Package 'wiggleplotr'

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Title Make read coverage plots from BigWig files

Version 1.29.0

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Description Tools to visualise read coverage from sequencing experiments together with genomic annotations (genes, transcripts, peaks). Introns of long transcripts can be rescaled to a fixed length for better visualisation of exonic read coverage.

Depends R (>= 3.6)

Imports dplyr, ggplot2 (>= 2.2.0), GenomicRanges, rtracklayer, cowplot, assertthat, purrr, S4Vectors, IRanges, GenomeInfoDb

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Contents

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getGenotypePalette	*Returns a three-colour palette suitable for visualising read coverage stratified by genotype*

Description

Returns a three-colour palette suitable for visualising read coverage stratified by genotype

Usage

```
getGenotypePalette(old = FALSE)
```

Arguments

old   Return old colour palette (now deprecated).

Value

Vector of three colours.

Examples

```
getGenotypePalette()
```

---

makeManhattanPlot   *Make a Manahattan plot of p-values*

Description

The Manhattan plots is compatible with wiggpleplotr read coverage and transcript strucutre plots. Can be appended to those using the cowplot::plot_grid() function.

Usage

```
makeManhattanPlot(pvalues_df, region_coords, color_R2 = FALSE,
  data_track = TRUE)
```

Arguments

pvalues_df	Data frame of association p-values (required columns: track_id, p_nominal, pos)
region_coords	Start and end coordinates of the region to plot.
color_R2	Color the points according to R2 from the lead variant. Require R2 column in the pvalues_df data frame.
data_track	If TRUE, then remove all information from x-axis. Makes it easy to append to read coverage or transcript strcture plots using cowplot::plot_grid().

Value

gglot2 object

Examples

```
data = dplyr::data_frame(track_id = "GWAS", pos = sample(c(1:1000), 200), p_nominal = runif(200, min = 0.0000001, 1
makeManhattanPlot(data, c(1,1000), data_track = FALSE)
```

---

ncoa7_cdss   *Coding sequences from 9 protein coding transcripts of NCOA7*

Description

A dataset containing start and end coordinates of coding sequences (CDS) from nine protein coding transcripts of NCOA7.

Usage

```
ncoa7_cdss
```

Format

A GRangesList object with 9 elements:

element CDS start and end coordinates for a single transcript (GRanges object) ...

Source

<http://www.ensembl.org/>

---

ncoa7_exons   *Exons from 9 protein coding transcripts of NCOA7*

Description

A dataset containing start and end coordinates of exons from nine protein coding transcripts of NCOA7.

Usage

```
ncoa7_exons
```

Format

A GRangesList object with 9 elements:

element Exon start and end coordinates for a single transcript (GRanges object) ...

Source

<http://www.ensembl.org/>

---

ncoa7_metadata   *Gene metadata for NCOA7*

Description

A a list of transcripts for NCOA7.

Usage

```
ncoa7_metadata
```

Format

A data.frame object with 4 columns:

transcript_id Ensembl transcript id.

gene_id Ensembl gene id.

gene_name Human readable gene name.

strand Strand of the transcript (either +1 or -1). ...

Source

<http://www.ensembl.org/>

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pasteFactors	*Paste two factors together and preserved their joint order.*

Description

Paste two factors together and preserved their joint order.

Usage

```
pasteFactors(factor1, factor2)
```

Arguments

factor1	First factor
factor2	Second factor

Value

Factors factor1 and factor2 pasted together.

---

plotCoverage	*Plot read coverage across genomic regions*

Description

Also supports rescaling introns to constant length. Does not work on Windows, because rtracklayer cannot read BigWig files on Windows.

Usage

```
plotCoverage(exons, cdss = NULL, transcript_annotations = NULL,
  track_data, rescale_introns = TRUE, new_intron_length = 50,
  flanking_length = c(50, 50), plot_fraction = 0.1, heights = c(0.75,
  0.25), alpha = 1, fill_palette = c("#a1dab4", "#41b6c4", "#225ea8"),
  mean_only = TRUE, connect_exons = TRUE, transcript_label = TRUE,
  return_subplots_list = FALSE, region_coords = NULL,
  coverage_type = "area")
```

Arguments

exons	list of GRanges objects, each object containing exons for one transcript. The list must have names that correspond to transcript_id column in transript_annotations data.frame.
cdss	list of GRanges objects, each object containing the coding regions (CDS) of a single transcript. The list must have names that correspond to transcript_id column in transript_annotations data.frame. If cdss is not specified then exons list will be used for both arguments. (default: NULL).
transcript_annotations	
	Data frame with at least three columns: transcript_id, gene_name, strand. Used to construct transcript labels. (default: NULL)
track_data	data.frame with the metadata for the bigWig read coverage files. Must contain the following columns:
	• sample_id - unique id for each sample.
	• track_id - if multiple samples (bigWig files) have the same track_id they will be overlayed on the same plot, track_id is also used as the facet label on the right.
	• bigWig - path to the bigWig file.
	• scaling_factor - normalisation factor for each sample, useful if different samples sequenced to different depth and bigWig files not normalised for that.
	• colour_group - additional column to group samples into, is used as the colour of the coverage track.
rescale_introns	
	Specifies if the introns should be scaled to fixed length or not. (default: TRUE)
new_intron_length	
	length (bp) of introns after scaling. (default: 50)
flanking_length	
	Lengths of the flanking regions upstream and downstream of the gene. (default: c(50,50))
plot_fraction	Size of the random sub-sample of points used to plot coverage (between 0 and 1). Smaller values make plotting significantly faster. (default: 0.1)
heights	Specifies the proportion of the height that is dedicated to coverage plots (first value) relative to transcript annotations (second value). (default: c(0.75,0.25))

alpha	Transparency (alpha) value for the read coverage tracks. Useful to set to something < 1 when overlaying multiple tracks (see track_id). (default: 1)
fill_palette	Vector of fill colours used for the coverage tracks. Length must be equal to the number of unique values in track_data$colour_group column.
mean_only	Plot only mean coverage within each combination of track_id and colour_group values. Useful for example for plotting mean coverage stratified by genotype (which is specified in the colour_group column) (default: TRUE).
connect_exons	Print lines that connect exons together. Set to FALSE when plotting peaks (default: TRUE).
transcript_label	If TRUE then transcript labels are printed above each transcript. (default: TRUE).
return_subplots_list	Instead of a joint plot return a list of subplots that can be joined together manually.
region_coords	Start and end coordinates of the region to plot, overrides flanking_length parameter.
coverage_type	Specifies if the read coverage is represented by either 'line', 'area' or 'both'. The 'both' option tends to give better results for wide regions. (default: area).

Value

Either object from cow_plot::plot_grid() function or a list of subplots (if return_subplots_list == TRUE)

Examples

```
require("dplyr")
require("GenomicRanges")
sample_data = dplyr::data_frame(sample_id = c("aipt_A", "aipt_C", "bima_A", "bima_C"),
    condition = factor(c("Naive", "LPS", "Naive", "LPS"), levels = c("Naive", "LPS")),
    scaling_factor = 1) %>%
  dplyr::mutate(bigWig = system.file("extdata", paste0(sample_id, ".str2.bw"), package = "wiggleplotr"))

track_data = dplyr::mutate(sample_data, track_id = condition, colour_group = condition)

selected_transcripts = c("ENST00000438495", "ENST00000392477") #Plot only two transcripts of the gens
## Not run:
plotCoverage(ncoa7_exons[selected_transcripts], ncoa7_cdss[selected_transcripts],
  ncoa7_metadata, track_data,
  heights = c(2,1), fill_palette = getGenotypePalette())

## End(Not run)
```

---

plotCoverageFromEnsembldb

Plot read coverage directly from ensembldb object.

Description

A wrapper around the plotCoverage function. See the documentation for ([plotCoverage](#)) for more information.

Usage

```
plotCoverageFromEnsembldb(ensembldb, gene_names, transcript_ids = NULL,
  ...)
```

Arguments

ensembldb	ensembldb object.
gene_names	List of gene names to be plotted.
transcript_ids	Optional list of transcript ids to be plotted.
...	Additional parameters to be passed to plotCoverage.

Value

ggplot2 object

Examples

```
require("EnsDb.Hsapiens.v86")
require("dplyr")
require("GenomicRanges")
sample_data = dplyr::data_frame(sample_id = c("aipt_A", "aipt_C", "bima_A", "bima_C"),
 condition = factor(c("Naive", "LPS", "Naive", "LPS"), levels = c("Naive", "LPS")),
 scaling_factor = 1) %>%
 dplyr::mutate(bigWig = system.file("extdata", paste0(sample_id, ".str2.bw"), package = "wiggleplotr"))

track_data = dplyr::mutate(sample_data, track_id = condition, colour_group = condition)
## Not run:
plotCoverageFromEnsembldb(EnsDb.Hsapiens.v86, "NCOA7", transcript_ids = c("ENST00000438495", "ENST00000392477"),
track_data, heights = c(2,1), fill_palette = getGenotypePalette())

## End(Not run)
```

plotCoverageFromUCSC *Plot read coverage directly from UCSC OrgDb and TxDb objects.*

Description

A wrapper around the plotCoverage function. See the documentation for ([`plotCoverage`](plotCoverage)) for more information.

Usage

```
plotCoverageFromUCSC(orgdb, txdb, gene_names, transcript_ids = NULL, ...)
```

Arguments

orgdb	UCSC OrgDb object.
txdb	UCSC TxDb obejct.
gene_names	List of gene names to be plotted.
transcript_ids	Optional list of transcript ids to be plotted.
...	Additional parameters to be passed to plotCoverage.

Value

ggplot2 object

Examples

```
require("dplyr")
require("GenomicRanges")
require("org.Hs.eg.db")
require("TxDb.Hsapiens.UCSC.hg38.knownGene")

orgdb = org.Hs.eg.db
txdb = TxDb.Hsapiens.UCSC.hg38.knownGene

sample_data = dplyr::data_frame(sample_id = c("aipt_A", "aipt_C", "bima_A", "bima_C"),
 condition = factor(c("Naive", "LPS", "Naive", "LPS"), levels = c("Naive", "LPS")),
 scaling_factor = 1) %>%
 dplyr::mutate(bigWig = system.file("extdata", paste0(sample_id, ".str2.bw"), package = "wiggleplotr"))

track_data = dplyr::mutate(sample_data, track_id = condition, colour_group = condition)
## Not run:
#Note: This example does not work, becasue UCSC and Ensembl use different chromosome names
plotCoverageFromUCSC(orgdb, txdb, "NCOA7", transcript_ids = c("ENST00000438495.6", "ENST00000368357.7"),
track_data, heights = c(2,1), fill_palette = getGenotypePalette())

## End(Not run)
```

plotTranscripts *Quickly plot transcript structure without read coverage tracks*

Description

Quickly plot transcript structure without read coverage tracks

Usage

```
plotTranscripts(exons, cdss = NULL, transcript_annotations = NULL,
  rescale_introns = TRUE, new_intron_length = 50,
  flanking_length = c(50, 50), connect_exons = TRUE,
  transcript_label = TRUE, region_coords = NULL)
```

Arguments

exons
: list of GRanges objects, each object containing exons for one transcript. The list must have names that correspond to transcript_id column in transript_annotations data.frame.

cdss
: list of GRanges objects, each object containing the coding regions (CDS) of a single transcript. The list must have names that correspond to transcript_id column in transript_annotations data.frame. If cdss is not specified then exons list will be used for both arguments. (default: NULL)

transcript_annotations
: Data frame with at least three columns: transcript_id, gene_name, strand. Used to construct transcript labels. (default: NULL)

rescale_introns
: Specifies if the introns should be scaled to fixed length or not. (default: TRUE)

new_intron_length
: length (bp) of introns after scaling. (default: 50)

flanking_length
: Lengths of the flanking regions upstream and downstream of the gene. (default: c(50,50))

connect_exons
: Print lines that connect exons together. Set to FALSE when plotting peaks (default: TRUE).

transcript_label
: If TRUE then transcript labels are printed above each transcript. (default: TRUE).

region_coords
: Start and end coordinates of the region to plot, overrides flanking_length parameter.

Value

ggplot2 object

Examples

```
plotTranscripts(ncoa7_exons, ncoa7_cdss, ncoa7_metadata, rescale_introns = FALSE)
```

---

plotTranscriptsFromEnsembldb

Plot transcripts directly from ensembldb object.

Description

A wrapper around the plotTranscripts function. See the documentation for ([plotTranscripts](#)) for more information.

Usage

```
plotTranscriptsFromEnsembldb(ensembldb, gene_names,
  transcript_ids = NULL, ...)
```

Arguments

ensembldb	ensembldb object.
gene_names	List of gene names to be plotted.
transcript_ids	Optional list of transcript ids to be plotted.
...	Additional parameters to be passed to plotTranscripts

Value

ggplot2 object

Examples

```
require("EnsDb.Hsapiens.v86")
plotTranscriptsFromEnsembldb(EnsDb.Hsapiens.v86, "NCOA7", transcript_ids = c("ENST00000438495", "ENST00000392477
```

---

plotTranscriptsFromUCSC

Plot transcripts directly from UCSC OrgDb and TxDb objects.

Description

A wrapper around the plotTranscripts function. See the documentation for ([plotTranscripts](#)) for more information. Note that this function is much slower than ([plotTranscripts](#)) or ([plotTranscriptsFromEnsembldb](#)) functions, because indivudally extracting exon coordinates from txdb objects is quite inefficient.

Usage

```
plotTranscriptsFromUCSC(orgdb, txdb, gene_names, transcript_ids = NULL,
   ...)
```

Arguments

orgdb	UCSC OrgDb object.
txdb	UCSC TxDb obejct.
gene_names	List of gene genaes to be plot.
transcript_ids	Optional list of transcript ids to be plot. (default = NULL)
...	Additional parameters to be passed to plotTranscripts

Value

Transcript plot.

Examples

```
#Load OrgDb and TxDb objects with UCSC gene annotations
require("org.Hs.eg.db")
require("TxDb.Hsapiens.UCSC.hg38.knownGene")
orgdb = org.Hs.eg.db
txdb = TxDb.Hsapiens.UCSC.hg38.knownGene

plotTranscriptsFromUCSC(orgdb, txdb, "NCOA7", transcript_ids = c("ENST00000438495.6", "ENST00000368357.7"))
```

---

wiggleplotr *wiggleplotr*

Description

wiggleplotr package provides tools to visualise transcript annotations (`plotTranscripts`) and plot sequencing read coverage over annotated transcripts (`plotCoverage`).

Details

You can also use covenient wrapper functions (`plotTranscriptsFromEnsembldb`), (`plotCoverageFromEnsembldb`), (`plotTranscriptsFromUCSC`) and (`plotCoverageFromUCSC`).

To learn more about wiggleplotr, start with the vignette: browseVignettes(package = "wiggleplotr")

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