Package: tidyCoverage (via r-universe)

November 1, 2026

Title Extract and aggregate genomic coverage over features of interest

Version 1.8.0

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 7.3.3

Depends R (>= 4.3.0), SummarizedExperiment

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

Suggests tidySummarizedExperiment, plyranges, TxDb.Mmusculus.UCSC.mm10.knownGene, AnnotationHub, GenomicFeatures, BiocStyle, hues, knitr, rmarkdown, sessioninfo, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

LazyData false

Config/pak/sysreqs libcairo2-dev libfontconfig1-dev libfreetype6-dev libfribidi-dev make libharfbuzz-dev libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libwebp-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

Date/Publication 2026-04-28 13:02:13 UTC

RemoteUrl https://github.com/bioc/tidyCoverage

RemoteRef RELEASE_3_23

RemoteSha b58be80181b28062086738b04cab5f3fe2d50905

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`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-AggregatedCoverage` *as_tibble*

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 *CoverageExperiment*

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 *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.

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 data frame.
...	<data-masking> Specification of columns to expand or complete. Columns can be atomic vectors or lists. • To find all unique combinations of x, y and z, including those not present in the data, supply each variable as a separate argument: expand(df, x, y, z) or complete(df, x, y, z).

- To find only the combinations that occur in the data, use `nesting`: `expand(df, nesting(x, y, z))`.
- You can combine the two forms. For example, `expand(df, nesting(school_id, student_id), date)` would produce a row for each present school-student combination for all possible dates.

When used with factors, `expand()` and `complete()` 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 `forcats::fct_drop()`.

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 `year = 2010:2020` or `year = full_seq(year,1)`.

`.name_repair` One of `"check_unique"`, `"unique"`, `"universal"`, `"minimal"`, `"unique_quiet"`, or `"universal_quiet"`. See `vec_as_names()` 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 aes(). 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().
alpha	Transparency level for geom_coverage() (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` *show method for* `CoverageExperiment` *and* `AggregatedCoverage` *objects*

Description

show method for `CoverageExperiment` and `AggregatedCoverage` objects

Arguments

`object`	a `CoverageExperiment` or `AggregatedCoverage` object
`setup`	a setup object returned from `pillar::tbl_format_setup()`.

Value

`Prints a message to the console describing the contents of the` CoverageExperimentor`AggregatedCoverage‘ objects.`

Examples

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

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