

# Package ‘tidyCoverage’

February 2, 2026

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

**Version** 1.7.1

**Date** 2023-11-09

**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

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**RoxygenNote** 7.3.3

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

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|                      |                                                                                        |
|----------------------|----------------------------------------------------------------------------------------|
| tidyCoverage-package | <i>tidyCoverage: Tidyomics-based analysis of coverage tracks over genomic features</i> |
|----------------------|----------------------------------------------------------------------------------------|

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Description

The tidyCoverage package provides a bridge between Bioconductor SummarizedExperiment objects and the tidyomics project.

Author(s)

Jacques Serizay

References

Serizay J, Koszul R., Epigenomics coverage data extraction and aggregation in R with tidyCoverage. Bioinformatics 40, btae487 (2024). [doi:10.1093/bioinformatics/btae487](https://doi.org/10.1093/bioinformatics/btae487)

See Also

Useful links:

- <https://github.com/js2264/tidyCoverage>
- Report bugs at <https://github.com/js2264/tidyCoverage/issues>

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|                    |                  |
|--------------------|------------------|
| AggregatedCoverage | <i>aggregate</i> |
|--------------------|------------------|

---

**Description**

Bin coverage contained in a CoverageExperiment into an AggregatedCoverage object.

**Usage**

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

**Arguments**

|     |                                                                                                          |
|-----|----------------------------------------------------------------------------------------------------------|
| x   | a CoverageExperiment object                                                                              |
| bin | an integer to bin each assay by. The width of the AggregatedCoverage object should be a multiple of bin. |
| ... | ignored                                                                                                  |

**Value**

an AggregatedCoverage object

**Examples**

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

---

|                              |
|------------------------------|
| as_tibble-AggregatedCoverage |
| <i>as_tibble</i>             |

---

**Description**

Coerce an CoverageExperiment or AggregatedCoverage object into a tibble

**Usage**

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

**Arguments**

|     |                                                                                           |
|-----|-------------------------------------------------------------------------------------------|
| x   | A data frame, list, matrix, or other object that could reasonably be coerced to a tibble. |
| ... | Unused, for extensibility.                                                                |

**Value**

tibble

**Row names**

The default behavior is to silently remove row names.

New code should explicitly convert row names to a new column using the `rownames` argument.

For existing code that relies on the retention of row names, call `pkgconfig::set_config("tibble::rownames" = NA)` in your script or in your package's `.onLoad()` function.

**Life cycle**

Using `as_tibble()` for vectors is superseded as of version 3.0.0, prefer the more expressive `as_tibble_row()` and `as_tibble_col()` variants for new code.

**See Also**

`tibble()` constructs a tibble from individual columns. `enframe()` converts a named vector to a tibble with a column of names and column of values. Name repair is implemented using `vctrs::vec_as_names()`.

**Examples**

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

---

|                    |                           |
|--------------------|---------------------------|
| CoverageExperiment | <i>CoverageExperiment</i> |
|--------------------|---------------------------|

---

**Description**

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.

**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 RleList or a <i>named</i> list of genomic tracks. |
| features      | A set of features imported as GRanges or a <i>named</i> GRangesList.            |
| ...           | Passed to the relevant method                                                   |
| x             | a CoverageExperiment 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 BiocParallel.                                                         |

### 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 data frame.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ...          | <p><a href="#">&lt;data-masking&gt;</a> Specification of columns to expand or complete. Columns can be atomic vectors or lists.</p> <ul style="list-style-type: none"> <li>• To find all unique combinations of x, y and z, including those not present in the data, supply each variable as a separate argument: <code>expand(df, x, y, z)</code> or <code>complete(df, x, y, z)</code>.</li> <li>• To find only the combinations that occur in the data, use <code>nesting</code>: <code>expand(df, nesting(x, y, z))</code>.</li> <li>• You can combine the two forms. For example, <code>expand(df, nesting(school_id, student_id), date)</code> would produce a row for each present school-student combination for all possible dates.</li> </ul> <p>When used with factors, <code>expand()</code> and <code>complete()</code> use the full set of levels, not just those that appear in the data. If you want to use only the values seen in the data, use <code>forcats::fct_drop()</code>.</p> <p>When used with continuous variables, you may need to fill in values that do not appear in the data: to do so use expressions like <code>year = 2010:2020</code> or <code>year = full_seq(year, 1)</code>.</p> |
| .name_repair | One of "check_unique", "unique", "universal", "minimal", "unique_quiet", or "universal_quiet". See <a href="#">vec_as_names()</a> for the meaning of these options.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

## Value

a tibble object

## Grouped data frames

With grouped data frames created by `dplyr::group_by()`, `expand()` operates *within* each group. Because of this, you cannot expand on a grouping column.

**See Also**

[complete\(\)](#) to expand list objects. [expand\\_grid\(\)](#) to input vectors rather than a data frame.

**Examples**

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

---

ggplot-tidyCoverage      *Plotting functions*

---

**Description**

Plotting functions for tidyCoverage objects. Two geoms are provided:

- `geom_coverage()`: for plotting coverages over individual loci.
- `geom_aggrcoverage()`: for plotting aggregated coverages with confidence intervals.

See the Details section for more information on the aesthetics used by each geom.

**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,  
  alpha = 0.6,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE,  
  raster = TRUE
```

```
)

scale_y_coverage()

scale_x_genome(unit = c("kb", "Mb", "b"))
```

### Arguments

|                                      |                                                                                                                                                                                                                                       |
|--------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mapping                              | Set of aesthetic mappings created by <code>aes()</code> . By default, no color/fill aesthetic is specified, but they can be assigned to a variable with <code>mapping = aes(...)</code> . Note that x and y are automatically filled. |
| data                                 | Data frame passed to <code>geom_*</code> . Typically a <code>CoverageExperiment</code> object (expanded to a tibble) or a <code>AggregatedCoverage</code> object.                                                                     |
| ..., na.rm, show.legend, inherit.aes | Argument passed to ggplot internal functions                                                                                                                                                                                          |
| unit                                 | Rounding of x axis (any of <code>c('b', 'kb', 'Mb')</code> ).                                                                                                                                                                         |
| 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> .                                                                                                                                                             |
| alpha                                | Transparency level for <code>geom_coverage()</code> (default: 0.6).                                                                                                                                                                   |
| raster                               | Should the plot be rasterized for faster rendering? (default: TRUE)                                                                                                                                                                   |

### Details

These geoms are drawn using `geom_line/ribbon/area()` so they support the same aesthetics: colour, linetype and linewidth. Both geoms also support the `unit` argument to control the x axis units (b, kb, Mb).

In addition, they each support additional arguments:

- `geom_coverage` uses a `type` argument to switch between line plot and area plots;
- `geom_aggrcoverage` uses a `ci` argument to toggle the confidence interval display.

### 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"),
  Scc1 = system.file("extdata", "Scc1.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 != 'Scc1', scales::oob_squish(coverage, c(0, 50)), coverage)) |>
  ggplot() +
  geom_coverage(aes(fill = track)) +
  facet_grid(track~features, scales = 'free')

```

---

|                   |                                                                          |
|-------------------|--------------------------------------------------------------------------|
| show-tidyCoverage | <i>show method for CoverageExperiment and AggregatedCoverage objects</i> |
|-------------------|--------------------------------------------------------------------------|

---

## Description

show method for CoverageExperiment and AggregatedCoverage objects

## Arguments

|        |                                                                        |
|--------|------------------------------------------------------------------------|
| object | a CoverageExperiment or AggregatedCoverage object                      |
| setup  | a setup object returned from <code>pillar::tbl_format_setup()</code> . |

**Value**

Prints a message to the console describing the contents of the `CoverageExperimentorAggregatedCoverage` objects.

**Examples**

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

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