

# Package ‘RiboCrypt’

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**Type** Package

**Title** Interactive visualization in genomics

**Version** 1.12.0

**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, 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

**VignetteBuilder** knitr

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---

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: <code>ifelse(two_dimensions, "bidir.max", "auto")</code> (Equal in both + / - direction, using max value + 0.5 of <code>meanCounts(in 1d) / rna(in 2d)</code> column of <code>dt</code> ). If you want <code>ggplot</code> to decide limit, set to "auto". For numeric vector, specify min and max x limit: like <code>c(-5, 5)</code>
ylim	numeric vector or character preset, default: "bidir.max" (Equal in both + / - direction, using max value + 0.5 of <code>LFC(in 1d) / rfp(in 2d)</code> column of <code>dt</code> ). If you want <code>ggplot</code> to decide limit, set to "auto". For numeric vector, specify min and max x limit: like <code>c(-5, 5)</code>
xlab	character, default: <code>ifelse(two_dimensions, "RNA fold change (log2)", "Mean counts (log2)")</code>
ylab	character, default: <code>ifelse(two_dimensions, "RFP fold change (log2)", "Fold change (log2)")</code>
two_dimensions	logical, default: <code>ifelse("LFC" %in% colnames(dt), FALSE, TRUE)</code> 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: <code>c("No change" = "black", "Significant" = "red", "Buffering" = "purple", "mRNA abundance" = "darkgreen", "Expression" = "blue", "Forwarded" = "yellow", "Inverse" = "aquamarine", "Translation" = "orange4")</code>

**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(gr1, gr2 = 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**

```
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(gr1)
```

**Arguments**

gr1      a GRangesList

**Value**

numeric, the track row index

---

getCoverageProfile	<i>Get coverage profile</i>
--------------------	-----------------------------

---

**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

---

getIndex	<i>Get index</i>
----------	------------------

---

**Description**

Get index

**Usage**

```
getIndex(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 DNAStrngSet

**Value**

integer vector, indices (named with pattern hit)



---

matchToGRanges	<i>Match to GRanges</i>
----------------	-------------------------

---

**Description**

Match to GRanges

**Usage**

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

**Arguments**

matches	integer vector, indices
ref_granges	GRanges

**Value**

GRanges object

---

multiOmicsPlot_animate	<i>Multi-omics animation using list input</i>
------------------------	---

---

**Description**

The animation will move with a play button, 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 <a href="#">GRangesList</a> or <a href="#">GRanges</a> object
annotation	the whole annotation which your target region is a subset, a <a href="#">GRangesList</a> or <a href="#">GRanges</a> object
reference_sequence	the genome reference, a <a href="#">FaFile</a> or <a href="#">FaFile</a> convertible object
reads	the NGS libraries, as a list of <a href="#">GRanges</a> 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 <a href="#">GRangesList</a> 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 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.
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**

<code>display_range</code>	the whole region to visualize, a <a href="#">GRangesList</a> or <a href="#">GRanges</a> object
<code>annotation</code>	the whole annotation which your target region is a subset, a <a href="#">GRangesList</a> or <a href="#">GRanges</a> object
<code>reference_sequence</code>	the genome reference, a <a href="#">FaFile</a> or <a href="#">FaFile</a> convertible object
<code>reads</code>	the NGS libraries, as a list of <a href="#">GRanges</a> with or without score column for replicates.
<code>viewMode</code>	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 <code>display_range</code> 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 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.
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 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 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,] #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 separated 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_150",
#                                   default_gene = "ATF4-ENSG00000128272"))
```

---

trimOverlaps

*Trim overlaps*

---

**Description**

Trim overlaps

**Usage**

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

*trimOverlaps*

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**Arguments**

overlaps      GRanges  
display\_range GRanges

**Value**

GRanges

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