# Package 'rGenomeTracks'

March 18, 2025

**Title** Integerated visualization of epigenomic data

**Version** 1.12.0

**Description** rGenomeTracks package leverages the power of pyGenomeTracks software with the interactivity of R.
pyGenomeTracks is a python software that offers robust method for visualizing epigenetic data files like narrowPeak, Hic matrix, TADs and arcs, however though, here is no way currently to use it within R interactive session.
rGenomeTracks wrapped the whole functionality of pyGenomeTracks with additional utilites to make to more pleasant for R users.

**Config/reticulate** list( packages = list( list(package = ``pyGenomeTracks", version = ``3.6") ) )

**License** GPL-3

**Depends** R (>= 4.1.0),

**Imports** imager, reticulate, methods, rGenomeTracksData

**SystemRequirements** pyGenomeTracks (prefered to use install_pyGenomeTracks())

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**Config/testthat/edition** 3

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---

`+,genome_track,genome_track-method`
*Adding genome_track Objects*

---

## Description

This method adds two "genome_track" objects together.

## Usage

```
## S4 method for signature 'genome_track,genome_track'
e1 + e2
```

## Arguments

| | |
|---|---|
| `e1` | genome_track object. |
| `e2` | genome_track object. |

## Value

genome_track object

## Author(s)

Omar Elashkar

## Examples

```
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
genes_dir <- system.file("extdata", "dm3_genes.bed.gz",
  package = "rGenomeTracks"
)
links_dir <- system.file("extdata", "test.arcs",
  package = "rGenomeTracks"
)
tads <- track_domains(tads_dir, color = "#cccccc", border_color = "red")
links_overlay <- track_links(links_dir,
  color = "red",
  line_width = 3, links_type = "loop",
  overlay_previous = "share-y"
)
links <- track_links(links_dir,
  color = "blue",
  line_width = 3, height = 3
)
genes <- track_bed(genes_dir,
  height = 7, style = "flybase",
  fontsize = 10
)
vlines <- track_vlines(genes_dir)
## Not run:
plot_gtracks(tads + links_overlay + links + genes + vlines, chr = "X", start = 30 * 10^5, end = 35 * 10^5)

## End(Not run)
```

---

`epilogos_json` *Generate epilogo json configuration file*

---

## Description

A convience function to generate epilogo json configuration file to be passed for `epi_logos()`

## Usage

```
epilogos_json(cat_df)
```

## Arguments

| | |
|---|---|
| `cat_df` | Dataframe with 3 columns of categories, names and colors |

## Details

The only argument passed to this function is data.frame or data.frame similar object. It should have 3 column: First is the state number of epilogos. The second is the label of the state. Finally, the desired colored of such state. Check the example provided for the structure of this data.frame.

## Value

Directory

## Author(s)

Omar Elashkar

## Examples

```
epilog_dir <- system.file("extdata", "epilog.qcat.bgz", package = "rGenomeTracks")
epi_cat <- data.frame(
  category = 1:15,
  label = c(
    "Active TSS",
    "Flanking Active TSS",
    "Transcr at gene 5 and 3",
    "Strong transcription",
    "Weak transcription",
    "Genic enhancers",
    "Enhancers",
    "ZNF genes & repeats",
    "Heterochromatin",
    "Bivalent/Poised TSS",
    "Flanking Bivalent TSS/Enh",
    "Bivalent Enhancer",
    "Repressed PolyComb",
    "Weak Repressed PolyComb",
    "Quiescent/Low"
  ),
  color = c(
    "#ff0000", "#ff4500", "#32cd32", "#008000",
    "#006400", "#c2e105", "#ffff00", "#66cdaa",
    "#8a91d0", "#cd5c5c", "#e9967a", "#bdb76b",
    "#808080", "#c0c0c0", "#ffffff"
  )
)
epilog <- track_epilogos(file = epilog_dir, categories_file = epilogos_json(epi_cat))
## Not run:
plot_gtracks(epilog, chr = "X", start = 3100000, 3150000)

## End(Not run)
```

---

`install_pyGenomeTracks` *Install pyGenomeTracks Dependency*

---

## Description

Install pyGenomeTracks dependency for plot_gtracks()

## Usage

```
install_pyGenomeTracks()
```

## Details

The function will install miniconda if does not exits and check pyGenomeTracks installation.

## Value

None

## Author(s)

Omar Elashkar

## Examples

```
## Not run:
install_pyGenomeTracks()

## End(Not run)
```

---

`plot_gtracks` *Plotting genomic tracks*

---

## Description

This is a generic function used to plot `genome_track` objects.

## Usage

```
plot_gtracks(
  obj,
  chr,
  start,
  end,
  dir = NULL,
  plot = TRUE,
  verbose = FALSE,
  dpi = 100,
  title = NULL,
  fontsize = NULL,
  width = 40,
  height = NULL,
  trackLabelFraction = 0.05,
  trackLabelHAlign = "left",
  ...
)

## S4 method for signature 'genome_track'
plot_gtracks(
  obj,
  chr,
  start,
  end,
  dir = NULL,
  plot = TRUE,
  verbose = FALSE,
  dpi = 100,
```

```
  title = NULL,
  fontsize = NULL,
  width = 40,
  height = NULL,
  trackLabelFraction = 0.05,
  trackLabelHAlign = "left",
  ...
)
```

## Arguments

| | |
|---|---|
| obj | genome_track object. Define all tracks to be plotted. |
| chr | String or numeric value to indicate the chromosome desire. |
| start | Numeric. Starting position of plotting on the defined chromosome. |
| end | Numeric. Starting position of plotting on the defined chromosome. |
| dir | String. Default is NULL. If defined, a string to directory and extension to which image is exported. Extension could be png, svg or pdf. |
| plot | Boolean. Default if TRUE. If FALSE, plot will not be generated, only exported. |
| verbose | If TRUE, print command that will be passed to pyGenomeTracks. |
| dpi | Numeric. Default is 100 |
| title | String. Title of the generated plot. Default is NULL. |
| fontsize | If set, global fontsize value overrides individual tracks.R . argument of all tracks passed. |
| width | Numeric. The width of the plot. Default is 40 |
| height | Numeric. Height of the plot. Default is NULL to set is based on tracks height. |
| trackLabelFraction | Numeric. Default is 0.05. |
| trackLabelHAlign | String. Position of labels aligment. Options are "left", "right" or "center". Default is "left". |
| ... | Extra arguments to be passed for generic plot(). |

## Value

None

None

## Note

For this function to run, you need pyGenomeTracks installed in R's loading enviroment. If not, please run install_pyGenomeTracks()

## Author(s)

Omar Elashkar

Omar Elashkar

## Examples

```
## Not run:
# Get example data directories
# Download h5 example
ah <- AnnotationHub()
query(ah, "rGenomeTracksData")
h5_dir <- ah[["AH95901"]]
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
arcs_dir <- system.file("extdata", "links2.links", package = "rGenomeTracks")
bw_dir <- system.file("extdata", "bigwig2_X_2.5e6_3.5e6.bw", package = "rGenomeTracks")
#
# Create HiC track from HiC matrix
h5 <- track_hic_matrix(
  file = h5_dir, depth = 250000, min_value = 5, max_value = 200,
  transform = "log1p", show_masked_bins = FALSE
)

# Create TADS track
tads <- track_domains(
  file = tads_dir, border_color = "black",
  color = "none", height = 5,
  line_width = 5,
  show_data_range = FALSE,
  overlay_previous = "share-y"
)

# Create arcs track
arcs <- track_links(
  file = arcs_dir, links_type = "triangles", line_style = "dashed",
  overlay_previous = "share-y",
  color = "darkred",
  line_width = 3,
  show_data_range = FALSE
)

# Create bigwig track
bw <- track_bigwig(
  file = bw_dir, color = "red",
  max_value = 50,
  min_value = 0,
  height = 4,
  overlay_previous = "yes",
  show_data_range = FALSE
)

# Create one object from HiC, arcs and bigwid
tracks <- h5 + arcs + bw

# Plot the tracks
plot_gtracks(tracks, chr = "X", start = 25 * 10^5, end = 31 * 10^5)
# Plot HiC, TADS and bigwig tracks
plot_gtracks(h5 + tads + bw, chr = "X", start = 25 * 10^5, end = 31 * 10^5)

## End(Not run)
```

track_bed *Generate bed track*

## Description

Generate genome_track object from a bed file.

## Usage

```
track_bed(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  fontsize = 12,
  orientation = NULL,
  line_width = 0.5,
  color = "#1f78b4",
  max_value = NULL,
  min_value = NULL,
  border_color = "black",
  prefered_name = "transcript_name",
  merge_transcripts = FALSE,
  labels = TRUE,
  style = "flybase",
  display = "stacked",
  max_labels = 60,
  global_max_row = FALSE,
  gene_rows = NULL,
  arrow_interval = 2,
  arrowhead_included = FALSE,
  color_utr = 0,
  height_utr = 1,
  arrow_length = 0,
  all_labels_inside = FALSE,
  labels_in_margin = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| fontsize | Numeric value to font size of tracks's text. |
| orientation | String. Set to "inverted" to make the track upside down. Default is NULL. |
| line_width | Numeric. Default is 0.5. |
| color | String. Hex color or string color. Default is "#1f78b4". |

`max_value` Numeric. Default is NULL. The max value cut-off for the numeric column.

`min_value` Numeric. Default is NULL. The max value cut-off for the numeric column.

`border_color` String. default is "black"

`prefered_name` String. Denote which column to get elements names. Default is "transcript_name".

`merge_transcripts` Boolean. Default is FALSE.

`labels` Boolean. Default is FALSE.

`style` String. Options are "flybase" (default), or "UCSV" or "tassarrow".

`display` String. options are "stacked" (default) or "collapsed", "triangles" or "interleaved".

`max_labels` Numeric. Any integer about 1. Default is 60.

`global_max_row` Boolean. Default is FALSE.

`gene_rows` Numeric. Default is NULL.

`arrow_interval` Numeric. Should be above 1. Default is 2

`arrowhead_included` Boolean. Default is FALSE

`color_utr` String. Hex color or string. Default is "grey"

`height_utr` Numeric. Between 0 and 1. Default is 1.

`arrow_length` Numeric. Default is NULL.

`all_labels_inside` Boolean. Default is FALSE

`labels_in_margin` Boolean. Default is FALSE.

## Details

`track_bed()` supports all common bed files with minimal of 3 columns and maximum of 12 columns.

## Value

genome_track

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
bed12_dir <- system.file("extdata", "dm3_genes.bed.gz",
  package = "rGenomeTracks"
)
bed4_dir <- system.file("extdata", "dm3_genes.bed4.gz",
  package = "rGenomeTracks"
)
bed6_dir <- system.file("extdata", "dm3_genes.bed6.gz",
```

```
  package = "rGenomeTracks"
)

# Create bed track using bed4 file
bed4 <- track_bed(
  file = bed4_dir, height = 3, title = "bed4", color = "cyan", ,
  border_color = "#9ACD32", line_width = 1.5
)

# Create bed track using bed6 file
bed6 <- track_bed(
  file = bed6_dir, height = 3, title = "bed4", fontsize = 8, color = "red",
  border_color = "yellow", arrowhead_included = TRUE
)

# Create bed track using bed12 file
bed12 <- track_bed(
  file = bed12_dir, height = 3, title = "bed12", style = "UCSC",
  arrow_interval = 10, fontsize = 10
)

# Create a spacer track
space <- track_spacer(height = 1)
## Not run:
# Plotting the tracks
plot_gtracks(bed4 + space + bed6 + space + bed12 + space,
  chr = "X", start = 300 * 10^4, end = 330 * 10^4, verbose = TRUE
)

## End(Not run)
```

---

`track_bedgraph` *Generate bedgraph track*

---

## Description

Generate genome_track object from bedgraph files.

## Usage

```
track_bedgraph(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  orientation = NULL,
  color = "#1f78b4",
  alpha = 1,
  max_value = NULL,
  min_value = NULL,
  use_middle = FALSE,
  show_data_range = TRUE,
  type = "fill",
```

```
  negative_color = NULL,
  nans_to_zeros = FALSE,
  summary_method = NULL,
  number_of_bins = 700,
  transform = "no",
  log_pseudocount = 0,
  y_axis_values = "transformed",
  second_file = NULL,
  operation = "file",
  grid = FALSE,
  rasterize = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| orientation | String. Default is NULL. Other option is "inverted". |
| color | String. Hex color or string color. Default is "#1f78b4". |
| alpha | Numeric variable between 0 and 1 to indicate level of transparancy. Default is 1. |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| min_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| use_middle | Boolean. Default is FALSE. |
| show_data_range | Boolean. Default is TRUE. |
| type | String. Options are "fill" (default),"line", "points". |
| negative_color | Hex color or string to indicate color of negative values. Default is NULL. |
| nans_to_zeros | Boolean. To convert empty values to zeros, set this to TRUE. Default is FALSE. |
| summary_method | String. summary_method applied over bin range. This parameter is set to NULL. See details for options. |
| number_of_bins | Numeric value to indicate summary method used over the bin range. Default is 700 |
| transform | String to indicate type of transformation applied. Default is "no". |
| log_pseudocount | Numeric. Default is 0. |
| y_axis_values | String with two options "transformed" (default) or "original". |
| second_file | Path for another file to be included in operations. This parameter is not set by default. |
| operation | Default is set to "file". See details. |
| grid | Boolean. Default is FALSE. |
| rasterize | Boolean. Default is FALSE. |

## Details

summary_method parameter can be choosen to be by "mean", "average", "max", "min", "stdev", "dev", "coverage", "cov" or "sum". Tranform paramter options are "no" (default) or "log", "log1p", "-log", "log2" or "log10". 'log1p': transformed_values = log(1 + initial_values) 'log': transformed_values = log(log_pseudocount + initial_values) 'log2': transformed_values = log2(log_pseudocount + initial_values) 'log10': transformed_values = log10(log_pseudocount + initial_values) '-log': transformed_values = log(log_pseudocount + initial_values) To compute operations on the fly on the file or between 2 bedgraph files, you can tweak operation parameter, it should contains file or file and second_file. It is adviced to use `nans_to_zeros = TRUE` to avoid unexpected results. Example value for operation are "0.89 * file", "- file", "file - second_file", "log2((1 + file) / (1 + second_file))" and "max(file, second_file)"

to add the preferred line width or point size : type = "line:lw" where lw (linewidth) is numeric value. Like `type = "line:0.5"` and `type = "points:0.5"`

By default the bedgraph is plotted at the base pair resolution. This can lead to very large pdf/svg files. If plotting large regions. If you want to decrase the size of your file. You can either rasterize the bedgraph profile by using: `rasterize = TRUE`

## Value

genome_track

## Note

`fontsize` parameter can be overriden by the same argument in `plot_gtracks()` `height` parameter will be ignored if `overlay_previous` is set.

## Author(s)

Omar Elashkar

## Examples

```
bg_dir <- system.file("extdata", "GSM3182416_E12DHL_WT_Hoxd11vp.bedgraph.gz",
  package = "rGenomeTracks"
)
bed_genes_dir <- system.file("extdata", "HoxD_cluster_regulatory_regions_mm10.bed",
  package = "rGenomeTracks"
)

bg <- track_bedgraph(bg_dir, color = "green", height = 5, max_value = 10)
bg_middle <- track_bedgraph(bg_dir,
  use_middle = TRUE, color = "blue",
  height = 5, max_value = 10
)
bed_genes <- track_bed(bed_genes_dir,
  title = "Regulatory regions", ,
  color = "red", height = 3
)

tracks <- track_x_axis(where = "top") + bg + bg_middle + bed_genes
## Not run:
plot_gtracks(tracks,
  chr = 2, start = 738 * 10^5, end = 750 * 10^5,
  trackLabelFraction = 0.2
```

```
)

## End(Not run)
```

---

`track_bedgraph_matrix` *Generate bedgraph matrix track*

---

## Description

A track for file like bedgraph but with more than 4 columns, like the insulation score from hicPlotTADs

## Usage

```
track_bedgraph_matrix(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  orientation = NULL,
  max_value = NULL,
  min_value = NULL,
  show_data_range = FALSE,
  type = "matrix",
  rasterize = TRUE,
  pos_score_in_bin = "center",
  plot_horizontal_lines = FALSE,
  colormap = "virdis"
)
```

## Arguments

| | |
|---|---|
| `file` | String. The location of the track file |
| `title` | String. If specificed, the title of the track to be displayed. |
| `height` | Numeric. The height of the plotted track in cm. |
| `overlay_previous` | String. Options are "no" (default) or "yes" or |
| `orientation` | String. Set to "inverted" to make the track upside down. Default is NULL. |
| `max_value` | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| `min_value` | Numeric. Default is NULL. The min value cut-off for the numeric column. |
| `show_data_range` | Boolean. Default is FALSE. |
| `type` | "matrix" (default) or "lines". |
| `rasterize` | Boolean. Default is TRUE |
| `pos_score_in_bin` | String value to indicate the position of score with respect to bin start and end. Possible values are either "center" (default) or "block". |
| `plot_horizontal_lines` | Boolean. Can be used only if type parameter is set to "lines". |
| `colormap` | String with matplotlib-compatible colormap. Default is set to "viridis". |

## Details

The different options for color maps can be found here: https://matplotlib.org/users/colormaps.html.

## Value

genome_track

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
IS_dir <- system.file("extdata", package = "rGenomeTracks", "tad_separation_score.bm.gz")
IS <- track_bedgraph_matrix(IS_dir)
## Not run:
plot_gtracks(IS, chr = "X", start = 2000000, end = 3500000)

## End(Not run)
```

---

# track_bigwig *Generate bigwig track*

---

## Description

Create genome_track object from bigwig file.

## Usage

```
track_bigwig(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  orientation = NULL,
  color = "#1f78b4",
  alpha = 1,
  max_value = NULL,
  min_value = NULL,
  show_data_range = TRUE,
  type = "fill",
  negative_color = NULL,
  nans_to_zeros = FALSE,
  summary_method = "mean",
  number_of_bins = 700,
  transform = "no",
  log_pseudocount = 0,
  y_axis_values = "transformed",
```

```
  second_file = NULL,
  operation = "file",
  grid = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. |
| overlay_previous | String. Options are "no" (default) or "yes" or |
| orientation | String. Set to "inverted" to make the track upside down. Default is NULL. |
| color | String. Hex color or string color. Default is "#1f78b4". |
| alpha | Numeric variable between 0 and 1 to indicate level of transparancy. Default is 1. |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| min_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| show_data_range | Boolean. Default is TRUE. |
| type | String. Options are "fill" (default),"line", "points". |
| negative_color | Hex color or string to indicate color of negative values. Default is NULL. |
| nans_to_zeros | Boolean. To convert empty values to zeros, set this to TRUE. Default is FALSE. |
| summary_method | String. summary_method applied over bin range. This parameter is set to NULL. See details for options. |
| number_of_bins | Numeric value to indicate summary method used over the bin range. Default is 700 |
| transform | String to indicate type of transformation applied. Default is "no". |
| log_pseudocount | Numeric. Default is 0. |
| y_axis_values | String with two options "transformed" (default) or "original". |
| second_file | Path for another file to be included in operations. This parameter is not set by default. |
| operation | Default is set to "file". See details. |
| grid | Boolean. Default is FALSE. |

## Details

summary_method parameter can be choosen to be by "mean", "average", "max", "min", "stdev", "dev", "coverage", "cov" or "sum". Tranform paramter options are "no" (default) or "log", "log1p", "-log", "log2" or "log10". 'log1p': transformed_values = log(1 + initial_values) 'log': transformed_values = log(log_pseudocount + initial_values) 'log2': transformed_values = log2(log_pseudocount + initial_values) 'log10': transformed_values = log10(log_pseudocount + initial_values) '-log': transformed_values = log(log_pseudocount + initial_values) To compute operations on the fly on the file or between 2 bedgraph files, you can tweak operation parameter, it should contains file or file and second_file. It is adviced to use `nans_to_zeros = TRUE` to avoid unexpected results. Example value for operation are "0.89 * file", "- file", "file - second_file", "log2((1 + file) / (1 + second_file))" and "max(file, second_file)"

## Value

None

**to add the preferred line width or point size : type = "line:lw" where lw (linewidth) is numeric value.**

Like type = "line:0.5" and type = "points:0.5"

## Author(s)

Omar Elashkar

## Examples

```
bw_dir <- system.file("extdata", "bigwig2_X_2.5e6_3.5e6.bw",
  package = "rGenomeTracks"
)
mean_bw <- track_bigwig(
  file = bw_dir, color = "gray",
 type = "point:1", summary_method = "mean", number_of_bins = 300, max_value = 200, min_value = -5
)
min_bw <- track_bigwig(
 file = bw_dir, color = "blue", type = "line:1", summary_method = "min", number_of_bins = 300,
  overlay_previous = "share-y", show_data_range = FALSE,
  max_value = 200, min_value = -5
)
max_bw <- track_bigwig(
 file = bw_dir, color = "red", type = "line:1", summary_method = "max", number_of_bins = 300,
  overlay_previous = "share-y", show_data_range = FALSE,
  max_value = 200, min_value = -5
)
hlines <- track_hlines(
  y_values = "10, 150",
  overlay_previous = "share-y",
  color = "blue", line_style = "dotted"
)
## Not run:
plot_gtracks(mean_bw + min_bw + max_bw + hlines, chr = "X", start = 27 * 10^5, end = 31 * 10^5)

## End(Not run)
```

---

`track_domains` *Generate domains track*

---

## Description

Domain files are bed files represents TADS in the case of HiC analysis.

## Usage

```
track_domains(
  file,
  title = NULL,
```

```
  height = 2,
  overlay_previous = "no",
  orientation = NULL,
  line_width = 0.5,
  color = "#1f78b4",
  max_value = NULL,
  show_data_range = TRUE,
  min_value = NULL,
  border_color = "black",
  prefered_name = "transcript_name",
  merge_transcripts = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| orientation | String. Set to "inverted" to make the track upside down. Default is NULL. |
| line_width | Numeric. Default is 0.5. |
| color | String. Hex color or string color. Default is "#1f78b4". |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| show_data_range | Boolean. Default is TRUE. |
| min_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| border_color | String. default is "black" |
| prefered_name | String. Denote which column to get elements names. Default is "transcript_name". |
| merge_transcripts | Boolean. Default is FALSE. |

## Details

To remove the border, set 'border_color' parameter to "none".

## Value

genome_track

## Author(s)

Omar Elashkar

## Examples

```
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
tads <- track_domains(
  file = tads_dir, border_color = "black",
```

```
  color = "#11FF34", height = 5
)
tads_i <- track_domains(
  file = tads_dir, border_color = "red",
  color = "#cccccc", height = 3, orientation = "inverted"
)
tracks <- track_x_axis(where = "top") +
  tads + tads_i
## Not run:
plot_gtracks(tracks, chr = "X", start = 30 * 10^5, end = 35 * 10^5)

## End(Not run)
```

---

`track_epilogos` *Generate epilogos track*

---

## Description

Generate epilogos genome_track from qcat file.

## Usage

```
track_epilogos(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  categories_file = NULL,
  orientation = NULL
)
```

## Arguments

| | |
|---|---|
| `file` | String. The location of the track file |
| `title` | String. If specificed, the title of the track to be displayed. |
| `height` | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| `overlay_previous` | String. Options are "no" (default) or "yes" or "share-y". |
| `categories_file` | Optionally pass a string of JSON custom colors configuration file directory. Default is NULL. |
| `orientation` | String. Set to "inverted" to make the track upside down. Default is NULL. |

## Details

Epilogos is used widely to represent multiple "states" across genome, like ChromHMM states. More details here `qcat` file is needed which can be generated using epilogos `track_epiolog` can optionally take categories_file parameter which specify the color scheme for the states present in `qcat` file. Check the example section for demonestration.

## Value

None

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
epilog_dir <- system.file("extdata", "epilog.qcat.bgz", package = "rGenomeTracks")
epi_cat <- data.frame(
  category = 1:15,
  label = c(
    "Active TSS",
    "Flanking Active TSS",
    "Transcr at gene 5 and 3",
    "Strong transcription",
    "Weak transcription",
    "Genic enhancers",
    "Enhancers",
    "ZNF genes & repeats",
    "Heterochromatin",
    "Bivalent/Poised TSS",
    "Flanking Bivalent TSS/Enh",
    "Bivalent Enhancer",
    "Repressed PolyComb",
    "Weak Repressed PolyComb",
    "Quiescent/Low"
  ),
  color = c(
    "#ff0000", "#ff4500", "#32cd32", "#008000",
    "#006400", "#c2e105", "#ffff00", "#66cdaa",
    "#8a91d0", "#cd5c5c", "#e9967a", "#bdb76b",
    "#808080", "#c0c0c0", "#ffffff"
  )
)
epilog <- track_epilogos(file = epilog_dir, categories_file = epilogos_json(epi_cat))
## Not run:
plot_gtracks(epilog, chr = "X", start = 3100000, 3150000)

## End(Not run)
```

---

# track_gtf *Generate gtf track*

---

## Description

Create genome_track object for gtf annotation files.

## Usage

```
track_gtf(
  file,
  title = NULL,
  height = 2,
  overlay_previous = "no",
  fontsize = 12,
  orientation = NULL,
  line_width = 0.5,
  color = "#1f78b4",
  border_color = "black",
  prefered_name = "transcript_name",
  merge_transcripts = FALSE,
  labels = FALSE,
  display = "stacked",
  max_labels = 60,
  global_max_row = FALSE,
  gene_rows = NULL,
  arrow_interval = 2,
  arrowhead_included = FALSE,
  color_utr = "grey",
  height_utr = 1,
  arrow_length = NULL,
  all_labels_inside = FALSE,
  labels_in_margin = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| fontsize | Numeric value to font size of tracks's text. |
| orientation | String. Set to "inverted" to make the track upside down. Default is NULL. |
| line_width | Numeric. Default is 0.5. |
| color | String. Hex color or string color. Default is "#1f78b4". |
| border_color | String. default is "black" |
| prefered_name | String. Denote which column to get elements names. Default is "transcript_name". |
| merge_transcripts | Boolean. Default is FALSE. |
| labels | Boolean. Default is FALSE. |
| display | String. options are "stacked" (default) or "collapsed", "triangles" or "interleaved". |
| max_labels | Numeric. Any integer about 1. Default is 60. |
| global_max_row | Boolean. Default is FALSE. |
| gene_rows | Numeric. Default is NULL. |

`arrow_interval` Numeric. Should be above 1. Default is 2

`arrowhead_included`
Boolean. Default is FALSE

`color_utr` String. Hex color or string. Default is "grey"

`height_utr` Numeric. Between 0 and 1. Default is 1.

`arrow_length` Numeric. Default is NULL.

`all_labels_inside`
Boolean. Default is FALSE

`labels_in_margin`
Boolean. Default is FALSE.

## Details

gtf files, unlike bed file, can provide richer annotation regarding levels of annotation where genomic features can be grouped based on the composing entity.

## Value

genome_track

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
gtf_dir <- system.file("extdata", "dm3_subset_BDGP5.78.gtf.gz",
  package = "rGenomeTracks"
)
gtf <- track_gtf(
  file = gtf_dir, height = 10,
  prefered_name = "gene_name", merge_transcripts = TRUE, fontsize = 12
)
## Not run:
plot_gtracks(gtf + track_spacer() +
  track_x_axis(), chr = "X", start = 30 * 10^5, end = 33 * 10^5)

## End(Not run)
```

---

# `track_hic_matrix` *Generate HiC track*

---

## Description

Create a genome_track for matrix files. Currently, only cool format and h5 format.

## Usage

```
track_hic_matrix(
  file,
  title = NULL,
  height = NULL,
  overlay_previous = "no",
  orientation = NULL,
  max_value = NULL,
  min_value = NULL,
  transform = "no",
  rasterize = TRUE,
  colormap = "RdYlBu_r",
  depth = 100000,
  show_masked_bins = FALSE,
  scale_factor = 1
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| orientation | String. Set to "inverted" to make the track upside down. Default is NULL. |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| min_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| transform | String to indicate type of transformation applied. Default is "no". |
| rasterize | Boolean. Default is FALSE. |
| colormap | String with matplotlib-compatible colormap. Default is set to "viridis". |
| depth | Numeric value above 1 to indicate the maximum distance that should be plotted. Default is 100000. |
| show_masked_bins | Boolean. If TRUE, showing masked bins as white lines. Default is FALSE. |
| scale_factor | Numeric factor by which matrix is to be scaled. |

## Details

This function expect cool or h5 format. Format converter like hicConvertFormat can help converting to supported formats. depth is the maximum distance that should be plotted. If it is more than 125% of the plotted region, it will be adjsted to this maximum value. colormap argument should be compatible with matplotlib. show_masked_bins plots bins not used during the corrections as white lines. Setting this argument to FALSE (default) extends neighboring bins to obtain an aesthetically pleasant output. scale argument scales the matrix by specific factor. This is useful if plotting multiple hic-matrices to be on the same scale.

## Value

genom_track

## Author(s)

Omar Elashkar

## Examples

```
## Not run:
# Get example data directories
# Download h5 example
ah <- AnnotationHub()
query(ah, "rGenomeTracksData")
h5_dir <- ah[["AH95901"]]
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
arcs_dir <- system.file("extdata", "links2.links", package = "rGenomeTracks")
bw_dir <- system.file("extdata", "bigwig2_X_2.5e6_3.5e6.bw", package = "rGenomeTracks")
#
# Create HiC track from HiC matrix
h5 <- track_hic_matrix(
  file = h5_dir, depth = 250000, min_value = 5, max_value = 200,
  transform = "log1p", show_masked_bins = FALSE
)

# Create TADS track
tads <- track_domains(
  file = tads_dir, border_color = "black",
  color = "none", height = 5,
  line_width = 5,
  show_data_range = FALSE,
  overlay_previous = "share-y"
)

# Create arcs track
arcs <- track_links(
  file = arcs_dir, links_type = "triangles", line_style = "dashed",
  overlay_previous = "share-y",
  color = "darkred",
  line_width = 3,
  show_data_range = FALSE
)

# Create bigwig track
bw <- track_bigwig(
  file = bw_dir, color = "red",
  max_value = 50,
  min_value = 0,
  height = 4,
  overlay_previous = "yes",
  show_data_range = FALSE
)

# Create one object from HiC, arcs and bigwid
tracks <- h5 + arcs + bw

# Plot the tracks
plot_gtracks(tracks, chr = "X", start = 25 * 10^5, end = 31 * 10^5)
```

```
# Plot HiC, TADS and bigwig tracks
plot_gtracks(h5 + tads + bw, chr = "X", start = 25 * 10^5, end = 31 * 10^5)

## End(Not run)
```

---

`track_hlines` *Generate a track with horizontal lines*

---

## Description

`track_hlines()` creates a genome_track with horizonal lines that can be overlayed on the previous track or, by default, track the lines in separate track.

## Usage

```
track_hlines(
  y_values,
  title = NULL,
  height = 0.5,
  overlay_previous = NULL,
  orientation = NULL,
  line_width = 0.5,
  line_style = "solid",
  color = "black",
  alpha = 1,
  max_value = NULL,
  min_value = NULL,
  show_data_range = TRUE
)
```

## Arguments

| | |
|---|---|
| `y_values` | String for y-values where horizontal lines should be plotted separated by comma. |
| `title` | String. If specificed, the title of the track to be displayed. |
| `height` | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| `overlay_previous` | String. Options are "no" (default) or "yes" or "share-y". |
| `orientation` | String. Default is NULL. Other option is "inverted". |
| `line_width` | Numeric value for line width. |
| `line_style` | String with options of either "solid", "dashed", "dotted", and "dashdot". |
| `color` | String. Hex color or string color. Default is "#1f78b4". |
| `alpha` | Numeric variable between 0 and 1 to indicate level of transparancy. Default is 1. |
| `max_value` | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| `min_value` | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| `show_data_range` | Boolean. Default is TRUE. |

## Details

y_values argument specify locations on the genome where where horizontal lines should be plotted separated by comma, like "50, 90"

## Value

genome_track

## Author(s)

Omar Elashkar

## Examples

```
bw_dir <- system.file("extdata", "bigwig2_X_2.5e6_3.5e6.bw",
  package = "rGenomeTracks"
)
mean_bw <- track_bigwig(
  file = bw_dir, color = "gray",
 type = "point:1", summary_method = "mean", number_of_bins = 300, max_value = 200, min_value = -5
)
min_bw <- track_bigwig(
 file = bw_dir, color = "blue", type = "line:1", summary_method = "min", number_of_bins = 300,
  overlay_previous = "share-y", show_data_range = FALSE,
  max_value = 200, min_value = -5
)
max_bw <- track_bigwig(
 file = bw_dir, color = "red", type = "line:1", summary_method = "max", number_of_bins = 300,
  overlay_previous = "share-y", show_data_range = FALSE,
  max_value = 200, min_value = -5
)
hlines <- track_hlines(
  y_values = "10, 150",
  overlay_previous = "share-y",
  color = "blue", line_style = "dotted"
)
## Not run:
plot_gtracks(mean_bw + min_bw + max_bw + hlines, chr = "X", start = 27 * 10^5, end = 31 * 10^5)

## End(Not run)
```

---

# track_links *Generate links track*

---

## Description

Generate links track from arc file.

## Usage

```
track_links(
  file,
  title = NULL,
```

```
  height = 2,
  overlay_previous = "no",
  orientation = NULL,
  links_type = "arcs",
  line_width = NULL,
  line_style = "solid",
  color = "blue",
  alpha = 0.8,
  max_value = NULL,
  min_value = NULL,
  ylim = NULL,
  show_data_range = FALSE,
  compact_arcs_level = 0,
  use_middle = FALSE
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| orientation | String. Default is NULL. Other option is "inverted". |
| links_type | String value with options "arcs" (default) or "triangles" or "loops". |
| line_width | Numeric value for line width. |
| line_style | String with options of either "solid", "dashed", "dotted", and "dashdot". |
| color | String. Hex color or string color. Default is "#1f78b4". |
| alpha | Numeric variable between 0 and 1 to indicate level of transparancy. Default is 1. |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| min_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| ylim | Numeric value above 0 to set arcs' height cutoff. Default is NULL |
| show_data_range | Boolean. Default is TRUE. |
| compact_arcs_level | Numeric value of either 0, 1 or 2 to indicate level of arcs' compactness by distance it travels. |
| use_middle | Boolean. Default is FALSE. |

## Details

Level of compactness relative to arcs' length can be manipulated using the argument compact_arcs_level where:

- compact_arcs_level = 0, The default where the height is proportional to distance
- compact_arcs_level = 1, the height is proportional to the square root of the distance
- compact_arcs_level = 2, the height is the same for all distances

ylim argument sets the cutoff for arcs' height. This could be handy if you have small arc overridden by larger arc.

## Value

genome_track

## Note

ylim argument is incompatible with compact_arcs_level = 2

## Author(s)

Omar Elashkar

## Examples

```
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
genes_dir <- system.file("extdata", "dm3_genes.bed.gz",
  package = "rGenomeTracks"
)
links_dir <- system.file("extdata", "test.arcs",
  package = "rGenomeTracks"
)
tads <- track_domains(tads_dir, color = "#cccccc", border_color = "red")
links_overlay <- track_links(links_dir,
  color = "red",
  line_width = 3, links_type = "loop",
  overlay_previous = "share-y"
)
links <- track_links(links_dir,
  color = "blue",
  line_width = 3, height = 3
)
genes <- track_bed(genes_dir,
  height = 7, style = "flybase",
  fontsize = 10
)
vlines <- track_vlines(genes_dir)
## Not run:
plot_gtracks(tads + links_overlay + links + genes + vlines, chr = "X", start = 30 * 10^5, end = 35 * 10^5)

## End(Not run)
```

---

# track_narrow_peak *Generate narrow peaks track*

---

## Description

Create genome_track object from narrow peak bed format.

## Usage

```
track_narrow_peak(
  file,
  title = NULL,
  height = 3,
  overlay_previous = "no",
  orientation = NULL,
  line_width = 1,
  color = "#FF000080",
  max_value = NULL,
  show_data_range = TRUE,
  show_labels = TRUE,
  use_summit = TRUE,
  width_adjust = 1.5,
  type = "peak"
)
```

## Arguments

| | |
|---|---|
| file | String. The location of the track file |
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |
| orientation | String. Default is NULL. Other option is "inverted". |
| line_width | Numeric value for line width. |
| color | String. Hex color or string color. Default is "#1f78b4". |
| max_value | Numeric. Default is NULL. The max value cut-off for the numeric column. |
| show_data_range | Boolean. Default is TRUE. |
| show_labels | Boolean. If TRUE, display labels on plotting which include peak tag, p-val and q-val. |
| use_summit | Boolean. If TRUE, peak summit data will be plotted. |
| width_adjust | Numeric value above 0 to adjust peaks' width. Default is 1.5. |
| type | String with options either "peak" or "box". |

## Details

narrowPeak file is bed file (4+3), where the 5th column is peak name, 6th column in p-value and 7th column in q-value. You might increase height it increased font size. narrowPeak format is very common with analysis pipelines involving MACS2. narrowPeak format provides the information of the peak summit. use_summit argument is used to deterimine if this information should be used. By default this information is used (use_summit = TRUE) although some peaks may look crooked. type argument specify if the plot will be:

- "box" which will plot a rectangle of the peak width
- or "peak" which will plot the shape of the peak, whose height is the narrowPeak file signal value (usually peak coverage)

## Value

genome_track

## Author(s)

Omar Elashkar

## Examples

```
np_bed_dir <- system.file("extdata", "test2.narrowPeak", package = "rGenomeTracks")

tracks <-
  track_scalebar() +
  track_narrow_peak(np_bed_dir,
    title = "peak type with summit",
    height = 3,
    type = "peak",
    color = "green"
  ) +

  track_spacer(height = 2) +
  track_narrow_peak(np_bed_dir,
    title = "peak type without summit",
    height = 3,
    type = "peak",
    color = "green",
    use_summit = FALSE
  ) +
  track_spacer(height = 2) +
  track_narrow_peak(np_bed_dir,
    title = "Box type with summit",
    height = 3,
    type = "box",
    color = "blue"
  ) +
  track_spacer(height = 2) +
  track_narrow_peak(np_bed_dir,
    title = "Box type without summit",
    height = 3,
    type = "box",
    color = "blue",
    use_summit = FALSE
  ) +
  track_x_axis()
## Not run:
plot_gtracks(tracks, chr = "X", start = 276 * 10^4, end = 280 * 10^4, trackLabelFraction = 0.2)

## End(Not run)
```

---

# track_scalebar *Generate scalebar track*

---

## Description

scalebar track is a track with a stretch that highlights specific distance on the genomic coordiantes

## Usage

```
track_scalebar(
  title = NULL,
  height = 2,
  overlay_previous = "no",
  where = "left",
  fontsize = 12,
  line_width = 0.5,
  color = "black",
  alpha = 1,
  x_center = NULL,
  size = NULL,
  scalebar_start_position = NULL,
  scalebar_end_position = NULL
)
```

## Arguments

| | |
|---|---|
| `title` | String. If specificed, the title of the track to be displayed. |
| `height` | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| `overlay_previous` | String. Options are "no" (default) or "yes" or "share-y". |
| `where` | "left" (default), "right", "top" or "bottom". |
| `fontsize` | Numeric value to font size of tracks's text. |
| `line_width` | 0.5 (default) or any float above 0. |
| `color` | String. Hex color or string color. Default is "#1f78b4". |
| `alpha` | Numeric variable between 0 and 1 to indicate level of transparancy. Default is 1. |
| `x_center` | Numeric value above 0. Default is NULL. |
| `size` | Numeric value above 0. Default is NULL. |
| `scalebar_start_position` | Numeric value above 0. Default is NULL. |
| `scalebar_end_position` | Numeric value above 0. Default is NULL. |

## Value

genome_track

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
np_bed_dir <- system.file("extdata", "test2.narrowPeak", package = "rGenomeTracks")

tracks <-
  track_scalebar(
    scalebar_start_position = 2785 * 10^3,
    scalebar_end_position = 2799 * 10^3
  ) +
  track_narrow_peak(np_bed_dir,
    title = "peak type with summit",
    height = 3,
    type = "peak",
    color = "green"
  ) + track_x_axis()
## Not run:
plot_gtracks(tracks, chr = "X", start = 276 * 10^4, end = 280 * 10^4, trackLabelFraction = 0.2)

## End(Not run)
```

---

# track_spacer *Generate spacing track*

---

## Description

Create spacing track with custom height.

## Usage

```
track_spacer(title = NULL, height = 2, overlay_previous = "no")
```

## Arguments

| | |
|---|---|
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |
| overlay_previous | String. Options are "no" (default) or "yes" or "share-y". |

## Value

None

## Author(s)

Omar Elashkar

## Examples

```
bed12_dir <- system.file("extdata", "dm3_genes.bed.gz",
  package = "rGenomeTracks"
)
bed4_dir <- system.file("extdata", "dm3_genes.bed4.gz",
  package = "rGenomeTracks"
)
```

```
bed6_dir <- system.file("extdata", "dm3_genes.bed6.gz",
  package = "rGenomeTracks"
)

# Create bed track using bed4 file
bed4 <- track_bed(
  file = bed4_dir, height = 3, title = "bed4", color = "cyan", ,
  border_color = "#9ACD32", line_width = 1.5
)

# Create bed track using bed6 file
bed6 <- track_bed(
  file = bed6_dir, height = 3, title = "bed4", fontsize = 8, color = "red",
  border_color = "yellow", arrowhead_included = TRUE
)

# Create bed track using bed12 file
bed12 <- track_bed(
  file = bed12_dir, height = 3, title = "bed12", style = "UCSC",
  arrow_interval = 10, fontsize = 10
)

# Create a spacer track
space <- track_spacer(height = 1)
## Not run:
# Plotting the tracks
plot_gtracks(bed4 + space + bed6 + space + bed12 + space,
  chr = "X", start = 300 * 10^4, end = 330 * 10^4, verbose = TRUE
)

## End(Not run)
```

---

`track_vlines` *Overlay vertical lines from a bed file*

---

## Description

`track_vlines()` overlay vertical lines over the whole plot. The only parameter to be passed is a bed file.

## Usage

```
track_vlines(file)
```

## Arguments

| | |
|---|---|
| `file` | String. The location of the track file |

## Value

genome_track

## Author(s)

Omar Elashkar

## Examples

```
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
genes_dir <- system.file("extdata", "dm3_genes.bed.gz",
  package = "rGenomeTracks"
)
links_dir <- system.file("extdata", "test.arcs",
  package = "rGenomeTracks"
)
tads <- track_domains(tads_dir, color = "#cccccc", border_color = "red")
links_overlay <- track_links(links_dir,
  color = "red",
  line_width = 3, links_type = "loop",
  overlay_previous = "share-y"
)
links <- track_links(links_dir,
  color = "blue",
  line_width = 3, height = 3
)
genes <- track_bed(genes_dir,
  height = 7, style = "flybase",
  fontsize = 10
)
vlines <- track_vlines(genes_dir)
## Not run:
plot_gtracks(tads + links_overlay + links + genes + vlines, chr = "X", start = 30 * 10^5, end = 35 * 10^5)

## End(Not run)
```

---

# track_x_axis *Specify x_axis option for genome_track.*

---

## Description

This track will specifiy the options for x-axis for location, height, font size and wheather to overlay previous track.

## Usage

```
track_x_axis(
  title = NULL,
  height = 2,
  overlay_previous = "no",
  where = "bottom",
  fontsize = 15
)
```

## Arguments

| | |
|---|---|
| title | String. If specificed, the title of the track to be displayed. |
| height | Numeric. The height of the plotted track in cm. Default is 2. See notes. |

`overlay_previous`
: String. Options are "no" (default) or "yes" or "share-y".

`where`
: String. Either "bottom" (default) or "top"

`fontsize`
: Numeric value to font size of tracks's text.

## Value

genome_track

## Note

`fontsize` argument can be overriden by the same argument in `plot_gtracks()`

## Author(s)

Omar Elashkar

## Examples

```
tads_dir <- system.file("extdata", "tad_classification.bed",
  package = "rGenomeTracks"
)
tads <- track_domains(
  file = tads_dir, border_color = "black",
  color = "#11FF34", height = 5
)
tads_i <- track_domains(
  file = tads_dir, border_color = "red",
  color = "#cccccc", height = 3, orientation = "inverted"
)
tracks <- track_x_axis(where = "top") +
  tads + tads_i
## Not run:
plot_gtracks(tracks, chr = "X", start = 30 * 10^5, end = 35 * 10^5)

## End(Not run)
```

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