

# Package ‘ribosomeProfilingQC’

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**Type** Package

**Title** Ribosome Profiling Quality Control

**Version** 1.18.0

**Description** Ribo-Seq (also named ribosome profiling or footprinting) measures translational activity (unlike RNA-Seq, which sequences the transcriptome) by direct quantification of the ribosome-protected fragments (RPFs). This package provides the tools for quality assessment of ribosome profiling. In addition, it can preprocess Ribo-Seq data for subsequent differential analysis.

**License** GPL (>=3) + file LICENSE

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|                    |                             |
|--------------------|-----------------------------|
| assignReadingFrame | <i>Assign reading frame</i> |
|--------------------|-----------------------------|

---

### Description

Set reading frame for each reads in CDS region to frame0, frame1 and frame2.

### Usage

```
assignReadingFrame(reads, CDS, txdb, ignore.seqlevelsStyle = FALSE)
```

**Arguments**

|                       |  |
|-----------------------|--|
| reads                 | Output of <a href="#">getPsiteCoordinates</a>  |
| CDS                   | Output of <a href="#">prepareCDS</a>   |
| txdb                  | A TxDb object. If it is set, assign reading frame for all reads. Default missing, only assign rading frame for reads in CDS. |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.   |

**Value**

An GRanges object of reads with reading frame information.

**Examples**

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=13)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   #   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   #   package="ribosomeProfilingQC"),
#   #   organism = "Danio rerio",
#   #   chrominfo = seqinfo(Drerio)["chr1"],
#   #   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
pc.sub <- assignReadingFrame(pc.sub, CDS)
```

---

codonBias

*Codon usage bias*

---

**Description**

Calculate the codon usage for the reads in the identified CDSs. And then compared to the reference codon usage.

**Usage**

```
codonBias(
  RPFs,
  gtf,
  genome,
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  ignore.seqlevelsStyle = FALSE,
```

```

summary = TRUE,
removeDuplicates = TRUE,
...
)

```

### Arguments

|                       |  |
|-----------------------|--|
| RPFs                  | Bam file names of RPFs.                              |
| gtf                   | GTF file name for annotation or a TxDb object.       |
| genome                | A BSgenome object.                                   |
| bestpsite             | P site position.                                     |
| readsLen              | Reads length to keep.                                |
| anchor                | 5end or 3end. Default is 5end.                       |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.     |
| summary               | Return the summary of codon usage bias or full list. |
| removeDuplicates      | Remove the PCR duplicates or not. Default TRUE.      |
| ...                   | Parameters pass to <a href="#">makeTxDbFromGFF</a>   |

### Value

A list of data frame of codon count table if summary is TRUE. list 'reads' means the counts by raw reads. list 'reference' means the counts by sequence extracted from reference by the coordinates of mapped reads. Otherwise, return the counts (reads/reference) table for each reads.

### Examples

```

path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
library(BSgenome.Drerio.UCSC.danRer10)
cb <- codonBias(RPFs[c(1,2)], gtf=gtf, genome=Drerio)

```

---

codonUsage

*Start or Stop codon usage*

---

### Description

Calculate the start or stop codon usage for the identified CDSs.

### Usage

```
codonUsage(reads, start = TRUE, genome)
```

### Arguments

|        |  |
|--------|--|
| reads  | Output of <a href="#">assignReadingFrame</a> . |
| start  | Calculate for start codon or stop codon.       |
| genome | A BSgenome object.                             |

**Value**

Table of codon usage.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))
library(BSgenome.Drerio.UCSC.danRer10)
codonUsage(pcs, genome=Drerio)
codonUsage(pcs, start=FALSE, genome=Drerio)
```

---

countReads

*Extract counts for RPFs and RNAs*

---

**Description**

Calculate the reads counts for gene level or transcript level.

**Usage**

```
countReads(
  RPFs,
  RNAs,
  gtf,
  level = c("tx", "gene"),
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

**Arguments**

|                       |   |
|-----------------------|---|
| RPFs                  | Bam file names of RPFs.   |
| RNAs                  | Bam file names of RNAseq.   |
| gtf                   | GTF file name for annotation.   |
| level                 | Transcript or gene level.   |
| bestpsite             | numeric(1). P site position.  |
| readsLen              | numeric(1). reads length to keep.   |
| anchor                | 5end or 3end. Default is 5end.  |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.  |
| ...                   | Parameters pass to <a href="#">featureCounts</a> except isGTFAnnotationFile, GTF.attrType, and annot.ext. |

**Value**

A list with reads counts.

**Examples**

```

path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names = TRUE)
cnts <- countReads(RPFs[1], gtf=gtf, level="gene", readsLen=29)
#cnts <- countReads(RPFs[1], RNAs[1], gtf=gtf, level="gene", readsLen=29)

```

coverageDepth

*Extract coverage depth for gene level or transcript level***Description**

Calculate the coverage depth for gene level or transcript level. Coverage for RPFs will be the best P site coverage. Coverage for RNAs will be the coverage for 5' end of reads.

**Usage**

```

coverageDepth(
  RPFs,
  RNAs,
  gtf,
  level = c("tx", "gene"),
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  region = "cds",
  ext = 5000,
  ignore.seqlevelsStyle = FALSE,
  ...
)

```

**Arguments**

|                       |  |
|-----------------------|--|
| RPFs                  | Bam file names of RPFs.  |
| RNAs                  | Bam file names of RNAseq.  |
| gtf                   | GTF file name for annotation or a TxDb object.   |
| level                 | Transcript or gene level.  |
| bestpsite             | P site position.   |
| readsLen              | Reads length to keep.  |
| anchor                | 5end or 3end. Default is 5end.   |
| region                | Annotation region. It could be "cds", "utr5", "utr3", "exon", "transcripts", "feature with extension". |
| ext                   | Extension region for "feature with extension".   |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.   |
| ...                   | Parameters pass to <a href="#">makeTxDbFromGFF</a>   |

**Value**

A cvgd object with coverage depth.

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], gtf=gtf, level="gene")
```

---

|               |                                |
|---------------|--------------------------------|
| coverageRates | <i>Calculate coverage rate</i> |
|---------------|--------------------------------|

---

**Description**

Coverage is a measure as percentage of position with reads along the CDS. Coverage rate calculate coverage rate for RPFs and mRNAs in gene level. Coverage will be calculated based on best P sites for RPFs and 5'end for RNA-seq.

**Usage**

```
coverageRates(cvgs, RPFsampleOrder, mRNAsampleOrder)
```

**Arguments**

cvgs                      Output of [coverageDepth](#)  
RPFsampleOrder, mRNAsampleOrder  
Sample order of RPFs and mRNAs. The parameters are used to make sure that the order of RPFs and mRNAs in cvgs is corresponding samples.

**Value**

A list with coverage rate.

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], gtf=gtf, level="gene")
cr <- coverageRates(cvgs)
```

---

|            |                     |
|------------|---------------------|
| cvgd-class | <i>Class "cvgd"</i> |
|------------|---------------------|

---

### Description

An object of class "cvgd" represents output of coverageDepth.

### Usage

```
cvgd(...)

## S4 method for signature 'cvgd'
x$name

## S4 replacement method for signature 'cvgd'
x$name <- value

## S4 method for signature 'cvgd,ANY,ANY'
x[[i, j, ..., exact = TRUE]]

## S4 replacement method for signature 'cvgd,ANY,ANY,ANY'
x[[i, j, ...]] <- value

## S4 method for signature 'cvgd'
show(object)
```

### Arguments

|        |  |
|--------|--|
| ...    | Each argument in ... becomes an slot in the new "cvgd"-class.    |
| x      | cvgd object.   |
| name   | A literal character string or a name (possibly backtick quoted). |
| value  | value to replace.  |
| i, j   | indexes specifying elements to extract or replace.               |
| exact  | see <a href="#">Extract</a>                                      |
| object | cvgd object.   |

### Value

A cvgd object.

### Slots

coverage "list", list of [CompressedRleList](#), specify the coverage of features of each sample.  
 granges [CompressedGRangesList](#), specify the features.

### Examples

```
cvgd()
```





```

#       package="ribosomeProfilingQC"),
#       organism = "Danio rerio",
#       chrominfo = seqinfo(Drerio)["chr1"],
#       taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
estimatePsite(bamfile, CDS, Drerio)

```

---

filterCDS

*Filter CDS by size*


---

### Description

Filter CDS by CDS size.

### Usage

```
filterCDS(CDS, sizeCutoff = 100L)
```

### Arguments

|            |   |
|------------|---|
| CDS        | Output of preparedCDS   |
| sizeCutoff | numeric(1). Cutoff size for CDS. If the size of CDS is less than the cutoff, it will be filtered out. |

### Value

A GRanges object with filtered CDS.

### Examples

```

#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",
#   chrominfo = seqinfo(Drerio)["chr1"],
#   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
filterCDS(CDS)

```

---

FLOSS *Fragment Length Organization Similarity Score (FLOSS)*

---

### Description

The FLOSS will be calculated from a histogram of read lengths for footprints on a transcript or reading frame.

### Usage

```
FLOSS(
  reads,
  ref,
  CDS,
  readLengths = c(26:34),
  level = c("tx", "gene"),
  draw = FALSE,
  ignore.seqlevelsStyle = FALSE
)
```

### Arguments

|                       |   |
|-----------------------|---|
| reads                 | Output of <a href="#">getPsiteCoordinates</a>   |
| ref                   | Reference id list. If level is set to tx, the id should be transcript names. If level is set to gene, the id should be gene id. |
| CDS                   | Output of <a href="#">prepareCDS</a>  |
| readLengths           | Read length used for calculation  |
| level                 | Transcript or gene level  |
| draw                  | Plot FLOSS vs total reads or not.   |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.  |

### Value

A data frame with colnames as id, FLOSS, totalReads, wilcox.test.pval, cook's distance.

### References

1: Ingolia NT, Brar GA, Stern-Ginossar N, Harris MS, Talhouarne GJ, Jackson SE, Wills MR, Weissman JS. Ribosome profiling reveals pervasive translation outside of annotated protein-coding genes. *Cell Rep.* 2014 Sep 11;8(5):1365-79. doi: 10.1016/j.celrep.2014.07.045. Epub 2014 Aug 21. PubMed PMID: 25159147; PubMed Central PMCID: PMC4216110.

### Examples

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
```

```

pc <- getPsiteCoordinates(bamfile, bestpsite=13)
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#      "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#      package="ribosomeProfilingQC"),
#      organism = "Danio rerio",
#      chrominfo = seqinfo(Drerio)["chr1"],
#      taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
      package="ribosomeProfilingQC"))

set.seed(123)
ref <- sample(unique(CDS$gene_id), 100)
fl <- FLOSS(pc, ref, CDS, level="gene")

```

---

frameCounts

*Extract counts for gene level or transcript level*


---

### Description

Calculate the reads counts or coverage rate for gene level or transcript level. Coverage is determined by measuring the proportion of in-frame CDS positions with  $\geq 1$  reads.

### Usage

```

frameCounts(
  reads,
  level = c("tx", "gene"),
  frame0only = TRUE,
  coverageRate = FALSE
)

```

### Arguments

|              |  |
|--------------|--|
| reads        | Output of <a href="#">assignReadingFrame</a> . |
| level        | Transcript or gene level                       |
| frame0only   | Only count for reading frame 0 or not          |
| coverageRate | Calculate for coverage or not                  |

### Value

A numeric vector with reads counts.

### Examples

```

pcs <- readRDS(system.file("extdata", "samplePc.rds",
      package="ribosomeProfilingQC"))
cnts <- frameCounts(pcs)
cnts.gene <- frameCounts(pcs, level="gene")
cvg <- frameCounts(pcs, coverageRate=TRUE)

```

---

|         |                                   |
|---------|-----------------------------------|
| getFPKM | <i>Get FPKM values for counts</i> |
|---------|-----------------------------------|

---

**Description**

Calculate Fragments Per Kilobase of transcript per Million mapped reads (FPKM) for counts.

**Usage**

```
getFPKM(counts, gtf, level = c("gene", "tx"))
```

**Arguments**

|        |  |
|--------|--|
| counts | Output of <a href="#">countReads</a> or <a href="#">normByRUVs</a> |
| gtf    | GTF file name for annotation.                                      |
| level  | Transcript or gene level.  |

**Value**

A list with FPKMs

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
```

---

|             |                           |
|-------------|---------------------------|
| getORFscore | <i>Calculate ORFscore</i> |
|-------------|---------------------------|

---

**Description**

To calculate the ORFscore, reads were counted at each position within the ORF.

$$ORFscore = \log_2\left(\left(\sum_{n=1}^3 \frac{(F_n - \bar{F})^2}{\bar{F}}\right) + 1\right)$$

where  $F_n$  is the number of reads in reading frame  $n$ ,  $\bar{F}$  is the total number of reads across all three frames divided by 3. If  $F_1$  is smaller than  $F_2$  or  $F_3$ ,  $ORFscore = -1 \times ORFscore$ .

**Usage**

```
getORFscore(reads)
```

**Arguments**

|       |   |
|-------|---|
| reads | Output of <a href="#">getPsiteCoordinates</a> |
|-------|---|

**Value**

A numeric vector with ORFscore.

**References**

1: Bazzini AA, Johnstone TG, Christiano R, Mackowiak SD, Obermayer B, Fleming ES, Vejnar CE, Lee MT, Rajewsky N, Walther TC, Giraldez AJ. Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. *EMBO J.* 2014 May 2;33(9):981-93. doi: 10.1002/embj.201488411. Epub 2014 Apr 4. PubMed PMID: 24705786; PubMed Central PMCID: PMC4193932.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))
ORFscore <- getORFscore(pcs)
```

---

getPsiteCoordinates    *Get P site coordinates*

---

**Description**

Extract P site coordinates from a bam file to a GRanges object.

**Usage**

```
getPsiteCoordinates(
  bamfile,
  bestpsite,
  anchor = "5end",
  param = ScanBamParam(what = c("qwidth"), tag = character(0), flag =
    scanBamFlag(isSecondaryAlignment = FALSE, isUnmappedQuery = FALSE,
    isNotPassingQualityControls = FALSE, isSupplementaryAlignment = FALSE))
)
```

**Arguments**

|           |  |
|-----------|--|
| bamfile   | A BamFile object.  |
| bestpsite | P site position. See <a href="#">estimatePsite</a>           |
| anchor    | 5end or 3end. Default is 5end.                               |
| param     | A ScanBamParam object. Please note the 'qwidth' is required. |

**Value**

A GRanges object with qwidth metadata which indicates the width of reads.

**Examples**

```

library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=13)

```

ggBar

*barplot by ggplot2***Description**

barplot with number in top.

**Usage**

```
ggBar(height, fill = "gray80", draw = TRUE, xlab, ylab, postfix)
```

**Arguments**

|                  |                                       |
|------------------|---------------------------------------|
| height           | data for plot                         |
| fill, xlab, ylab | parameters pass to ggplot.            |
| draw             | plot or not                           |
| postfix          | Postfix of text labled in top of bar. |

**Value**

ggplot object.

**Examples**

```
ribosomeProfilingQC::ggBar(sample.int(100, 3))
```

metaPlot

*Metagene analysis plot***Description**

Plot the average coverage of UTR5, CDS and UTR3.

**Usage**

```

metaPlot(
  UTR5coverage,
  CDScoverage,
  UTR3coverage,
  sample,
  xaxis = c("RPFs", "mRNA"),
  bins = c(UTR5 = 100, CDS = 500, UTR3 = 100),
  ...
)

```

**Arguments**

UTR5coverage, CDScoverage, UTR3coverage  
 Coverages of UTR5, CDS, and UTR3 region. Output of [coverageDepth](#)

sample  
 character(1). Sample name to plot.

xaxis  
 What to plot for x-axis.

bins  
 Bins for UTR5, CDS and UTR3.

...  
 Parameter pass to plot.

**Value**

A list contain the data for plot.

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], RNAs[1], gtf)
cvgs.utr3 <- coverageDepth(RPFs[1], RNAs[1], gtf, region="utr3")
cvgs.utr5 <- coverageDepth(RPFs[1], RNAs[1], gtf, region="utr5")
metaPlot(cvgs.utr5, cvgs, cvgs.utr3, sample=1)

## End(Not run)
```

---

normalizeTEbyLoess      *Normalize the TE by Loess*

---

**Description**

Fitting the translational efficiency values with the mRNA value by [loess](#).

**Usage**

```
normalizeTEbyLoess(
  TE,
  log2 = TRUE,
  pseudocount = 0.001,
  span = 2/3,
  family.loess = "symmetric"
)
```

**Arguments**

TE  
 output of [translationalEfficiency](#).

log2  
 logical(1L). Do log2 transform for TE or not. If TE value is not log2 transformed, please set it as TRUE.

pseudocount  
 The number will be add to sum of reads count to avoid X/0.

span, family.loess  
 Parameters will be passed to [loess](#)



**Value**

A list with RPFs, mRNA levels and TE as a matrix with log2 transformed translational efficiency.

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)
te1 <- normalizeTEbyLoess(te)
plotTE(te)
plotTE(te1, log2=FALSE)
```

---

|        |   |
|--------|---|
| normBy | <i>Normalization by edgeR, DESeq2 or RUVSeq</i> |
|--------|---|

---

**Description**

Normalization by multiple known methods

**Usage**

```
normBy(counts, method = c("edgeR", "DESeq2", "RUVs", "fpkm", "vsn"), ...)
```

**Arguments**

|        |  |
|--------|--|
| counts | Output of <a href="#">countReads</a>   |
| method | Character(1L) to indicate the method for normalization.                            |
| ...    | parameters will be passed to <a href="#">normByRUVs</a> or <a href="#">getFPKM</a> |

**Value**

Normalized counts list

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
cnts <- readRDS(file.path(path, "cnts.rds"))
norm <- normBy(cnts, method = 'edgeR')
norm2 <- normBy(cnts, method = 'DESeq2')
norm3 <- normBy(cnts, 'vsn')
```

---

normByRUVs                      *Normalization by RUVSeq*

---

### Description

Normalization by RUVSeq:RUVs methods

### Usage

```
normByRUVs(counts, RPFgroup, mRNAgroup = RPFgroup, k = 1)
```

### Arguments

counts                      Output of [countReads](#)  
RPFgroup, mRNAgroup  
                              Groups for RPF and mRNA files  
k                              The number of factor of unwanted variation to be estimated from the data. See [RUVs](#)

### Value

Normalized counts list

### Examples

```
## Not run: ##waiting for EDASeq fix the issue.
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
gp <- c("KD1", "KD1", "WT", "WT")
norm <- normByRUVs(cnts, gp, gp)

## End(Not run)
```

---

PAmotif                      *Metaplot of P site distribution*

---

### Description

Metaplot of P site distribution in all the CDS aligned by the start codon or stop codon.

### Usage

```
PAmotif(reads, genome, plot = TRUE, ignore.seqlevelsStyle = FALSE)
```

**Arguments**

reads            Output of [assignReadingFrame](#) or [shiftReadsByFrame](#).  
 genome          A BSgenome object.  
 plot            Plot the motif or not.  
 ignore.seqlevelsStyle    Ignore the sequence name style detection or not.

**Value**

A [pcm](#) object

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
  package="ribosomeProfilingQC"))
library(BSgenome.Drerio.UCSC.danRer10)
#PAmotif(pcs, Drerio)
```

---

plotDistance2Codon    *Metaplot of P site distribution*

---

**Description**

Metaplot of P site distribution in all the CDS aligned by the start codon or stop codon.

**Usage**

```
plotDistance2Codon(
  reads,
  start = TRUE,
  anchor = 50,
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")
)
```

**Arguments**

reads            Output of [assignReadingFrame](#).  
 start            Plot for start codon or stop codon.  
 anchor          The maximal xlim or (min, max) position for plot.  
 col             Colors for different reading frame.

**Value**

Invisible height of the barplot.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
  package="ribosomeProfilingQC"))
plotDistance2Codon(pcs)
#plotDistance2Codon(pcs, start=FALSE)
#plotDistance2Codon(pcs, anchor=c(-10, 20))
```

---

|                  |  |
|------------------|--|
| plotFrameDensity | <i>Plot density for each reading frame</i> |
|------------------|--|

---

**Description**

Plot density for each reading frame.

**Usage**

```
plotFrameDensity(  
  reads,  
  density = TRUE,  
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")  
)
```

**Arguments**

|         |  |
|---------|--|
| reads   | Output of <a href="#">assignReadingFrame</a> |
| density | Plot density or counts                       |
| col     | Colors for reading frames                    |

**Value**

A ggplot object.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",  
  package="ribosomeProfilingQC"))  
plotFrameDensity(pcs)
```

---

|                 |                          |
|-----------------|--------------------------|
| plotSpliceEvent | <i>Plot splice event</i> |
|-----------------|--------------------------|

---

**Description**

Plot the splice event

**Usage**

```
plotSpliceEvent(  
  se,  
  tx_name,  
  coverage,  
  group1,  
  group2,  
  cutoffFDR = 0.05,  
  resetIntronWidth = TRUE  
)
```

**Arguments**

|                  |  |
|------------------|--|
| se               | Output of <a href="#">spliceEvent</a>  |
| tx_name          | Transcript name.   |
| coverage         | Coverages of feature region with extensions. Output of <a href="#">coverageDepth</a> |
| group1, group2   | The sample names of group 1 and group 2  |
| cutoffFDR        | Cutoff of FDR  |
| resetIntronWidth | logical(1). If set to true, reset the region with no read to minimal width.          |

**Value**

A ggplot object.

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
coverage <- coverageDepth(RPFs, gtf=gtf, level="gene",
                           region="feature with extension")
group1 <- c("RPF.KD1.1", "RPF.KD1.2")
group2 <- c("RPF.WT.1", "RPF.WT.2")
se <- spliceEvent(coverage, group1, group2)
plotSpliceEvent(se, se$feature[1], coverage, group1, group2)

## End(Not run)
```

---

plotTE

*Plot translational efficiency*


---

**Description**

Scatterplot of RNA/RPFs level compared to the translational efficiency.

**Usage**

```
plotTE(
  TE,
  sample,
  xaxis = c("mRNA", "RPFs"),
  removeZero = TRUE,
  log2 = TRUE,
  theme = theme_classic(),
  type = "histogram",
  margins = "y",
  ...
)
```

**Arguments**

|                    |   |
|--------------------|---|
| TE                 | Output of <a href="#">translationalEfficiency</a> |
| sample             | Sample names to plot.                             |
| xaxis              | What to plot for x-axis.                          |
| removeZero         | Remove the 0 values from plots.                   |
| log2               | Do log2 transform for TE or not.                  |
| theme              | Theme for ggplot2.                                |
| type, margins, ... | Parameters pass to ggMarginal                     |

**Value**

A ggExtraPlot object.

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)
plotTE(te, 1)
```

---

plotTranscript

*Plot reads P site abundance for a specific transcript*

---

**Description**

Plot the bundances of P site on a transcript.

**Usage**

```
plotTranscript(
  reads,
  tx_name,
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")
)
```

**Arguments**

|         |  |
|---------|--|
| reads   | Output of <a href="#">assignReadingFrame</a> |
| tx_name | Transcript names.                            |
| col     | Colors for reading frames                    |

**Value**

Invisible heights of the barplot.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))

plotTranscript(pcs, c("ENSDART00000152562", "ENSDART00000054987"))
```

---

```
prepareCDS
```

---

```
Prepare CDS
```

---

**Description**

Prepare CDS library from a TxDb object.

**Usage**

```
prepareCDS(txdb, withUTR = FALSE)
```

**Arguments**

|         |                                   |
|---------|-----------------------------------|
| txdb    | A TxDb object.                    |
| withUTR | Including UTR information or not. |

**Value**

A GRanges object with metadata which include: tx\_id: transcript id; tx\_name: transcript name; gene\_id: gene id; isFirstExonInCDS: is first exon in CDS or not; idFirstExonInCDS: the id for the first exon; isLastExonInCDS: is last exon in CDS or not; wid.cumsu: cumulative sums of number of bases in CDS; internalPos: offset position from 1 base;

**Examples**

```
library(GenomicFeatures)
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
CDS <- prepareCDS(txdb)
```

---

```
readsDistribution
```

---

```
Plot reads distribution in genomic elements
```

---

**Description**

Plot the percentage of reads in CDS, 5'UTR, 3'UTR, introns, and other elements.

**Usage**

```
readsDistribution(
  reads,
  txdb,
  upstreamRegion = 3000,
  downstreamRegion = 3000,
  plot = TRUE,
  precedence = NULL,
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

**Arguments**

|                                  |   |
|----------------------------------|---|
| reads                            | Output of <code>getPsiteCoordinates</code>  |
| txdb                             | A TxDb object   |
| upstreamRegion, downstreamRegion | The range for promoter region and downstream region.  |
| plot                             | Plot the distribution or not  |
| precedence                       | If no precedence specified, double count will be enabled, which means that if the reads overlap with both CDS and 5'UTR, both CDS and 5'UTR will be incremented. If a precedence order is specified, for example, if promoter is specified before 5'UTR, then only promoter will be incremented for the same example. The values could be any combinations of "CDS", "UTR5", "UTR3", "OtherExon", "Intron", "upstream", "downstream" and "InterGenic", Default=NULL |
| ignore.seqlevelsStyle            | Ignore the sequence name style detection or not.  |
| ...                              | Not use.  |

**Value**

The reads with distribution assignment

**Examples**

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=11)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
txdb <- makeTxDbFromGFF(system.file("extdata",
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
                                   package="ribosomeProfilingQC"),
                       organism = "Danio rerio",
                       chrominfo = seqinfo(Drerio)["chr1"],
                       taxonomyId = 7955)
pc.sub <- readsDistribution(pc.sub, txdb, las=2)
pc.sub <- readsDistribution(pc.sub, txdb, las=2,
```



```

precedence=c(
"CDS", "UTR5", "UTR3", "OtherExon",
"Intron", "upstream", "downstream",
"InterGenic"
))

```

---

|              |                                |
|--------------|--------------------------------|
| readsEndPlot | <i>Plot start/stop windows</i> |
|--------------|--------------------------------|

---

### Description

Plot the reads shifted from start/stop position of CDS.

### Usage

```

readsEndPlot(
  bamfile,
  CDS,
  toStartCodon = TRUE,
  fiveEnd = TRUE,
  shift = 0,
  window = c(-29, 30),
  readLen = 25:30,
  ignore.seqlevelsStyle = FALSE
)

```

### Arguments

|                       |  |
|-----------------------|--|
| bamfile               | A BamFile object.  |
| CDS                   | Output of <a href="#">prepareCDS</a>   |
| toStartCodon          | What to search: start or end codon   |
| fiveEnd               | Search from five or three ends of the reads.   |
| shift                 | number(1). Search from 5' end or 3' end of given number. if fiveEnd set to false, please set the shift as a negative number. |
| window                | The window of CDS region to plot   |
| readLen               | The reads length used to plot  |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not.   |

### Value

The invisible list with counts numbers and reads in GRanges.

**Examples**

```

library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",
#   chrominfo = seqinfo(Drerio)["chr1"],
#   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
re <- readsEndPlot(bamfile, CDS, toStartCodon=TRUE)
readsEndPlot(re$reads, CDS, toStartCodon=TRUE, fiveEnd=FALSE)
#re <- readsEndPlot(bamfile, CDS, toStartCodon=FALSE)
#readsEndPlot(re$reads, CDS, toStartCodon=FALSE, fiveEnd=FALSE)
readsEndPlot(bamfile, CDS, shift=13)
#readsEndPlot(bamfile, CDS, fiveEnd=FALSE, shift=-16)

```

readsLenToKeep

*Get reads length to keep by cutoff percentage***Description**

Set the percentage to filter the reads.

**Usage**

```
readsLenToKeep(readsLengthDensity, cutoff = 0.8)
```

**Arguments**

```
readsLengthDensity      Output of summaryReadsLength
cutoff                  Cutoff value.
```

**Value**

Reads length to be kept.

**Examples**

```

reads <- GRanges("chr1", ranges=IRanges(seq.int(100), width=1),
                 qwidth=sample(25:31, size = 100, replace = TRUE,
                               prob = c(.01, .01, .05, .1, .77, .05, .01)))
readsLenToKeep(summaryReadsLength(reads, plot=FALSE))

```

---

ribosomeReleaseScore *Ribosome Release Score (RRS)*

---

### Description

RRS is calculated as the ratio of translational efficiency in the CDS with RPFs in the 3'UTR.

### Usage

```
ribosomeReleaseScore(
  cdsTE,
  utr3TE,
  CDSsampleOrder,
  UTR3sampleOrder,
  pseudocount = 0,
  log2 = FALSE
)
```

### Arguments

cdsTE, utr3TE      Translational efficiency of CDS and UTR3 region. Output of [translationalEfficiency](#)

CDSsampleOrder, UTR3sampleOrder  
                     Sample order of cdsTE and utr3TE. The parameters are used to make sure that the order of CDS and UTR3 in TE is corresponding samples.

pseudocount        The number will be add to sum of reads count to avoid X/0.

log2                Do log2 transform or not.

### Value

A vector of RRS.

### Examples

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs, RNAs, gtf)
cvgs.utr3 <- coverageDepth(RPFs, RNAs, gtf, region="utr3")
TE90 <- translationalEfficiency(cvgs, window = 90)
TE90.utr3 <- translationalEfficiency(cvgs.utr3, window = 90)
rrs <- ribosomeReleaseScore(TE90, TE90.utr3)

## End(Not run)
```

---

shiftReadsByFrame      *Shift reads by reading frame*

---

### Description

Shift reads P site position by reading frame. After shifting, all reading frame will be set as 0

### Usage

```
shiftReadsByFrame(reads, txdb, ignore.seqlevelsStyle = FALSE)
```

### Arguments

reads                      Output of [getPsiteCoordinates](#)  
txdb                        A TxDb object.  
ignore.seqlevelsStyle      Ignore the sequence name style detection or not.

### Value

Reads with reading frame information

### Examples

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=11)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
txdb <- makeTxDbFromGFF(system.file("extdata",
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
                                   package="ribosomeProfilingQC"),
                       organism = "Danio rerio",
                       chrominfo = seqinfo(Drerio)["chr1"],
                       taxonomyId = 7955)
pc.sub <- shiftReadsByFrame(pc.sub, txdb)
```

---

simulateRPF                      *Simulation function*

---

### Description

Simulate the RPFs reads in CDS, 5'UTR and 3'UTR

**Usage**

```
simulateRPF(
  txdb,
  outputPath,
  genome,
  samples = 6,
  group1 = c(1, 2, 3),
  group2 = c(4, 5, 6),
  readsPerSample = 1e+06,
  readsLen = 28,
  psite = 13,
  frame0 = 0.9,
  frame1 = 0.05,
  frame2 = 0.05,
  DRegions = GRanges(),
  size = 1,
  sd = 0.02,
  minDElevel = log2(2),
  includeReadsSeq = FALSE
)
```

**Arguments**

|                        |   |
|------------------------|---|
| txdb                   | A TxDb object   |
| outputPath             | Output folder for the bam files                               |
| genome                 | A BSgenome object   |
| samples                | Total samples to simulate.                                    |
| group1, group2         | Numeric to index the sample groups.                           |
| readsPerSample         | Total reads number per sample.                                |
| readsLen               | Reads length, default 100bp.                                  |
| psite                  | P-site position. default 13.                                  |
| frame0, frame1, frame2 | Percentage of reads distribution in frame0, frame1 and frame2 |
| DRegions               | The regions with differential reads in exon, utr5 and utr3.   |
| size                   | Dispersion parameter. Must be strictly positive.              |
| sd                     | Standard deviations.  |
| minDElevel             | Minimal differential level. default: log2(2).                 |
| includeReadsSeq        | logical(1). Include reads sequence or not.                    |

**Value**

An invisible list of GAlignments.

**Examples**

```
library(GenomicFeatures)
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
  package="GenomicFeatures")
```

```
txdb <- loadDb(txdb_file)
simulateRPF(txdb, samples=1, readsPerSample = 1e3)
## Not run:
cds <- prepareCDS(txdb, withUTR = TRUE)
cds <- cds[width(cds)>200]
DEregions <- cds[sample(seq_along(cds), 10)]
simulateRPF(txdb, samples=6, readsPerSample = 1e5, DEregions=DEregions)

## End(Not run)
```

---

spliceEvent

*Get splicing events*


---

### Description

Get differential usage of alternative Translation Initiation Sites, alternative Polyadenylation Sites or alternative splicing sites

### Usage

```
spliceEvent(coverage, group1, group2)
```

### Arguments

coverage            Coverages of feature region with extensions. Output of [coverageDepth](#)  
group1, group2      The sample names of group 1 and group 2

### Value

A GRanges object of splice events.

### Examples

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
coverage <- coverageDepth(RPFs, gtf=gtf,
                          level="gene", region="feature with extension")
group1 <- c("RPF.KD1.1", "RPF.KD1.2")
group2 <- c("RPF.WT.1", "RPF.WT.2")
se <- spliceEvent(coverage, group1, group2)

## End(Not run)
```

strandPlot

*Plot the distribution of reads in sense and antisense strand***Description**

Plot the distribution of reads in sense and antisense strand to check the mapping is correct.

**Usage**

```
strandPlot(
  reads,
  CDS,
  col = c("#009E73", "#D55E00"),
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

**Arguments**

|                       |  |
|-----------------------|--|
| reads                 | Output of <a href="#">getPsiteCoordinates</a>    |
| CDS                   | Output of <a href="#">prepareCDS</a>             |
| col                   | Color for sense and antisense strand.            |
| ignore.seqlevelsStyle | Ignore the sequence name style detection or not. |
| ...                   | Parameter passed to barplot                      |

**Value**

A ggplot object.

**Examples**

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=11)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
txdb <- makeTxDbFromGFF(system.file("extdata",
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
                                   package="ribosomeProfilingQC"),
                      organism = "Danio rerio",
                      chrominfo = seqinfo(Drerio)["chr1"],
                      taxonomyId = 7955)
CDS <- prepareCDS(txdb)
strandPlot(pc.sub, CDS)
```

---

summaryReadsLength      *Summary the reads lengths*

---

### Description

Plot the reads length distribution

### Usage

```
summaryReadsLength(reads, widthRange = c(20:35), plot = TRUE, ...)
```

### Arguments

|            |                               |
|------------|-------------------------------|
| reads      | Output of getPsiteCoordinates |
| widthRange | The reads range to be plot    |
| plot       | Do plot or not                |
| ...        | Not use.                      |

### Value

The reads length distribution

### Examples

```
reads <- GRanges("chr1", ranges=IRanges(seq.int(100), width=1),
                 qwidth=sample(25:31, size = 100, replace = TRUE,
                               prob = c(.01, .01, .05, .1, .77, .05, .01)))
summaryReadsLength(reads)
```

---

translationalEfficiency  
*Translational Efficiency*

---

### Description

Calculate Translational Efficiency (TE). TE is defined as the ratios of the absolute level of ribosome occupancy divided by RNA levels for transcripts.

### Usage

```
translationalEfficiency(
  x,
  window,
  RPFsampleOrder,
  mRNAsampleOrder,
  pseudocount = 1,
  log2 = FALSE,
  normByLibSize = FALSE,
  shrink = FALSE,
  ...
)
```



**Arguments**

|                                 |   |
|---------------------------------|---|
| x                               | Output of <code>getFPKM</code> or <code>normByRUVs</code> . if window is set, it must be output of <code>coverageDepth</code> .                     |
| window                          | numeric(1). window size for maximal counts.   |
| RPFsampleOrder, mRNAsampleOrder | Sample order of RPFs and mRNAs. The parameters are used to make sure that the order of RPFs and mRNAs in cvgs is corresponding samples.             |
| pseudocount                     | The number will be add to sum of reads count to avoid X/0.  |
| log2                            | Do log2 transform or not.   |
| normByLibSize                   | Normalization by library size or not. If window size is provided and normByLibSize is set to TRUE, the coverage will be normalized by library size. |
| shrink                          | Shrink the TE or not.   |
| ...                             | Parameters will be passed to ash function from ash.   |

**Value**

A list with RPFs, mRNA levels and TE as a matrix with translational efficiency

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\.[12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cnts <- countReads(RPFs, RNAs, gtf, level="gene")
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)

## End(Not run)
```

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