Package ‘wiggleplotr’

May 4, 2024

Title Make read coverage plots from BigWig files

Version 1.28.0

Author Kaur Alasoo [aut, cre]

Maintainer Kaur Alasoo <kaur.alasoo@gmail.com>

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

License Apache License 2.0

LazyData true

RoxygenNote 6.1.1

Suggests knitr, markdown, biomaRt, GenomicFeatures, testthat, ensemblDb, Ensembl.Hsapiens.v86, org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg38.knownGene, AnnotationDbi, AnnotationFilter

VignetteBuilder knitr

biocViews Immunology, Coverage, RNASeq, ChIPSeq, Sequencing, Visualization, GeneExpression, Transcription, AlternativeSplicing

git_url https://git.bioconductor.org/packages/wiggleplotr

git_branch RELEASE_3_19

git_last_commit 0bcb1de

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-03
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

**Description**

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

**Usage**

```r
code = 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 structure plots using cowplot::plot_grid().

**Value**

ggplot2 object

**Examples**

```r
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

**Description**

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

**Usage**

```r
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/

---

**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 transcript_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 transcript_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))
plotCoverage

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

```r
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("ENST00000392477", "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) for more information.

Usage

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

Arguments

orgdb         UCSC OrgDb object.
txdb          UCSC TxDb 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

```r
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, because 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 transcript_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 transcript_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

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

### Description

A wrapper around the `plotTranscripts` function. See the documentation for `plotTranscripts` for more information.

### Usage

```r
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

```r
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 individually extracting exon coordinates from txdb objects is quite inefficient.

**Usage**

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

**Arguments**

- `orgdb` : UCSC OrgDb object.
- `txdb` : UCSC TxDb object.
- `gene_names` : List of gene names 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**

```r
#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"))
```
Description

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

Details

You can also use convenient wrapper functions (\texttt{plotTranscriptsFromEnsembldb}), (\texttt{plotCoverageFromEnsembldb}), (\texttt{plotTranscriptsFromUCSC}) and (\texttt{plotCoverageFromUCSC}).

To learn more about wiggleplotr, start with the vignette: \texttt{browseVignettes(package = "wiggleplotr")}
Index

* datasets
  - ncoa7_cdss, 3
  - ncoa7_exons, 4
  - ncoa7_metadata, 4

getGenotypePalette, 2

makeManhattanPlot, 3

ncoa7_cdss, 3
ncoa7_exons, 4
ncoa7_metadata, 4

pasteFactors, 5
plotCoverage, 5, 8, 9, 13
plotCoverageFromEnsemblDb, 8, 13
plotCoverageFromUCSC, 9, 13
plotTranscripts, 10, 11–13
plotTranscriptsFromEnsemblDb, 11, 12, 13
plotTranscriptsFromUCSC, 12, 13

wiggleplotr, 13
wiggleplotr-package (wiggleplotr), 13