

# Package ‘wigggleplotr’

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**Title** Make read coverage plots from BigWig files  
**Version** 1.33.0  
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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

|                              |   |
|------------------------------|---|
| getGenotypePalette . . . . . | 2 |
| makeManhattanPlot . . . . .  | 2 |

|                                        |           |
|----------------------------------------|-----------|
| ncoa7_cdss . . . . .                   | 3         |
| ncoa7_exons . . . . .                  | 4         |
| ncoa7_metadata . . . . .               | 4         |
| pasteFactors . . . . .                 | 5         |
| plotCoverage . . . . .                 | 5         |
| plotCoverageFromEnsemblDb . . . . .    | 7         |
| plotCoverageFromUCSC . . . . .         | 8         |
| plotTranscripts . . . . .              | 9         |
| plotTranscriptsFromEnsemblDb . . . . . | 10        |
| plotTranscriptsFromUCSC . . . . .      | 10        |
| wiggleplotr . . . . .                  | 11        |
| <b>Index</b>                           | <b>12</b> |

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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()

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|                   |                                    |
|-------------------|------------------------------------|
| makeManhattanPlot | Make a Manahattan plot of p-values |
|-------------------|------------------------------------|

---

**Description**

The Manhattan plots is compatible with wiggleplotr 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**

ggplot2 object

**Examples**

```
data = dplyr::data_frame(track_id = "GWAS", pos = sample(c(1:1000), 200), p_nominal = runif(200, min = 0.000000)
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 | <i>Exons from 9 protein coding transcripts of NCOA7</i> |
|-------------|---------------------------------------------------------|

---

**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 | <i>Gene metadata for NCOA7</i> |
|----------------|--------------------------------|

---

**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 | <i>Paste two factors together and preserved their joint order.</i> |
|--------------|--------------------------------------------------------------------|

---

**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 | <i>Plot read coverage across genomic regions</i> |
|--------------|--------------------------------------------------|

---

**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: <ul style="list-style-type: none"> <li>• sample_id - unique id for each sample.</li> <li>• 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.</li> <li>• bigWig - path to the bigWig file.</li> <li>• scaling_factor - normalisation factor for each sample, useful if different samples sequenced to different depth and bigWig files not normalised for that.</li> <li>• colour_group - additional column to group samples into, is used as the colour of the coverage track.</li> </ul> |
| 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 = "wigglyplotr"))

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(ensemldb, gene_names, transcript_ids = NULL,
  ...)
```

**Arguments**

|                |                                                     |
|----------------|-----------------------------------------------------|
| ensemldb       | ensemldb 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 = "wigglyplotr"))

track_data = dplyr::mutate(sample_data, track_id = condition, colour_group = condition)
## Not run:
plotCoverageFromEnsemblDb(EnsDb.Hsapiens.v86, "NCOA7", transcript_ids = c("ENST00000438495", "ENST0000039247"),
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

|                             |                                                                   |
|-----------------------------|-------------------------------------------------------------------|
| <code>orgdb</code>          | UCSC OrgDb object.                                                |
| <code>txdb</code>           | UCSC TxDb object.                                                 |
| <code>gene_names</code>     | List of gene names to be plotted.                                 |
| <code>transcript_ids</code> | Optional list of transcript ids to be plotted.                    |
| <code>...</code>            | Additional parameters to be passed to <code>plotCoverage</code> . |

## 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("a1pt_A", "a1pt_C", "b1ma_A", "b1ma_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 = "wigglyplotr"))

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 | <i>Quickly plot transcript structure without read coverage tracks</i> |
|-----------------|-----------------------------------------------------------------------|

---

## 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

```
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", "ENST0000039
```

---

```
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

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

**Arguments**

|                             |                                                                    |
|-----------------------------|--------------------------------------------------------------------|
| <code>orgdb</code>          | UCSC OrgDb object.                                                 |
| <code>txdb</code>           | UCSC TxDb object.                                                  |
| <code>gene_names</code>     | List of gene names to be plot.                                     |
| <code>transcript_ids</code> | Optional list of transcript ids to be plot. (default = NULL)       |
| <code>...</code>            | Additional parameters to be passed to <code>plotTranscripts</code> |

**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"))
```

---

wigglyplotr

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*wigglyplotr*


---

**Description**

wigglyplotr package provides tools to visualise transcript annotations ([plotTranscripts](#)) and plot sequencing read coverage over annotated transcripts ([plotCoverage](#)).

**Details**

You can also use convenient wrapper functions ([plotTranscriptsFromEnsemblDb](#)), ([plotCoverageFromEnsemblDb](#)), ([plotTranscriptsFromUCSC](#)) and ([plotCoverageFromUCSC](#)).

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

# Index

## \* datasets

- ncoa7\_cdss, [3](#)
- ncoa7\_exons, [4](#)
- ncoa7\_metadata, [4](#)

getGenotypePalette, [2](#)

makeManhattanPlot, [2](#)

ncoa7\_cdss, [3](#)

ncoa7\_exons, [4](#)

ncoa7\_metadata, [4](#)

pasteFactors, [5](#)

plotCoverage, [5](#), [7](#), [8](#), [11](#)

plotCoverageFromEnsemblDb, [7](#), [11](#)

plotCoverageFromUCSC, [8](#), [11](#)

plotTranscripts, [9](#), [10](#), [11](#)

plotTranscriptsFromEnsemblDb, [10](#), [10](#), [11](#)

plotTranscriptsFromUCSC, [10](#), [11](#)

wiggleplotr, [11](#)

wiggleplotr-package (wiggleplotr), [11](#)