

# Package ‘wiggplotr’

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

**Version** 1.35.2

**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 ( $\geq 3.6$ )

**Imports** dplyr, ggplot2 ( $\geq 2.2.0$ ), GenomicRanges, rtracklayer, cowplot, assertthat, purrr, S4Vectors, IRanges, GenomeInfoDb

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## Contents

extractCoverageData	2
getGenotypePalette	4
makeManhattanPlot	4
ncoa7_cdss	5
ncoa7_exons	5
ncoa7_metadata	6
pasteFactors	6
plotCoverage	7
plotCoverageData	9
plotCoverageFromEnsemblDb	10
plotCoverageFromUCSC	11
plotTranscripts	12
plotTranscriptsFromEnsemblDb	13
plotTranscriptsFromUCSC	14
wiggleplotr	15
<b>Index</b>	<b>16</b>

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extractCoverageData	<i>Extract read coverage data from the bigWig files</i>
---------------------	---

---

### Description

Does not work on Windows, because rtracklayer cannot read BigWig files on Windows.

### Usage

```
extractCoverageData(
  exons,
  cdss = NULL,
  transcript_annotatons = NULL,
  track_data,
  rescale_introns = TRUE,
  new_intron_length = 50,
  flanking_length = c(50, 50),
  plot_fraction = 0.1,
  mean_only = 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_annotatons 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_annotatons data.frame. If cdss is not specified then exons list will be used for both arguments. (default: NULL).

transcript_annotatations	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 overlaid 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)
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).
region_coords	Start and end coordinates of the region to plot, overrides flanking_length parameter. The 'both' option tends to give better results for wide regions. (default: area).

**Value**

List containing all of the necessary data for the plotCoverageData function ()

**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:
extractCoverageData(ncoa7_exons[selected_transcripts], ncoa7_cdss[selected_transcripts], ncoa7_metadata, track_data)
## End(Not run)
```

---

getGenotypePalette	<i>Returns a three-colour palette suitable for visualising read coverage stratified by genotype</i>
--------------------	---

---

**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	<i>Make a Manhattan plot of p-values</i>
-------------------	--

---

**Description**

The Manhattan plots is compatible with wiggpleplotr read coverage and transcript structure 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 structure 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

*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	<i>Plot read coverage across a genomic region</i>
--------------	---

---

## Description

Also supports rescaling introns to constant length. Extracts read coverage from bigWig files with `extractCoverageData` and plots it with `plotCoverageData`. Custom visualisations can be created by modifying the `plotCoverageData` function. Does not work on Windows, because `rtracklayer` cannot read BigWig files on Windows.

## Usage

```
plotCoverage(
  exons,
  cdss = NULL,
  transcript_annotiations = 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",
  show_legend = FALSE
)
```

## Arguments

- |                                      |  |
|--------------------------------------|--|
| <code>exons</code>                   | list of <code>GRanges</code> objects, each object containing exons for one transcript. The list must have names that correspond to <code>transcript_id</code> column in <code>transcript_annotiations</code> <code>data.frame</code> .   |
| <code>cdss</code>                    | list of <code>GRanges</code> objects, each object containing the coding regions (CDS) of a single transcript. The list must have names that correspond to <code>transcript_id</code> column in <code>transcript_annotiations</code> <code>data.frame</code> . If <code>cdss</code> is not specified then <code>exons</code> list will be used for both arguments. (default: <code>NULL</code> ). |
| <code>transcript_annotiations</code> | <code>Data frame</code> with at least three columns: <code>transcript_id</code> , <code>gene_name</code> , <code>strand</code> . Used to construct transcript labels. (default: <code>NULL</code> )  |
| <code>track_data</code>              | <code>data.frame</code> with the metadata for the bigWig read coverage files. Must contain the following columns: <ul style="list-style-type: none"> <li><code>sample_id</code> - unique id for each sample.</li> </ul>  |

- track\_id - if multiple samples (bigWig files) have the same track\_id they will be overlaid 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).
show_legend	display legend for the colour_group next to the read coverage plot (default: FALSE).

### 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)

```

---

plotCoverageData      *Plot read coverage across a genomic region*

---

**Description**

Does not work on Windows, because rtracklayer cannot read BigWig files on Windows.

**Usage**

```

plotCoverageData(
  coverage_data_list,
  heights = c(0.75, 0.25),
  alpha = 1,
  fill_palette = c("#a1dab4", "#41b6c4", "#225ea8"),
  connect_exons = TRUE,
  transcript_label = TRUE,
  return_subplots_list = FALSE,
  coverage_type = "area",
  show_legend = FALSE
)

```

**Arguments**

coverage\_data\_list

List of required from the extractCoverageData function:

- exons - list of GRanges objects, each object containing exons for one transcript.
- cdss - list of GRanges objects, each object containing the coding regions (CDS) of a single transcript.
- plotting\_annotatons - Transcript labels for plotting.
- tx\_annotatons - Transcript coordinates for plotting.
- xlabel - Label of the x-axis.

- coverage\_df - Read coverage data frame.
- limits - x-axis limits.

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.
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.
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).
show_legend	display legend for the colour_group next to the read coverage plot (default: FALSE).

### 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:
cov_data = extractCoverageData(ncoa7_exons[selected_transcripts], ncoa7_cdss[selected_transcripts], ncoa7_me
plotCoverageData(cov_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("aigt_A", "aigt_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**

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 = "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

*Quickly plot transcript structure without read coverage tracks*

---

**Description**

Quickly plot transcript structure without read coverage tracks

**Usage**

```
plotTranscripts(
  exons,
  cdss = NULL,
  transcript_annotatons = 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_annotatons 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_annotatons data.frame. If cdss is not specified then exons list will be used for both arguments. (default: NULL)
transcript_annotatons	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**

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 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**

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"))
```

---

*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 convenient wrapper functions ([plotTranscriptsFromEnsemblDb](#)), ([plotCoverageFromEnsemblDb](#)), ([plotTranscriptsFromUCSC](#)) and ([plotCoverageFromUCSC](#)).

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

# Index

## \* datasets

- ncoa7\_cdss, [5](#)
- ncoa7\_exons, [5](#)
- ncoa7\_metadata, [6](#)

extractCoverageData, [2](#)

getGenotypePalette, [4](#)

makeManhattanPlot, [4](#)

ncoa7\_cdss, [5](#)

ncoa7\_exons, [5](#)

ncoa7\_metadata, [6](#)

pasteFactors, [6](#)

plotCoverage, [7](#), [11](#), [15](#)

plotCoverageData, [9](#)

plotCoverageFromEnsemblDb, [10](#), [15](#)

plotCoverageFromUCSC, [11](#), [15](#)

plotTranscripts, [12](#), [13–15](#)

plotTranscriptsFromEnsemblDb, [13](#), [14](#), [15](#)

plotTranscriptsFromUCSC, [14](#), [15](#)

wiggleplotr, [15](#)