

# Package ‘tidyCoverage’

February 4, 2025

**Title** Extract and aggregate genomic coverage over features of interest

**Version** 1.3.0

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**Description** `tidyCoverage` framework enables tidy manipulation of collections of genomic tracks and features using `tidySummarizedExperiment` methods. It facilitates the extraction, aggregation and visualization of genomic coverage over individual or thousands of genomic loci, relying on `CoverageExperiment` and `AggregatedCoverage` classes. This accelerates the integration of genomic track data in genomic analysis workflows.

**License** MIT + file LICENSE

**URL** <https://github.com/js2264/tidyCoverage>

**BugReports** <https://github.com/js2264/tidyCoverage/issues>

**biocViews** Software, Sequencing, Coverage,

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Depends** R (>= 4.3.0), SummarizedExperiment

**Imports** S4Vectors, IRanges, GenomicRanges, GenomeInfoDb, BiocParallel, BiocIO, rtracklayer, methods, tidy, ggplot2, dplyr, fansi, pillar, rlang, scales, cli, purrr, vctrs, stats

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AggregatedCoverage	<i>aggregate</i>
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## Description

Bin coverage contained in a CoverageExperiment into an AggregatedCoverage object.

## Usage

```
## S4 method for signature 'CoverageExperiment'
aggregate(x, bin = 1, ...)
```

## Arguments

<code>x</code>	a CoverageExperiment object
<code>bin</code>	an integer to bin each assay by. The width of the AggregatedCoverage object should be a multiple of bin.
<code>...</code>	ignored

## Value

an AggregatedCoverage object

## Examples

```
data(ce)
aggregate(ce, bin = 10)
```

---

as\_tibble-methods      *as\_tibble*


---

**Description**

Coerce an CoverageExperiment or AggregatedCoverage object into a tibble

**Usage**

```
## S3 method for class 'AggregatedCoverage'
as_tibble(x, ...)
```

**Arguments**

```
x                    an CoverageExperiment object
...                  ignored
```

**Value**

tibble

**Examples**

```
data(ac)
as_tibble(ac)
```

---

CoverageExperiment      *CoverageExperiment*


---

**Description**

```
#' @description
```

**Usage**

```
CoverageExperiment(tracks, features, ...)

coarsen(x, window, ...)

## S4 method for signature 'BigWigFileList,GRangesList'
CoverageExperiment(
  tracks,
  features,
  width = NULL,
  center = FALSE,
  scale = FALSE,
```

```
    ignore.strand = TRUE,  
    window = 1,  
    BPPARAM = BiocParallel::bpparam()  
  )  
  
## S4 method for signature 'BigWigFileList,GRanges'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'BigWigFileList,list'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'BigWigFile,GRangesList'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'BigWigFile,GRanges'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'BigWigFile,list'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'list,GRangesList'  
CoverageExperiment(  
  tracks,  
  features,  
  width = NULL,  
  center = FALSE,  
  scale = FALSE,  
  ignore.strand = TRUE,  
  window = 1,  
  BPPARAM = BiocParallel::bpparam()  
)  
  
## S4 method for signature 'list,GRanges'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'list,list'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'RleList,GRangesList'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'RleList,GRanges'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'RleList,list'  
CoverageExperiment(tracks, features, ...)  
  
## S4 method for signature 'CoverageExperiment'
```

```
coarsen(x, window = 1, BPPARAM = BiocParallel::bpparam())
```

### Arguments

tracks	A genomic track imported as a <code>RleList</code> or a <i>named</i> list of genomic tracks.
features	A set of features imported as <code>GRanges</code> or a <i>named</i> <code>GRangesList</code> .
...	Passed to the relevant method
x	a <code>CoverageExperiment</code> object
window	an integer to coarsen coverage by.
width	Width to resize each set of genomic features
scale, center	Logical, whether to scale and/or center tracks prior to summarization
ignore.strand	Logical, whether to not take the features strand information
BPPARAM	Passed to <code>BiocParallel</code> .

### Details

`CoverageExperiment` objects store coverages for individual tracks over different sets of features. The coverage assay contains a separate matrix for each combination of track x features. `CoverageExperiment` objects are instantiated using the `CoverageExperiment()` #' function, and can be coarsened using the `coarsen()` function.

### Value

A `CoverageExperiment` object

### Examples

```
library(rtracklayer)
library(purrr)
library(plyranges)
TSSs_bed <- system.file("extdata", "TSSs.bed", package = "tidyCoverage")
features <- import(TSSs_bed) |> filter(strand == '+')

#####
## 1. Creating a `CoverageExperiment` object from a single BigWigFile
#####

RNA_fwd <- system.file("extdata", "RNA.fwd.bw", package = "tidyCoverage")
tracks <- BigWigFile(RNA_fwd)
CoverageExperiment(tracks, features, width = 5000)

#####
## 2. Creating a `CoverageExperiment` object from a BigWigFileList
#####

RNA_rev <- system.file("extdata", "RNA.rev.bw", package = "tidyCoverage")
tracks <- BigWigFileList(list(RNA_fwd = RNA_fwd, RNA_rev = RNA_rev))
CoverageExperiment(tracks, features, width = 5000)
```

```
#####
## 3. Creating a `CoverageExperiment` object from imported bigwig files
#####

tracks <- list(
  RNA_fwd = system.file("extdata", "RNA.fwd.bw", package = "tidyCoverage"),
  RNA_rev = system.file("extdata", "RNA.rev.bw", package = "tidyCoverage")
) |> map(import, as = 'Rle')
CoverageExperiment(tracks, features, width = 5000)

#####
## 4. Correct for strandness when recovering coverage
#####

TSSs_bed <- system.file("extdata", "TSSs.bed", package = "tidyCoverage")
features <- list(
  TSS_fwd = import(TSSs_bed) |> filter(strand == '+'),
  TSS_rev = import(TSSs_bed) |> filter(strand == '-')
)
tracks <- list(
  RNA_fwd = system.file("extdata", "RNA.fwd.bw", package = "tidyCoverage"),
  RNA_rev = system.file("extdata", "RNA.rev.bw", package = "tidyCoverage")
) |> map(import, as = 'Rle')
CoverageExperiment(tracks, features, width = 5000, ignore.strand = FALSE)

#####
## Aggregating a `CoverageExperiment` object
#####
data(ce)
coarsen(ce, window = 10)
```

---

data

*Example CoverageExperiment and AggregatedCoverage objects*


---

## Description

Two example objects are provided in the tidyCoverage package:

- ce: a CoverageExperiment dataset containing stranded RNA-seq coverage (forward and reverse) over Scc1 peaks ( $\pm$  1kb).
- ac: an AggregatedCoverage object obtained with aggregate(ce).

## Usage

```
data(ce)
```

```
data(ac)
```

**Format**

CoverageExperiment object containing 1 features set and 2 tracks.

AggregatedCoverage object containing 1 features set and 2 tracks.

**Details**

Data was generated in yeast (S288c) and aligned to reference R64-1-1.

---

expand, CoverageExperiment

*Expand a CoverageExperiment object*

---

**Description**

A CoverageExperiment object can be coerced into a tibble using the tidySummarizedExperiment package, but this will not turn each coverage matrix into a "long" format. The expand function provided here allows one to coerce a CoverageExperiment object into a long data frame, and adds the ranges and seqnames to the resulting tibble.

**Usage**

```
## S3 method for class 'CoverageExperiment'  
expand(data, ..., .name_repair = NULL)
```

**Arguments**

```
data          a CoverageExperiment object  
..., .name_repair  
              ignored
```

**Value**

a tibble object

**Examples**

```
data(ce)  
ce  
  
expand(ce)
```

---

**ggplot-tidyCoverage** *Plotting functions*

---

**Description**

```
#' @description
```

**Usage**

```
geom_aggrcoverage(  
  mapping = NULL,  
  data = NULL,  
  ...,  
  unit = c("kb", "Mb", "b"),  
  ci = TRUE,  
  grid = FALSE,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)  
  
geom_coverage(  
  mapping = NULL,  
  data = NULL,  
  ...,  
  type = c("area", "line"),  
  unit = c("kb", "Mb", "b"),  
  grid = FALSE,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)  
  
scale_y_coverage()  
  
scale_x_genome(unit = c("kb", "Mb", "b"))
```

**Arguments**

mapping	Aesthetics for geom_*. By default, no color/fill aesthetic is specified, but they can be assigned to a variable with mapping = aes(...). Note that x and y are automatically filled.
data	Data frame passed to geom_*. Typically a CoverageExperiment object (expanded to a tibble) or a AggregatedCoverage object.
..., na.rm, show.legend, inherit.aes	Argument passed to ggplot internal functions



unit	Rounding of x axis (any of c('b', 'kb', 'Mb')).
ci	Should the confidence interval be plotted by <code>geom_aggrcoverage()</code> ? (default: TRUE)
grid	Should the plot grid be displayed? (default: FALSE).
type	Choose between "line" and "area" style for <code>geom_coverage()</code> .

## Details

Plotting functions for tidyCoverage objects

## Value

A ggplot object

## Examples

```
library(rtracklayer)
library(plyranges)
library(ggplot2)
library(purrr)
TSSs_bed <- system.file("extdata", "TSSs.bed", package = "tidyCoverage")
features <- list(
  TSS_fwd = import(TSSs_bed) |> filter(strand == '+'),
  TSS_rev = import(TSSs_bed) |> filter(strand == '-'),
  conv_sites = import(system.file("extdata", "conv_transcription_loci.bed", package = "tidyCoverage"))
)
tracks <- list(
  RNA_fwd = system.file("extdata", "RNA.fwd.bw", package = "tidyCoverage"),
  RNA_rev = system.file("extdata", "RNA.rev.bw", package = "tidyCoverage"),
  Sccl = system.file("extdata", "Sccl1.bw", package = "tidyCoverage")
) |> map(import, as = 'Rle')
ce <- CoverageExperiment(tracks, features, width = 5000, center = TRUE, scale = TRUE)
ac <- aggregate(ce)

#####
## 1. Plotting aggregated coverage
#####

ac |>
  as_tibble() |>
  ggplot() +
  geom_aggrcoverage(aes(col = track)) +
  facet_grid(track ~ features) +
  geom_vline(xintercept = 0, color = 'black', linetype = 'dashed', linewidth = 0.5)

#####
## 2. Plotting track coverages over individual loci
#####

ce2 <- CoverageExperiment(
  tracks,
```

```
GRangesList(list(locus1 = "II:400001-455000", locus2 = "IV:720001-775000"),
  window = 50
)
expand(ce2) |>
  mutate(coverage = ifelse(track != 'Sccl', scales::oob_squish(coverage, c(0, 50)), coverage)) |>
  ggplot() +
  geom_coverage(aes(fill = track)) +
  facet_grid(track~features, scales = 'free')
```

---

reexports

*Objects exported from other packages*


---

### Description

These objects are imported from other packages. Follow the links below to see their documentation.

**dplyr** [as\\_tibble](#)

**S4Vectors** [aggregate](#)

**tidyr** [expand](#)

### Value

Depending on the re-exported function

### Examples

```
1 + 1
```

---

show

*show*


---

### Description

show method for CoverageExperiment and AggregatedCoverage objects

### Usage

```
## S4 method for signature 'CoverageExperiment'
show(object)
```

```
## S4 method for signature 'AggregatedCoverage'
show(object)
```

```
## S3 method for class 'CoverageExperiment'
print(x, ..., n = NULL)
```

```
## S3 method for class 'AggregatedCoverage'  
print(x, ..., n = NULL)  
  
## S3 method for class 'tidyCoverageExperiment'  
tbl_format_header(x, setup, ...)  
  
## S3 method for class 'tidyAggregatedCoverage'  
tbl_format_header(x, setup, ...)
```

### Arguments

object	a CoverageExperiment or AggregatedCoverage object
x	Object to format or print.
...	Passed on to <code>tbl_format_setup()</code> .
n	Number of rows to show. If NULL, the default, will print all rows if less than the <code>print_max</code> option. Otherwise, will print as many rows as specified by the <code>print_min</code> option.
setup	a setup object returned from <code>pillar::tbl_format_setup()</code> .

### Value

Prints a message to the console describing the contents of the CoverageExperiment or AggregatedCoverage objects.

### Examples

```
data(ce)  
print(ce)  
data(ac)  
print(ac)
```

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