Package 'ggsc'

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Title Visualizing Single Cell Data

Version 1.0.2

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`ggsc-package` *ggsc: Visualizing Single Cell Data*

Description

Useful functions to visualize single cell and spatial data. It supports both 'SingleCellExperiment' and 'Seurat' objects. It also supports visualizing the data using grammar of graphics implemented in 'ggplot2'.

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See Also

Useful links:

- https://github.com/YuLab-SMU/ggsc
- Report bugs at https://github.com/YuLab-SMU/ggsc/issues

`CalWkdeCpp` *Two-Dimensional Weighted Kernel Density Estimation And Mapping the Result To Original Dimension*

Description

Two-Dimensional Weighted Kernel Density Estimation And Mapping the Result To Original Dimension

Usage

```
CalWkdeCpp(x, w, l, h, adjust = 1, n = 400L)
```

Arguments

`x`	The 2-D coordinate matrix
`w`	The weighted sparse matrix, the number columns the same than the number rows than x.
`l`	The limits of the rectangle covered by the grid as c(xl, xu, yl, yu)
`h`	The vector of bandwidths for x and y directions, defaults to normal reference bandwidth (see bandwidth.nrd), A scalar value will be taken to apply to both directions (see ks::hpi).
`adjust`	numeric value to adjust to bandwidth, default is 1.
`n`	number of grid points in the two directions, default is 400.

`reexports` *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

ggplot2 `aes`, `theme`

Value

Depending on the re-exported function

sc_dim *sc_dim*

Description

sc_dim

Usage

```
sc_dim(
  object,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ...
)

## S4 method for signature 'Seurat'
sc_dim(
  object,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ...
)

## S4 method for signature 'SingleCellExperiment'
sc_dim(
  object,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ...
)
```

Arguments

object	Seurat object
dims	selected dimensions (must be a two-length vector) that are used in visualization
reduction	reduction method, default is NULL and will use the default setting store in the object

cells	selected cells to plot (default is all cells)
slot	slot to pull expression data from (e.g., 'count' or 'data')
mapping	aesthetic mapping
...	additional parameters pass to 'scattermore::geom_scattermore()'

Value

dimension reduction plot

See Also

geom_scattermore;

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP', mapping = aes(colour = Cell_Cycle))
p2 <- sc_dim(sce, reduction = 'UMAP')
f1 <- p1 + sc_dim_geom_label()
f2 <- p2 +
      sc_dim_geom_label(
        geom = shadowtext::geom_shadowtext,
        color='black',
        bg.color='white'
      )
```

---

sc_dim_count *sc_dim_count*

Description

sc_dim_count

Usage

```
sc_dim_count(sc_dim_plot)
```

Arguments

sc_dim_plot	dimension reduction plot of single cell data

Value

a bar plot to present the cell numbers of different clusters

See Also

sc_dim()

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p <- sc_dim(sce, reduction = 'UMAP')
p1 <- sc_dim_count(p)
```

---

sc_dim_geom_ellipse *sc_dim_geom_ellipse*

Description

sc_dim_geom_ellipse

Usage

```
sc_dim_geom_ellipse(mapping = NULL, level = 0.95, ...)
```

Arguments

mapping	aesthetic mapping
level	the level at which to draw an ellipse
...	additional parameters pass to the stat_ellipse

Value

layer of ellipse

See Also

stat_ellipse;

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP', mapping = aes(colour = Cell_Cycle))
p2 <- sc_dim(sce, reduction = 'UMAP')
f1 <- p1 + sc_dim_geom_ellipse()
```

---

sc_dim_geom_feature *sc_dim_geom_feature*

Description

sc_dim_geom_feature

Usage

```
sc_dim_geom_feature(
  object,
  features,
  dims = c(1, 2),
  ncol = 3,
  ...,
  .fun = function(.data) dplyr::filter(.data, .data$value > 0)
)
```

Arguments

object	Seurat or SingleCellExperiment object
features	selected features (i.e., genes)
dims	selected dimensions (must be a two-length vector) that are used in visualization
ncol	number of facet columns if 'length(features) > 1'
...	additional parameters pass to 'scattermore::geom_scattermore()'
.fun	user defined function that will be applied to selected features (default is to filter out genes with no expression values)

Value

layer of points for selected features

See Also

sc_feature()

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP')
set.seed(123)
genes <- rownames(sce) |> sample(6)
f1 <- p1 +
      sc_dim_geom_feature(
        object = sce,
        features = genes
      )
```

---

sc_dim_geom_label *sc_dim_geom_label*

Description

sc_dim_geom_label

Usage

```
sc_dim_geom_label(geom = ggplot2::geom_text, ...)
```

Arguments

geom	geometric layer (default: geom_text) to display the lables
...	additional parameters pass to the geom

Value

layer of labels

See Also

sc_dim_geom_label()

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP', mapping = aes(colour = Cell_Cycle))
p2 <- sc_dim(sce, reduction = 'UMAP')
f1 <- p1 + sc_dim_geom_label()
```

---

sc_dim_geom_sub *sc_dim_geom_subset*

Description

sc_dim_geom_subset

Usage

```
sc_dim_geom_sub(mapping = NULL, subset, .column = "ident", ...)
```

Arguments

mapping	aesthetic mapping
subset	subset of clusters to be displayed
.column	which column represents cluster (e.g., 'ident')
...	additional parameters pass to sc_geom_point

Value

plot with a layer of specified clusters

See Also

sc_dim_geom_sub

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
```

```
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP')
f1 <- p1 + sc_dim_geom_sub(subset = c(1, 2), .column = 'label')
```

---

sc_dim_sub *sc_dim_sub*

Description

sc_dim_sub

Usage

```
sc_dim_sub(subset, .column = "ident")
```

Arguments

subset	subset of clusters to be displayed
.column	which column represents cluster (e.g., 'ident')

Value

update plot with only subset displayed

See Also

sc_dim

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
p1 <- sc_dim(sce, reduction = 'UMAP')
f1 <- p1 + sc_dim_sub(subset = c(1, 2), .column = 'label')
```

sc_feature *sc_feature*

Description

sc_feature

Usage

```
sc_feature(
  object,
  features,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ncol = 3,
  density = FALSE,
  grid.n = 100,
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  ...
)

## S4 method for signature 'Seurat'
sc_feature(
  object,
  features,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ncol = 3,
  density = FALSE,
  grid.n = 100,
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  ...
)

## S4 method for signature 'SingleCellExperiment'
sc_feature(
  object,
```

```
  features,
  dims = c(1, 2),
  reduction = NULL,
  cells = NULL,
  slot = "data",
  mapping = NULL,
  ncol = 3,
  density = FALSE,
  grid.n = 100,
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  ...
)
```

Arguments

object	Seurat object
features	selected features (i.e., genes)
dims	selected dimensions (must be a two-length vector) that are used in visualization
reduction	reduction method, default is NULL and will use the default setting store in the object
cells	selected cells to plot (default is all cells)
slot	slot to pull expression data from (e.g., 'count' or 'data')
mapping	aesthetic mapping
ncol	number of facet columns if 'length(features) > 1'
density	whether plot the 2D weighted kernel density, default is FALSE.
grid.n	number of grid points in the two directions to estimate 2D weighted kernel density, default is 100.
joint	whether joint the multiple features with `joint.fun`, default is FALSE.
joint.fun	how to joint the multiple features if `joint=TRUE`, default is prod.
common.legend	whether to use `facet_wrap` to display the multiple `features`, default is TRUE.
...	additional parameters pass to 'scattermore::geom_scattermore()'

Value

dimension reduction plot colored by selected features

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
```

```
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runTSNE(sce, assay.type = 'logcounts')
set.seed(123)
genes <- rownames(sce) |> sample(6)
p1 <- sc_feature(sce, genes[1], slot='logcounts', reduction = 'TSNE')
p2 <- sc_feature(sce, genes, slot='logcounts', reduction = 'TSNE')
f1 <- sc_dim(sce, slot='logcounts', reduction = 'TSNE') +
      sc_dim_geom_feature(sce, genes[1], color='black')
f2 <- sc_dim(sce, alpha=.3, slot='logcounts', reduction = 'TSNE') +
    ggnewscale::new_scale_color() +
    sc_dim_geom_feature(sce, genes, mapping=aes(color=features)) +
    scale_color_viridis_d()
p1 + p2 + f1 + f2
```

`sc_geom_point` *sc_geom_point*

Description

sc_geom_point

Usage

```
sc_geom_point(mapping = NULL, ...)
```

Arguments

`mapping`	aesthetic mapping
`...`	additional parameters pass to 'scattermore::geom_scattermore()'

Value

layer of points

See Also

`sc_dim()` and `sc_feature()`

Examples

```
library(ggplot2)
ggplot(iris,
 aes(x= Sepal.Length, y = Petal.Width, color=Species)
) +
sc_geom_point()
```

sc_spatial *sc_spatial*

Description

sc_spatial

Usage

```
sc_spatial(
  object,
  features = NULL,
  sample.id = NULL,
  image.id = NULL,
  slot = "data",
  image.plot = TRUE,
  image.first.operation = "rotate",
  image.rotate.degree = NULL,
  image.mirror.axis = NULL,
  remove.point = FALSE,
  mapping = NULL,
  ncol = 6,
  density = FALSE,
  grid.n = 100,
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  point.size = 5,
  ...
)

## S4 method for signature 'Seurat'
sc_spatial(
  object,
  features = NULL,
  sample.id = NULL,
  image.id = NULL,
  slot = "data",
  image.plot = TRUE,
  image.first.operation = "rotate",
  image.rotate.degree = NULL,
  image.mirror.axis = NULL,
  remove.point = FALSE,
  mapping = NULL,
  ncol = 6,
  density = FALSE,
  grid.n = 100,
```

```
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  point.size = 5,
  ...
)

## S4 method for signature 'SingleCellExperiment'
sc_spatial(
  object,
  features = NULL,
  sample.id = NULL,
  image.id = NULL,
  slot = "data",
  image.plot = TRUE,
  image.first.operation = "rotate",
  image.rotate.degree = NULL,
  image.mirror.axis = NULL,
  remove.point = FALSE,
  mapping = NULL,
  ncol = 6,
  density = FALSE,
  grid.n = 100,
  joint = FALSE,
  joint.fun = prod,
  common.legend = TRUE,
  point.size = 5,
  ...
)
```

Arguments

object	Seurat object
features	selected features to be visualized
sample.id	the index name of sample id, which only work with SingleCellExperiment or SpatialExperiment.
image.id	the index name of image id, which only work with SingleCellExperiment or SpatialExperiment.
slot	if plotting a feature, which data will be used (e.g., 'data', 'counts'), the assay name if object is SingleCellExperiment or SpatialExperiment.
image.plot	whether to display the issue image as background.
image.first.operation	character which the first operation to image, 'rotate' or 'mirror', default is 'rotate'.
image.rotate.degree	integer the degree to ratate image, default is NULL.

image.mirror.axis	character the direction to mirror the image, default is 'h'.
remove.point	whether to remove the spot points, it is nice if your just view the issue image, default is FALSE.
mapping	aesthetic mapping, default is NULL.
ncol	integer number of facet columns if 'length(features) > 1', default is 6.
density	whether plot the 2D weighted kernel density, default is FALSE.
grid.n	number of grid points in the two directions to estimate 2D weighted kernel density, default is 100.
joint	whether joint the multiple features with joint.fun, default is FALSE.
joint.fun	how to joint the multiple features if joint = TRUE, default is prod.
common.legend	whether to use facet_wrap to display the multiple features, default is TRUE.
point.size	the size of point, default is 5.
...	additional parameters.

Value

ggplot object

Examples

```
## Not run:
library(STexampleData)
# create ExperimentHub instance
eh <- ExperimentHub()
# query STexampleData datasets
myfiles <- query(eh, "STexampleData")
spe <- myfiles[["EH7538"]]
spe <- spe[, colData(spe)$in_tissue == 1]
set.seed(123)
genes <- rownames(spe) |> sample(6)
p <- sc_spatial(spe, features = genes,
                image.rotate.degree = -90,
                image.mirror.axis = NULL,
                ncol = 3)

## End(Not run)
```

---

sc_violin *sc_violin*

Description

sc_violin

Usage

```
sc_violin(
  object,
  features,
  cells = NULL,
  slot = "data",
  .fun = NULL,
  mapping = NULL,
  ncol = 3,
  ...
)

## S4 method for signature 'Seurat'
sc_violin(
  object,
  features,
  cells = NULL,
  slot = "data",
  .fun = NULL,
  mapping = NULL,
  ncol = 3,
  ...
)

## S4 method for signature 'SingleCellExperiment'
sc_violin(
  object,
  features,
  cells = NULL,
  slot = "data",
  .fun = NULL,
  mapping = NULL,
  ncol = 3,
  ...
)
```

Arguments

object	Seurat object
features	selected features
cells	selected cells to plot (default is all cells)
slot	slot to pull expression data from (e.g., 'count' or 'data')
.fun	user defined function that will be applied to selected features (default is NULL and there is no data operation)
mapping	aesthetic mapping
ncol	number of facet columns if 'length(features) > 1'
...	additional parameters pass to 'ggplot2::geom_geom_violin()'

Value

violin plot to visualize feature expression distribution

See Also

geom_violin;

Examples

```
library(scuttle)
library(scater)
library(scran)
library(ggplot2)
sce <- mockSCE()
sce <- logNormCounts(sce)
clusters <- clusterCells(sce, assay.type = 'logcounts')
colLabels(sce) <- clusters
sce <- runUMAP(sce, assay.type = 'logcounts')
set.seed(123)
genes <- rownames(sce) |> sample(6)
sc_violin(sce, genes[1], slot = 'logcounts')
sc_violin(sce, genes[1], slot = 'logcounts',
     .fun=function(d) dplyr::filter(d, value > 0)
     ) +
     ggforce::geom_sina(size=.1)
sc_violin(sce, genes, slot = 'logcounts') +
  theme(axis.text.x = element_text(angle=45, hjust=1))
```

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