrite=TRUE, remove=FALSE)

bedUtils(bedInput = bedfile, maxFragLen = 100, chrFilterList = NULL) %>%
atacPeakCalling %>% atacFripQC(bsgenome=BSgenome.Hsapiens.UCSC.hg19)

```

```
dir(td)
```

| | |
|--------------|---|
| getMotifInfo | <i>Generate PFMatrix or PFMatrixList from file.</i> |
|--------------|---|

Description

atacMotifScan and atacMotifScanPair accept PFM in a list, this function convert JASPAR PFM file to [PFMatrix](#) or [PFMatrixList](#).

Usage

```
getMotifInfo(motif.file = NULL)
```

Arguments

motif.file Motif PFM file downloaded from JASPAR.

Details

Generate [PFMatrix](#) or [PFMatrixList](#).

Value

[PFMatrix](#) or [PFMatrixList](#).

Author(s)

Wei Zhang

Examples

```
motif_file <- system.file("extdata", "CustomizedMotif.txt", package="esATAC")
pfm <- getMotifInfo(motif.file = motif_file)
```


Description

The function calculate the nonredundant fraction of reads (NRF). Its definition is number of distinct uniquely mapping reads (i.e. after removing duplicates) / Total number of reads. The function also Calculate PCR Bottlenecking Coefficient 1 (PBC1) and PCR Bottlenecking Coefficient 2 (PBC2). $PBC1=M1/M_DISTINCT$ and $PBC2=M1/M2$, where M1: number of genomic locations where exactly one read maps uniquely, M2: number of genomic locations where two reads map uniquely M_DISTINCT: number of distinct genomic locations to which some read maps uniquely.

Usage

```

atacLibComplexQC(
  atacProc,
  reportOutput = NULL,
  samInput = NULL,
  singleEnd = FALSE,
  subsampleSize = Inf,
  ...
)

## S4 method for signature 'ATACProc'
atacLibComplexQC(
  atacProc,
  reportOutput = NULL,
  samInput = NULL,
  singleEnd = FALSE,
  subsampleSize = Inf,
  ...
)

libComplexQC(
  samInput,
  reportOutput = NULL,
  singleEnd = FALSE,
  subsampleSize = Inf,
  ...
)

```

Arguments

| | |
|---------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacBowtie2Mapping bowtie2Mapping |
| reportOutput | Character scalar. The report file path |
| samInput | Character scalar. The SAM file input path. |
| singleEnd | Character scalar. Single end data if TRUE. Paired end data if FALSE. |
| subsampleSize | Integer scalar. Down sample reads if the number is less than total number when subsample is TRUE |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use [libComplexQC](#) instead.

Value

An invisible [libComplexQC](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacBowtie2Mapping](#) [bowtie2Mapping](#)

Examples

```
library(R.utils)
td <- tempdir()
setTmpDir(td)

sambzfile <- system.file(package="esATAC", "extdata", "Example.sam.bz2")
samfile <- file.path(td,"Example.sam")
bunzip2(sambzfile,destname=samfile,overwrite=TRUE,remove=FALSE)
atacproc<-libComplexQC(samInput = samfile)
```

PeakCallingFseq

Use F-seq to call peak

Description

Use F-seq to call peak

Usage

```
atacPeakCalling(
  atacProc,
  bedInput = NULL,
  background = NULL,
  genomicReadsCount = NULL,
  fragmentSize = 0,
  featureLength = NULL,
  bedOutput = NULL,
  ploidyDir = NULL,
  fileformat = c("bed", "wig", "npf"),
  wiggleTrackStep = NULL,
  threshold = NULL,
  verbose = TRUE,
```

```

        wgThresholdSet = NULL,
        ...
    )

## S4 method for signature 'ATACProc'
atacPeakCalling(
    atacProc,
    bedInput = NULL,
    background = NULL,
    genomicReadsCount = NULL,
    fragmentSize = 0,
    featureLength = NULL,
    bedOutput = NULL,
    ploidyDir = NULL,
    fileformat = c("bed", "wig", "npf"),
    wiggleTrackStep = NULL,
    threshold = NULL,
    verbose = TRUE,
    wgThresholdSet = NULL,
    ...
)

peakCalling(
    bedInput,
    background = NULL,
    genomicReadsCount = NULL,
    fragmentSize = 0,
    featureLength = NULL,
    bedOutput = NULL,
    ploidyDir = NULL,
    fileformat = c("bed", "wig", "npf"),
    wiggleTrackStep = NULL,
    threshold = NULL,
    verbose = TRUE,
    wgThresholdSet = NULL,
    ...
)

```

Arguments

| | |
|-------------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed , atacBedUtils . |
| bedInput | Character scalar. BED file input path. |
| background | Character scalar. background directory default: NULL (none) |
| genomicReadsCount | Integer scalar. genomic count of sequence reads. default: NULL (calculated) |
| fragmentSize | Integer scalar. fragment size. set NULL to estimat from data. default:0 |
| featureLength | Character scalar. feature length default: NULL (600) |
| bedOutput | Character scalar. the output bed file path |
| ploidyDir | Character scalar. ploidy/input directory. default: NULL |
| fileformat | Character scalar. File format of result. default: bed |

| | |
|-----------------|---|
| wiggleTrackStep | Integer scalar. wiggle track step default: NULL (1) |
| threshold | Numeric scalar. threshold (standard deviations) default: NULL (4.0) |
| verbose | Logical scalar. verbose output if TRUE. |
| wgThresholdSet | Character scalar. wg threshold set default: NULL (calculated) |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `peakCalling` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [samToBed](#) [atacBedUtils](#) [bedUtils](#)

Examples

```
library(R.utils)
library(magrittr)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)

bedUtils(bedInput = bedfile,maxFragLen = 100, chrFilterList = NULL) %>%
  atacPeakCalling

dir(td)
```

PeakCallingMACS2

Use MACS2 to call peak

Description

Use MACS2 installed by to call peak

Usage

```

atacPeakCallingMACS2(
  atacProc,
  bedInput = NULL,
  background = NULL,
  outputPrefix = NULL,
  genomeSize = NULL,
  pvalueThreshold = 0.01,
  extsize = 150,
  shift = -round(extsize/2),
  ...
)

## S4 method for signature 'ATACProc'
atacPeakCallingMACS2(
  atacProc,
  bedInput = NULL,
  background = NULL,
  outputPrefix = NULL,
  genomeSize = NULL,
  pvalueThreshold = 0.01,
  extsize = 150,
  shift = -round(extsize/2),
  ...
)

peakCallingMACS2(
  bedInput,
  background = NULL,
  outputPrefix = NULL,
  genomeSize = NULL,
  pvalueThreshold = 0.01,
  extsize = 150,
  shift = -round(extsize/2),
  ...
)

testPeakCallingMACS2()

```

Arguments

| | |
|--------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed , atacBedUtils . |
| bedInput | Character scalar. BED file input path. |
| background | Character scalar. background directory default: NULL (none) |
| outputPrefix | Character scalar. the output bed file path |
| extsize | Logical scalar. verbose output if TRUE. |
| shift | Character scalar. wg threshold set default: NULL (calculated) |
| ... | Additional arguments, currently unused. |
| genomeSize | Numeric scalar. the size of genome |

pvalueThreshold

Numeric scalar. threshold (standard deviations) default: NULL (4.0)

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `peakCalling` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [samToBed](#) [atacBedUtils](#) [bedUtils](#)

Examples

```
library(R.utils)
library(magrittr)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)

bedUtils(bedInput = bedfile,maxFragLen = 100, chrFilterList = NULL) %>%
  atacPeakCalling

dir(td)
```

PeakQC

Quality control for peak overlap

Description

These functions are used to calculate the overlap ratio in specific quality control region. Blacklist and DHS region are provided. You can also set your own BED file as quality control region.

Usage

```
atacPeakQC(
  atacProc,
  bsgenome = NULL,
  reportOutput = NULL,
  qcbedInput = c("DHS", "blacklist", "path/to/bed"),
```

```

    bedInput = NULL,
    newStepType = "PeakQC",
    ...
)

## S4 method for signature 'ATACProc'
atacPeakQC(
  atacProc,
  bsgenome = NULL,
  reportOutput = NULL,
  qcbedInput = c("DHS", "blacklist", "path/to/bed"),
  bedInput = NULL,
  newStepType = "PeakQC",
  ...
)

peakQC(
  bedInput,
  bsgenome = NULL,
  reportOutput = NULL,
  qcbedInput = c("DHS", "blacklist", "path/to/bed"),
  newStepType = "PeakQC",
  ...
)

```

Arguments

| | |
|--------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed , atacBedUtils . |
| bsgenome | BSGenome object scalar. BSGenome object for specific species. |
| reportOutput | Character scalar. The report file path. |
| qcbedInput | Character scalar. It can be "DHS", "blacklist" or Other quality control BED file input path. |
| bedInput | Character scalar. BED file input path for quality control. |
| newStepType | Character scalar. New step type name for different default parameters. |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object or generated based on known parameters if their values are default (e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `peakQC` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [atacBedUtils](#)

Examples

```
library(R.utils)
library(magrittr)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)
blacklistfile <- system.file(package="esATAC", "extdata", "hg19.blacklist.bed")
library(BSgenome.Hsapiens.UCSC.hg19)
bedUtils(bedInput = bedfile,maxFragLen = 100, chrFilterList = NULL) %>%
atacPeakCalling %>% atacPeakQC(qcbedInput = blacklistfile, bsgenome = BSgenome.Hsapiens.UCSC.hg19)
dir(td)
```

RemoveAdapter

Use AdapterRemoval to remove adapters

Description

Use AdapterRemoval to remove adapters

Usage

```
atacRemoveAdapter(
  atacProc,
  adapter1 = NULL,
  adapter2 = NULL,
  fastqOutput1 = NULL,
  reportPrefix = NULL,
  fastqOutput2 = NULL,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  paramList = NULL,
  findParamList = NULL,
  ...
)

## S4 method for signature 'ATACProc'
atacRemoveAdapter(
  atacProc,
  adapter1 = NULL,
  adapter2 = NULL,
  fastqOutput1 = NULL,
  reportPrefix = NULL,
  fastqOutput2 = NULL,
```



```

    fastqInput1 = NULL,
    fastqInput2 = NULL,
    interleave = FALSE,
    threads = getThreads(),
    paramList = NULL,
    findParamList = NULL,
    ...
)

removeAdapter(
  fastqInput1,
  fastqInput2,
  adapter1,
  adapter2,
  fastqOutput1 = NULL,
  reportPrefix = NULL,
  fastqOutput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  paramList = NULL,
  findParamList = NULL,
  ...
)

```

Arguments

| | |
|--------------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacRenamer renamer atacUnzipAndMerge unzipAndMerge |
| adapter1 | Character. It is an adapter sequence for file1. For single end data, it is required. |
| adapter2 | Character. It is an adapter sequence for file2. |
| fastqOutput1 | Character. The trimmed mate1 reads output file path for fastqInput2. Default: <code>basename.pair1.truncated</code> (paired-end), <code>basename.truncated</code> (single-end), or <code>basename.paired.truncated</code> (interleaved) |
| reportPrefix | Character. The prefix of report files path. Default: generate from known parameters |
| fastqOutput2 | Character. The trimmed mate2 reads output file path for fastqInput2. Default: <code>BASENAME.pair2.truncated</code> (only used in PE mode, but not if <code>-interleaved-output</code> is enabled) |
| fastqInput1 | Character vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2 And it can also be interleaved file paths when argument <code>interleaved=TRUE</code> |
| fastqInput2 | Character vector. It contains file paths with #2 mates paired with file paths in fastqInput1 For single-end sequencing files and interleaved paired-end sequencing files(argument <code>interleaved=TRUE</code>), it must be NULL. |
| interleave | Logical. Set TRUE when files are interleaved paired-end sequencing data. |
| threads | Numeric. The max threads allowed to be used by this step. Default: <code>getThreads()</code> |
| paramList | Additional arguments to be passed on to the binaries for removing adapter. See below for details. |

`findParamList` Additional arguments to be passed on to the binaries for identifying adapter. See below for details.

... Additional arguments, currently unused.

Details

The parameter related to input and output file path will be automatically obtained from `ATACProc-class` object or generated based on known parameters if their values are default (e.g. `NULL`). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `removeAdapter` instead. You can put all additional arguments in one `Character` (e.g. `"-threads 8"`) with white space splited just like command line, or put them in `Character` vector (e.g. `c("-threads","8")`). Note that some arguments (`"-file1","-file2","-adapter1","-adapter2","-output1","-output2","-basename","-interleaved","thread"`) to the `paramList` and `findParamList` are invalid if they are already handled as explicit function arguments. See the output of `adapterremoval_usage()` for details about available parameters.

Value

An invisible `ATACProc-class` object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacRenamer](#) [renamer](#) [atacUnzipAndMerge](#) [unzipAndMerge](#) [atacBowtie2Mapping](#)

Examples

```
library(magrittr)
td <- tempdir()
setTmpDir(td)

# Identify adapters
prefix<-system.file(package="esATAC", "extdata", "uzmg")
(reads_1 <-file.path(prefix,"m1",dir(file.path(prefix,"m1"))))
(reads_2 <-file.path(prefix,"m2",dir(file.path(prefix,"m2"))))

reads_merged_1 <- file.path(td,"reads1.fastq")
reads_merged_2 <- file.path(td,"reads2.fastq")
atacproc <-
atacUnzipAndMerge(fastqInput1 = reads_1,fastqInput2 = reads_2) %>%
atacRenamer %>% atacFindAdapter %>% atacRemoveAdapter

dir(td)
```

| | |
|---------|-----------------------------------|
| Renamer | <i>Rename reads name in fastq</i> |
|---------|-----------------------------------|

Description

Rename reads name in fastq with increasing integer

Usage

```

atacRenamer(
  atacProc,
  fastqOutput1 = NULL,
  fastqOutput2 = NULL,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  ...
)

## S4 method for signature 'ATACProc'
atacRenamer(
  atacProc,
  fastqOutput1 = NULL,
  fastqOutput2 = NULL,
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  ...
)

renamer(
  fastqInput1 = NULL,
  fastqInput2 = NULL,
  fastqOutput1 = NULL,
  fastqOutput2 = NULL,
  interleave = FALSE,
  threads = getThreads(),
  ...
)

```

Arguments

| | |
|--------------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacUnzipAndMerge unzipAndMerge |
| fastqOutput1 | Character scalar. The output file path of renamed fastqInput1. |
| fastqOutput2 | Character scalar. The output file path of renamed fastqInput2. |
| fastqInput1 | Character scalar. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file path with #1 mates paired with file path in file2 And it can also be interleaved file paths when argument interleave=TRUE |

| | |
|-------------|--|
| fastqInput2 | Character scalar. It contains file path with #2 mates paired with file paths in fastqInput1 For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. |
| interleave | Character scalar. Set TRUE when files are interleaved paired-end sequencing data. |
| threads | Integer scalar. The threads will be created in this process. default: 1 |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use renamer instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacUnzipAndMerge](#) [unzipAndMerge](#) [atacQCReport](#) [atacRemoveAdapter](#)

Examples

```
ignoreCheck() # warning: run this for fast test only
library(magrittr)
td <- tempdir()
setTmpDir(td)

# Identify adapters
prefix<-system.file(package="esATAC", "extdata", "uzmg")
(reads_1 <-file.path(prefix,"m1",dir(file.path(prefix,"m1"))))
(reads_2 <-file.path(prefix,"m2",dir(file.path(prefix,"m2"))))

reads_merged_1 <- file.path(td,"reads1.fastq")
reads_merged_2 <- file.path(td,"reads2.fastq")
atacproc <-
atacUnzipAndMerge(fastqInput1 = reads_1,fastqInput2 = reads_2) %>%
atacRenamer

dir(td)
```

Description

Ranking functional groups based on a set of genes. For more information, please see [enrichGO](#).

Usage

```
atacGOAnalysis(  
  atacProc,  
  gene = NULL,  
  OrgDb = NULL,  
  keytype = "ENTREZID",  
  ont = "MF",  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe = NULL,  
  qvalueCutoff = 0.2,  
  readable = FALSE,  
  pool = FALSE,  
  goOutput = NULL,  
  ...  
)  
  
## S4 method for signature 'ATACProc'  
atacGOAnalysis(  
  atacProc,  
  gene = NULL,  
  OrgDb = NULL,  
  keytype = "ENTREZID",  
  ont = "MF",  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe = NULL,  
  qvalueCutoff = 0.2,  
  readable = FALSE,  
  pool = FALSE,  
  goOutput = NULL,  
  ...  
)  
  
goanalysis(  
  gene,  
  OrgDb = NULL,  
  keytype = "ENTREZID",  
  ont = "MF",  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  universe = NULL,  
  qvalueCutoff = 0.2,
```

```

readable = FALSE,
pool = FALSE,
goOutput = NULL,
...
)

```

Arguments

| | |
|---------------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakAnno . |
| gene | A vector of entrez gene id. |
| OrgDb | Genome wide annotation database. |
| keytype | Keytype of input gene. |
| ont | One of "MF", "BP", and "CC" subontologies. "MF" for molecular function, "BP" for biological process, "CC" for cellular component. |
| pvalueCutoff | pvalueCutoff. |
| pAdjustMethod | One of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". |
| universe | Background genes. |
| qvalueCutoff | qvalue cutoff. |
| readable | whether mapping gene ID to gene Name. |
| pool | If ont='ALL', whether pool 3 GO sub-ontologies. |
| goOutput | Character scalar. Output file path. Default:in the same folder as your input file with the suffix "df". |
| ... | Additional arguments, currently unused. |

Details

This function using [enrichGO](#) to do GO analysis but fixed some parameters. If atacProc is not NULL, it will read the gene ID from the output of [atacPeakAnno](#).

Value

An invisible [ATACProc-class](#) object scalar.

Author(s)

Wei Zhang

References

Guangchuang Yu., Li-Gen Wang, Yanyan Han, Qing-Yu He. clusterProfiler: an R package for comparing biological themes among gene clusters. OMICS: A Journal of Integrative Biology. 2012, 16(5):284-287

See Also

[atacPeakAnno](#) [enrichGO](#) function [enrichGO](#) in package "clusterProfiler"

Examples

```
## Not run:
library(org.Hs.eg.db)
# generate simulated geneID
geneId <- as.character(sample(seq(10000), 100))
goanalysis(gene = geneId, OrgDb = 'org.Hs.eg.db')

## End(Not run)
```

RMotifScan*Search Motif Position in Given Regions*

Description

Search motif position in genome according thr given motif and peak information.

Usage

```
atacMotifScan(
  atacProc,
  peak = NULL,
  genome = NULL,
  motifs = NULL,
  p.cutoff = 1e-06,
  scan0.dir = NULL,
  prefix = NULL,
  ...
)

## S4 method for signature 'ATACProc'
atacMotifScan(
  atacProc,
  peak = NULL,
  genome = NULL,
  motifs = NULL,
  p.cutoff = 1e-06,
  scan0.dir = NULL,
  prefix = NULL,
  ...
)

motifscan(
  peak = NULL,
  genome = NULL,
  motifs = NULL,
  p.cutoff = 1e-06,
  scan0.dir = NULL,
  prefix = NULL,
  ...
)
```

Arguments

| | |
|-----------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling . |
| peak | Character scalar. Input region path. UCSC bed file is recommended. Other file should be able to import as GRanges objects through import in package rtracklayer . |
| genome | BSgenome object, Default: from getRefRc . |
| motifs | either PFMatrix , PFMatrixList , PWMMatrix , PWMMatrixList . |
| p.cutoff | p-value cutoff for returning motifs. |
| scan0.dir | Character scalar. the output file directory. This function will use the name in motifs as the file name to save the motif position information in separate files. |
| prefix | prefix for Output file. |
| ... | Additional arguments, currently unused. |

Details

This function scan motif position in a given genome regions.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also

[atacPeakCalling](#) [atacCutSiteCount](#)

Examples

```
## Not run:
library(R.utils)
library(BSgenome.Hsapiens.UCSC.hg19)
peak.path <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
peak.path <- as.vector(bunzip2(filename = peak.path, destname = file.path(getwd(), "Example_peak1.bed"), ext=
motif <- readRDS(system.file("extdata", "MotifPFM.rds", package="esATAC"))

motifscan(peak = peak.path, genome = BSgenome.Hsapiens.UCSC.hg19, motifs = motif)

## End(Not run)
```

| | |
|----------------|---|
| RMotifScanPair | <i>Search Motif Position in Given Regions</i> |
|----------------|---|

Description

Search motif position in genome according thr given motif and peak information.

Usage

```
atacMotifScanPair(  
  atacProc,  
  peak1 = NULL,  
  peak2 = NULL,  
  background = NULL,  
  genome = NULL,  
  motifs = NULL,  
  p.cutoff = 1e-04,  
  scan0.dir = NULL,  
  prefix = NULL,  
  ...  
)  
  
## S4 method for signature 'ATACProc'  
atacMotifScanPair(  
  atacProc,  
  peak1 = NULL,  
  peak2 = NULL,  
  background = NULL,  
  genome = NULL,  
  motifs = NULL,  
  p.cutoff = 1e-04,  
  scan0.dir = NULL,  
  prefix = NULL,  
  ...  
)  
  
motifscanpair(  
  peak1 = NULL,  
  peak2 = NULL,  
  background = NULL,  
  genome = NULL,  
  motifs = NULL,  
  p.cutoff = 1e-04,  
  scan0.dir = NULL,  
  prefix = NULL,  
  ...  
)
```

Arguments

atacProc [ATACProc-class](#) object scalar. It has to be the return value of upstream process: [atacPeakComp](#).

| | |
|------------|---|
| peak1 | peak file path. |
| peak2 | peak file path. |
| background | background peak file path. |
| genome | BSgenome object, Default: from getRefRc . |
| motifs | either PFMatrix , PFMatrixList , PWMMatrix , PWMMatrixList . |
| p.cutoff | p-value cutoff for returning motifs. |
| scan0.dir | Character scalar. the output file directory. This function will use the name in motifs as the file name to save the motif position information in separate files. |
| prefix | prefix for Output file. Order: peak1, peak2, background. |
| ... | Additional arguments, currently unused. |

Details

This function scan motif position in a given genome regions.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also

[atacPeakComp](#)

Examples

```
## Not run:
library(R.utils)
library(BSgenome.Hsapiens.UCSC.hg19)
p1bz <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
p2bz <- system.file("extdata", "Example_peak2.bed.bz2", package="esATAC")
peak1_path <- as.vector(bunzip2(filename = p1bz,
  destname = file.path(getwd(), "Example_peak1.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE , remove = FALSE))
peak2_path <- as.vector(bunzip2(filename = p2bz,
  destname = file.path(getwd(), "Example_peak2.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
peakcom.output <- peakcomp.bedInput1 = peak1_path, bedInput2 = peak2_path,
  olap.rate = 0.1)

motif <- readRDS(system.file("extdata", "MotifPFM.rds", package="esATAC"))
output <- atacMotifScanPair(atacProc = peakcom.output,
  genome = BSgenome.Hsapiens.UCSC.hg19, motifs = motif)

## End(Not run)
```

RPeakAnno

Annotate ATAC-seq Peak

Description

This function annotates ATAC-seq peak by a given annotation database. For more information, please see [annotatePeak](#).

Usage

```

atacPeakAnno(
  atacProc,
  peakInput = NULL,
  tssRegion = c(-1000, 1000),
  TxDb = NULL,
  level = "transcript",
  genomicAnnotationPriority = c("Promoter", "5UTR", "3UTR", "Exon", "Intron",
    "Downstream", "Intergenic"),
  annoDb = NULL,
  addFlankGeneInfo = FALSE,
  flankDistance = 5000,
  sameStrand = FALSE,
  ignoreOverlap = FALSE,
  ignoreUpstream = FALSE,
  ignoreDownstream = FALSE,
  overlap = "TSS",
  annoOutput = NULL,
  ...
)

## S4 method for signature 'ATACProc'
atacPeakAnno(
  atacProc,
  peakInput = NULL,
  tssRegion = c(-1000, 1000),
  TxDb = NULL,
  level = "transcript",
  genomicAnnotationPriority = c("Promoter", "5UTR", "3UTR", "Exon", "Intron",
    "Downstream", "Intergenic"),
  annoDb = NULL,
  addFlankGeneInfo = FALSE,
  flankDistance = 5000,
  sameStrand = FALSE,
  ignoreOverlap = FALSE,
  ignoreUpstream = FALSE,
  ignoreDownstream = FALSE,
  overlap = "TSS",
  annoOutput = NULL,
  ...
)

```

```

peakanno(
  peakInput,
  tssRegion = c(-1000, 1000),
  TxDb = NULL,
  level = "transcript",
  genomicAnnotationPriority = c("Promoter", "5UTR", "3UTR", "Exon", "Intron",
    "Downstream", "Intergenic"),
  annoDb = NULL,
  addFlankGeneInfo = FALSE,
  flankDistance = 5000,
  sameStrand = FALSE,
  ignoreOverlap = FALSE,
  ignoreUpstream = FALSE,
  ignoreDownstream = FALSE,
  overlap = "TSS",
  annoOutput = NULL,
  ...
)

```

Arguments

| | |
|---------------------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling . |
| peakInput | Character scalar. Input peak file path. UCSC bed file is recommended. Other file should be able to import as GRanges objects through import in package rtracklayer . |
| tssRegion | Region range of TSS, default:c(-1000, 1000). |
| TxDb | TxDb object, annotation database. |
| level | "transcript" or "gene". |
| genomicAnnotationPriority | genomic annotation priority. |
| annoDb | Gene annotation database. |
| addFlankGeneInfo | logical, add flanking gene information from the peaks. |
| flankDistance | distance of flanking sequence. |
| sameStrand | logical, whether find nearest/overlap gene in the same strand. |
| ignoreOverlap | logical, whether ignore overlap of TSS with peak. |
| ignoreUpstream | logical, if True only annotate gene at the 3' of the peak. |
| ignoreDownstream | logical, if True only annotate gene at the 5' of the peak. |
| overlap | one of 'TSS' or 'all', if overlap="all", then gene overlap with peak will be reported as nearest gene, no matter the overlap is at TSS region or not. |
| annoOutput | Character scalar. the output file path. |
| ... | Additional arguments, currently unused. |

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

References

Guangchuan Yu, Li-Gen Wang, Qing-Yu He. CHIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization. *Bioinformatics* 2015, 31(14):2382-2383

See Also

[atacPeakCalling](#) [atacGOAnalysis](#)

Examples

```
library(R.utils)
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
p1bz <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
peak1_path <- as.vector(bunzip2(filename = p1bz,
  destname = file.path(getwd(), "Example_peak1.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
#peakanno(peakInput = peak1_path, TxDb = TxDb.Hsapiens.UCSC.hg19.knownGene,
#annoDb = 'org.Hs.eg.db')
```

RPeakComp

Find the overlap or differential peaks between two samples.

Description

This function compares two peak file and report overlap or differential peaks according to the parameter "operation".

Usage

```
atacPeakComp(
  atacProcPeak1,
  atacProcPeak2,
  bedInput1 = NULL,
  bedInput2 = NULL,
  bedOutput = NULL,
  olap.rate = 0.2,
  ...
)

## S4 method for signature 'ATACProc'
atacPeakComp(
  atacProcPeak1,
  atacProcPeak2,
  bedInput1 = NULL,
  bedInput2 = NULL,
  bedOutput = NULL,
```

```

    olap.rate = 0.2,
    ...
)

peakcomp(
  bedInput1 = NULL,
  bedInput2 = NULL,
  bedOutput = NULL,
  olap.rate = 0.2,
  ...
)

```

Arguments

| | |
|---------------|---|
| atacProcPeak1 | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling . |
| atacProcPeak2 | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling . |
| bedInput1 | Character scalar. Input peak file path. UCSC bed file is recommended. Other file should be able to import as GRanges objects through <code>import</code> in package <code>rtracklayer</code> . |
| bedInput2 | Character scalar. Input peak file path. UCSC bed file is recommended. Other file should be able to import as GRanges objects through <code>import</code> in package <code>rtracklayer</code> . |
| bedOutput | The output file path for overlap peaks. |
| olap.rate | Overlap rate, if the overlap region between 2 peak is more than this rate of the short peak, these two peak are considered to be overlap and will be merged to a bigger peak. Default: 0.2. NOTICE: multi-peak will be merged together! |
| ... | Additional arguments, currently unused. |

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also

[atacPeakCalling](#)

Examples

```

library(R.utils)
p1bz <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
p2bz <- system.file("extdata", "Example_peak2.bed.bz2", package="esATAC")
## Not run:
peak1_path <- as.vector(bunzip2(filename = p1bz,
  destname = file.path(getwd(), "Example_peak1.bed"),
  ext="bz2", FUN=bzfile, overwrite=TRUE , remove = FALSE))
peak2_path <- as.vector(bunzip2(filename = p2bz,

```

```

destname = file.path(getwd(), "Example_peak2.bed"),
ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
output <- peakcomp.bedInput1 = peak1_path, bedInput2 = peak2_path,
olap.rate = 0.1)

## End(Not run)

```

RSNPs

*Find whether snps are in the given regions.***Description**

Find snps(user providing) in given regions. This function do not consider strand.

Usage

```

atacSNPAnno(
  atacProc,
  snp.info = NULL,
  region.info = NULL,
  annoOutput = NULL,
  ...
)

## S4 method for signature 'ATACProc'
atacSNPAnno(
  atacProc,
  snp.info = NULL,
  region.info = NULL,
  annoOutput = NULL,
  ...
)

spanno(snp.info = NULL, region.info = NULL, annoOutput = NULL, ...)

```

Arguments

| | |
|-------------|---|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacPeakCalling atacMotifScan . If from atacPeakCalling , the output file would contain the snps in given region. If from atacMotifScan , the output file would contain file path to the output of every motif. |
| snp.info | Character scalar. Input snp info path. There are two type of input files(you can specify by parameter withend). 1.The first 2 column must be chr, position. e.g. chr13 39776775 rs7993214. Other columns could be other information about snps. 2.The first 3 column must be chr, start, end. e.g. chr13 39776775 39776775 rs7993214. Other columns could be other information about snps. When genome is hg19, using human disease as default. |
| region.info | Character scalar. Input region info path. The first 3 column must be chr, position, end. The standard BED format is recommended. |
| annoOutput | Character scalar. Output path. |
| ... | withend Your snp data has only one position column or 2. |

Value

An invisible [ATACProc-class](#) object scalar.

Author(s)

Wei Zhang

See Also

[atacPeakCalling](#) [atacMotifScan](#)

Examples

```
library(R.utils)
p1bz <- system.file("extdata", "Example_peak1.bed.bz2", package="esATAC")
peak1_path <- as.vector(bunzip2(filename = p1bz,
destname = file.path(getwd(), "Example_peak1.bed"),
ext="bz2", FUN=bzfile, overwrite=TRUE, remove = FALSE))
snps <- system.file("extdata", "snp_info", package="esATAC")
#snpanno(snp.info = snps, region.info = peak1_path)
```

Rsortbam

Sort bam file and rebuild bai index.

Description

Sort bamfile and build index.

Usage

```
atacBamSort(atacProc, bamInput = NULL, bamOutput = NULL, ...)
```

```
## S4 method for signature 'ATACProc'
```

```
atacBamSort(atacProc, bamInput = NULL, bamOutput = NULL, ...)
```

```
bamsort(bamInput = NULL, bamOutput = NULL, ...)
```

Arguments

| | |
|-----------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSam2Bam . |
| bamInput | Character scalar. Input bam file path. |
| bamOutput | Character scalar. Output bam file path. |
| ... | Additional arguments, currently unused. |

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also[atacSam2Bam](#) [atacBam2Bed](#)**Examples**

```
library(Rsamtools)
ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
bamsort(bamInput = ex1_file)
```

SamToBam*Convert sam format to bam format.*

Description

This function convert a sam file into a bam file.

Usage

```
atacSam2Bam(atacProc, samInput = NULL, bamOutput = NULL, isSort = TRUE, ...)

## S4 method for signature 'ATACProc'
atacSam2Bam(atacProc, samInput = NULL, bamOutput = NULL, isSort = TRUE, ...)

sam2bam(samInput, bamOutput = NULL, isSort = TRUE, ...)
```

Arguments

| | |
|------------------------|---|
| <code>atacProc</code> | ATACProc-class object scalar. It has to be the return value of upstream process: atacBowtie2Mapping . |
| <code>samInput</code> | Character scalar. Sam file input path. |
| <code>bamOutput</code> | Character scalar. Bam file output path. If ignored, bed file will be put in the same path as the sam file. |
| <code>isSort</code> | Logical scalar. Sort bam. |
| <code>...</code> | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) `object(atacProc)` or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use `bamToBed` instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Wei Zhang

See Also[atacBowtie2Mapping](#) [atacBam2Bed](#) [atacBamSort](#)**Examples**

```
library(R.utils)
sam_bz <- system.file("extdata", "Example.sam.bz2", package="esATAC")
sam_path <- as.vector(bunzip2(filename = sam_bz,
destname = file.path(getwd(), "Example.sam"),
ext="bz2", FUN=bzfile, remove = FALSE))
sam2bam(samInput = sam_path)
```

SamToBed

Convert SAM file to BED file

Description

This function is used to convert SAM file to BED file and merge interleaved paired end reads, shift reads, filter reads according to chromosome, filter reads according to fragment size, sort, remove duplicate reads before generating BED file.

Usage

```
atacSamToBed(
  atacProc,
  reportOutput = NULL,
  merge = c("auto", "yes", "no"),
  posOffset = +4,
  negOffset = -5,
  chrFilterList = "chrM",
  samInput = NULL,
  bedOutput = NULL,
  sortBed = TRUE,
  minFragLen = 0,
  maxFragLen = 100,
  saveExtLen = FALSE,
  uniqueBed = TRUE,
  ...
)

## S4 method for signature 'ATACProc'
atacSamToBed(
  atacProc,
  reportOutput = NULL,
  merge = c("auto", "yes", "no"),
  posOffset = +4,
```

```

    negOffset = -5,
    chrFilterList = "chrM",
    samInput = NULL,
    bedOutput = NULL,
    sortBed = TRUE,
    minFragLen = 0,
    maxFragLen = 100,
    saveExtLen = FALSE,
    uniqueBed = TRUE,
    ...
)

samToBed(
  samInput,
  reportOutput = NULL,
  merge = c("auto", "yes", "no"),
  posOffset = +4,
  negOffset = -5,
  chrFilterList = "chrM",
  bedOutput = NULL,
  sortBed = TRUE,
  minFragLen = 0,
  maxFragLen = 100,
  saveExtLen = FALSE,
  uniqueBed = TRUE,
  ...
)

```

Arguments

| | |
|---------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacBowtie2Mapping bowtie2Mapping |
| reportOutput | Character scalar report file path |
| merge | Logical scalar Merge paired end reads. |
| posOffset | Integer scalar The offset that positive strand reads will shift. |
| negOffset | Integer scalar The offset that negative strand reads will shift. |
| chrFilterList | Character vector The chromatin(or regex of chromatin) will be discard |
| samInput | Character scalar. SAM file input path. |
| bedOutput | Character scalar. Bed file output path. |
| sortBed | Logical scalar Sort bed file in the order of chromatin, start, end |
| minFragLen | Integer scalar The minimum fragment size will be retained. |
| maxFragLen | Integer scalar The maximum fragment size will be retained. |
| saveExtLen | Logical scaler Save the fragment that are not in the range of minFragLen and maxFragLen |
| uniqueBed | Logical scalar Remove duplicates reads in bed if TRUE. default: FALSE |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object(atacProc) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, you can use samToBed instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacBowtie2Mapping](#) [bowtie2Mapping](#) [atacFragLenDistr](#) [atacExtractCutSite](#) [atacPeakCalling](#)
[atacBedUtils](#) [atacTSSQC](#) [atacBedToBigWig](#)

Examples

```
library(R.utils)
library(magrittr)
td <- tempdir()
setTmpDir(td)

sambzfile <- system.file(package="esATAC", "extdata", "Example.sam.bz2")
samfile <- file.path(td,"Example.sam")
bunzip2(sambzfile,destname=samfile,overwrite=TRUE,remove=FALSE)
samToBed(samInput = samfile)
```

SingleRepReport

Final report for single group of regions

Description

When user call all steps in the pipeline, the final report can be generated.

Usage

```
atacSingleRepReport(prevStep, htmlOutput = NULL, createHTML = TRUE, ...)

## S4 method for signature 'Step'
atacSingleRepReport(prevStep, htmlOutput = NULL, createHTML = TRUE, ...)
```

Arguments

prevStep [Step-class](#) object scalar. Any steps object in this package is acceptable when the pipeline is ready.

htmlOutput Character scalar. HTML report file directory Default: NULL ("Report.html")

createHTML Logical scalar. If create HTML file. Default: TRUE. This parameter needs to be set FALSE when pandoc or other dependence softwares are not available for markdown package.

... Additional arguments, currently unused.

Details

The report is HTML format. All link in HTML file is the relative directory in report step folder and other step folder. If user want to move HTML file and keep all link access available, they should move the whole pipeline folder at the same time.

Value

An invisible [ATACProc-class](#) object ([Step-class](#) based) scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacPipe](#)

| | |
|-------|---|
| TSSQC | <i>Quality control for transcription start site(TSS) reads enrichment</i> |
|-------|---|

Description

These functions are used to generate the reads coverage plot around TSS.

Usage

```

atacTSSQC(
  atacProc,
  txdbKnownGene = NULL,
  bsgenome = NULL,
  reportPrefix = NULL,
  bedInput = NULL,
  fragLenRange = c(0, 2000),
  tssUpdownstream = 1000,
  newStepType = "TSSQC",
  ...
)

## S4 method for signature 'ATACProc'
atacTSSQC(
  atacProc,
  txdbKnownGene = NULL,
  bsgenome = NULL,
  reportPrefix = NULL,
  bedInput = NULL,

```

```

    fragLenRange = c(0, 2000),
    tssUpdownstream = 1000,
    newStepType = "TSSQC",
    ...
)

tssQC(
  bedInput,
  txdbKnownGene = NULL,
  bsgenome = NULL,
  reportPrefix = NULL,
  fragLenRange = c(0, 2000),
  tssUpdownstream = 1000,
  newStepType = "TSSQC",
  ...
)

```

Arguments

| | |
|-----------------|--|
| atacProc | ATACProc-class object scalar. It has to be the return value of upstream process: atacSamToBed , atacBedUtils . |
| txdbKnownGene | TxDB object scalar. TxDb object for specific species. |
| bsgenome | BSGenome object scalar. BSGenome object for specific species. |
| reportPrefix | Character scalar. The prefix of report files path. |
| bedInput | Character scalar. BED file input path. |
| fragLenRange | Integer vector of 2 element. The fragment length ranges. |
| tssUpdownstream | Integer scalar. The upstream and downstream from TSS locations. |
| newStepType | Character scalar. New class name |
| ... | Additional arguments, currently unused. |

Details

The parameter related to input and output file path will be automatically obtained from [ATACProc-class](#) object([atacProc](#)) or generated based on known parameters if their values are default(e.g. NULL). Otherwise, the generated values will be overwritten. If you want to use this function independently, [atacProc](#) should be set NULL or you can use [tssQC](#) instead.

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacSamToBed](#) [samToBed](#) [atacBedUtils](#) [bedUtils](#)

Examples

```

library(R.utils)
td <- tempdir()
setTmpDir(td)

bedbzfile <- system.file(package="esATAC", "extdata", "chr20.50000.bed.bz2")
bedfile <- file.path(td,"chr20.50000.bed")
bunzip2(bedbzfile,destname=bedfile,overwrite=TRUE,remove=FALSE)
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(BSgenome.Hsapiens.UCSC.hg19)
tssQC(bedfile,TxDb.Hsapiens.UCSC.hg19.knownGene,BSgenome.Hsapiens.UCSC.hg19,fragLenRange=c(180,247))

dir(td)

```

UnzipAndMerge

Unzip and merge fastq files

Description

Unzip and merge fastq files that are in format of bzip, gzip or fastq

Usage

```

atacUnzipAndMerge(
  fastqInput1,
  fastqInput2 = NULL,
  fastqOutput1 = NULL,
  fastqOutput2 = NULL,
  interleave = FALSE,
  ...
)

unzipAndMerge(
  fastqInput1,
  fastqInput2 = NULL,
  fastqOutput1 = NULL,
  fastqOutput2 = NULL,
  interleave = FALSE,
  ...
)

```

Arguments

| | |
|--------------|--|
| fastqInput1 | Character vector. For single-end sequencing, it contains sequence file paths. For paired-end sequencing, it can be file paths with #1 mates paired with file paths in fastqInput2 And it can also be interleaved file paths when argument interleaved=TRUE |
| fastqInput2 | Character vector. It contains file paths with #2 mates paired with file paths in fastqInput1 For single-end sequencing files and interleaved paired-end sequencing files(argument interleaved=TRUE), it must be NULL. |
| fastqOutput1 | Character. The trimmed mate1 reads output file path for fastqInput2. |

| | |
|--------------|--|
| fastqOutput2 | Character. The trimmed mate2 reads output file path for fastqInput2. |
| interleave | Logical. Set TRUE when files are interleaved paired-end sequencing data. |
| ... | Additional arguments, currently unused. |

Value

An invisible [ATACProc-class](#) object scalar for downstream analysis.

Author(s)

Zheng Wei

See Also

[atacRenamer](#) [atacQCReport](#)

Examples

```
ignoreCheck() # warning: run this for fast test only

td<-tempdir()
setTmpDir(td)

# Identify adapters
prefix<-system.file(package="esATAC", "extdata", "uzmg")
(reads_1 <-file.path(prefix,"m1",dir(file.path(prefix,"m1"))))
(reads_2 <-file.path(prefix,"m2",dir(file.path(prefix,"m2"))))

reads_merged_1 <- file.path(td,"reads_1.fq")
reads_merged_2 <- file.path(td,"reads_2.fq")
atacproc <- atacUnzipAndMerge(fastqInput1 = reads_1,fastqInput2 = reads_2)
dir(td)
```


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