Package ‘RiboCrypt’

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Type Package
Title Interactive visualization in genomics
Version 1.8.0
License MIT + file LICENSE
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, GenomInfoDb, GenomicFeatures, GenomicRanges, ggplot2,
   htmlwidgets, httr, IRanges, jsonlite, knitr, markdown,
   NGLVieweR, plotly, rlang, RCurl, shiny, shinyjqui, stringr

Suggests testthat, rmarkdown, BiocStyle, BSgenome,

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**Author**  Michal Swirski [aut, cre, cph],
Haakon Tjeldnes [aut, ctb],
Kornel Labun [ctb]

**Maintainer**  Michal Swirski <michal.swirski@uw.edu.pl>

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**Description**

Get antisense

**Usage**

antisense(gr1)

**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"),
)```
DEG_plot

'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**

```r
distanceToFollowing(gr1, gr12 = gr1, ignore.strand = FALSE)
```

**Arguments**

- `gr1` a GRangesList
- `gr12` a GRangesList, default `gr1`
- `ignore.strand` logical, default FALSE

**Value**

numeric vector of distance

---

### fetch_JS_seq

**Fetch Javascript sequence**

**Description**

Fetch Javascript sequence

**Usage**

```r
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

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

Description
Get index

Usage
gGetIndexes(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**

```r
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**

```r
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**

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

**Arguments**

- `matches` integer vector, indices
- `ref_granges` GRanges

**Value**

GRanges object

### multiOomicsPlot_animate

**Multi-omics animation using list input**

**Description**

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

**Usage**

```r
multiOomicsPlot_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.
**multiOmicsPlot_animate**

- **kmers_type**: character, function used for kmers sliding window. Default: "mean", alternative: "sum"
- **ylables**: character, default NULL. 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). 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**

```r
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
multiOmicsPlot_list

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 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). Alternative: custom name for region.

plot_title character, default NULL. A title for plot.
**multiOmicsPlot_list**

**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.
multiOmicsPlot_ORFikExp

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 multicore, 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 display 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,self] #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
trimOverlaps

Value

GRanges
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