Package: tidyCoverage (via r-universe)

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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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BugReports https://github.com/js2264/tidyCoverage/issues

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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-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Using `as_tibble()` for vectors is superseded as of version 3.0.0, prefer the more expressive `as_tibble_row()` and `as_tibble_col()` variants for new code.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 *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.

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 data frame.
`...`	<`data-masking`> Specification of columns to expand or complete. Columns can be atomic vectors or lists. • To find all unique combinations of `x`, `y` and `z`, including those not present in the data, supply each variable as a separate argument: `expand(df, x, y, z)` or `complete(df, x, y, z)`.

- To find only the combinations that occur in the data, use `nesting`: `expand(df, nesting(x, y, z))`.
- You can combine the two forms. For example, `expand(df, nesting(school_id, student_id), date)` would produce a row for each present school-student combination for all possible dates.

When used with factors, `expand()` and `complete()` 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 `forcats::fct_drop()`.

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 `year = 2010:2020` or `year = full_seq(year,1)`.

`.name_repair` One of `"check_unique"`, `"unique"`, `"universal"`, `"minimal"`, `"unique_quiet"`, or `"universal_quiet"`. See `vec_as_names()` 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 aes(). 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()`.
`alpha`	Transparency level for `geom_coverage()` (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"),
    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')
```

`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` CoverageExperimentorAggregatedCoverage‘ objects.

Examples

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

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