Package ‘tidyCoverage’

January 30, 2026

Title Extract and aggregate genomic coverage over features of interest

Version 1.6.0

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.

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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, tidyr, ggplot2, dplyr, fansi, pillar, rlang, scales, cli, purrr, vctrs, stats

Suggests tidySummarizedExperiment, plyranges, TxDb.Hsapiens.UCSC.hg19.knownGene, AnnotationHub, GenomicFeatures, BiocStyle, hues, knitr, rmarkdown, sessioninfo, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

LazyData false

git_url https://git.bioconductor.org/packages/tidyCoverage

git_branch RELEASE_3_22

git_last_commit 56ab248

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-29

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Contents

`AggregatedCoverage` *aggregate*

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-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 `RleList` or a *named* list of genomic tracks.
`features`	A set of features imported as `GRanges` or a *named* `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.

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 (± 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 `geom_aggrcoverage()`? (default: TRUE)
`grid`	Should the plot grid by displayed? (default: FALSE).
`type`	Choose between "line" and "area" style for `geom_coverage()`.

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"),
    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')
```

`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 `tbl_format_setup()`.
`n`	Number of rows to show. If `NULL`, the default, will print all rows if less than the `print_max` option. Otherwise, will print as many rows as specified by the `print_min` option.
`setup`	a setup object returned from `pillar::tbl_format_setup()`.

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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