

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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tidyCoverage-package *tidyCoverage: Tidyomics-based analysis of coverage tracks over genomic features*

Description

The tidyCoverage package provides a bridge between Bioconductor SummarizedExperiment objects and the tidyomics project.

Author(s)

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References

Serizay J, Koszul R., Epigenomics coverage data extraction and aggregation in R with tidyCoverage. *Bioinformatics* 40, btae487 (2024). doi:10.1093/bioinformatics/btae487

See Also

Useful links:

- <https://github.com/js2264/tidyCoverage>
- Report bugs at <https://github.com/js2264/tidyCoverage/issues>

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 <i>named</i> list of genomic tracks.
features	A set of features imported as GRanges or a <i>named</i> 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 (\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

<code>data</code>	A data frame.
<code>...</code>	<p><data-masking> Specification of columns to expand or complete. Columns can be atomic vectors or lists.</p> <ul style="list-style-type: none"> • To find all unique combinations of <code>x</code>, <code>y</code> and <code>z</code>, including those not present in the data, supply each variable as a separate argument: <code>expand(df, x, y, z)</code> or <code>complete(df, x, y, z)</code>. • To find only the combinations that occur in the data, use <code>nesting</code>: <code>expand(df, nesting(x, y, z))</code>. • You can combine the two forms. For example, <code>expand(df, nesting(school_id, student_id), date)</code> would produce a row for each present school-student combination for all possible dates. <p>When used with factors, <code>expand()</code> and <code>complete()</code> 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 <code>forcats::fct_drop()</code>.</p> <p>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 <code>year = 2010:2020</code> or <code>year = full_seq(year, 1)</code>.</p>
<code>.name_repair</code>	One of "check_unique", "unique", "universal", "minimal", "unique_quiet", or "universal_quiet". See <code>vec_as_names()</code> 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 <code>aes()</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.
data	Data frame passed to <code>geom_*</code> . 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 <code>c('b', 'kb', 'Mb')</code>).
ci	Should the confidence interval be plotted by <code>geom_aggrcoverage()</code> ? (default: TRUE)
grid	Should the plot grid by displayed? (default: FALSE).
type	Choose between "line" and "area" style for <code>geom_coverage()</code> .
alpha	Transparency level for <code>geom_coverage()</code> (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"),
  Sccl = system.file("extdata", "Sccl.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')
```

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 CoverageExperiment or AggregatedCoverage objects.

Examples

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

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