Package: tidyCoverage (via r-universe)

June 30, 2024

Title Extract and aggregate genomic coverage over features of interest

Version 1.1.0

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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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Depends R (>= 4.3.0), SummarizedExperiment

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BiocIO, rtracklayer, methods, tidyr, dplyr, fansi, pillar,
rlang, cli, purrr, vctrs, stats

Suggests tidySummarizedExperiment, plyranges, ggplot2,
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sessioninfo, testthat (>= 3.0.0)

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VignetteBuilder knitr

LazyData false

Repository https://bioc.r-universe.dev

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

RemoteRef HEAD

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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)
```

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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,
  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,
  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)
```

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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