Package 'tidyCoverage'

January 20, 2026

Title Extract and aggregate genomic coverage over features of interest

Version 1.6.0

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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.

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

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

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pillar, rlang, scales, cli, purrr, vctrs, stats

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TxDb.Hsapiens.UCSC.hg19.knownGene, AnnotationHub,
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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 CoverageExperi-mentorAggregatedCoverage' objects.

Examples

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

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