

Package ‘dupRadar’

May 5, 2024

Type Package

Title Assessment of duplication rates in RNA-Seq datasets

Version 1.34.0

Date 2015-09-26

Author Sergi Sayols <sergisayolspuig@gmail.com>, Holger Klein
<holger.klein@gmail.com>

Maintainer Sergi Sayols <sergisayolspuig@gmail.com>, Holger Klein
<holger.klein@gmail.com>

Description Duplication rate quality control for RNA-Seq datasets.

URL <https://www.bioconductor.org/packages/dupRadar>,
<https://ssayols.github.io/dupRadar/index.html>

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, AnnotationHub

Depends R (>= 3.2.0)

Imports Rsubread (>= 1.14.1), KernSmooth

LazyData true

License GPL-3

biocViews Technology, Sequencing, RNASeq, QualityControl,
ImmunoOncology

NeedsCompilation no

Encoding UTF-8

RoxygenNote 7.2.3

git_url <https://git.bioconductor.org/packages/dupRadar>

git_branch RELEASE_3_19

git_last_commit 8dad41

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-05

Contents

| | |
|---------------------------------------------|----|
| analyzeDuprates | 2 |
| bamutilMarkDuplicates | 3 |
| cumulativeDuprateBarplot | 4 |
| dm | 5 |
| dm.bad | 5 |
| dupRadar | 6 |
| dupRadar_examples | 6 |
| duprateExpBoxplot | 6 |
| duprateExpDensPlot | 7 |
| duprateExpFit | 8 |
| duprateExpIdentify | 9 |
| duprateExpPlot | 9 |
| expressionHist | 10 |
| getBinDuplication | 11 |
| getBinRpkMean | 12 |
| getDupMatBin | 12 |
| getDupMatStats | 13 |
| getDynamicRange | 13 |
| getRpkBinReadCountFraction | 14 |
| getRpkCumulativeReadCountFraction | 15 |
| markDuplicates | 15 |
| picardMarkDuplicates | 16 |
| readcountExpBoxplot | 17 |

| | |
|--------------|-----------|
| Index | 19 |
|--------------|-----------|

| | |
|-----------------|------------------------------------------------------------------------------------------------|
| analyzeDuprates | <i>Read in a BAM file and count the tags falling on the features described in the GTF file</i> |
|-----------------|------------------------------------------------------------------------------------------------|

Description

analyzeDuprates returns a data.frame with tag counts

Usage

```
analyzeDuprates(
  bam,
  gtf,
  stranded = 0,
  paired = FALSE,
  threads = 1,
  verbose = FALSE,
  ...
)
```

Arguments

| | |
|----------|------------------------------------------------------|
| bam | The bam file containing the duplicate-marked reads |
| gtf | The gtf file describing the features |
| stranded | Whether the reads are strand specific |
| paired | Paired end experiment? |
| threads | The number of threads to be used for counting |
| verbose | Whether to output Rsubread messages into the console |
| ... | Other params sent to featureCounts |

Details

This function makes use of the Rsubread package to count tags on the GTF features in different scenarios. The scenarios are the 4 possible combinations of allowing multimappers (yes/no) and duplicate reads (yes/no).

Value

A data.frame with counts on features, with and without taking into account multimappers/duplicated reads

Examples

```
bam <- system.file("extdata",
                  "wgEncodeCaltechRnaSeqGm12878R1x75dAlignsRep2V2_duprm.bam",
                  package="dupRadar")
gtf <- system.file("extdata", "genes.gtf", package="dupRadar")
stranded <- 2 # '0' (unstranded), '1' (stranded) and '2' (reverse)
paired <- FALSE
threads <- 4

# call the duplicate marker and analyze the reads
dm <- analyzeDuprates(bam,gtf,stranded,paired,threads)
```

bamutilMarkDuplicates *Mark duplicates using bamutil*

Description

bamutilMarkDuplicates Mark duplicated reads from a BAM file by calling bamutil

Usage

```
bamutilMarkDuplicates(bam, out, path, verbose)
```

Arguments

| | |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| bam | The bam file to mark duplicates from |
| out | Regular expression describing the transformation on the original filename to get the output filename. By default, a "_duprm" suffix is added before the bam extension |
| path | Path to the duplicate marker binaries |
| verbose | Redirect all the program output to the R console |

Details

This function is supposed to be called through the markDuplicatess wrapper

Value

The return code of the system call

cumulativeDuprateBarplot

Barplot showing the cumulative read counts fraction

Description

cumulativeDuprateBarplot Barplot showing the cumulative read counts fraction

Usage

```
cumulativeDuprateBarplot(DupMat, stepSize = 0.05, ...)
```

Arguments

| | |
|----------|------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| stepSize | The size of the windows used for plotting |
| ... | Other params sent to barplot |

Details

This function makes a barplot showing the cumulative read counts fraction from the duplication matrix calculated by analyzeDuprates.

Value

nothing

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:  
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)  
attach(dupRadar_examples)  
  
# call the plot  
cumulativeDuprateBarplot(DupMat=dm)
```

| | |
|----|-------------------------------------------------------|
| dm | <i>Duplication matrix of a good RNASeq experiment</i> |
|----|-------------------------------------------------------|

Description

A dataset containing the duplication matrix of a good RNASeq experiment, in terms of duplicates. Comes from the GM12878 SR1x75 replicate 2 from Caltech (UCSC's table Browser name: wgEncodeCaltechRnaSeqGm12878R1x75dAlignsRep2V2)

Usage

```
data(dupRadar_examples)
```

Format

A data frame with 23228 rows and 14 variables

| | |
|--------|---------------------------------------------------------|
| dm.bad | <i>Duplication matrix of a failed RNASeq experiment</i> |
|--------|---------------------------------------------------------|

Description

A dataset containing the duplication matrix of a failed RNASeq experiment, containing unusual duplication rate. Comes from the HCT116 PE2x75 replicate 1 from Caltech (UCSC's table Browser name: wgEncodeCaltechRnaSeqHct116R2x75II200AlignsRep1V2)

Usage

```
data(dupRadar_examples)
```

Format

A data frame with 23228 rows and 14 variables

| | |
|----------|------------------|
| dupRadar | <i>dupRadar.</i> |
|----------|------------------|

Description

Duplication rate quality control for RNA-Seq datasets.

| | |
|-------------------|--------------------------------------------------------------------------------|
| dupRadar_examples | <i>Example data containing precomputed matrices for two RNASeq experiments</i> |
|-------------------|--------------------------------------------------------------------------------|

Description

Precomputed duplication matrices for two RNASeq experiments used as examples of a good and a failed (in terms of high redundancy of reads) experiments. The experiments come from the ENCODE project, as a source of a broad variety of protocols, library types and sequencing facilities.

Usage

```
data(dupRadar_examples)
```

Format

A list with two example duplication matrices

| | |
|-------------------|------------------------------------------------------------------|
| duprateExpBoxplot | <i>Duplication rate ~ total reads per kilobase (RPK) boxplot</i> |
|-------------------|------------------------------------------------------------------|

Description

duprateExpBoxplot Duplication rate ~ total reads per kilobase (RPK) boxplot

Usage

```
duprateExpBoxplot(DupMat, stepSize = 0.05, ...)
```

Arguments

| | |
|----------|------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| stepSize | Expression bin size for the boxplot |
| ... | Other params sent to boxplot |

Details

This function makes a boxplot showing the distribution of per gene duplication rate versus the reads per kilobase (RPK) inside gene expression bins.

Value

nothing

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# duprate boxplot
duprateExpBoxplot(DupMat=dm)
```

duprateExpDensPlot *Duplication rate ~ total read count plot*

Description

duprateExpDensPlot Duplication rate ~ total read count plot

Usage

```
duprateExpDensPlot(
  DupMat,
  pal = c("cyan", "blue", "green", "yellow", "red"),
  tNoAlternative = TRUE,
  tRPKM = TRUE,
  tRPKMval = 0.5,
  tFit = TRUE,
  addLegend = TRUE,
  ...
)
```

Arguments

| | |
|----------------|------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| pal | The color palette to use to display the density |
| tNoAlternative | Display threshold of 1000 reads per kilobase |
| tRPKM | Display threshold at a given RPKM level |
| tRPKMval | The given RPKM level |
| tFit | Whether to fit the model |
| addLegend | Whether to add a legend to the plot |
| ... | Other parameters sent to plot() |

Details

This function makes a scatter plot showing the per gene duplication rate versus the total read count.

Value

nothing

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# duprate plot
duprateExpDensPlot(DupMat=dm)
```

duprateExpFit *Duplication rate ~ total read count fit model*

Description

duprateExpDensPlot Duplication rate ~ total read count fit model

Usage

```
duprateExpFit(DupMat)
```

Arguments

DupMat The duplication matrix calculated by analyzeDuprates

Details

Fit a Generalized Linear Model using a logit function between the gene duplication rate and the total read count.

Value

The GLM and the coefficients of the fitted logit function

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# duprate plot
duprateExpFit(DupMat=dm)
```

duprateExpIdentify *Identify genes plotted by duprateExpPlot*

Description

duprateExpIdentify Identify genes plotted by duprateExpPlot

Usage

```
duprateExpIdentify(DupMat, idCol = "ID")
```

Arguments

| | |
|--------|--------------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| idCol | The column from the duplication matrix containing the labels |

Details

This function makes a barplot showing the cumulative read counts fraction from the duplication matrix calculated by analyzeDuprates.

Value

The identified points. x and y values match the ones from duprateExpPlot

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# call the plot and identify genes
duprateExpPlot(DupMat=dm)
duprateExpIdentify(DupMat=dm)
```

duprateExpPlot *Duplication rate ~ total read count plot*

Description

duprateExpPlot Duplication rate ~ total read count plot

Usage

```
duprateExpPlot(
  DupMat,
  tNoAlternative = TRUE,
  tRPKM = TRUE,
  tRPKMval = 0.5,
  addLegend = TRUE,
  ...
)
```

Arguments

| | |
|----------------|------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| tNoAlternative | Display threshold of 1000 reads per kilobase |
| tRPKM | Display threshold at a given RPKM level |
| tRPKMval | The given RPKM level |
| addLegend | Whether to add a legend to the plot |
| ... | Other parameters sent to smoothScatter() |

Details

This function makes a smooth scatter plot showing the per gene duplication rate versus the total read count.

Value

nothing

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# duprate plot
duprateExpPlot(DupMat=dm)
```

expressionHist *Draw histogram with the expression values*

Description

expressionHist Draw histogram with the expression values

Usage

```
expressionHist(DupMat, value = "RPK", ...)
```

Arguments

| | |
|--------|-------------------------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| value | The column from the duplication matrix containing the expression values |
| ... | Other parameters sent to hist() |

Details

This function draws a histogram of the expression values from the duplication matrix calculated by analyzeDuprates.

Value

nothing

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# histogram of expression values for annotation
expressionHist(DupMat=dm)
```

getBinDuplication *Helper function used in duprateExpBoxplot*

Description

getBinDuplication get duplication rate for a subset of the duplication matrix

Usage

```
getBinDuplication(p, stepSize, DupMat)
```

Arguments

| | |
|----------|------------------------------------------------------|
| p | The vector of bins |
| stepSize | The window size |
| DupMat | The duplication matrix calculated by analyzeDuprates |

Value

The duplication rate per bin

getBinRpkMean *Helper function used in duprateExpBoxplot*

Description

getBinRpkMean get mean duplication rate per bin

Usage

```
getBinRpkMean(p, stepSize, DupMat)
```

Arguments

| | |
|----------|------------------------------------------------------|
| p | The vector of bins |
| stepSize | The window size |
| DupMat | The duplication matrix calculated by analyzeDuprates |

Value

The averaged RPK per bin

getDupMatBin *Helper function used in getBinDuplication and getBinRpkMean*

Description

getDupMatBin get a subset of the matrix for values in a specific bin defined by the upper bound p and stepSize

Usage

```
getDupMatBin(p, stepSize = 0.05, value = "allCounts", DupMat)
```

Arguments

| | |
|----------|------------------------------------------------------|
| p | The vector of bins |
| stepSize | The window size |
| value | The column to be subset |
| DupMat | The duplication matrix calculated by analyzeDuprates |

Value

The subseted matrix

| | |
|----------------|--------------------------------------------|
| getDupMatStats | <i>Report duplication stats on regions</i> |
|----------------|--------------------------------------------|

Description

getDupMatStats Report duplication stats based on the data calculated in the duplication matrix

Usage

```
getDupMatStats(DupMat)
```

Arguments

DupMat The duplication matrix calculated by analyzeDuprates

Value

A data.frame containing the stats about the number of genes covered (1+ tags) and the number of genes containing duplicates (1+)

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# call the plot and identify genes
getDupMatStats(DupMat=dm)
```

| | |
|-----------------|----------------------|
| getDynamicRange | <i>Dynamic range</i> |
|-----------------|----------------------|

Description

getDynamicRange Calculate the dynamic range of the RNAseq experiment

Usage

```
getDynamicRange(dm)
```

Arguments

dm The duplication matrix calculated by analyzeDuprates

Details

This function calculates the dynamic range of the RNAseq experiment

Value

A list with 2 elements, containing the dynamic range counting all reads and the dynamic range after removing duplicates.

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)
attach(dupRadar_examples)

# calculate the dynamic range
getDynamicRange(dm)
```

getRpkBinReadCountFraction

Helper function used in readcountExpressionBoxplot

Description

readcountExpressionBoxplot Calculates the fraction of total reads in a vector of bins

Usage

```
getRpkBinReadCountFraction(p, stepSize = stepSize, DupMat = DupMat)
```

Arguments

| | |
|----------|------------------------------------------------------|
| p | The vector of bins |
| stepSize | The window size |
| DupMat | The duplication matrix calculated by analyzeDuprates |

Value

The fraction of total reads in a vector of bins

```
getRpkCumulativeReadCountFraction
```

Helper function used in readcountExpressionBoxplot

Description

getRpkCumulativeReadCountFraction get the cumulative read count fraction

Usage

```
getRpkCumulativeReadCountFraction(p, DupMat = DupMat)
```

Arguments

| | |
|--------|------------------------------------------------------|
| p | The vector of bins |
| DupMat | The duplication matrix calculated by analyzeDuprates |

Value

The cumulative read count fraction

```
markDuplicates
```

Program dispatchers to mark duplicated reads from a BAM file

Description

markDuplicates Mark duplicated reads from a BAM file by calling widely used tools.

Usage

```
markDuplicates(
  dupremover = c("bamutil", "picard"),
  bam = NULL,
  out = gsub("\\.bam$", "_duprm.bam", bam),
  rminput = TRUE,
  path = ".",
  verbose = TRUE,
  ...
)
```

Arguments

| | |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dupremover | The tool to be called. Currently, "picard" and "bamutils" are supported |
| bam | The bam file to mark duplicates from |
| out | Regular expression describing the transformation on the original filename to get the output filename. By default, a "_duprm" suffix is added before the bam extension |
| rminput | Whether to keep the original, non duplicate-marked, bam file |
| path | Path to the duplicate marker binaries |
| verbose | Redirect all the program output to the R console |
| ... | Other parameters sent to the caller function |

Details

This function works as a wrapper for several tools widely adopted to mark duplicated reads in a BAM file. Currently, it supports PICARD and BamUtils.

Value

The output filename

Examples

```
## Not run:
bam <- system.file("extdata", "sample1Aligned.out.bam", package="dupRadar")
gtf <- "genes.gtf"
stranded <- 2 # '0' (unstranded), '1' (stranded) and '2' (reverse)
paired <- FALSE
threads <- 4

# call the duplicate marker and analyze the reads
bamDuprm <- markDuplicates(dupremover="bamutil", bam,
                           path="/opt/bamUtil-master/bin", rminput=FALSE)
dm <- analyzeDuprates(bamDuprm, gtf, stranded, paired, threads)

## End(Not run)
```

picardMarkDuplicates *Mark duplicates using Picard tools*

Description

picardMarkDuplicates Mark duplicated reads from a BAM file by calling picard tools

Usage

```
picardMarkDuplicates(bam, out, path, verbose, threads = 1, maxmem = "4g")
```


Arguments

| | |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| bam | The bam file to mark duplicates from |
| out | Regular expression describing the transformation on the original filename to get the output filename. By default, a "_duprm" suffix is added before the bam extension |
| path | Path to the duplicate marker binaries |
| verbose | Redirect all the program output to the R console |
| threads | Number of threads to use |
| maxmem | Max memory assigned to the jvm |

Details

This function is supposed to be called through the markDuplicates wrapper

Value

The return code of the system call

readcountExpBoxplot *Barplot of percentage of reads falling into expression bins*

Description

readcountExpBoxplot Barplot of percentage of reads falling into expression bins

Usage

```
readcountExpBoxplot(DupMat, stepSize = 0.05, ...)
```

Arguments

| | |
|----------|------------------------------------------------------|
| DupMat | The duplication matrix calculated by analyzeDuprates |
| stepSize | The number of bars to be shown |
| ... | Other parameters sent to barplot() |

Details

This function makes a barplot of percentage of reads falling into expression bins

Value

nothing Other parameters sent to barplot()

Examples

```
# dm is a duplication matrix calculated by analyzeDuprates:  
# R> dm <- analyzeDuprates(bamDuprm,gtf,stranded,paired,threads)  
attach(dupRadar_examples)
```

```
# barplot of percentage of reads falling into expression bins  
readcountExpBoxplot(DupMat=dm)
```

Index

* datasets

dm, 5

dm.bad, 5

dupRadar_examples, 6

analyzeDuprates, 2

bamutilMarkDuplicates, 3

cumulativeDuprateBarplot, 4

dm, 5

dm.bad, 5

dupRadar, 6

dupRadar_examples, 6

duprateExpBoxplot, 6

duprateExpDensPlot, 7

duprateExpFit, 8

duprateExpIdentify, 9

duprateExpPlot, 9

expressionHist, 10

getBinDuplication, 11

getBinRpkMean, 12

getDupMatBin, 12

getDupMatStats, 13

getDynamicRange, 13

getRpkBinReadCountFraction, 14

getRpkCumulativeReadCountFraction, 15

markDuplicates, 15

picardMarkDuplicates, 16

readcountExpBoxplot, 17