

# Package ‘RLSeq’

January 16, 2022

**Type** Package

**Title** RLSeq: An analysis package for R-loop mapping data

**Version** 1.0.0

**Description** RLSeq is a toolkit for analyzing and evaluating R-loop mapping datasets.

RLSeq serves two primary purposes: (1) to facilitate the evaluation of dataset quality, and (2) to enable R-loop analysis in the context of publicly-available data sets from RLBase.

The package is intended to provide a simple pipeline, called with the `RLSeq()` function, which performs all main analyses. Individual functions are also accessible and provide custom analysis capabilities. Finally an HTML report is generated with `report()`.

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**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

**Suggests** AnnotationDbi, BiocStyle, covr, lintr, rcmdcheck, DT, httr, jsonlite, kableExtra, kernlab, knitr, magick, MASS, org.Hs.eg.db, R.utils, randomForest, readr, rmarkdown, rpart, testthat (>= 3.0.0), tibble, tidyr, TxDb.Hsapiens.UCSC.hg19.knownGene, futile.logger

**Config/testthat/edition** 3

**Depends** R (>= 4.1.0)

**Imports** dplyr, ggplot2, RColorBrewer, grid, regioneR, valr, caretEnsemble, GenomicFeatures, rtracklayer, GenomicRanges, GenomeInfoDb, ComplexHeatmap, AnnotationHub, VennDiagram, callr, circlize, ggplotify, ggprism, methods, stats, RLHub, aws.s3, pheatmap

**VignetteBuilder** knitr

**biocViews** Sequencing, Coverage, Epigenetics, Transcriptomics, Classification

**URL** <https://github.com/Bishop-Laboratory/RLSeq>,  
<https://bishop-laboratory.github.io/RLSeq/>

**BugReports** <https://github.com/Bishop-Laboratory/RLSeq/issues>

**BiocType** Software**git\_url** <https://git.bioconductor.org/packages/RLSeq>**git\_branch** RELEASE\_3\_14**git\_last\_commit** 191326e**git\_last\_commit\_date** 2021-10-26**Date/Publication** 2022-01-16

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analyzeRLFS

*Analyze RLFS***Description**

Analyzes the enrichment of ranges within R-loop forming sequences (RLFS). See *details*.

**Usage**

```
analyzeRLFS(
  object,
  mask = NULL,
  quiet = FALSE,
  useMask = TRUE,
  noZ = FALSE,
  ntimes = 100,
  stepsize = 50,
  ...
)
```

**Arguments**

object	An <a href="#">RLRanges</a> object.
mask	GRanges object containing masked genomic ranges. Not needed unless masked genome unavailable (see <a href="#">genomeMasks</a> ). Custom masks can be generated using <a href="#">regioneR::getMask</a> .
quiet	If TRUE, messages are suppressed. Default: FALSE.
useMask	If FALSE, masked genome is not used. This is not recommended unless a mask is unavailable as it can lead to spurious results. Default: TRUE.
noZ	If TRUE, Z-score distribution is not calculated. Default: FALSE.
ntimes	Number of permutations to perform (default: 100).
stepsize	The step size for calculating the Z score distribution. Default: 50. See also <a href="#">regioneR::localZScore</a> .
...	Arguments passed to <a href="#">regioneR::permTest</a> .

**Details**

R-loop forming sequences are regions of the genome with sequences that are favorable for R-loop formation. They are computationally predicted with the [QmRLFS-finder](#) software program and serve as a data-independent test of whether a sample has mapped R-loops robustly or not.

**Method:**

Permutation testing is implemented via [regioneR::permTest](#) such that, for each permutation, R-loop peaks were randomized using [regioneR::circularRandomizeRegions](#) and then the number of overlaps with RLFS are counted. 100 permutations are used by default to build an empirical

distribution for peak/RLFS overlap. Then the true number of overlaps from non-randomized peaks and RLFS are compared to the null distribution to calculate Z-score and significance of enrichment. Finally, a Z-score distribution was calculated (using `regioneR::localZScore`) 5kb upstream and downstream of the average RLFS midpoint.

These results are subsequently used in the binary classification of the sample as "POS" (maps R-loops) or "NEG" (does not map R-loops). See also `predictCondition`.

## Value

An `RLRanges` object with RLFS analysis results accessible via `RLSeq::rlresult(object, "rlfsRes")`. Contains the following structure:

- `perTestResults`
  - An object of the class `permTestResultsList` from `regioneR` with the results of permutation testing. See also `regioneR::permTest` for full description.
- `Z-scores`
  - An object of the class `localZScoreResultsList` from `regioneR`. Contains the results of local Z-score analysis +/-5kb around each RLFS. See also `regioneR::localZScore`.

## Examples

```
# Example dataset
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Perform RLFS analysis (remove ntimes=2 and noZ=TRUE for a typical analysis)
rlr <- analyzeRLFS(rlr, ntimes = 2, noZ = TRUE)
```

---

auxdata

*Auxiliary Data*

---

## Description

A list containing data used by `RLSeq` functions. It can also be useful for checking the available modes and genomes in `RLSeq`. See also the `data-raw/auxdata.R` script that was used to create it.

## Usage

```
auxdata
```

## Format

An object of class `list` of length 10.

## Details

### Structure:

A named list containing the following entries:

- db\_cols
  - A tbl with colors associated with each database in RLHub useful for plotting. See also [RLHub::annotations](#).
- annotypes
  - A tbl containing the annotation databases and annotation types available from RLBase. See also [RLHub::annotations](#).
- ip\_cols
  - A tbl containing the colors associated with each "Immunoprecipitation type" (ip\_type) in RLBase. See also [RLHub::rlbase\\_samples](#).
- mode\_cols
  - A tbl containing the colors associated with each R-loop mapping mode in [RLHub::rlbase\\_samples](#).
- heat\_cols
  - A tbl containing the colors associated with user-supplied data and RLBase data when running [corrHeatmap](#).
- label\_cols
  - A tbl containing the colors associated with the labels in [RLBase](#). See also [RLHub::rlbase\\_samples](#).
- prediction\_cols
  - A tbl containing the colors associated with the predictions in [RLBase](#). See also [RLHub::rlbase\\_samples](#).
- available\_modes
  - A tbl containing the modes available in RLBase and associated metadata. See also [RLHub::rlbase\\_samples](#).
- available\_genomes
  - A character showing all the official UCSC genomes available for use with RLSeq. See also [available\\_genomes](#).
- misc\_modes
  - A character showing the R-loop mapping modes that are lumped into the 'misc' category for simplification of plotting.

## Examples

```
auxdata
```

---

available_genomes	<i>Available Genomes</i>
-------------------	--------------------------

---

## Description

Contains metadata about all the genomes available in UCSC. It contains derived metadata, such as the effective genome sizes as well. See also the `data-raw/available_genomes.R` script to see processing steps.

**Usage**

available\_genomes

**Format**

An object of class `data.frame` with 199 rows and 27 columns.

**Details****Structure:**

available\_genomes is a `data.frame` with the following columns:

- UCSC\_orgID
  - Official UCSC ID of the genome
- description
  - Verbose description of the assembly, source, and year/month of entry.
- nibPath
  - Endpoint of the genome in UCSC gbdb.
- organism
  - Name of the organism.
- defaultPos
  - Default location of genome browser view for this genome.
- active
  - Description not available.
- orderKey
  - Description not available.
- genome
  - The name of the genome.
- scientificName
  - The scientific name of the organism.
- htmlPath
  - Path in UCSC gbdb to the `description.html` file for the genome.
- hgNearOk
  - Description not available.
- hgPbOk
  - Description not available.
- sourceName
  - Name of organization providing the genome.
- taxId
  - The taxonomy ID of the organism.
- genes\_available
  - If TRUE, the gene annotations are available in GTF format.
- year
  - The year the genome assembly was added.

- `eff_genome_size_XXbp`
  - The effective genome size of this genome. Calculated at various read lengths with `khmer` and used to improve the accuracy of analysis. See the `data-raw/available_genomes.R` script to see how this calculation was performed.
- `genome_length`
  - The total length of the genome.
- `rlfs_available`
  - If TRUE, R-loop forming sequences annotations are available in the RLBase AWS S3 repository.

### Examples

```
available_genomes
```

---

<code>checkRLFSAnno</code>	<i>Check RLFS</i>
----------------------------	-------------------

---

### Description

Helper function that checks whether a genome has RLFS available.

### Usage

```
checkRLFSAnno(genome)
```

### Arguments

`genome`            the UCSC genome name to check

### Value

A logical, TRUE if available, FALSE if not

---

<code>corrAnalyze</code>	<i>Analyze Correlations</i>
--------------------------	-----------------------------

---

### Description

Finds the pairwise correlation in signal around gold-standard R-Loop sites between the query sample and the coverage tracks in the `RLBase` database. See *details*.

### Usage

```
corrAnalyze(object, force = FALSE)
```

## Arguments

object	An RLRanges object.
force	Force corrAnalyze to run, even if on Windows. Default: FALSE.

## Details

Currently, this does not work on windows.

### Method:

The corrAnalyze function performs a correlation test that can be used to assess sample-sample similarity by calculating coverage signal (from genomic alignments) around “gold standard” R-loop sites (PMID: [33411340](#)). The resulting correlation matrix is useful for determining how well a supplied sample correlates with previously-published datasets.

During the [RLBase-data workflow](#), the signal for each R-loop mapping sample within “gold standard” R-loop sites was calculated see [RLHub::gs\\_signal](#).

The corrAnalyze function loads [RLHub::gs\\_signal](#) and accepts an [RLRanges](#) object with a valid coverage slot. It then does the following:

1. The coverage is quantified within the “gold standard” sites and added as a column to the signal matrix from [RLHub::gs\\_signal](#).
2. Then, the [stats::cor](#) function is used to calculate the Pearson correlation pairwise between all samples, yielding a correlation matrix
3. Finally, the correlation matrix is stashed in the in the correlationMat slot of the [RLResults](#) and returned.

## Value

An RLRanges object with correlation results included as a matrix. The correlation matrix is accessed via `rlresults(object, "correlationMat")`.

## Examples

```
# Example RLRanges object
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# corrAnalyze does not work on Windows OS
if (.Platform$OS.type != "windows") {

  # run corrAnalyze
  rlr <- corrAnalyze(rlr)
}
```



---

corrHeatmap	<i>Plot Correlation Results</i>
-------------	---------------------------------

---

**Description**

Plots a heatmap to visualize the pairwise Pearson correlation matrix generated via [corrAnalyze](#).

**Usage**

```
corrHeatmap(object, returnData = FALSE, complex = TRUE, ...)
```

**Arguments**

object	An RLRanges with <a href="#">corrAnalyze</a> already run.
returnData	If TRUE, plot data is returned instead of plotting. Default: FALSE
complex	If TRUE, <a href="#">ComplexHeatmap::Heatmap</a> will be used for plotting. Otherwise, <a href="#">pheatmap::pheatmap</a> is used. Default: TRUE
...	For internal use.

**Value**

A plot object or plotting data (if returnData is TRUE).

**Examples**

```
# Example RLRanges data with corrAnalyze() already run.
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Corr heatmap
corrHeatmap(rlr)
```

---

featureEnrich	<i>Test Genomic Feature Enrichment</i>
---------------	--

---

**Description**

Tests the enrichment of genomic features in supplied peaks. See *details*.

**Usage**

```
featureEnrich(
  object,
  annotype = c("primary", "full"),
  annotations = NULL,
  downsample = 10000,
  quiet = FALSE
)
```

**Arguments**

object	An RLRanges object.
annotype	The type of annotations to use. Can be one of "primary" or "full". Default: "primary". See <a href="#">RLHub::annotations</a> for greater detail.
annotations	A custom annotation list of the same structure described in <a href="#">RLHub::annotations</a> .
downsample	If a numeric, data will be down sampled to the requested number of peaks. This improves the speed of genomic shuffling and helps prevent p-value inflation. If FALSE, then downsampling will not be performed. Default: 10000.
quiet	If TRUE, messages will be suppressed. Default: FALSE

**Details****Method:**

Annotations relevant to R-loops were curated as part of the [RLBase-data](#) workflow and are provided via [RLHub::annotations](#).

In featureEnrich, each annotation "type" (e.g., "Exons", "Introns", etc) is compared to the supplied RLRanges, yielding enrichment statistics with the following procedure:

1. For each annotation type, the peaks are overlapped with the annotations.
2. Then, [valr::bed\\_reldist](#) is used to find the relative distance distribution between the peaks and the annotations for both the supplied RLRanges and shuffled RLRanges (via [valr::bed\\_shuffle](#)). Significance of the relative distance is calculated via [stats::ks.test](#).
3. Then, Fisher's exact test is implemented via [valr::bed\\_fisher](#) to obtain the significance of the overlap and the odds ratio.

**Value**

An RLRanges object containing the results of the enrichment test accessed via `rlresult(object, "featureEnrichment")`. The results are in tbl format. For a full description of all columns in the output table see [RLHub::feat\\_enrich\\_samples](#).

**Examples**

```
# Example RLRanges dataset
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# RL Region Test
featureEnrich(rlr)

# With custom annotations
small_anno <- list(
  "Centromeres" = readr::read_csv(
    system.file("extdata", "Centromeres.csv.gz", package="RLSeq"),
    show_col_types = FALSE
  )
)
featureEnrich(rlr, annotations = small_anno)
```

---

feature_ggplot	<i>Feature ggplot</i>
----------------	-----------------------

---

**Description**

The core plotting component of plotEnrichment

**Usage**

```
feature_ggplot(x, usamp, limits, splitby)
```

**Arguments**

x	A tbl containing data for plotting.
usamp	The name of the user-supplied sample
limits	Specify limits on data. Useful for controlling infinite estimation of odds ratio resulting from fisher's exact test. To remove limits, set c(-Inf, Inf). Default: c(-10, 15).
splitby	Metadata by which to split plots. Can be "none", "prediction", or "label".

**Value**

A ggplot2 object.

---

geneAnnotation	<i>Annotate R-Loops with Genes</i>
----------------	------------------------------------

---

**Description**

Annotates RLRanges with entrez ids for overlapping genes. See *details*.

**Usage**

```
geneAnnotation(object, txdb = NULL)
```

**Arguments**

object	An RLRanges object.
txdb	The TxDb or EnsDb object containing gene annotations. If not supplied, annotations will be automatically downloaded from AnnotationHub. See also <a href="#">GenomicFeatures::TxDb</a> .

## Details

The `geneAnnotation` function provides a simple procedure for annotating `RLRanges` with gene IDs by overlap.

### Annotations:

First, gene annotations are automatically downloaded using `AnnotationHub::query` with the following pattern:

```
AnnotationHub::query(
  x = ah,
  pattern = c("TxDb", "UCSC", "knownGene", genome)
)
```

Where `genome` is the UCSC genome id for the `RLRanges` object. If these annotations are unavailable, they should be provided using the `txdb` parameter. See also `GenomicFeatures::TxDb`.

### Overlaps:

The annotations are subsequently overlapped with the ranges in the supplied `RLRanges` object using `valr::bed_intersect` and saved in the `RLResults` object as a `tbl` with a mapping of peak names to `gene_id` (entrez gene IDs).

## Value

An `RLRanges` object with gene overlaps included. The results are available via `rlresult(object, "geneAnnoRes")`. The result object is a `tbl` with a mapping of `peak_name` (peak names from `names(object)`) to `gene_id` (entrez gene IDs).

## Examples

```
# Example RLRanges data
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Perform gene annotation
rlr <- geneAnnotation(rlr)

# Supply custom TxDb if needed
if (GenomeInfoDb::genome(rlr)[1] == "hg19") {
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  rlr <- geneAnnotation(rlr, txdb = TxDb.Hsapiens.UCSC.hg19.knownGene)
}
```

---

genomeMasks

*Genome Masks*

---

## Description

A collection of genome masks for use with `analyzeRLFS`. See the `data-raw/genome_masks.R` script for the processing steps.

**Usage**

```
genomeMasks
```

**Format**

An object of class `list` of length 8.

**Details****Structure:**

`genomeMasks` is a named list of `GRanges` objects. Each entry in the list follows the naming convention: `<genome>.masked`, where `<genome>` is an official UCSC genome ID. Each entry contains a `GRanges` object with the masked ranges from `<genome>`. The genomes provided correspond to the masked genomes available in [BSgenome::available.genomes](#).

**Examples**

```
genomeMasks
```

---

getChromSizes

*Get Chrom Sizes*

---

**Description**

Helper function which extracts chrom sizes from an `RLRanges` object.

**Usage**

```
getChromSizes(object)
```

**Arguments**

`object` An `RLRanges` object.

**Value**

A tibble containing chrom sizes

---

`getGSSignal`*Get GS Signal*

---

**Description**

Extract signal around "gold-standard" R-loop sites

**Usage**

```
getGSSignal(coverage, gssignal)
```

**Arguments**

<code>coverage</code>	The path to a .bigWig file (can be a URL)
<code>gssignal</code>	The GS signal obtained from RLHub.

**Value**

A named list containing the results of correlation analysis.

---

`getRLFSAnno`*Get RLFS*

---

**Description**

Helper function that retrieves R-loop-forming sequences as GRanges

**Usage**

```
getRLFSAnno(object)
```

**Arguments**

<code>object</code>	An RLRanges object.
---------------------	---------------------

**Value**

A GRanges object with RLFS for that species.

---

peak_stats	<i>Build peak statistics tibble</i>
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---

### Description

A helper function for building the peak statistics tibble

### Usage

```
peak_stats(x, xshuff, y, chromSizeTbl, quiet = FALSE)
```

### Arguments

x	The R-loop peaks to test.
xshuff	x, but shuffled around the genome to build a control peakset.
y	The annotations against which to test x.
chromSizeTbl	A tibble containing the sizes of each chromosome in x and y.
quiet	If TRUE, messages will be suppressed. Default: FALSE

### Value

A tibble containing the test results.

---

plotEnrichment	<i>Plot Enrichment Test Results</i>
----------------	-------------------------------------

---

### Description

Creates a list of plots, one for each annotation database (see [RLHub::annotations](#)). These plots show the feature enrichment for the user-supplied sample in comparison to the samples in [RLBase](#). This will only work if you did not use custom annotations with [featureEnrich](#).

### Usage

```
plotEnrichment(
  object,
  pred_POS_only = TRUE,
  label_POS_only = FALSE,
  splitby = c("none", "prediction", "label"),
  limits = c(-10, 15),
  returnData = FALSE,
  ...
)
```

**Arguments**

object	An RLRanges object with <a href="#">featureEnrich</a> already run.
pred_POS_only	If TRUE, only "POS" predicted samples included (see also <a href="#">predictCondition</a> ). Default: TRUE.
label_POS_only	If TRUE, only "POS" labeled samples included (samples which are expected to robustly map R-loops, e.g., "D210N" condition R-ChIP data). Default: FALSE.
splitby	Metadata by which to split plots. Can be "none", "prediction", or "label".
limits	Specify limits on data range. This is used for controlling the infinite estimation of odds ratio resulting from fisher's exact test. To remove limits, set <code>c(-Inf, Inf)</code> . Default: <code>c(-10, 15)</code> .
returnData	If TRUE, plot data is returned instead of plot objects. Default: FALSE
...	For internal use.

**Value**

A named list of `ggplot2::ggplot` objects. Names correspond to the annotations provided. See also [featureEnrich](#).

**Examples**

```
# Example dataset with featureEnrich() already run.
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Make plots, split by prediction
plotEnrichment(rlr, pred_POS_only = FALSE, splitby = "prediction")
```

---

plotRLFSRes

*Plot RLFS analysis results*

---

**Description**

Plots the results of the R-loop-forming sequences (RLFS) analysis. The plot is a metaplot of the Z score distribution around RLFS with the p value from permutation testing annotated. See also [analyzeRLFS](#).

**Usage**

```
plotRLFSRes(object, plotName = NULL, fft = FALSE, ...)
```

**Arguments**

object	An RLRanges object with <a href="#">analyzeRLFS</a> already run. Alternatively, can be the RLFS results object from an RLRanges (from <code>rlresult(object, "rlfsRes")</code> ).
plotName	A Sample name used for plotting. If blank, the RLRanges <code>sampleName</code> metadata entry is used (see <a href="#">RLRanges</a> ).
fft	If TRUE, the Fourier transform of the Z-score is plotted instead. Default: FALSE.
...	Additional parameters passed to <code>ggplot2::ggplot</code> .



**Value**

A `ggplot` object. See also [ggplot2::ggplot](#).

**Examples**

```
# Example RLRanges dataset with analyzeRLFS() already run.
r1r <- readRDS(system.file("extdata", "r1rsmall.rds", package = "RLSeq"))

# Plot RLFS res
plotRLFSRes(r1r)

# Plot the Fourier transform instead
plotRLFSRes(r1r, fft = TRUE)
```

---

`plotRLRegionOverlap` *Plot RL-Region overlap with RLRanges*

---

**Description**

Convenience function for plotting the overlap between `RLRanges` and R-loop regions (RL regions) as calculated by [rlRegionTest](#).

**Usage**

```
plotRLRegionOverlap(object, returnData = FALSE, rlregions_table = NULL, ...)
```

**Arguments**

<code>object</code>	An <code>RLRanges</code> object with <a href="#">rlRegionTest</a> already run.
<code>returnData</code>	If TRUE, plot data is returned instead of plotting. Default: FALSE
<code>rlregions_table</code>	The table of <code>RLRegions</code> to overlap sample ranges with. Obtained from <code>RLHub</code> using <a href="#">RLHub::rlregions_meta</a> . Loaded from <code>RLHub</code> if not supplied. Default: NULL.
<code>...</code>	Additional arguments passed to <a href="#">VennDiagram::venn.diagram</a>

**Value**

A `ggplot2::ggplot` object containing the venn diagram. Built using [ggplotify::as.ggplot](#).

**Examples**

```
# Example dataset with rlRegionTest() already run.
r1r <- readRDS(system.file("extdata", "r1rsmall.rds", package = "RLSeq"))

# Plot RL-Region overlap
plotRLRegionOverlap(r1r)
```

```
# Return data only
plotRLRegionOverlap(rlr, returnData = TRUE)
```

---

predictCondition      *Predict Condition*

---

## Description

Uses the results of [analyzeRLFS](#) to predict whether a sample is "POS" (robust R-loop mapping) or "NEG" (poor R-loop mapping). See *details*.

## Usage

```
predictCondition(object, rlfsRes = NULL, ...)
```

## Arguments

object	An RLRanges object with <a href="#">analyzeRLFS</a> already run. Ignored if rlfsRes is provided.
rlfsRes	If object not supplied, provide the rlfsRes list which is obtained from <code>rlresult(object, "rlfsRes")</code> .
...	Internal use only.

## Details

Following R-loop forming sequences (RLFS) analysis, the quality model (see [RLHub::models](#)) is implemented for predicting the sample condition in coordination with other results from [analyzeRLFS](#). A prediction of "POS" indicates robust R-loop mapping, whereas "NEG" indicates poor R-loop mapping. The succeeding sections describe this process in greater detail.

### Application of binary classification model:

First, the binary classifier is applied, yielding a preliminary prediction of quality. This is accomplished via the following steps:

1. Calculate the Fourier transform of the Z-score distribution (see [analyzeRLFS](#)).
2. Reduce the dimensions to the engineered feature set (see table below).
3. Apply the preprocessing model (see [RLHub::models](#)) to normalize these features
4. Apply the classifier (see [RLHub::models](#)) to render a quality prediction.

*Engineered feature set:*

Abbreviations: Z, Z-score distribution; ACF, autocorrelation function; FT, Fourier Transform.

feature	description
Z1	mean of Z
Z2	variance of Z
Zacf1	mean of Z ACF
Zacf2	variance of Z ACF
ReW1	mean of FT of Z (real part)
ReW2	variance of FT of Z (real part)

ImW1	mean of FT of Z (imaginary part)
ImW2	variance of FT of Z (imaginary part)
ReWacf1	mean of FT of Z ACF (real part)
ReWacf2	variance of FT of Z ACF (real part)
ImWacf1	mean of FT of Z ACF (imaginary part)
ImWacf2	variance of FT of Z ACF (imaginary part)

**Final quality prediction:**

The results from the binary classifier are combined with other results from [analyzeRLFS](#) to yield a final prediction. To yield a prediction of “POS” all the following must be TRUE:

1. The RLFS Permutation test P value is significant ( $p < .05$ ). Stored as PVal Significant in the results object.
2. The Z-score distribution at 0bp is  $> 0$ . Stored as ZApex  $> 0$  in the results object.
3. The Z-score distribution at 0bp is  $>$  the start and the end. Stored as ZApex  $>$  ZEdges in the results object.
4. binary The classifier predicts a label of “POS”. Stored as Predicted 'POS' in the results object.

**Value**

An RLRanges object with predictions accessible via `r1result(object, "predictRes")`.

**Structure:**

The results object is a named list of the structure:

- Features
  - A tbl with three columns that describe the engineered features used for prediction:
    - \* feature: the name of the feature (see *details*).
    - \* raw\_value: The raw value of that feature in the supplied object.
    - \* processed\_value: The normalized value of that feature after preprocessing (see *details*).
- Criteria
  - The four criteria which must all be TRUE to render a prediction of "POS" (see *details*).
- prediction
  - The final prediction. "POS" indicates robust R-loop mapping, "NEG" indicates poor R-loop mapping.

**Examples**

```
# Example data with analyzeRLFS already run
r1r <- readRDS(system.file("extdata", "r1rsmall.rds", package = "RLSeq"))

# predict condition
r1r <- predictCondition(r1r)

# With r1fsRes
predRes <- predictCondition(r1fsRes = r1result(r1r, "r1fsRes"))
```

---

report	<i>RLSeq Report</i>
--------	---------------------

---

**Description**

Builds an HTML report to showcase the results available in the supplied [RLRanges](#) object (see also [RLResults](#)).

**Usage**

```
report(object, reportPath = "rlreport.html", quiet = FALSE, ...)
```

**Arguments**

object	An RLRanges object.
reportPath	A path indicating the report output HTML file. Default: "rlreport.html"
quiet	If TRUE, messages are suppressed. Default: FALSE.
...	Arguments passed to <code>rmarkdown::render()</code>

**Value**

TRUE

**Examples**

```
# Example data with RLSeq() already run.
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Get a TMP file (only for example usae)
tmp <- tempfile()

# Generate the report
report(rlr, reportPath = tmp)
```

---

RLRanges-class	<i>Construct RLRanges Dataset</i>
----------------	-----------------------------------

---

**Description**

RLRanges is a subclass of GRanges, which stores R-loop peaks and metadata about the R-loop-mapping experiment, along with results from the analyses in [RLSeq](#).

**Usage**

```
RLRanges(
  peaks = GenomicRanges::GRanges(),
  coverage = character(1),
  genome = character(1),
  mode = character(1),
  label = character(1),
  sampleName = "User-selected sample",
  qcol = NULL
)
```

**Arguments**

peaks	Path/URL to peak file or a GRanges object. This file should be in "broadPeak" format if possible. If not, then qcol should be specified.
coverage	Path/URL to the corresponding coverage file (in "bigWig" format). If not supplied, correlation tests will be skipped.
genome	UCSC genome ID. Acceptable types are listed in <a href="#">auxdata</a> (available_genomes entry).
mode	Type of R-loop mapping from which peaks and coverage were derived. Acceptable types are listed in <a href="#">auxdata</a> (available_modes entry). Can be unspecified.
label	"POS" (positive R-loop-mapping sample; e.g., DRIP-Seq S9.6 -RNH1) or "NEG" (negative control sample; e.g., DRIP-Seq S9.6 +RNH1 or Input). Can be unspecified.
sampleName	A unique name for identifying this sample. Can be unspecified.
qcol	The name of the metadata column which contains the score or significance of each peak. For broadPeak (preferred), this is the qvalue (column 11 after accounting for extra columns created during peakset building). If not specified, the last column will be chosen by default. <b>NOTE:</b> if supplying narrowPeak form peaks, the last column will NOT be appropriate and QCol should be specified as 11. If FALSE or if no metadata columns exist, it will be left blank and some operations in report() will not fully run.

**Value**

An object of class RLRanges. These objects are an extension of GRanges with the addition of sample metadata entries and [RLResults](#).

**Examples**

```
# Example dataset
rlbase <- "https://rlbase-data.s3.amazonaws.com"
cvg <- file.path(rlbase, "coverage", "SRX7671349_hg38.bw")
pks <- system.file("extdata", "SRX7671349_hg38.broadPeak", package="RLSeq")

# Get RLRanges object
rlr <- RLRanges(pks,
```

```

coverage = cvg, genome = "hg38", label = "NEG",
mode = "RDIP", sampleName = "RDIP-Seq +RNH1", qcol = 9
)

```

---

RLRangesFromRLBase      *Access RLBase samples as RLRanges*

---

### Description

Accessor function which returns any sample in **RLBase** as an **RLRanges** object for use with **RLSeq**. For a full list of available samples, see [RLHub::rlbase\\_samples](#).

### Usage

```
RLRangesFromRLBase(acc, rlsamples = NULL)
```

### Arguments

**acc**                      The sample ID of the RLBase object. See the `rlsample` column in [RLHub::rlbase\\_samples](#).

**rlsamples**                The tibble provided by [RLHub::rlbase\\_samples](#). Providing these data ahead of time speeds up this operation. Default: `NULL`.

### Value

An **RLRanges** object with all results available.

### Examples

```
r1r <- RLRangesFromRLBase("SRX1070676")
```

---

rlRegionTest              *R-Loop region test*

---

### Description

Tests the overlap of user-supplied ranges with R-loop regions (RL regions).

### Usage

```
rlRegionTest(object)
```

### Arguments

**object**                    An **RLRanges** object with genome "hg38".

**Details**

R-loop regions (RL regions) are consensus sites of R-loop formation. For more information, see [RLHub:rlregions](#). The `rlRegionTest` is a simple function which finds the overlap of user-supplied samples with RL regions and calculates Fisher's exact test via `valr::bed_fisher`.

**Value**

An `RLRanges` object with test results accessible via `rlresult(object, "rlRegionRes")`.

**Structure:**

The structure of the results is a named `list` containing the following:

- `Overlap`
  - A `tbl` showing the overlap between RL regions and user-supplied ranges.
  - Column description:
    - \* `chrom` - The chromosome name
    - \* `start__peaks` - The starting position of the user-supplied peak in the overlap.
    - \* `end__peaks` - Same as above for end position.
    - \* `name__peaks` - The name of the user-supplied peak in the overlap (from `names(object)`).
    - \* `start/end/name__rlregion` - Same as above for RL regions.
    - \* `strand__rlregion` - The genomic strand of the RL region in the overlap.
    - \* `.overlap` - The size of the overlap.
- `Test_results`
  - A `tbl` showing the results of the Fisher's exact test. See `valr::bed_fisher`.

**Examples**

```
# Example RLRanges data
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# RL Region Test
rlRegionTest(rlr)
```

---

`rlresult`
*RLSeq Results*


---

**Description**

Functions for creating and accessing the R-loop results (RL Results). These are a type of object used for holding the results of the tests implemented in `RLSeq`. They can be accessed using the `rlresult` function.

**Usage**

```
rlresult(object, resultName)
```

## Arguments

- object            [RLRanges](#) object.
- resultName       Name of the result slot to access. See *details*.

## Details

### Slot descriptions:

- featureEnrichment
  - The tbl generated from running [featureEnrich](#).
  - The structure and column descriptions are provided in detail within [RLHub::feat\\_enrich\\_samples](#).
- correlationMat
  - The matrix generated from running [corrAnalyze](#).
  - Contains pairwise pearson correlations between all samples in [RLBase](#) and the supplied [RLRanges](#) object.
- rlfRes
  - The list generated from running [analyzeRLFS](#).
  - See [analyzeRLFS](#) for description of structure.
- geneAnnoRes
  - The tbl generated from running [geneAnnotation](#).
- predictRes
  - The list generated from running [predictCondition](#).
- rlRegionRes
  - The list generated from running [rlRegionTest](#).

## Value

The contents of the requested slot.

## Examples

```
r1r <- readRDS(system.file("extdata", "r1rsmall.rds", package = "RLSeq"))
r1result(r1r, "predictRes")
```

---

RLSeq

*RLSeq*

---

## Description

Executes the RLSeq analysis workflow.

## Usage

```
RLSeq(object, quiet = FALSE, skip = NULL, ...)
```



## Arguments

object	An <a href="#">RLRanges</a> object.
quiet	If TRUE, messages are suppressed. Default: FALSE.
skip	Analysis steps to skip. Default: NULL. See <i>details</i> for options.
...	Arguments passed to <a href="#">analyzeRLFS</a> .

## Details

The `RLSeq()` function does all of the following by default:

1. **RLFS Perm Test.** Runs the [analyzeRLFS](#) function to test the enrichment of user-supplied ranges within R-loop-forming sequences. *Cannot be skipped.*
2. **Predict Condition.** Runs the [predictCondition](#) function to predict whether the user-supplied sample robustly maps R-loops or not. *Cannot be skipped.*
3. **Feature enrichment test.** Runs the [featureEnrich](#) function to test the enrichment of user-supplied ranges within R-loop-relevant genomic features. Skip with `skip="featureEnrich"`.
4. **Correlation Analysis.** Runs the [corrAnalyze](#) function to test the correlation of user-supplied R-loop signal with other samples in RLBse around "gold-standard" R-loop regions. Skip with `skip="corrAnalyze"`.
5. **Gene annotation.** Runs the [geneAnnotation](#) function to find the overlap of genes with the user-supplied ranges. Skip with `skip="geneAnnotation"`.
6. **R-loop Region Analysis.** Runs the [rlRegionTest](#) function to find the overlap of user-supplied ranges with consensus R-loop sites (RL-Regions). Skip with `skip="rlRegionTest"`.

## Value

An [RLRanges](#) object with results available (see [rlresult](#)).

## Examples

```
# Example RLRanges
rlr <- readRDS(system.file("extdata", "rlrsmall.rds", package = "RLSeq"))

# Run RLSeq
# `useMask=FALSE`, `ntime=10`, and `skip=` for demonstration purposes here.
rlr <- RLSeq(
  rlr, useMask = FALSE, ntimes = 10,
  skip=c('featureEnrich', 'corrAnalyze', 'geneAnnotation', 'rlRegionTest')
)
```

---

tableToRegions	<i>Table to Regions</i>
----------------	-------------------------

---

**Description**

Helper function to Convert "table" format to "regions" format.

**Usage**

```
tableToRegions(table)
```

**Arguments**

table	A tibble in "Table" format from RLHub.
-------	--

**Value**

A tibble in "regions" format.

---

urlExists	<i>Check if URL exists</i>
-----------	----------------------------

---

**Description**

Check if URL exists

**Usage**

```
urlExists(urlcon)
```

**Arguments**

urlcon	URL to check
--------	--------------

**Value**

logical. TRUE if status code 200, FALSE if not

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