Package: SummarizedHeatmap (via r-universe)

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Title Heatmaps for SummarizedExperiment Objects

Version 1.0.0

Description Represents a heatmap as a SummarizedExperiment-derived object, holding a single assay together with its row and column annotations and any hierarchical clustering. Assay values, annotations, display order, and dendrograms stay synchronized as the object is subsetted or reclustered, so a heatmap's components cannot drift out of step with each other. Each visual component (the main heatmap, annotation strips, dendrograms) is returned as an ordinary ggplot2 plot, and these can be composed, laid out, and customized using patchwork.

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`SummarizedHeatmap-package`
SummarizedHeatmap

Description

A `SummarizedExperiment`-derived representation of clustered assays and their feature and sample annotations. Plotting functions return ordinary ggplot2 and patchwork objects that remain open to standard customization.

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See Also

`SummarizedHeatmap()`, `plotHeatmap()`, `SummarizedExperiment::SummarizedExperiment()`

`[,SummarizedHeatmap,ANY,ANY,ANY-method`
Subset a SummarizedHeatmap

Description

Subsetting follows SummarizedExperiment semantics. If row membership or order changes, the row dendrogram is cleared and row order resets to the natural order of the subset. The same rule applies independently to columns. Clustering for an unchanged dimension is preserved. Subsetting never reclusters implicitly; call `clusterRows()`, `clusterCols()`, or `clusterHeatmap()` when new clustering is desired.

Usage

```
## S4 method for signature 'SummarizedHeatmap,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]
```

Arguments

`x`	A SummarizedHeatmap object.
`i`	Row indices, names, or logical selector.
`j`	Column indices, names, or logical selector.
`...`	Additional subsetting arguments.
`drop`	Whether to drop dimensions. Defaults to `FALSE` to preserve the SummarizedHeatmap class.

Value

A valid SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(20), 5, dimnames = list(letters[1:5], LETTERS[1:4]))
x <- SummarizedHeatmap(mat)
x[1:3, 1:2]
```

assay-set-SummarizedHeatmap *Replace the assay of a SummarizedHeatmap*

Description

Assay replacement follows SummarizedExperiment semantics: dimensions and dimnames must be preserved. Because a stored dendrogram and its implied order are only valid for the assay values they were computed from, replacing the assay never silently reclusters. Instead, whenever a dendrogram is currently stored for an axis, it is cleared and that axis's order resets to its natural order; when no dendrogram is stored (e.g. a manually-supplied or default order), the existing order is left untouched. The same rule is applied independently to rows and columns. Call `clusterRows()`, `clusterCols()`, or `clusterHeatmap()` afterwards to recompute clustering against the new values.

Usage

```
## S4 replacement method for signature 'SummarizedHeatmap,missing'
assay(x, i, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'SummarizedHeatmap,numeric'
assay(x, i, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'SummarizedHeatmap,character'
assay(x, i, withDimnames = TRUE, ...) <- value
```

Arguments

x	A SummarizedHeatmap object.
i	Optional name or index of the assay to replace. Since a SummarizedHeatmap always holds exactly one assay, this must (when supplied) identify that single assay.
withDimnames	A logical value indicating whether value's dimnames must be respected. Passed through to the SummarizedExperiment method.
...	Additional arguments passed to the SummarizedExperiment method.
value	A numeric, non-complex matrix with the same dimensions and dimnames as the current assay.

Value

An updated, valid SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
x <- SummarizedHeatmap(mat)
assay(x) <- mat * 2
rowDendro(x)
```

assays-set-SummarizedHeatmap *Replace the assays of a SummarizedHeatmap*

Description

Assay replacement follows SummarizedExperiment semantics: dimensions and dimnames must be preserved. Because a stored dendrogram and its implied order are only valid for the assay values they were computed from, replacing the assay never silently reclusters. Instead, whenever a dendrogram is currently stored for an axis, it is cleared and that axis's order resets to its natural order; when no dendrogram is stored (e.g. a manually-supplied or default order), the existing order is left untouched. The same rule is applied independently to rows and columns. Call `clusterRows()`, `clusterCols()`, or `clusterHeatmap()` afterwards to recompute clustering against the new values.

Usage

```
## S4 replacement method for signature 'SummarizedHeatmap,list'
assays(x, withDimnames = TRUE, ...) <- value

## S4 replacement method for signature 'SummarizedHeatmap,SimpleList'
assays(x, withDimnames = TRUE, ...) <- value
```

Arguments

x	A SummarizedHeatmap object.
withDimnames	A logical value indicating whether value's dimnames must be respected. Passed through to the SummarizedExperiment method.
...	Additional arguments passed to the SummarizedExperiment method.
value	A list or SimpleList of exactly one assay, with the same dimensions and dimnames as the current assay.

Value

An updated, valid SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
x <- SummarizedHeatmap(mat)
assays(x) <- list(matrix = mat * 2)
rowDendro(x)
```

clusterCols *Cluster columns*

Description

Compute a hierarchical clustering across assay columns and update the stored column dendrogram and display order.

Usage

```
clusterCols(x, distMethod = "euclidean", hclustMethod = "average")
```

Arguments

x	A SummarizedHeatmap object.
distMethod	Distance method passed to stats::dist().
hclustMethod	Linkage method passed to stats::hclust().

Value

The updated SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
clusterCols(SummarizedHeatmap(mat))
```

clusterHeatmap *Cluster rows and columns*

Description

Cluster rows and columns

Usage

```
clusterHeatmap(x, distMethod = "euclidean", hclustMethod = "average")
```

Arguments

x	A SummarizedHeatmap object.
distMethod	Distance method passed to stats::dist().
hclustMethod	Linkage method passed to stats::hclust().

Value

The updated SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
clusterHeatmap(SummarizedHeatmap(mat))
```

`clusterRows` *Cluster rows*

Description

Compute a hierarchical clustering across assay rows and update the stored row dendrogram and display order. Clustering is deterministic for a fixed assay and set of methods.

Usage

```
clusterRows(x, distMethod = "euclidean", hclustMethod = "average")
```

Arguments

`x`	A SummarizedHeatmap object.
`distMethod`	Distance method passed to `stats::dist()`.
`hclustMethod`	Linkage method passed to `stats::hclust()`.

Value

The updated SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
clusterRows(SummarizedHeatmap(mat))
```

colDendro *Access stored column dendrogram*

Description

Access stored column dendrogram

Usage

```
colDendro(x)

## S4 method for signature 'SummarizedHeatmap'
colDendro(x)
```

Arguments

x	A SummarizedHeatmap object.

Value

A dendrogram, or NULL if columns are not clustered.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
colDendro(SummarizedHeatmap(mat))
```

colOrder *Access column display order*

Description

Access column display order

Usage

```
colOrder(x)

## S4 method for signature 'SummarizedHeatmap'
colOrder(x)
```

Arguments

x	A SummarizedHeatmap object.

Value

Integer column indices in display order.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
colOrder(SummarizedHeatmap(mat))
```

---

plotColData *Plot column annotations*

Description

Each selected column annotation is represented by an independent ggplot, labelled with its variable name as axis text next to the annotation tiles. A single variable returns a ggplot; multiple variables return an (unwrapped) patchwork stacking the independent plots (see `plotRowData()` for alignment and safe-composition details).

Usage

```
plotColData(
  x,
  vars = NULL,
  side = "right",
  tileColor = "white",
  palette = NULL,
  showNames = FALSE
)
```

Arguments

`x`	A SummarizedHeatmap object.
`vars`	Character vector of `rowData` names. A named vector uses its names as displayed labels.
`side`	Which side of the annotation tiles the variable-name label is drawn on: `"left"` or `"right"` for column annotations (the tiles are always laid out with column identifiers on the horizontal axis, matching the heatmap's columns, so the label sits on that axis's left or right edge). `"left"` places the label where it is more prone to clipping when combined with `patchwork::free(type = "space")`; see Details.
`tileColor`	Tile border colour.
`palette`	Optional named values passed to `scale_fill_manual()`.
`showNames`	Whether to display row or column names on the annotation axis.

Value

A ggplot for one variable, a patchwork for multiple variables, or a spacer when no column annotations are present.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
cd <- S4Vectors::DataFrame(
    group = c("A", "B", "A"), row.names = LETTERS[1:3]
)
plotColData(SummarizedHeatmap(mat, colData = cd))
```

---

plotColDendro *Plot the stored column dendrogram*

Description

Plot the stored column dendrogram

Usage

```
plotColDendro(x, side = "top", linewidth = 0.5)
```

Arguments

x	A SummarizedHeatmap object.
side	Side on which the dendrogram is oriented. The default places leaves toward the heatmap when shown to its left.
linewidth	Dendrogram line width.

Value

A ggplot object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
plotColDendro(SummarizedHeatmap(mat))
```

plotHeatmap *Compose a complete heatmap with patchwork*

Description

The component plots remain available through their individual plotting functions. This helper arranges them around the main heatmap panel, constructing the components in a deterministic order (the main heatmap, then column dendrogram, column annotation, then row dendrogram, row annotation) so that, when `collectGuides = TRUE`, their legends are always collected into the shared guide area in that same order, regardless of which side of the heatmap each panel is placed on. `guide_area()` (the `M` panel) only controls *where* the collected guides are drawn, not the order they are collected in; see `.orderPanelsForGuides()` for the ordering itself. Column annotation plots are stacked vertically. The row dendrogram and row annotation panels move to whichever side of the heatmap `rowDendroSide`/ `rowAnnotationSide` request (`"left"` or `"right"`, both defaulting to `"left"`); the column dendrogram and column annotation panels likewise move with `colDendroSide`/`colAnnotationSide` (`"top"` or `"bottom"`, both defaulting to `"top"`). When a dendrogram and its matching annotation share a side, the annotation sits adjacent to the heatmap and the dendrogram sits further out; by default this puts both on the same side for each axis. Pass named variable vectors to `rowVars` or `colVars` to control annotation strip labels; pass `NULL` to `rowAnnotationSide`/ `colAnnotationSide` to omit that annotation panel entirely. Any omitted panel – an annotation set to `NULL`, a dendrogram hidden with `showRowDendro`/`showColDendro = FALSE`, or a dendrogram that was never stored – is dropped from the grid rather than left as a blank but still-sized slot, so the remaining panels use the reclaimed space.

Usage

```
plotHeatmap(
  x,
  rowVars = NULL,
  colVars = NULL,
  showRowDendro = TRUE,
  showColDendro = TRUE,
  rowDendroSide = "left",
  colDendroSide = "top",
  rowAnnotationSide = "left",
  colAnnotationSide = "top",
  collectGuides = TRUE,
  guideWidth = 3,
  ...
)
```

Arguments

`x`	A SummarizedHeatmap object.
`rowVars`, `colVars`	Optional annotation variables to display. `NULL` includes all available variables.

showRowDendro, showColDendro
: Whether to display stored dendrograms.

rowDendroSide
: "left" or "right": which side of the heatmap the row dendrogram panel is placed on (and oriented toward).

colDendroSide
: "top" or "bottom": which side of the heatmap the column dendrogram panel is placed on (and oriented toward).

rowAnnotationSide, colAnnotationSide
: Which side of the heatmap the annotation panel is placed on, restricted to "left"/"right" (rows) or "top"/"bottom" (columns); this only controls panel placement; see Details for how it affects the variable-name label's position. "right" (rows) places the annotation's variable-name label where it can be clipped if the figure is too small; see Details. Set to NULL to omit the annotation panel entirely.

collectGuides
: Collect guides into a shared guide area.

guideWidth
: Relative width of the guide area column, on the same scale as the dendrogram/annotation (1) and heatmap body (8) column widths. Increase this when stacked legends (e.g. several annotation variables) overflow their column and collide with the heatmap's row labels or with each other.

...
: Additional arguments passed to plotHeatmapMain(), such as low/mid/high/midpoint (fill scale) or fillTitle (legend title). flip is not accepted here – flipping only the main panel would misalign it against the annotation and dendrogram panels arranged around it; call plotHeatmapMain() directly for a flipped main panel on its own.

Details

Each annotation strip's variable-name axis text is wrapped with patchwork::free(type = "space") so it packs tightly against the heatmap instead of forcing extra column/row width (see plotColData()/plotRowData() for the axis text itself). Because "space" reserves no room for that text, it can get clipped at the edge of the plotting device if there isn't enough surrounding space to draw it – most likely with the non-default rowAnnotationSide = "right", which anchors the row annotation's variable-name label at the bottom of its strip, where it competes for space with the heatmap's own column identifier labels (the column annotation's variable-name label always sits to the right of its strip, matching the heatmap's own row labels, regardless of colAnnotationSide). Increase the figure's height or width if labels are clipped in that configuration.

Value

A patchwork object.

Examples

```
mat <- matrix(
    rnorm(24), 6,
    dimnames = list(paste0("f", 1:6), paste0("s", 1:4))
)
x <- SummarizedHeatmap(mat)
plotHeatmap(x)
```

`plotHeatmapMain` *Plot the assay as a ggplot heatmap*

Description

The returned object is an ordinary ggplot and can be modified with standard ggplot2 layers and scales. The display follows the stored row and column orders.

Usage

```
plotHeatmapMain(
  x,
  tileColor = "white",
  high = "red3",
  mid = "white",
  low = "blue4",
  midpoint = 0,
  fillTitle = "Value",
  flip = FALSE
)
```

Arguments

`x`	A SummarizedHeatmap object.
`tileColor`	Tile border colour.
`high`, `mid`, `low`	Colours for high, midpoint, and low assay values.
`midpoint`	Assay value mapped to `mid`.
`fillTitle`	Title for the fill legend.
`flip`	If `TRUE`, transpose the visual orientation.

Value

A ggplot object.

Examples

```
mat <- matrix(
    rnorm(24), 6,
    dimnames = list(paste0("f", 1:6), paste0("s", 1:4))
)
plotHeatmapMain(SummarizedHeatmap(mat))
```

plotRowData *Plot row annotations*

Description

Each selected row annotation is represented by an independent ggplot, labelled with its variable name as axis text next to the annotation tiles (in addition to its legend title). A single variable returns a ggplot; multiple variables return an (unwrapped) patchwork stacking the independent plots, so the result stays aligned with sibling panels and its guides can still be collected by an enclosing `plot_layout(guides = "collect")` – see `plotHeatmap()`.

Usage

```
plotRowData(
  x,
  vars = NULL,
  side = "top",
  tileColor = "white",
  palette = NULL,
  showNames = FALSE
)
```

Arguments

x	A SummarizedHeatmap object.
vars	Character vector of `rowData` names. A named vector uses its names as displayed labels.
side	Which side of the annotation tiles the variable-name label is drawn on: `"top"` or `"bottom"` for row annotations (the tiles are always laid out with row identifiers on the vertical axis, matching the heatmap's rows, so the label sits on that narrow axis's top or bottom edge). `"bottom"` places the label where it is more prone to clipping when combined with `patchwork::free(type = "space")`; see Details.
tileColor	Tile border colour.
palette	Optional named values passed to `scale_fill_manual()`.
showNames	Whether to display row or column names on the annotation axis.

Details

Combining a multiple-variable result directly with another plot using patchwork operators (`+`, `/`, `|`) can silently flatten its panel list into the parent's, which may break a `plot_layout(heights = ...)`/`plot_layout(design = ...)` built around an expected panel count. Use `patchwork::wrap_plots(list(annotation, otherPlot), ...)` instead of an operator to combine them safely (this is how `plotHeatmap()` does it internally).

When composing a custom layout, wrap the result with `patchwork::free(type = "space")` so its variable-name axis text packs tightly against neighbouring panels instead of forcing extra column/row width (`plotHeatmap()` does this for every annotation strip). Because `"space"` reserves no room for that text, it can get clipped at the edge of the plotting device when there isn't enough surrounding space – most likely with `side = "right"` or `side = "bottom"`, where the (possibly rotated) label competes for space with other axis labels. Increase the figure's height or width if labels are clipped in that configuration.

Value

A ggplot for one variable, a patchwork for multiple variables, or a spacer when no row annotations are present.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
rd <- S4Vectors::DataFrame(
    kind = rep(c("gene", "control"), 2), row.names = letters[1:4]
)
plotRowData(SummarizedHeatmap(mat, rowData = rd))
```

---

plotRowDendro *Plot the stored row dendrogram*

Description

Plot the stored row dendrogram

Usage

```
plotRowDendro(x, side = "left", linewidth = 0.5)
```

Arguments

`x`	A SummarizedHeatmap object.
`side`	Side on which the dendrogram is oriented. The default places leaves toward the heatmap when shown to its left.
`linewidth`	Dendrogram line width.

Value

A ggplot object.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
plotRowDendro(SummarizedHeatmap(mat))
```

rowDendro *Access stored row dendrogram*

Description

Access stored row dendrogram

Usage

```
rowDendro(x)

## S4 method for signature 'SummarizedHeatmap'
rowDendro(x)
```

Arguments

x	A SummarizedHeatmap object.

Value

A dendrogram, or NULL if rows are not clustered.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
rowDendro(SummarizedHeatmap(mat))
```

rowOrder *Access row display order*

Description

Access row display order

Usage

```
rowOrder(x)

## S4 method for signature 'SummarizedHeatmap'
rowOrder(x)
```

Arguments

x	A SummarizedHeatmap object.

Value

Integer row indices in display order.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
rowOrder(SummarizedHeatmap(mat))
```

---

show,SummarizedHeatmap-method *Display a concise summary of a SummarizedHeatmap*

Description

Display a concise summary of a SummarizedHeatmap

Usage

```
## S4 method for signature 'SummarizedHeatmap'
show(object)
```

Arguments

object	A SummarizedHeatmap object.

Value

The method displays a summary and returns invisibly.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
show(SummarizedHeatmap(mat))
```

SummarizedHeatmap *Create a SummarizedHeatmap*

Description

Create a heatmap representation from a numeric matrix or from a single assay of a SummarizedExperiment object. Rows and columns are clustered by default when their sizes permit; stored orders are integer indices into the assay dimensions. Missing dimension names are filled with stable sequential identifiers when x is a matrix.

Usage

```
SummarizedHeatmap(
  x,
  assay = NULL,
  rowOrder = NULL,
  colOrder = NULL,
  clusterRows = TRUE,
  clusterCols = TRUE,
  distMethod = "euclidean",
  hclustMethod = "average",
  ...
)
```

Arguments

x	A numeric matrix, or a SummarizedExperiment object.
assay	When x is a SummarizedExperiment, the name or integer index of the assay to use. Required when x has more than one assay; optional but still validated when x has exactly one. Unused when x is a matrix. The selected assay's original name is preserved in the resulting SummarizedHeatmap (falling back to "matrix" when the source assay is unnamed).
rowOrder	Optional manual row order, as integer indices or row names. Supplying it leaves the row dendrogram unset and takes precedence over clusterRows.
colOrder	Optional manual column order, as integer indices or column names. Supplying it leaves the column dendrogram unset and takes precedence over clusterCols.
clusterRows	Whether to compute a row dendrogram and clustering order. Ignored (with no dendrogram computed) when rowOrder is supplied. When FALSE and rowOrder is not supplied, rows keep their natural order and no dendrogram is stored.
clusterCols	Whether to compute a column dendrogram and clustering order. Ignored (with no dendrogram computed) when colOrder is supplied. When FALSE and colOrder is not supplied, columns keep their natural order and no dendrogram is stored.
distMethod	Distance method passed to stats::dist().
hclustMethod	Linkage method passed to stats::hclust(). Defaults to average linkage, matching the original constructor.
...	Additional arguments passed to SummarizedExperiment::SummarizedExperiment(), such as rowData and colData. Only used when x is a matrix; ignored when x is a SummarizedExperiment, whose own annotations are preserved instead.

Details

A SummarizedHeatmap always holds exactly one assay. When x is a SummarizedExperiment with a single assay, that assay is used automatically. When it has multiple assays, assay must be supplied to select one by name or position. Either way, the selected assay's original name is preserved in the resulting SummarizedHeatmap; rowData, colData, and metadata are carried over from x unchanged.

Value

A valid SummarizedHeatmap object.

Examples

```
mat <- matrix(rnorm(24),
    nrow = 6,
    dimnames = list(paste0("feature", 1:6), paste0("sample", 1:4))
)
x <- SummarizedHeatmap(mat)
validObject(x)

se <- SummarizedExperiment::SummarizedExperiment(
    assays = list(counts = mat)
)
y <- SummarizedHeatmap(se)
validObject(y)
SummarizedExperiment::assayNames(y) # "counts", preserved from se
```

SummarizedHeatmap-class

SummarizedHeatmap class

Description

A single assay and its row and column annotations, display orders, and optional hierarchical clusterings. The class extends SummarizedExperiment but is restricted to exactly one assay; use SummarizedHeatmap() to build one from a matrix or from a SummarizedExperiment (selecting an assay when it holds more than one).

Slots

rowDendro Row dendrogram, or NULL when rows are not clustered.

colDendro Column dendrogram, or NULL when columns are not clustered.

rowOrder Integer indices giving row display order.

colOrder Integer indices giving column display order.

Examples

```
mat <- matrix(rnorm(12), 4, dimnames = list(letters[1:4], LETTERS[1:3]))
show(SummarizedHeatmap(mat))
```

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