

Package ‘tidyCoverage’

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Title Extract and aggregate genomic coverage over features of interest

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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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Author Jacques Serizay [aut, cre]

Maintainer Jacques Serizay <jacquessserizay@gmail.com>

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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-methods *as_tibble*

Description

Coerce an `CoverageExperiment` or `AggregatedCoverage` object into a `tibble`

Usage

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

Arguments

<code>x</code>	an <code>CoverageExperiment</code> object
<code>...</code>	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::bparam()  
)
```

```

## 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::bparam()
)

## 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::bparam())

```

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 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 ($\pm 1\text{kb}$).
- `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

<i>data</i>	a <i>CoverageExperiment</i> object
<i>..., .name_repair</i>	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 <code>mapping = aes(...)</code> . Note that x and y are automatically filled.
data	Data frame passed to geom_*. 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 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` object⁴

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')

```

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	<i>show</i>
------	-------------

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 <code>CoverageExperiment</code> or <code>AggregatedCoverage</code> object
x	Object to format or print.
...	Passed on to <code>tbl_format_setup()</code> .
n	Number of rows to show. If <code>NULL</code> , 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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