Package 'RiboCrypt'

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Type Package

Title Interactive visualization in genomics

Version 1.10.0

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Description R Package for interactive visualization and browsing NGS data.
It contains a browser for both transcript and genomic coordinate view.
In addition a QC and general metaplots are included, among others differential translation plots and gene expression plots. The package is still under development.

biocViews Software, Sequencing, RiboSeq, RNASeq,

Encoding UTF-8

LazyData true

BugReports https://github.com/m-swirski/RiboCrypt/issues

URL https://github.com/m-swirski/RiboCrypt

Depends R (>= 3.6.0), ORFik (>= 1.13.12)

Imports bslib, BiocGenerics, BiocParallel, Biostrings, data.table, dplyr, GenomeInfoDb, GenomicFeatures, GenomicRanges, ggplot2, htmlwidgets, httr, IRanges, jsonlite, knitr, markdown, NGLVieweR, plotly, rlang, RCurl, shiny, shinycssloaders, shinyhelper, shinyjqui, stringr

Suggests testthat, rmarkdown, BiocStyle, BSgenome, BSgenome.Hsapiens.UCSC.hg19

RoxygenNote 7.2.3

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Contents

`antisense` *Get antisense*

Description

Get antisense

Usage

```
antisense(grl)
```

Value

a GRangesList

createSeqPanelPattern *Create sequence panel for RiboCrypt*

Description

Create sequence panel for RiboCrypt

Usage

```
createSeqPanelPattern(
  sequence,
  start_codons = "ATG",
  stop_codons = c("TAA", "TAG", "TGA"),
  frame = 1,
  custom_motif = NULL
)
```

Arguments

start_codons	character vector, default "ATG"
stop_codons	character vector, default c("TAA", "TAG", "TGA")
custom_motif	character vector, default NULL.

Value

a ggplot object

DEG_plot *Differential expression plots (1D or 2D)*

Description

Gives you interactive 1D or 2D DE plots

Usage

```
DEG_plot(
  dt,
  draw_non_regulated = FALSE,
  xlim = ifelse(two_dimensions, "bidir.max", "auto"),
  ylim = "bidir.max",
  xlab = ifelse(two_dimensions, "RNA fold change (log2)", "Mean counts (log2)"),
  ylab = ifelse(two_dimensions, "RFP fold change (log2)", "Fold change (log2)"),
  two_dimensions = ifelse("LFC" %in% colnames(dt), FALSE, TRUE),
 color.values = c(`No change` = "black", Significant = "red", Buffering = "purple",
```

```
   `mRNA abundance` = "darkgreen", Expression = "blue", Forwarded = "yellow", Inverse =
    "aquamarine", Translation = "orange4")
)
```

Arguments

dt	a data.table with results from a differential expression run. Normally from: `ORFik::DTEG.analysis(df1, df2)`
draw_non_regulated	logical, default FALSE. Should non-regulated rows be included in the plot? Will make the plot faster to render if skipped (FALSE)
xlim	numeric vector or character preset, default: `ifelse(two_dimensions, "bidir.max", "auto")` (Equal in both + / - direction, using max value + 0.5 of meanCounts(in 1d) / rna(in 2d) column of dt). If you want ggplot to decide limit, set to "auto". For numeric vector, specify min and max x limit: like c(-5, 5)
ylim	numeric vector or character preset, default: "bidir.max" (Equal in both + / - direction, using max value + 0.5 of LFC(in 1d) / rfp(in 2d) column of dt). If you want ggplot to decide limit, set to "auto". For numeric vector, specify min and max x limit: like c(-5, 5)
xlab	character, default: `ifelse(two_dimensions, "RNA fold change (log2)", "Mean counts (log2)")`
ylab	character, default: `ifelse(two_dimensions, "RFP fold change (log2)", "Fold change (log2)")`
two_dimensions	logical, default: `ifelse("LFC" %in% colnames(dt), FALSE, TRUE)` Is this two dimensional, like: Ribo-seq vs RNA-seq. Alternative, FALSE: Then Log fold change vs mean counts
color.values	named character vector, default: `c("No change" = "black", "Significant" = "red","Buffering" = "purple", "mRNA abundance" = "darkgreen","Expression" = "blue", "Forwarded" = "yellow","Inverse" = "aquamarine", "Translation" = "orange4")`

Value

plotly object

Examples

```
# Load experiment
df <- ORFik.template.experiment()
# 1 Dimensional analysis
dt <- DEG.analysis(df[df$libtype == "RNA",])
dt$Regulation[1] <- "Significant" # Fake sig level
DEG_plot(dt, draw_non_regulated = TRUE)
# 2 Dimensional analysis
dt_2d <- DTEG.analysis(df[df$libtype == "RFP",], df[df$libtype == "RNA",],
                    output.dir = NULL)
dt_2d$Regulation[4] <- "Translation" # Fake sig level
dt_2d$Regulation[5] <- "Buffering" # Fake sig level
DEG_plot(dt_2d, draw_non_regulated = TRUE)
```

distanceToFollowing *Distance to following range*

Description

Distance to following range

Usage

```
distanceToFollowing(grl, grl2 = grl, ignore.strand = FALSE)
```

Arguments

grl	a GRangesList
grl2	a GRangesList, default 'grl'
ignore.strand	logical, default FALSE

Value

numeric vector of distance

fetch_JS_seq *Fetch Javascript sequence*

Description

Fetch Javascript sequence

Usage

```
fetch_JS_seq(
  target_seq,
  nplots,
  distance = 50,
  display_dist,
  aa_letter_code = "one_letter"
)
```

Arguments

target_seq	the target sequence
nplots	number of plots
distance	numeric, default 50.
display_dist	display distance
aa_letter_code	"one_letter"

Value

a list of 2 lists, the nt list (per frame, total 3) and AA list (per frame, total 3)

`fetch_summary` *Fetch summary of uniprot id*

Description

Fetch summary of uniprot id

Usage

```
fetch_summary(qualifier, provider = "alphafold")
```

Arguments

`qualifier`	uniprot ids
`provider`	"pdbe", alternatives: "alphafold", "all"

Value

a character of json

`geneTrackLayer` *How many rows does the gene track need*

Description

How many rows does the gene track need

Usage

```
geneTrackLayer(grl)
```

Arguments

`grl`	a GRangesList

Value

numeric, the track row index

getCoverageProfile *Get coverage profile*

Description

Get coverage profile

Usage

```
getCoverageProfile(grl, reads, kmers = 1, kmers_type = "mean")
```

Arguments

grl	a GRangesList
reads	GRanges
kmers	1
kmers_type	"mean"

Value

data.table of coverage

getIndexes *Get index*

Description

Get index

Usage

```
getIndexes(ref_granges)
```

Arguments

ref_granges	a GRanges object

Value

integer vector, indices

ggplotlyHover *Call ggplotly with hoveron defined*

Description

Call ggplotly with hoveron defined

Usage

```
ggplotlyHover(x, ...)
```

Arguments

x	a a ggplot argument
...	additional arguments for ggplotly

Value

a ggplotly object

matchMultiplePatterns *Match multiple patterns*

Description

Match multiple patterns

Usage

```
matchMultiplePatterns(patterns, Seq)
```

Arguments

patterns	character
Seq	a DNAStringSet

Value

integer vector, indices (named with pattern hit)

`matchToGRanges` *Match to GRanges*

Description

Match to GRanges

Usage

```
matchToGRanges(matches, ref_granges)
```

Arguments

`matches`	integer vector, indices
`ref_granges`	GRanges

Value

GRanges object

`multiOmicsPlot_animate` *Multi-omics animation using list input*

Description

The animation will move with a play butten, there is 1 transition per library given.

Usage

```
multiOmicsPlot_animate(
  display_range,
  annotation = display_range,
  reference_sequence,
  reads,
  viewMode = c("tx", "genomic")[1],
  custom_regions = NULL,
  leader_extension = 0,
  trailer_extension = 0,
  withFrames = NULL,
  frames_type = "lines",
  colors = NULL,
  kmers = NULL,
  kmers_type = c("mean", "sum")[1],
  ylabels = NULL,
```

```
  lib_to_annotation_proportions = c(0.8, 0.2),
  lib_proportions = NULL,
  annotation_proportions = NULL,
  width = NULL,
  height = NULL,
  plot_name = "default",
  plot_title = NULL,
  display_sequence = c("both", "nt", "aa", "none")[1],
  seq_render_dist = 100,
  aa_letter_code = c("one_letter", "three_letters")[1],
  annotation_names = NULL,
  start_codons = "ATG",
  stop_codons = c("TAA", "TAG", "TGA"),
  custom_motif = NULL,
  BPPARAM = BiocParallel::SerialParam()
)
```

Arguments

display_range	the whole region to visualize, a GRangesList or GRanges object
annotation	the whole annotation which your target region is a subset, a GRangesList or GRanges object
reference_sequence	the genome reference, a FaFile or FaFile convertible object
reads	the NGS libraries, as a list of GRanges with or without score column for replicates.
viewMode	character, default "tx" (transcript coordinates, first position is 1, exons are merged into a single sequence) Alternative: "genomic" (genomic coordinates, first position is first position in display_range argument. Introns are displayed).
custom_regions	a GRangesList or NULL, default: NULL. The alternative annotation, like self defined uORFs etc. The vertical annotation bars will have a different color.
leader_extension	integer, default 0. (How much to extend view upstream)
trailer_extension	integer, default 0. (How much to extend view downstream)
withFrames	a logical vector, default NULL. Alternative: a length 1 or same length as list length of "reads" argument.
frames_type	character, default "lines". Alternative: - columns - stacks - area
colors	character, default NULL (automatic colouring). If "withFrames" argument is TRUE, colors are set to to c("red", "green", "blue") for the 3 frames. Alternative: Character vector of length 1 or length of "reads" list argument.
kmers	numeric (integer), bin positions into kmers.

`kmers_type` character, function used for kmers sliding window. default: "mean", alternative: "sum"

`ylabels` character, default NULL. Name of libraries in "reads" list arugment.

`lib_to_annotation_proportions` numeric vector of length 2. relative sizes of profiles and annotation.

`lib_proportions` numeric vector of length equal to displayed libs. Relative sizes of profiles displayed

`annotation_proportions` numeric vector of length 3 (seq displayed), or 2 (seq not displayed). Relative sizes of annotation tracks.

`width` numeric, default NULL. Width of plot.

`height` numeric, default NULL. Height of plot.

`plot_name` = character, default "default" (will create name from display_range name). Alternative: custom name for region.

`plot_title` character, default NULL. A title for plot.

`display_sequence` character/logical, default `c("both","nt", "aa", "none")[1]`. If TRUE or "both", display nucleotide and aa sequence in plot.

`seq_render_dist` integer, default 100. The sequences will appear after zooming below this threshold.

`aa_letter_code` character, when set to "three_letters", three letter amino acid code is used. One letter by default.

`annotation_names` character, default NULL. Alternative naming for annotation.

`start_codons` character vector, default "ATG"

`stop_codons` character vector, default c("TAA", "TAG", "TGA")

`custom_motif` character vector, default NULL.

`BPPARAM` how many cores/threads to use? default: `BiocParallel::SerialParam()`. To see number of threads used for multicores, do `BiocParallel::bpparam()$workers`. You can also add a time remaining bar, for a more detailed pipeline.

Value

the plot object

Examples

```
library(RiboCrypt)
df <- ORFik.template.experiment()[9:10,]
cds <- loadRegion(df, "cds")
mrna <- loadRegion(df, "mrna")
# multiOmicsPlot_animate(mrna[1], annotation = cds[1], reference_sequence = findFa(df),
#                  frames_type = "columns", leader_extension = 30, trailer_extension = 30,
#                    reads = outputLibs(df, type = "pshifted", output.mode = "envirlist",
#                                       naming = "full", BPPARAM = BiocParallel::SerialParam()))
```

`multiOmicsPlot_list` *Multi-omics plot using list input*

Description

Customizable html plots for visualizing genomic data.

Usage

```
multiOmicsPlot_list(
  display_range,
  annotation = display_range,
  reference_sequence,
  reads,
  viewMode = c("tx", "genomic")[1],
  custom_regions = NULL,
  leader_extension = 0,
  trailer_extension = 0,
  withFrames = NULL,
  frames_type = "lines",
  colors = NULL,
  kmers = NULL,
  kmers_type = c("mean", "sum")[1],
  ylabels = NULL,
  lib_to_annotation_proportions = c(0.8, 0.2),
  lib_proportions = NULL,
  annotation_proportions = NULL,
  width = NULL,
  height = NULL,
  plot_name = "default",
  plot_title = NULL,
  display_sequence = c("both", "nt", "aa", "none")[1],
  seq_render_dist = 100,
  aa_letter_code = c("one_letter", "three_letters")[1],
  annotation_names = NULL,
  start_codons = "ATG",
  stop_codons = c("TAA", "TAG", "TGA"),
  custom_motif = NULL,
  AA_code = Biostrings::GENETIC_CODE,
  BPPARAM = BiocParallel::SerialParam(),
  summary_track = FALSE,
  summary_track_type = frames_type,
  export.format = "svg"
)
```

Arguments

`display_range` the whole region to visualize, a `GRangesList` or `GRanges` object

`annotation` the whole annotation which your target region is a subset, a `GRangesList` or `GRanges` object

`reference_sequence`
the genome reference, a `FaFile` or `FaFile` convertible object

`reads` the NGS libraries, as a list of `GRanges` with or without score column for replicates.

`viewMode` character, default "tx" (transcript coordinates, first position is 1, exons are merged into a single sequence)
Alternative: "genomic" (genomic coordinates, first position is first position in `display_range` argument. Introns are displayed).

`custom_regions` a GRangesList or NULL, default: NULL. The alternative annotation, like self defined uORFs etc. The vertical annotation bars will have a different color.

`leader_extension`
integer, default 0. (How much to extend view upstream)

`trailer_extension`
integer, default 0. (How much to extend view downstream)

`withFrames` a logical vector, default NULL. Alternative: a length 1 or same length as list length of "reads" argument.

`frames_type` character, default "lines". Alternative:
- columns
- stacks
- area

`colors` character, default NULL (automatic colouring). If "withFrames" argument is TRUE, colors are set to to c("red", "green", "blue") for the 3 frames. Alternative: Character vector of length 1 or length of "reads" list argument.

`kmers` numeric (integer), bin positions into kmers.

`kmers_type` character, function used for kmers sliding window. default: "mean", alternative: "sum"

`ylabels` character, default NULL. Name of libraries in "reads" list arugment.

`lib_to_annotation_proportions`
numeric vector of length 2. relative sizes of profiles and annotation.

`lib_proportions`
numeric vector of length equal to displayed libs. Relative sizes of profiles displayed

`annotation_proportions`
numeric vector of length 3 (seq displayed), or 2 (seq not displayed). Relative sizes of annotation tracks.

`width` numeric, default NULL. Width of plot.

`height` numeric, default NULL. Height of plot.

`plot_name` = character, default "default" (will create name from display_range name). Alternative: custom name for region.

`plot_title` character, default NULL. A title for plot.

`display_sequence`
: character/logical, default `c("both","nt", "aa", "none")[1]`. If TRUE or "both", display nucleotide and aa sequence in plot.

`seq_render_dist`
: integer, default 100. The sequences will appear after zooming below this threshold.

`aa_letter_code`
: character, when set to "three_letters", three letter amino acid code is used. One letter by default.

`annotation_names`
: character, default NULL. Alternative naming for annotation.

`start_codons`
: character vector, default "ATG"

`stop_codons`
: character vector, default c("TAA", "TAG", "TGA")

`custom_motif`
: character vector, default NULL.

`AA_code`
: Genetic code for amino acid display. Default is SGC0 (standard: Vertebrate). See `Biostrings::GENETIC_CODE_TABLE` for options. To change to bacterial, do: `Biostrings::getGeneticCode("11")`

`BPPARAM`
: how many cores/threads to use? default: `BiocParallel::SerialParam()`. To see number of threads used for multicores, do `BiocParallel::bpparam()$workers`. You can also add a time remaining bar, for a more detailed pipeline.

`summary_track`
: logical, default FALSE. Display a top track, that is the sum of all tracks.

`summary_track_type`
: character, default is same as 'frames_type' argument

`export.format`
: character, default: "svg". alternative: "png". when you click the top right image button export, what should it export as?

Value

the plot object

Examples

```
library(RiboCrypt)
df <- ORFik.template.experiment()[9:10,]
cds <- loadRegion(df, "cds")
mrna <- loadRegion(df, "mrna")
multiOmicsPlot_list(mrna[1], annotation = cds[1], reference_sequence = findFa(df),
                 frames_type = "columns", leader_extension = 30, trailer_extension = 30,
                   reads = outputLibs(df, type = "pshifted", output.mode = "envirlist",
                               naming = "full", BPPARAM = BiocParallel::SerialParam()))
```

multiOmicsPlot_ORFikExp *Multi-omics plot using ORFik experiment input*

Description

Customizable html plots for visualizing genomic data.

Usage

```
multiOmicsPlot_ORFikExp(
  display_range,
  df,
  annotation = "cds",
  reference_sequence = findFa(df),
 reads = outputLibs(df, type = "pshifted", output.mode = "envirlist", naming = "full",
    BPPARAM = BiocParallel::SerialParam()),
  viewMode = c("tx", "genomic")[1],
  custom_regions = NULL,
  leader_extension = 0,
  trailer_extension = 0,
 withFrames = libraryTypes(df, uniqueTypes = FALSE) %in% c("RFP", "RPF", "LSU"),
  frames_type = "lines",
  colors = NULL,
  kmers = NULL,
  kmers_type = c("mean", "sum")[1],
  ylabels = bamVarName(df),
  lib_to_annotation_proportions = c(0.8, 0.2),
  lib_proportions = NULL,
  annotation_proportions = NULL,
  width = NULL,
  height = NULL,
  plot_name = "default",
  plot_title = NULL,
  display_sequence = c("both", "nt", "aa", "none")[1],
  seq_render_dist = 100,
  aa_letter_code = c("one_letter", "three_letters")[1],
  annotation_names = NULL,
  start_codons = "ATG",
  stop_codons = c("TAA", "TAG", "TGA"),
  custom_motif = NULL,
  BPPARAM = BiocParallel::SerialParam(),
  input_id = "",
  summary_track = FALSE,
  summary_track_type = frames_type,
  export.format = "svg"
)
```

Arguments

display_range	the whole region to visualize, a GRangesList or GRanges object
df	an ORFik experiment or a list containing ORFik experiments. Usually a list when you have split Ribo-seq and RNA-seq etc.
annotation	the whole annotation which your target region is a subset, a GRangesList or GRanges object
reference_sequence	the genome reference, default ORFik::findFa(df)
reads	the NGS libraries, as a list of GRanges with or without 'score' column for replicates. Can also be a covRle object of precomputed coverage. Default: outputLibs(df, type = "pshifted", output.mode = "envirlist",naming = "full", BPPARAM = BiocParallel::SerialParam())
viewMode	character, default "tx" (transcript coordinates, first position is 1, exons are merged into a single sequence) Alternative: "genomic" (genomic coordinates, first position is first position in display_range argument. Introns are displayed).
custom_regions	a GRangesList or NULL, default: NULL. The alternative annotation, like self defined uORFs etc. The vertical annotation bars will have a different color.
leader_extension	integer, default 0. (How much to extend view upstream)
trailer_extension	integer, default 0. (How much to extend view downstream)
withFrames	a logical vector, default libraryTypes(df, uniqueTypes = FALSE) %in% c("RFP", "RPF", "LSU") Alternative: a length 1 or same length as list length of "reads" argument.
frames_type	character, default "lines". Alternative: - columns - stacks - area
colors	character, default NULL (automatic colouring). If "withFrames" argument is TRUE, colors are set to to c("red", "green", "blue") for the 3 frames. Alternative: Character vector of length 1 or length of "reads" list argument.
kmers	numeric (integer), bin positions into kmers.
kmers_type	character, function used for kmers sliding window. default: "mean", alternative: "sum"
ylabels	character, default bamVarName(df). Name of libraries in "reads" list argument.
lib_to_annotation_proportions	numeric vector of length 2. relative sizes of profiles and annotation.
lib_proportions	numeric vector of length equal to displayed libs. Relative sizes of profiles displayed
annotation_proportions	numeric vector of length 3 (seq displayed), or 2 (seq not displayed). Relative sizes of annotation tracks.

width	numeric, default NULL. Width of plot.
height	numeric, default NULL. Height of plot.
plot_name	character, default "default" (will create name from display_range name).
plot_title	character, default NULL. A title for plot.
display_sequence	character/logical, default `c("both","nt", "aa", "none")[1]`. If TRUE or "both", display nucleotide and aa sequence in plot.
seq_render_dist	integer, default 100. The sequences will appear after zooming below this threshold.
aa_letter_code	character, when set to "three_letters", three letter amino acid code is used. One letter by default.
annotation_names	character, default NULL. Alternative naming for annotation.
start_codons	character vector, default "ATG"
stop_codons	character vector, default c("TAA", "TAG", "TGA")
custom_motif	character vector, default NULL.
BPPARAM	how many cores/threads to use? default: `BiocParallel::SerialParam()`. To see number of threads used for multicores, do `BiocParallel::bpparam()$workers`. You can also add a time remaining bar, for a more detailed pipeline.
input_id	character path, default: "", id for shiny to disply structures, should be "" for local users.
summary_track	logical, default FALSE. Display a top track, that is the sum of all tracks.
summary_track_type	character, default is same as 'frames_type' argument
export.format	character, default: "svg". alternative: "png". when you click the top right image button export, what should it export as?

Value

the plot object

Examples

```
library(RiboCrypt)
df <- ORFik.template.experiment()[9,] #Use third library in experiment only
cds <- loadRegion(df, "cds")
multiOmicsPlot_ORFikExp(extendLeaders(extendTrailers(cds[1], 30), 30), df = df,
                        frames_type = "columns")
```

organism_input_select *Select box for organism*

Description

Select box for organism

Usage

```
organism_input_select(genomes, ns)
```

Arguments

genomes	name of genomes, returned from list.experiments()
ns	the ID, for shiny session

Value

selectizeInput object

RiboCrypt_app *Create RiboCrypt app*

Description

Create RiboCrypt app

Usage

```
RiboCrypt_app(
  validate.experiments = TRUE,
  options = list(launch.browser = ifelse(interactive(), TRUE, FALSE)),
  all_exp = list.experiments(validate = validate.experiments),
  browser_options = c(),
  init_tab_focus = "browser"
)
```

Arguments

validate.experiments	logical, default TRUE, set to FALSE to allow starting the app with malformed experiments, be careful will crash if you try to load that experiment!
options	list of arguments, default `list("launch.browser" = ifelse(interactive(), TRUE, FALSE))`

all_exp	a data.table, default: list.experiments(validate = validate.experiments). Which experiments do you want to allow your app to see, default is all in your system config path.
browser_options	named character vector of browser specific arguments: - default_experiment : Which experiment to select, default: first one - default_gene : Which genes to select, default: first one - default_libs : Which libraries to select: first one, else a single string, where libs are seperated by "|", like "RFP_WT_r1|RFP_WT_r2". - default_kmer : K-mer windowing size, default: 1 - default_frame_type : Ribo-seq line type, default: "lines" - plot_on_start : Plot when starting, default: "FALSE"
init_tab_focus	character, default "browser". Which tab to open on init.

Value

RiboCrypt shiny app

Examples

```
## Default run
# RiboCrypt_app()
## Plot on start
# RiboCrypt_app(browser_options = c(plot_on_start = "TRUE"))
## Init with an experiment and gene (you must of course have the experiment)

#RiboCrypt_app(validate.experiments = FALSE,
#       browser_options = c(plot_on_start = "TRUE",
#                           default_experiment = "human_all_merged_l50",
#                           default_gene = "ATF4-ENSG00000128272"))
```

---

trimOverlaps *Trim overlaps*

Description

Trim overlaps

Usage

```
trimOverlaps(overlaps, display_range)
```

Arguments

overlaps	GRanges
display_range	GRanges

Value

GRanges

Index