

Package ‘tidyCoverage’

January 20, 2025

Title Extract and aggregate genomic coverage over features of interest

Version 1.3.0

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 devel

git_last_commit defcab5
git_last_commit_date 2024-10-29
Repository Bioconductor 3.21
Date/Publication 2025-01-19
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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 SccI 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

<code>mapping</code>	Aesthetics for <code>geom_*</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.
<code>data</code>	Data frame passed to <code>geom_*</code> . Typically a <code>CoverageExperiment</code> object (expanded to a tibble) or a <code>AggregatedCoverage</code> object.
<code>..., na.rm, show.legend, inherit.aes</code>	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"),
  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 != '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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