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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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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