

# Package ‘RNAsShapeQC’

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**Type** Package

**Title** RNA Coverage-Shape-Based Quality Control Metrics

**Version** 1.0.0

**Description** RNAsShapeQC provides coverage-shape-based quality control (QC) metrics for mRNA-seq and total RNA-seq data. It supports per-gene pileup construction from BAM files as well as toy datasets for quick-start examples. The package implements protocol-specific metrics, including decay rate (DR), degradation score (DS), mean coverage depth (MCD), window coefficient of variation (wCV), area under the curve (AUC), and shape-based sample-level indices. RNAsShapeQC also includes HPC-friendly functions for per-gene batch processing and cross-study pileup generation. This package enables interpretable, protocol-specific QC assessments for diverse RNA-seq workflows.

**License** MIT + file LICENSE

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---

`.build_pileupExon`      *Core helper to build exon-only pileup*

---

## Description

Core helper to build exon-only pileup

## Usage

```
.build_pileupExon(pileupPath, cases = NULL, study = NULL)
```

## Arguments

<code>pileupPath</code>	file paths of coverage pileupData including .RData file names
<code>cases</code>	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
<code>study</code>	a character of study abbreviation in the pileupList. Default is NULL.

## Value

a numeric matrix of exon-only coverage (rows: exon positions, columns: samples).

## References

Choi, H.Y., Jo, H., Zhao, X. et al. SCISSOR: a framework for identifying structural changes in RNA transcripts. *Nat Commun* 12, 286 (2021).

## Examples

```
## Requires a base-level coverage pileup .RData file
try(
  .build_pileupExon(pileupPath="path/to/pileup.RData"), silent=TRUE
)
```

---

`combine_vecObj`*Combine vectors as a matrix from objects*

---

**Description**

Combine vectors as a matrix from objects

**Usage**

```
combine_vecObj(  
  filePath,  
  objName = NULL,  
  header = NULL,  
  skip = NULL,  
  txtCol = NULL,  
  margin,  
  rowNames,  
  colNames,  
  nCores = 2  
)
```

**Arguments**

<code>filePath</code>	file paths including .RData file names
<code>objName</code>	a character of object name
<code>header</code>	logical; whether the text files have a header line.
<code>skip</code>	integer; number of lines to skip before reading data from ‘.txt’ files.
<code>txtCol</code>	integer; column index in the text file that contains the numeric vector to be extracted.
<code>margin</code>	1 and 2 return for gene- and sample-level vectors, respectively.
<code>rowNames</code>	a vector of gene names
<code>colNames</code>	a vector of sample names
<code>nCores</code>	the number of cores for parallel computing. Default is 2.

**Value**

a gene x sample matrix

**Examples**

```
## API illustration only  
invisible(NULL)
```

---

compute\_DIIwt                      *Core helper to compute a degraded/intact index using gene weight*

---

## Description

Core helper to compute a degraded/intact index using gene weight

## Usage

```
compute_DIIwt(DR, alpha = 2, cutoff = 3, TPM, thr = 5, pct = 40, genelength)
```

## Arguments

DR	a the number of genes x the number of samples matrix of decay rates
alpha	a positive numeric exponent factor to weight the magnitude of decay rates. Default is 2.
cutoff	numeric threshold on projection depth used to classify samples.
TPM	a numeric matrix of TPM values with the same genes in rows and the same samples in columns as DR.
thr	threshold. Default is 5.
pct	percent. Default is 40.
genelength	a gene length (bp) vector with names as gene IDs.

## Value

a matrix of with decay rate with filtered genes; a matrix including a vector of DII; a data frame of gene info; and a scale factor.

## Examples

```
data("TOY_mrna_mat")

compute_DIIwt(
  DR      = TOY_mrna_mat$DR,
  TPM     = TOY_mrna_mat$TPM,
  genelength = TOY_mrna_mat$gene_length
)
```

---

`compute_DR`*Core helper to compute decay rate*

---

**Description**

Core helper to compute decay rate

**Usage**

```
compute_DR(  
  pileupData,  
  exonRanges,  
  sampleInfo,  
  cases = NULL,  
  logshiftVal = 10,  
  plotNormalization = FALSE  
)
```

**Arguments**

<code>pileupData</code>	exon-only coverage pileup matrix for a single gene.
<code>exonRanges</code>	GRanges object specifying exon coordinates for the gene.
<code>sampleInfo</code>	a sample information table including sample id. The number of rows is equal to the number of samples.
<code>cases</code>	optional character vector specifying a subset of samples. used for handling missing coverage.
<code>logshiftVal</code>	numeric; passed to <code>process_pileup()</code> .
<code>plotNormalization</code>	logical; passed to <code>process_pileup()</code> .

**Details**

The arguments `pileupData`, `exonRanges`, `logshiftVal`, and `plotNormalization` are passed directly to `process_pileup()`; see its documentation for details.

**Value**

a numeric vector of decay rates, one value per sample.

**References**

Choi, H.Y., Jo, H., Zhao, X. et al. SCISSOR: a framework for identifying structural changes in RNA transcripts. *Nat Commun* 12, 286 (2021).

**Examples**

```
## API illustration only
## Exon-only pileup matrix (rows: exon positions, columns: samples)
## Typically obtained via get_pileupExon()
pileupData <- matrix(c(10, 12, 8, 9, 5, 6, 4, 5), nrow=2, byrow=TRUE)
colnames(pileupData) <- c("S1", "S2", "S3", "S4")

sampleInfo <- data.frame(SampleID=colnames(pileupData))

exonRanges <- list(
  Gene      = "KEAP1",
  cRanges   = data.frame(e.start=c(1), e.end=c(50001), row.names="exon1"),
  regions    = "chr19:10600000-10650000:+",
  new.regions = "chr19:10600000-10650000:+",
  strand     = "+"
)

compute_DR(
  pileupData = pileupData,
  exonRanges = exonRanges,
  sampleInfo = sampleInfo
)
```

---

compute\_MCD

*Core helper to compute a mean coverage depth*


---

**Description**

Core helper to compute a mean coverage depth

**Usage**

```
compute_MCD(pileupData, sampleInfo, cases = NULL)
```

**Arguments**

pileupData	exon-only coverage pileup matrix for a single gene.
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
cases	optional character vector specifying a subset of samples. used for handling missing coverage.

**Value**

a numeric vector of mean coverage depth, one value per sample.

**Examples**

```
## API illustration only
## Exon-only pileup matrix (rows: exon positions, columns: samples)
## Typically obtained via get_pileupExon()
pileupData <- matrix(c(10, 12, 8, 9, 5, 6, 4, 5), nrow=2, byrow=TRUE)
colnames(pileupData) <- c("S1", "S2", "S3", "S4")

sampleInfo <- data.frame(SampleID=colnames(pileupData))

compute_MCD(pileupData=pileupData, sampleInfo=sampleInfo)
```

---

compute\_SOI

*Core helper to compute a suboptimal/optimal index*


---

**Description**

Core helper to compute a suboptimal/optimal index

**Usage**

```
compute_SOI(MCD, wCV, rstPct = 20, obsPct = 50, cutoff = 3)
```

**Arguments**

MCD	a mean coverage depth is a the number of genes x the number of samples matrix.
wCV	a window coefficient of variation is a the number of genes x the number of samples matrix.
rstPct	restricted percent (one-side) to restrict genes by log transformed MC. Default is 20.
obsPct	span includes the percent of observations in each local regression. Default is 50.
cutoff	numeric threshold on projection depth used to classify samples.

**Value**

a matrix including a vector of SOI; a coordinate matrix of smoothed data; and a range of MCD.

**Examples**

```
data("TOY_total_mat")

compute_SOI(MCD=TOY_total_mat$MCD, wCV=TOY_total_mat$wCV)
```

---

`compute_wCV`*Core helper to compute a window coefficient of variation*

---

## Description

Core helper to compute a window coefficient of variation

## Usage

```
compute_wCV(  
  pileupData,  
  sampleInfo,  
  rnum = 100,  
  method = 1,  
  winSize = 20,  
  egPct = 10,  
  cases = NULL  
)
```

## Arguments

<code>pileupData</code>	exon-only coverage pileup matrix for a single gene.
<code>sampleInfo</code>	a sample information table including sample id. The number of rows is equal to the number of samples.
<code>rnum</code>	the number of regions for uniformly dividing the x-axis. Default is 100.
<code>method</code>	1 and 2 return the raw read depth and the interpolated read depth at the normalized genomic position, respectively. Default is 1.
<code>winSize</code>	window size of the rolling window. Default is 20.
<code>egPct</code>	edge percent (one-side) to calculate the trimmed mean. Default is 10.
<code>cases</code>	optional character vector specifying a subset of samples. used for handling missing coverage.

## Value

a numeric vector of window coefficients of variation, one value per sample.

## Examples

```
## API illustration only  
## Exon-only pileup matrix (rows: exon positions, columns: samples)  
## Typically obtained via get_pileupExon()  
pileupData <- matrix(c(10, 12, 8, 9, 5, 6, 4, 5), nrow=2, byrow=TRUE)  
colnames(pileupData) <- c("S1", "S2", "S3", "S4")  
  
sampleInfo <- data.frame(SampleID=colnames(pileupData))
```

```
compute_wCV(
  pileupData = pileupData,
  sampleInfo = sampleInfo,
  rnum       = 10,
  winSize    = 2
)
```

---

construct_pileup	<i>Construct a per-gene pileup from BAM files (for single-study or multi-study)</i>
------------------	---

---

### Description

Construct a per-gene pileup from BAM files (for single-study or multi-study)

### Usage

```
construct_pileup(
  Gene,
  studylist,
  regionsFile,
  regionsFormat = c("auto", "SCISSOR_gaf", "gencode.regions"),
  geneCol = 1,
  regionsCol = NULL,
  bamFilesList,
  caseIDList,
  max_depth = 1e+05,
  strand.specific = FALSE,
  nCores = 2,
  outFile = NULL
)
```

### Arguments

Gene	a character of gene name
studylist	a character vector of study IDs or abbreviation/name
regionsFile	either a file path or a data.frame specifying gene regions. If a file path is given, it is read using <code>read.table()</code> with automatic handling of header/non-header cases.
regionsFormat	character; one of "auto", "SCISSOR_gaf", or "gencode.regions". In "auto" mode, the function attempts to detect whether the file uses SCISSOR-style columns <code>gene_name</code> and <code>regions</code> , falling back to "gencode.regions" otherwise.
geneCol	integer; column index for the gene identifier when <code>regionsFormat="gencode.regions"</code> . Default is 1.
regionsCol	integer; column index for the regions string when <code>regionsFormat="gencode.regions"</code> . Default is NULL, which is interpreted as 2.

bamFilesList	named list of character vectors of BAM file paths
caseIDList	named list of character vectors of sample IDs corresponding to bamFilesList
max_depth	integer; max depth parameter for Rsamtools::PileupParam. Default is 100000.
strand.specific	Logical; whether to use strand-specific pileup. If TRUE, only the "+" strand is retained (when strand information is available). Default is FALSE.
nCores	the number of cores for parallel computing. Default is 2.
outFile	a directory with a file name to save outputs. Default is NULL.

**Value**

a pileup matrix, regions, and ranges of genomic positions

**Examples**

```
## API illustration only
invisible(NULL)
```

---

extract_RData	<i>Extract an object from .RData</i>
---------------	--------------------------------------

---

**Description**

Extract an object from .RData

**Usage**

```
extract_RData(file, object)
```

**Arguments**

file	.RData file
object	object name

**Value**

the object

**References**

<https://stackoverflow.com/questions/65964064/programmatically-extract-an-object-from-collection-of-rdata-files>

**Examples**

```
tmp <- tempfile(fileext=".RData")
x <- 1
save(x, file=tmp)
extract_RData(tmp, "x")
```

---

filter\_lowExpGenes      *Filter low expressed genes*

---

**Description**

Filter low expressed genes

**Usage**

```
filter_lowExpGenes(genelist, TPM, thr = 5, pct = 40)
```

**Arguments**

genelist	a vector of gene names
TPM	a gene expression counts matrix transformed by TPM
thr	threshold. Default is 5.
pct	percent. Default is 40.

**Value**

a vector of filtered gene names

**Examples**

```
data("TOY_mrna_mat")
filter_lowExpGenes(genelist=TOY_mrna_mat$genes, TPM=TOY_mrna_mat$TPM)
```

---

gen\_DR      *Get a decay rate for genes and samples (for a single gene)*

---

**Description**

Get a decay rate for genes and samples (for a single gene)

**Usage**

```
gen_DR(Gene, pileupPath, sampleInfo, cases = NULL, Study = NULL, outFile)
```

**Arguments**

Gene	a character of gene name
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
Study	a character of study abbreviation in the pileupList. Default is NULL.
outFile	a directory with a file name to save outputs

**Value**

Invisibly returns NULL; results are saved to outFile.

**References**

Choi, H.Y., Jo, H., Zhao, X. et al. SCISSOR: a framework for identifying structural changes in RNA transcripts. Nat Commun 12, 286 (2021).

**Examples**

```
## API illustration only
invisible(NULL)
```

---

gen_MCD	<i>Get a mean coverage depth for genes and samples (for a single gene)</i>
---------	--

---

**Description**

Get a mean coverage depth for genes and samples (for a single gene)

**Usage**

```
gen_MCD(Gene, pileupPath, sampleInfo, cases = NULL, Study = NULL, outFile)
```

**Arguments**

Gene	a character of gene name
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
Study	a character of study abbreviation in the pileupList. Default is NULL.
outFile	a directory with a file name to save outputs

**Value**

Invisibly returns NULL; results are saved to outFile.

**Examples**

```
## API illustration only
invisible(NULL)
```

---

gen_wCV	<i>Get a window coefficient of variation for genes and samples (for a single gene)</i>
---------	--

---

**Description**

Get a window coefficient of variation for genes and samples (for a single gene)

**Usage**

```
gen_wCV(
  Gene,
  pileupPath,
  sampleInfo,
  rnum = 100,
  method = 1,
  winSize = 20,
  egPct = 10,
  cases = NULL,
  Study = NULL,
  outFile
)
```

**Arguments**

Gene	a character of gene name
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
rnum	the number of regions for uniformly dividing the x-axis for gene length normalization. Default is 100.
method	1 and 2 return the raw read depth and the interpolated read depth at the normalized genomic position, respectively. Default is 1.
winSize	window size of the rolling window. Default is 20.
egPct	edge percent (one-side) to calculate the trimmed mean. Default is 10.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
Study	a character of study abbreviation in the pileupList. Default is NULL.
outFile	a directory with a file name to save outputs

**Value**

Invisibly returns NULL; results are saved to outFile.

**Examples**

```
## API illustration only
invisible(NULL)
```

---

get_DIIhc	<i>Get a degraded/intact index for samples using hierarchical clustering</i>
-----------	--

---

**Description**

Get a degraded/intact index for samples using hierarchical clustering

**Usage**

```
get_DIIhc(DR, topPct = 5)
```

**Arguments**

DR	a the number of genes x the number of samples matrix of decay rates
topPct	top percentages of decay rates defined as degrateGrp=1. Default is 5.

**Value**

a matrix of binary converted decay rates; hierarchical clustering outputs of samples; and a vector of DII per sample.

**Examples**

```
data("TOY_mrna_mat")
get_DIIhc(DR=TOY_mrna_mat$DR)
```

---

get\_DIIwt

*Get a degraded/intact index for samples using gene weight*


---

### Description

Get a degraded/intact index for samples using gene weight

### Usage

```
get_DIIwt(
  DR,
  alpha = 2,
  cutoff = 3,
  TPM = NULL,
  thr = 5,
  pct = 40,
  genelength = NULL,
  assay.DR = "DR",
  assay.TPM = "TPM"
)
```

### Arguments

DR	a the number of genes x the number of samples matrix of decay rates
alpha	a positive numeric exponent factor to weight the magnitude of decay rates. Default is 2.
cutoff	numeric threshold on projection depth used to classify samples.
TPM	a numeric matrix of TPM values with the same genes in rows and the same samples in columns as DR.
thr	threshold. Default is 5.
pct	percent. Default is 40.
genelength	a gene length (bp) vector with names as gene IDs.
assay.DR	character string specifying the assay name containing the DR matrix in a SummarizedExperiment object.
assay.TPM	character string specifying the assay name containing the TPM matrix in a SummarizedExperiment object.

### Value

a matrix of with decay rate with filtered genes; a matrix including a vector of DII; a data frame of gene info; and a scale factor.

**Examples**

```
data("TOY_mrna_se")
get_DIIwt(TOY_mrna_se)
```

---

get_DR	<i>Get a decay rate for genes and samples (for a genelist)</i>
--------	--

---

**Description**

Get a decay rate for genes and samples (for a genelist)

**Usage**

```
get_DR(genelist, pileupPath, sampleInfo, cases = NULL, nCores = 2)
```

**Arguments**

genelist	a vector of gene names
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
nCores	the number of cores for parallel computing. Default is 2.

**Value**

DR is a the number of genes x the number of samples matrix.

**References**

Choi, H.Y., Jo, H., Zhao, X. et al. SCISSOR: a framework for identifying structural changes in RNA transcripts. Nat Commun 12, 286 (2021).

**Examples**

```
## NOTE:
## This example demonstrates the function interface only.
## Meaningful results require coverage pileup files generated
## from BAM files (see vignette for a full workflow).
data("TOY_mrna_mat")

## Interface-only example (no meaningful output is produced)
try(
  get_DR(
    genelist = TOY_mrna_mat$genes,
```

```

        pileupPath = rep(NA, length(TOY_mrna_mat$genes)),
        sampleInfo = data.frame(SampleID=TOY_mrna_mat$samples),
        nCores      = 2
    ),
    silent=TRUE
)

```

---

get\_MCD

*Get a mean coverage depth for genes and samples (for a genelist)*


---

## Description

Get a mean coverage depth for genes and samples (for a genelist)

## Usage

```
get_MCD(genelist, pileupPath, sampleInfo, cases = NULL, nCores = 2)
```

## Arguments

genelist	a vector of gene names
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
nCores	the number of cores for parallel computing. Default is 2.

## Value

MCD is a the number of genes x the number of samples matrix.

## Examples

```

## NOTE:
## This example demonstrates the function interface only.
## Meaningful results require coverage pileup files generated
## from BAM files (see vignette for a full workflow).
data("TOY_total_mat")

## Interface-only example (no meaningful output is produced)
try(
  get_MCD(
    genelist  = TOY_total_mat$genes,
    pileupPath = rep(NA, length(TOY_total_mat$genes)),
    sampleInfo = data.frame(SampleID=TOY_total_mat$samples),
    nCores     = 2
  ),
  silent=TRUE
)

```

---

get_pileupExon	<i>Get a focused pileup of exon location (for single-study)</i>
----------------	---

---

**Description**

Get a focused pileup of exon location (for single-study)

**Usage**

```
get_pileupExon(g, pileupPath, cases = NULL)
```

**Arguments**

g	the gene order in genelist
pileupPath	file paths of coverage pileupData including .RData file names
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.

**Value**

a focused pileup is a the number of exon locations x the number of samples matrix for the g-th gene.

**Examples**

```
## Requires a base-level coverage pileup .RData file
try(
  get_pileupExon(g=1, pileupPath=c("path/to/pileup1.RData", "path/to/pileup2.RData")), silent=TRUE
)
```

---

get_SOI	<i>Get a suboptimal/optimal index for samples</i>
---------	---

---

**Description**

Get a suboptimal/optimal index for samples

**Usage**

```
get_SOI(
  MCD,
  wCV = NULL,
  rstPct = 20,
  obsPct = 50,
  cutoff = 3,
  assay.MCD = "MCD",
  assay.wCV = "wCV"
)
```

**Arguments**

MCD	a mean coverage depth is a the number of genes x the number of samples matrix.
wCV	a window coefficient of variation is a the number of genes x the number of samples matrix.
rstPct	restricted percent (one-side) to restrict genes by log transformed MC. Default is 20.
obsPct	span includes the percent of observations in each local regression. Default is 50.
cutoff	numeric threshold on projection depth used to classify samples.
assay.MCD	character string specifying the assay name containing the MCD matrix in a SummarizedExperiment object.
assay.wCV	character string specifying the assay name containing the wCV matrix in a SummarizedExperiment object.

**Value**

a matrix including a vector of SOI; a coordinate matrix of smoothed data; and a range of MCD.

**Examples**

```
data("TOY_total_se")
get_SOI(TOY_total_se)
```

---

get_wCV	<i>Get a window coefficient of variation for genes and samples (for a genelist)</i>
---------	---

---

**Description**

Get a window coefficient of variation for genes and samples (for a genelist)

**Usage**

```
get_wCV(
  genelist,
  pileupPath,
  sampleInfo,
  rnum = 100,
  method = 1,
  winSize = 20,
  egPct = 10,
  cases = NULL,
  nCores = 2
)
```

**Arguments**

genelist	a vector of gene names
pileupPath	file paths of coverage pileupData including .RData file names
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
rnum	the number of regions for uniformly dividing the x-axis for gene length normalization. Default is 100.
method	1 and 2 return the raw read depth and the interpolated read depth at the normalized genomic position, respectively. Default is 1.
winSize	window size of the rolling window. Default is 20.
egPct	edge percent (one-side) to calculate the trimmed mean. Default is 10.
cases	a vector of specific samples among all samples in pileup. If NULL, all samples are selected. Default is NULL.
nCores	the number of cores for parallel computing. Default is 2.

**Value**

wCV is a the number of genes x the number of samples matrix.

**Examples**

```
## NOTE:
## This example demonstrates the function interface only.
## Meaningful results require coverage pileup files generated
## from BAM files (see vignette for a full workflow).
data("TOY_total_mat")

## Interface-only example (no meaningful output is produced)
try(
  get_wCV(
    genelist = TOY_total_mat$genes,
    pileupPath = rep(NA, length(TOY_total_mat$genes)),
    sampleInfo = data.frame(SampleID=TOY_total_mat$samples),
    nCores = 2
  ),
  silent=TRUE
)
```

---

plot\_DIIwt

*Plot degraded/intact index outputs*


---

**Description**

Plot degraded/intact index outputs

**Usage**

```
plot_DIIwt(DR, DIIresult, cutoff = 3, outFile = NULL)
```

**Arguments**

DR	a the number of genes x the number of samples matrix of decay rates
DIIresult	outputs from get_DII function
cutoff	numeric threshold on projection depth used to classify samples.
outFile	a directory with a file name to save outputs. Default is NULL.

**Value**

figures for the distribution of DII by PD; and the heatmap of DR.

**References**

<https://jtr13.github.io/cc21fall2/raincloud-plot-101-density-plot-or-boxplotwhy-not-do-both.html>

**Examples**

```
data("TOY_mrna_se")

res <- get_DIIwt(TOY_mrna_se)

try(
  plot_DIIwt(
    DR      = TOY_mrna_se$DR,
    DIIresult = res,
    outFile  = tempfile(fileext=".png")
  ),
  silent=TRUE
)
```

---

plot\_GBC

*Plot gene body coverage*

---

**Description**

Plot gene body coverage

**Usage**

```
plot_GBC(
  pileupPath,
  geneNames,
  rnum = 100,
  method = 1,
```

```

    scale = TRUE,
    stat = 2,
    plot = TRUE,
    sampleInfo
  )

```

### Arguments

pileupPath	file paths of coverage pileupData including .RData file names
geneNames	gene names per file. If NULL, Gene i with the same length of pileupPath be set. Default is NULL.
rnum	the number of regions for uniformly dividing the x-axis. Default is 100.
method	1 and 2 return the raw read depth and the interpolated read depth at the normalized genomic position, respectively. Default is 1.
scale	TRUE/FALSE returns the scaled/unscaled normalized transcript coverage. Default is TRUE.
stat	1 and 2 return median and mean normalized coverage curves per sample, respectively. Default is 1.
plot	TRUE/FALSE turns on/off the normalized transcript coverage plot. Default is TRUE.
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.

### Value

a matrix and a plot, or a matrix for the gene body coverage where plot is TRUE or FALSE, respectively.

### Examples

```

## Interface-only example
try(
  plot_GBC(
    pileupPath = NA,
    geneNames = "GENE1",
    sampleInfo = data.frame(
      SampleID = c("S1", "S2"),
      CODING_BASES = c(1, 1),
      INTRONIC_BASES = c(1, 1)
    ),
    plot = FALSE
  ),
  silent=TRUE
)

```

---

plot\_GBCos                      *Plot gene body coverage with optimal samples*

---

### Description

Plot gene body coverage with optimal samples

### Usage

```
plot_GBCos(stat = 2, plot = TRUE, sampleInfo, GBCresult, auc.vec)
```

### Arguments

stat	1 and 2 return median and mean normalized coverage curves per sample, respectively. Default is 1.
plot	TRUE/FALSE turns on/off the normalized transcript coverage plot. Default is TRUE.
sampleInfo	a sample information table including sample id. The number of rows is equal to the number of samples.
GBCresult	results of the gene body coverage with all samples
auc.vec	a vector with SOI per sample

### Value

a matrix and a plot, or a matrix for the gene body coverage where plot is TRUE or FALSE, respectively.

### Examples

```
## Interface-only example
GBCresult <- list(
  GBP=data.frame(
    region      = 1:2,
    sample      = c("S1", "S2"),
    scale.geom  = c(1, 1),
    RatioIntron = c(1, 1)
  )
)

auc.vec <- data.frame(
  Sample = c("S1", "S2"),
  PD     = c(0, 0),
  SOI    = c("Optimal", "Optimal")
)

try(
  plot_GBCos(
    sampleInfo = data.frame(SampleID=c("S1", "S2")),
```

```
        GBCresult = GBCresult,  
        auc.vec   = auc.vec,  
        plot      = FALSE  
    ),  
    silent=TRUE  
)
```

---

plot\_SOI

*Plot suboptimal/optimal index outputs*

---

### Description

Plot suboptimal/optimal index outputs

### Usage

```
plot_SOI(SOIresult, cutoff = 3, outFile = NULL)
```

### Arguments

SOIresult        outputs from get\_SOI function  
cutoff           numeric threshold on projection depth used to classify samples.  
outFile         a directory with a file name to save outputs. Default is NULL.

### Value

figures for the distribution of SOI by PD; and the relation of wCV and MCD.

### References

<https://jtr13.github.io/cc21fall2/raincloud-plot-101-density-plot-or-boxplotwhy-not-do-both.html>

### Examples

```
data("TOY_total_se")  
  
res <- get_SOI(TOY_total_se)  
  
plot_SOI(SOIresult=res, outFile=tempfile(fileext=".png"))
```

---

 TOY\_mrna\_mat

*Toy mRNA-seq-like dataset for RNAshapeQC (matrix input)*


---

### Description

A small synthetic dataset mimicking mRNA-seq coverage-based quality control (QC) inputs. It is used in the vignette to demonstrate degradation-based metrics such as decay rate (DR), degradation score (DS), and the degraded/intact index (DII).

### Format

A list with 6 components:

**DR** A numeric matrix of decay rates; genes in rows and samples in columns. In this toy dataset, it is a 100 (genes) x 10 (samples) matrix with row names like "Gene001" and column names like "T01".

**genes** A character vector of length 100 containing gene IDs used as row names in DR and TPM.

**samples** A character vector of length 10 containing sample IDs used as column names in DR and TPM.

**protocol** A single character string indicating the protocol used, here "mRNA-seq".

**TPM** A numeric matrix of TPM values; same dimension and dimnames as DR.

**genelength** A gene length (bp) vector with names matching the row names of DR.

### Details

All values are synthetic and were generated solely for demonstration and testing. They do not correspond to any real samples or cohorts.

### Examples

```
data("TOY_mrna_mat")
str(TOY_mrna_mat)
```

---

 TOY\_mrna\_se

*Toy mRNA-seq-like dataset for RNAshapeQC (SE input)*


---

### Description

A small synthetic SummarizedExperiment object mimicking mRNA-seq coverage-based quality control (QC) inputs. It is used in the vignette to demonstrate degradation-based metrics such as decay rate (DR), degradation score (DS), and the degraded/intact index (DII).

**Format**

A SummarizedExperiment object with:

**assays** Two matrices:

**DR** A numeric matrix of decay rates (genes x samples).

**TPM** A numeric matrix of TPM expression values with the same dimension and dimnames as DR.

**rowData** A DataFrame containing gene-level metadata, including gene\_length (bp).

**Details**

The dataset contains 100 synthetic genes and 10 synthetic samples. All values were generated solely for demonstration and testing purposes and do not correspond to real biological data.

**Examples**

```
data(TOY_mrna_se)
TOY_mrna_se
```

---

TOY_total_mat	<i>Toy total RNA-seq-like dataset for RNAscopeQC (matrix input)</i>
---------------	---

---

**Description**

A small synthetic dataset mimicking total RNA-seq coverage-based quality control (QC) inputs. It is used in the vignette to demonstrate coverage-shape metrics such as mean coverage depth (MCD), window coefficient of variation (wCV), and the suboptimal/optimal index (SOI).

**Format**

A list with 5 components:

**MCD** A numeric matrix of mean coverage depth; genes in rows and samples in columns. In this toy dataset, it is a 100 (genes) x 10 (samples) matrix with row names like "Gene001" and column names like "A01".

**wCV** A numeric matrix of window coefficients of variation; same dimension and dimnames as MCD.

**genes** A character vector of length 100 containing gene IDs used as row names in MCD and wCV.

**samples** A character vector of length 10 containing sample IDs used as column names in MCD and wCV.

**protocol** A single character string indicating the protocol used, here "total RNA-seq".

**Details**

All values are synthetic and were generated solely for demonstration and testing. They do not correspond to any real samples or cohorts.

**Examples**

```
data("TOY_total_mat")
str(TOY_total_mat)
```

---

TOY\_total\_se

*Toy total RNA-seq-like dataset for RNAscapeQC (SE input)*

---

**Description**

A small synthetic SummarizedExperiment object mimicking total RNA-seq coverage-based quality control (QC) inputs. It is used in the vignette to demonstrate coverage-shape metrics such as mean coverage depth (MCD), window coefficient of variation (wCV), and the suboptimal/optimal index (SOI).

**Format**

A SummarizedExperiment object with:

**assays** Two matrices:

**MCD** A numeric matrix of mean coverage depth (genes x samples).

**wCV** A numeric matrix of window coefficients of variation with the same dimension and dimnames as MCD.

**Details**

The dataset contains 100 synthetic genes and 10 synthetic samples. All values were generated solely for demonstration and testing purposes and do not correspond to real biological data.

**Examples**

```
data(TOY_total_se)
TOY_total_se
```

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