Package ‘wiggleplotr’

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Title  Make read coverage plots from BigWig files
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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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Suggests  knitr, rmarkdown, biomaRt, GenomicFeatures, testthat, ensemblDb, EnsDb.Hsapiens.v86, org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg38.knownGene, AnnotationDbi, AnnotationFilter
VignetteBuilder  knitr
biocViews  ImmunoOncology, Coverage, RNASeq, ChIPSeq, Sequencing, Visualization, GeneExpression, Transcription, AlternativeSplicing
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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

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

### Arguments

- `old` 
  Return old colour palette (now deprecated).

### Value

Vector of three colours.

### Examples

```r
getGenotypePalette()
```
### makeManhattanPlot

**Make a Manhattan plot of p-values**

#### 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
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

gglot2 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

**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

```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 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.
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))
alpha  Transparency (alpha) value for the read coverage tracks. Useful to set to some-
thing < 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 (de-
fault: 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 manu-
ally.

region_coords  Start and end coordinates of the region to plot, overrides flanking_length param-
eter.

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**

```r
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**

```r
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(sample_data, 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) 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**

```
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 (de-
fault: 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 param-
eter.

Value

ggplot2 object
Examples

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

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 indivudually 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 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

# 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 covenient wrapper functions (\texttt{plotTranscriptsFromEnsemblDb}), (\texttt{plotCoverageFromEnsemblDb}), (\texttt{plotTranscriptsFromUCSC}) and (\texttt{plotCoverageFromUCSC}).

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